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PROBLEMS AND SOLUTIONS IN APPLIED STATISTICS

Contents

1
Introduction

This book will hold a collection of problems, and my solutions to them, in applied statistics with R. These come from my courses STAC32 and STAD29 at the University of Toronto Scarborough.

The problems were originally written in Sweave (that is, LaTeX with R code chunks), using the `exam` document class, using data sets stolen from numerous places (textbooks, websites etc). I wrote a Perl program to strip out the LaTeX and turn each problem into R Markdown for this book. You will undoubtedly see bits of LaTeX still embedded in the text. I am trying to update my program to catch them, but I am sure to miss some. If you see anything, file an issue on the Github page for now. I want to fix problems programmatically at first, but when the majority of the problems have been caught, I will certainly take pull requests. I will acknowledge all the people who catch things.

working on stuff from assignments 9/9a

look at heat data

rejig the crickets questions so less duplication

bodyfat and bodyfat-sign duplication

2

Getting used to R and R Studio

We begin with this:

```
library(tidyverse)
```

```
## -- Attaching packages ---- tidyverse 1.2.1 --
```

```
## v ggplot2 3.0.0     v purrr   0.2.5
## v tibble  1.4.2     v dplyr   0.7.6
## v tidyr   0.8.1     v stringr 1.3.1
## v readr   1.1.1     v forcats 0.3.0
```

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

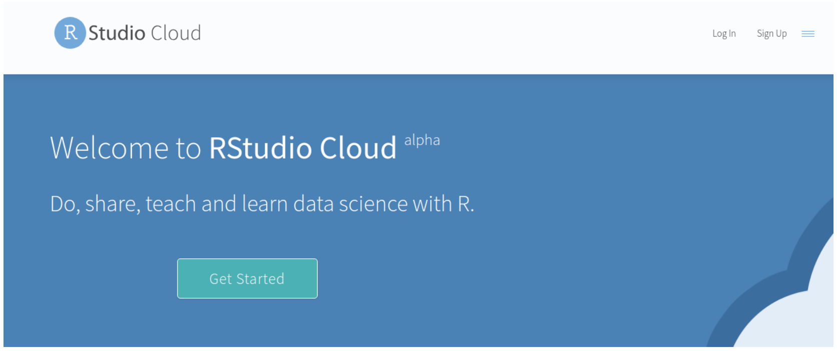
and so to the problems:

2.1 *Getting an R Studio Cloud account*

Follow these steps to get an R Studio Cloud account.

(a) Point your web browser at link. (If you already have R and R Studio installed on your computer, you can use that instead, throughout the course; just do part (d) of this question. Any references to R Studio Cloud in this assignment also apply to R Studio on your computer.)

Solution
You should see this:



Welcome to RStudio Cloud alpha

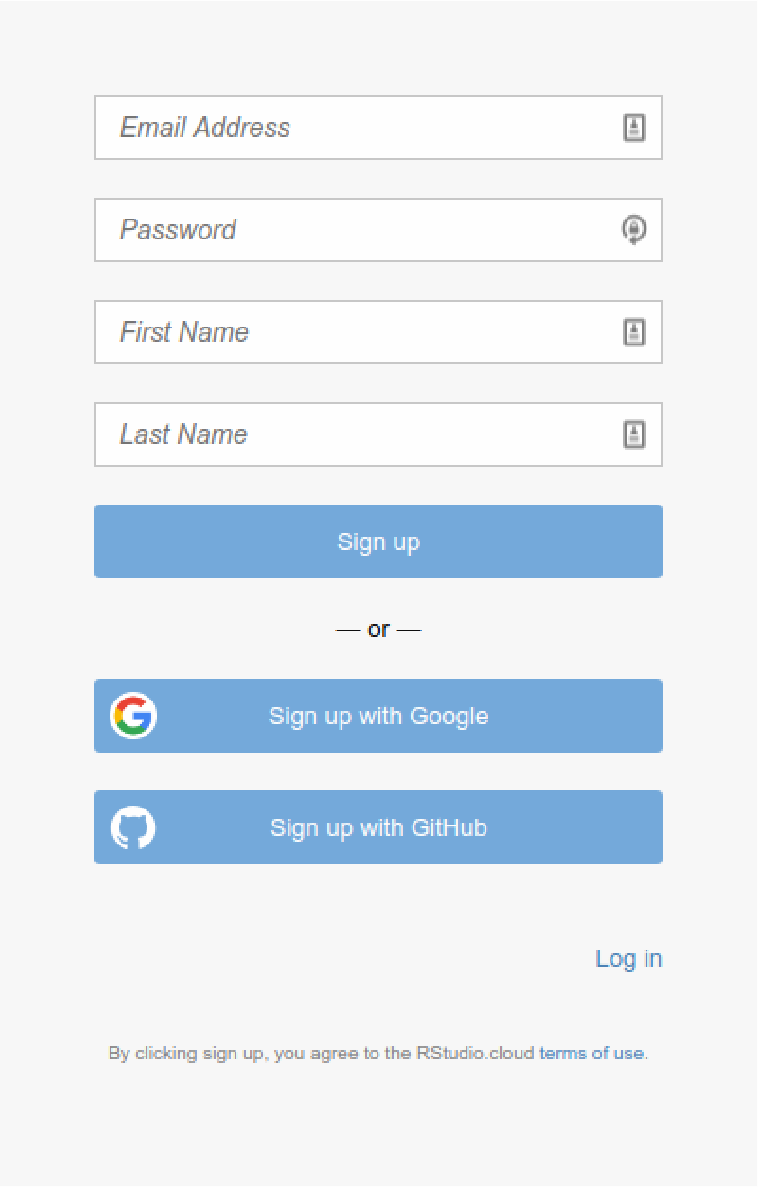
Do, share, teach and learn data science with R.

. Click on Get Started. You might instead see the screen in the next part.

(b) Choose an account to use.

Solution

Here's what you should see now:

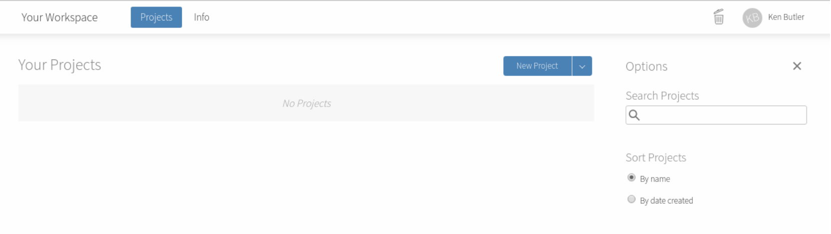


By clicking sign up, you agree to the RStudio.cloud terms of use.

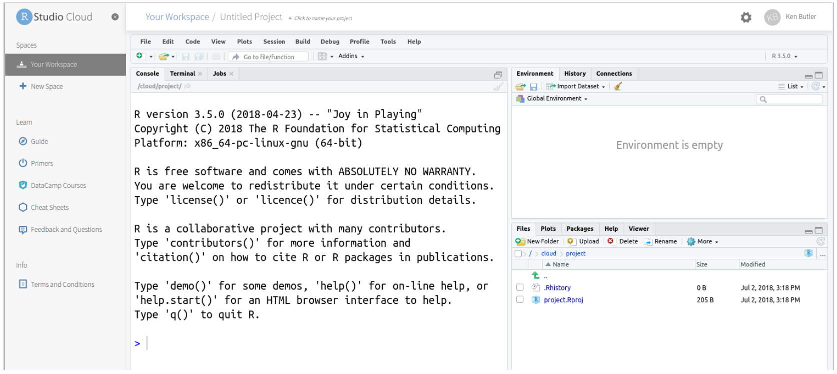
If you're happy with using your Google account, click that button. You will probably have to enter your Google password. (If you are doing this on your own computer, you might not have to do that.) If you have a GitHub account and you want to use *that*, same principle. You can also use an email address as your login to R Studio Cloud. (You can use any e-mail address; I'm not checking.) Enter it in the top box, and enter a password to use with R Studio Cloud in the second. (This does not have to be, and indeed probably should not be, the same as your email password.) Below that, enter your first and last name. This will appear at the top right of the screen when you are logged in. Then click Sign Up. After that, you will have to make a unique account name (which *you* actually never use, but which `rstudio.cloud` uses to name your files). After that, you are automatically logged in.

(c) Take a look around, and create a new Project. Give the new project any name you like.

Solution
This is what you see now:



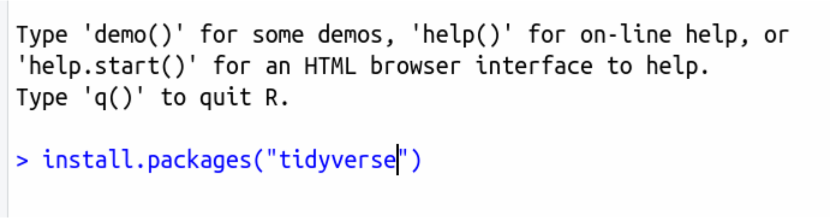
Click on the blue New Project button to create a new Project. (A project is a self-contained piece of work, like for example an assignment.) You will see the words "Loading Project" and spinning circles for a few moments. Then you see this:



```
R version 3.5.0 (2018-04-23) -- "Joy in Playing"
Copyright (C) 2018 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

>
```

To give your project a name, click at the top where it says Untitled Project and type a name like Assignment 0 into the box.

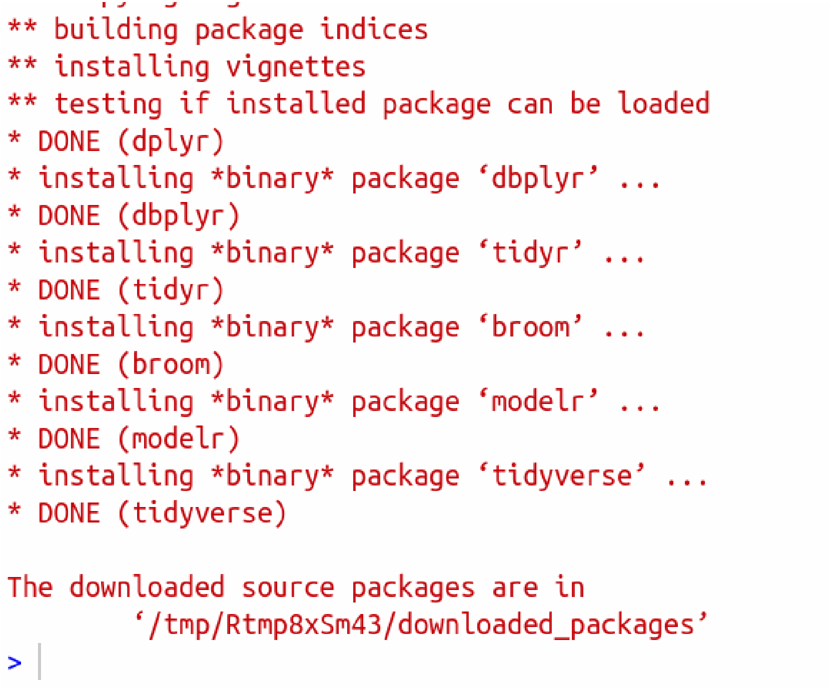
(d) Before we get to work, look for the blue > at the bottom left. Click next to it to get a flashing cursor, and then type what you see here (in blue):



```
Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

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

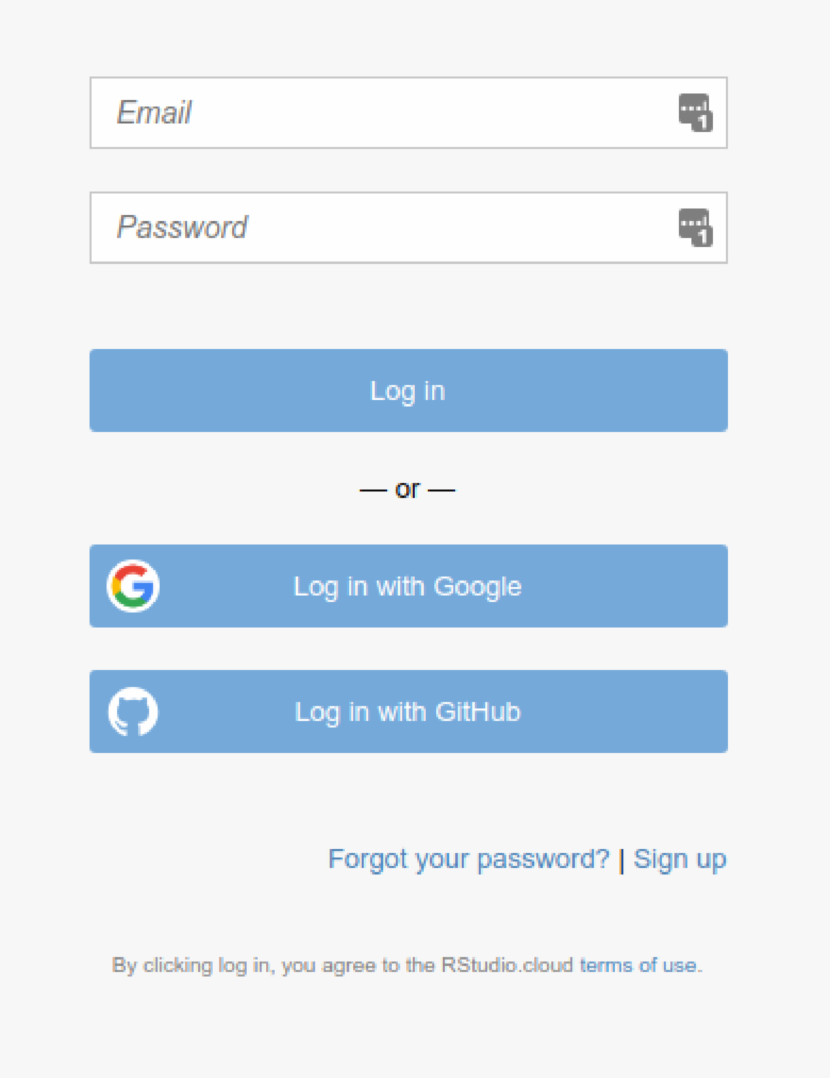
Then press Enter.
Solution

This lets it install a bunch of things. It may take some time. If you are watching it, look out for lines beginning with g++, which are C++ code that needs to be compiled. This is the end of what I had. Look out for the word DONE near the bottom:



```
** building package indices
** installing vignettes
** testing if installed package can be loaded
* DONE (dplyr)
* installing *binary* package 'dbplyr' ...
* DONE (dbplyr)
* installing *binary* package 'tidyr' ...
* DONE (tidyr)
* installing *binary* package 'broom' ...
* DONE (broom)
* installing *binary* package 'modelr' ...
* DONE (modelr)
* installing *binary* package 'tidyverse' ...
* DONE (tidyverse)

The downloaded source packages are in
        '/tmp/Rtmp8xSm43/downloaded_packages'
> 
```

(e) Not for now, but for later: if you are on a lab computer, you should probably log out when you are done. To do that, find your name at the top right. Click on it, and two things should pop out to the right: Profile and Log Out. Select Log Out. You should be returned to one of the screens you began with, possibly the Welcome to R Studio Cloud one. To log back in, now or next time, look for Log In at the top right. Click it, to get this:



By clicking log in, you agree to the RStudio.cloud terms of use.

and then you can log in with your email and password, or Google or Github IDs, whichever you used. Now we can get down to some actual work.

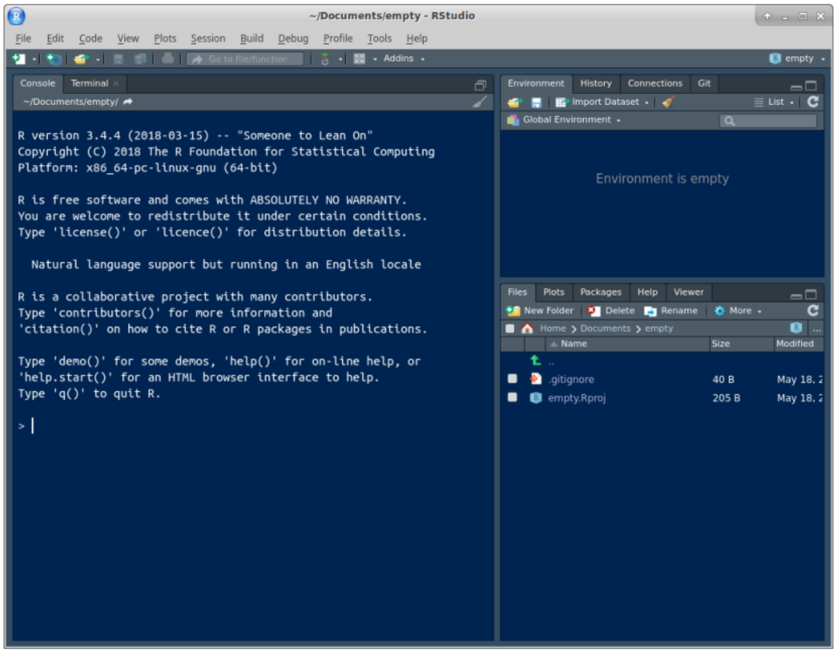
2.2 *Getting started*

This question is to get you started using R.

(a) Start R Studio Cloud, in some project. (If you started up a new project in the previous question and are still logged in, use that; if not, create a new project.)

Solution

You ought to see something like this. I have a dark blue background here, which you probably do not.



```
R version 3.4.4 (2018-03-15) -- "Someone to Lean On"
Copyright (C) 2018 The R Foundation for Statistical Computing
Platform: x86_64-pc-linux-gnu (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

  Natural language support but running in an English locale

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> |
```

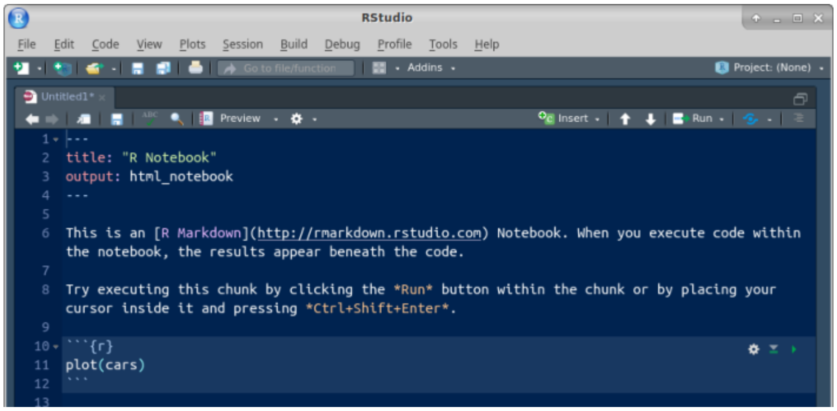
Name	Size	Modified
..		
.gitignore	40 B	May 18, 2
empty.Rproj	205 B	May 18, 2

It won't look exactly like that (for example, the background will probably be white) but there should be one thing on the left half, and at the top right it'll say "Environment is empty". Extra: if you want to tweak things, select Tools (at the top of the screen) and from it Global Options, then click Appearance. You can make the text bigger or smaller via Editor Font Size, and choose a different colour scheme by picking one of the Editor Themes (which previews on the right). My favourite is Tomorrow Night Blue. Click Apply or OK when you have found something you like. (I spend a lot of time in R Studio, and I like having a dark background to be easier on my eyes.)

(b) We're going to do some stuff in R here, just to get used to it. First, make an R Notebook by selecting File, New File and R Notebook.

Solution

The first time, you'll be invited to "install some packages" to make the Notebook thing work. Let it do that by clicking Yes. After that, you'll have this:



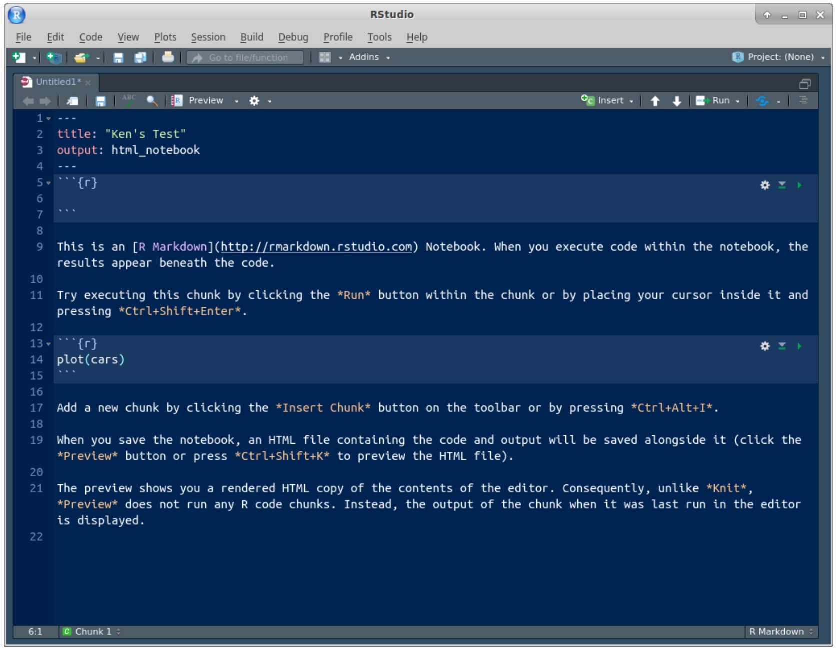
````
1  ---
2  title: "R Notebook"
3  output: html_notebook
4  ---
5
6  This is an [R Markdown](http://rmarkdown.rstudio.com) Notebook. When you execute code within
   the notebook, the results appear beneath the code.
7
8  Try executing this chunk by clicking the *Run* button within the chunk or by placing your
   cursor inside it and pressing *Ctrl+Shift+Enter*.
9
10 ```{r}
11 plot(cars)
12 ```
13
````

Find the Insert and Run buttons along the top of the R Notebook window. We'll be using them shortly. (The template notebook may or may not be maximized; it doesn't matter either way. You might see all four panes or as few as one. If you want to control that, select View at the top, then Panes, then either Show All Panes or Zoom Source, as you prefer. In the menus, you'll also see keyboard shortcuts for these, which you might find worth learning.)

(c) Change the title to something of your choosing. Then go down to line 5, click on the Insert button and select R. You should see a "code chunk" appear at line 5, which we are going to use in a moment.

Solution

Something like this:



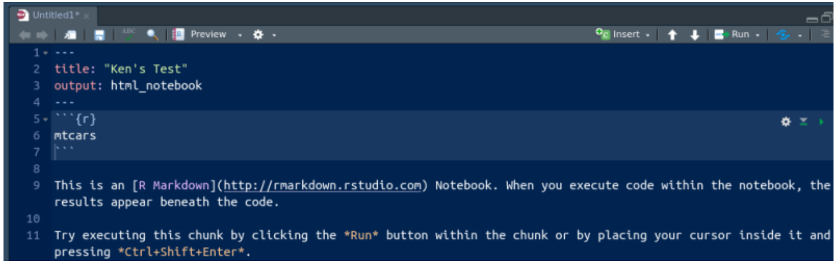
````
1  ---
2  title: "Ken's Test"
3  output: html_notebook
4  ---
5  ```{r}
6
7  ```
8
9  This is an [R Markdown](http://rmarkdown.rstudio.com) Notebook. When you execute code within the notebook, the
   results appear beneath the code.
10
11 Try executing this chunk by clicking the *Run* button within the chunk or by placing your cursor inside it and
   pressing *Ctrl+Shift+Enter*.
12
13 ```{r}
14 plot(cars)
15 ```
16
17 Add a new chunk by clicking the *Insert Chunk* button on the toolbar or by pressing *Ctrl+Alt+I*.
18
19 When you save the notebook, an HTML file containing the code and output will be saved alongside it (click the
   *Preview* button or press *Ctrl+Shift+K* to preview the HTML file).
20
21 The preview shows you a rendered HTML copy of the contents of the editor. Consequently, unlike *Knit*,
   *Preview* does not run any R code chunks. Instead, the output of the chunk when it was last run in the editor
   is displayed.
22
````

(d) Type the line of code shown below into the chunk in the R Notebook:

```
mtcars
```

Solution

What this will do: get hold of a built-in data set with information about some different models of car, and display it.



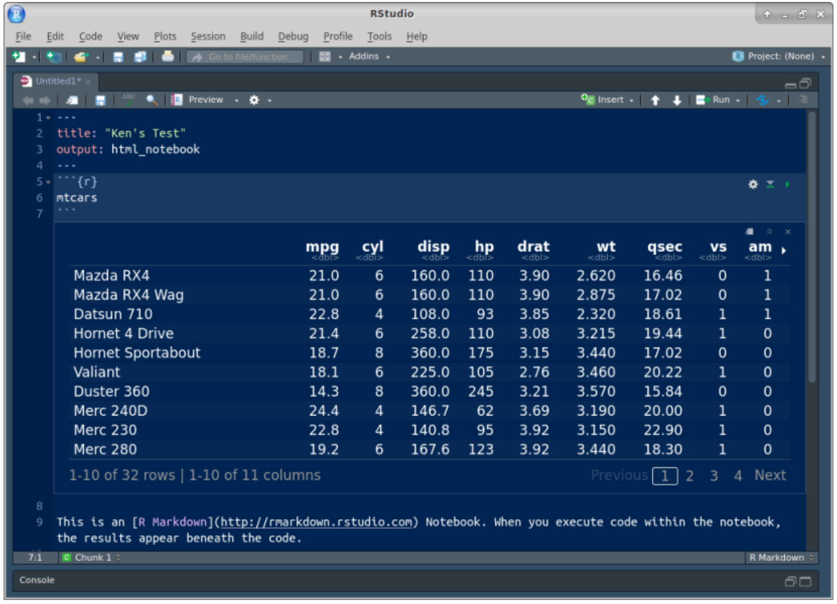
~~~
---
title: "Ken's Test"
output: html_notebook
---
```{r}
mtcars
```

This is an [R Markdown](http://rmarkdown.rstudio.com) Notebook. When you execute code within the notebook, the
results appear beneath the code.

Try executing this chunk by clicking the *Run* button within the chunk or by placing your cursor inside it and
pressing *Ctrl+Shift+Enter*.
~~~

In approximately five seconds, you'll be demonstrating that for yourself.

(e) Run this command. To do that, look at the top right of your code chunk block (shaded in a slightly different colour). You should see a gear symbol, a down arrow and a green "play button". Click the play button. This will run the code, and show the output below the code chunk.

Solution

Here's what I get (yours will be the same).



~~~
---
title: "Ken's Test"
output: html_notebook
---
```{r}
mtcars
```
~~~

```
                      mpg   cyl   disp    hp   drat     wt   qsec    vs    am
                    <dbl> <dbl>  <dbl> <dbl>  <dbl>  <dbl>  <dbl> <dbl> <dbl>
Mazda RX4            21.0     6  160.0   110   3.90  2.620  16.46     0     1
Mazda RX4 Wag        21.0     6  160.0   110   3.90  2.875  17.02     0     1
Datsun 710           22.8     4  108.0    93   3.85  2.320  18.61     1     1
Hornet 4 Drive       21.4     6  258.0   110   3.08  3.215  19.44     1     0
Hornet Sportabout    18.7     8  360.0   175   3.15  3.440  17.02     0     0
Valiant              18.1     6  225.0   105   2.76  3.460  20.22     1     0
Duster 360           14.3     8  360.0   245   3.21  3.570  15.84     0     0
Merc 240D            24.4     4  146.7    62   3.69  3.190  20.00     1     0
Merc 230             22.8     4  140.8    95   3.92  3.150  22.90     1     0
Merc 280             19.2     6  167.6   123   3.92  3.440  18.30     1     0
1-10 of 32 rows | 1-10 of 11 columns                  Previous 1 2 3 4 Next
```

```
This is an [R Markdown](http://rmarkdown.rstudio.com) Notebook. When you execute code within the notebook,
the results appear beneath the code.
```

This is a rectangular array of rows and columns, with individuals in rows and variables in columns, known as a "data frame". When you display a data frame in an R Notebook, you see 10 rows and as many columns as will fit on the screen. At the bottom, it says how many rows and columns there are altogether (here 32 rows and 11 columns), and which ones are being displayed. You can see more rows by clicking on Next, and if there are more columns, you'll see a little arrow next to the rightmost column (as here next to `am`) that you can click on to see more columns. Try it and see. Or if you want to go to a particular collection of rows, click one of the numbers between Previous and Next: 1 is rows 1–10, 2 is rows 11–20, and so on. The column on the left without a header (containing the names of the cars) is called "row names". These have a funny kind of status, kind of a column and kind of not a column; usually, if we need to use the names, we have to put them in a column first. In future solutions, rather than showing you a screenshot, expect me to show you something like this:

```
mtcars
```

```
## # A tibble: 32 x 11
##      mpg   cyl  disp    hp  drat    wt  qsec
##  * <dbl> <dbl> <dbl> <dbl> <dbl> <dbl> <dbl>
##  1  21       6  160    110  3.9   2.62  16.5
##  2  21       6  160    110  3.9   2.88  17.0
##  3  22.8     4  108     93  3.85  2.32  18.6
##  4  21.4     6  258    110  3.08  3.22  19.4
##  5  18.7     8  360    175  3.15  3.44  17.0
##  6  18.1     6  225    105  2.76  3.46  20.2
##  7  14.3     8  360    245  3.21  3.57  15.8
##  8  24.4     4  147.    62  3.69  3.19  20
##  9  22.8     4  141.    95  3.92  3.15  22.9
## 10  19.2     6  168.   123  3.92  3.44  18.3
## # ... with 22 more rows, and 4 more
## #   variables: vs <dbl>, am <dbl>,
## #   gear <dbl>, carb <dbl>
```

The top bit is the code, the bottom bit with the `##` the output. In this kind of display, you only see the first ten rows (by default).

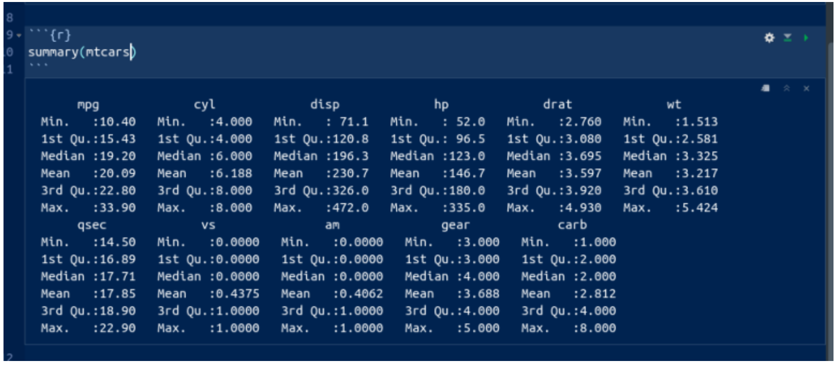
If you don't see the "play button", make sure that what you have really is a code chunk. (I often accidentally delete one of the special characters above or below the code chunk). If you can't figure it out, delete this code chunk and make a new one. Sometimes R Studio gets confused.

On the code chunk, the other symbols are the settings for this chunk (you have the choice to display or not display the code or the output or to not actually run the code). The second one, the down arrow, runs all the chunks prior to this one (but not this one).

The output has its own little buttons. The first one pops the output out into its own window; the second one shows or hides the output, and the third one deletes the output (so that you have to run the chunk again to get it back). Experiment. You can't do much damage here.

(f) Something a little more interesting: `summary` obtains a summary of whatever you feed it (the five-number summary plus the mean for numerical variables). Obtain this for our data frame. To do this, create a new code chunk below the previous one, type `summary(mtcars)` into the code chunk, and run it.

Solution
This is what you should see:



~~~
```{r}
summary(mtcars)
```
~~~

```
      mpg             cyl             disp             hp             drat             wt       
 Min.   :10.40   Min.   :4.000   Min.   : 71.1   Min.   : 52.0   Min.   :2.760   Min.   :1.513  
 1st Qu.:15.43   1st Qu.:4.000   1st Qu.:120.8   1st Qu.: 96.5   1st Qu.:3.080   1st Qu.:2.581  
 Median :19.20   Median :6.000   Median :196.3   Median :123.0   Median :3.695   Median :3.325  
 Mean   :20.09   Mean   :6.188   Mean   :230.7   Mean   :146.7   Mean   :3.597   Mean   :3.217  
 3rd Qu.:22.80   3rd Qu.:8.000   3rd Qu.:326.0   3rd Qu.:180.0   3rd Qu.:3.920   3rd Qu.:3.610  
 Max.   :33.90   Max.   :8.000   Max.   :472.0   Max.   :335.0   Max.   :4.930   Max.   :5.424  
      qsec             vs               am              gear             carb      
 Min.   :14.50   Min.   :0.0000   Min.   :0.0000   Min.   :3.000   Min.   :1.000  
 1st Qu.:16.89   1st Qu.:0.0000   1st Qu.:0.0000   1st Qu.:3.000   1st Qu.:2.000  
 Median :17.71   Median :0.0000   Median :0.0000   Median :4.000   Median :2.000  
 Mean   :17.85   Mean   :0.4375   Mean   :0.4062   Mean   :3.688   Mean   :2.812  
 3rd Qu.:18.90   3rd Qu.:1.0000   3rd Qu.:1.0000   3rd Qu.:4.000   3rd Qu.:4.000  
 Max.   :22.90   Max.   :1.0000   Max.   :1.0000   Max.   :5.000   Max.   :8.000  
```

or the other way:

```
summary(mtcars)

##       mpg             cyl       
##  Min.   :10.40   Min.   :4.000  
##  1st Qu.:15.43   1st Qu.:4.000  
##  Median :19.20   Median :6.000  
##  Mean   :20.09   Mean   :6.188  
##  3rd Qu.:22.80   3rd Qu.:8.000  
##  Max.   :33.90   Max.   :8.000  
##       disp             hp       
##  Min.   : 71.1   Min.   : 52.0  
##  1st Qu.:120.8   1st Qu.: 96.5  
##  Median :196.3   Median :123.0  
##  Mean   :230.7   Mean   :146.7  
##  3rd Qu.:326.0   3rd Qu.:180.0  
##  Max.   :472.0   Max.   :335.0  
##       drat             wt       
##  Min.   :2.760   Min.   :1.513  
##  1st Qu.:3.080   1st Qu.:2.581  
##  Median :3.695   Median :3.325  
```

```
##  Mean   :3.597   Mean   :3.217  
##  3rd Qu.:3.920   3rd Qu.:3.610  
##  Max.   :4.930   Max.   :5.424  
##       qsec             vs        
##  Min.   :14.50   Min.   :0.0000  
##  1st Qu.:16.89   1st Qu.:0.0000  
##  Median :17.71   Median :0.0000  
##  Mean   :17.85   Mean   :0.4375  
##  3rd Qu.:18.90   3rd Qu.:1.0000  
##  Max.   :22.90   Max.   :1.0000  
##        am              gear      
##  Min.   :0.0000   Min.   :3.000  
##  1st Qu.:0.0000   1st Qu.:3.000  
##  Median :0.0000   Median :4.000  
##  Mean   :0.4062   Mean   :3.688  
##  3rd Qu.:1.0000   3rd Qu.:4.000  
##  Max.   :1.0000   Max.   :5.000  
##       carb      
##  Min.   :1.000  
##  1st Qu.:2.000  
##  Median :2.000  
##  Mean   :2.812  
##  3rd Qu.:4.000  
##  Max.   :8.000  
```

For the gas mileage column mpg, the mean is bigger than the median, and the largest value is unusually large compared with the others, suggesting a distribution that is skewed to the right.

There are 11 numeric (quantitative) variables, so we get the five-number summary plus mean for each one. Categorical variables, if we had any here, would be displayed a different way.

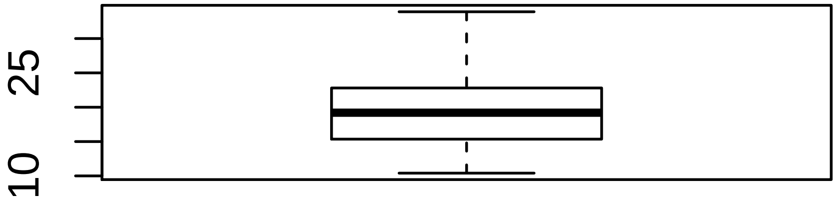
(In case you are wondering, the way without screenshots is obtained by *my* writing a notebook with code chunks and running them, so this output genuinely *is* obtained by running the code you see.)

(g) Let’s make a boxplot of the gas mileage data. This is a “poor man’s boxplot”; we’ll see a nicer-looking way later. To do it this way, make another new code chunk, enter the code boxplot(mtcars$mpg) into it, and run the chunk.

Solution

This is what you should see:

```
boxplot(mtcars$mpg)
```



The long upper whisker supports our guess from before that the distribution is right-skewed.

(h) Some aesthetics to finish with: delete the template notebook (all the stuff you didn't type below your code chunks and output). Then add some narrative text above and below your code chunks. Above the code chunk is where you say what you are going to do (and maybe why you are doing it), and below is where you say what you conclude from the output you just obtained.

Solution

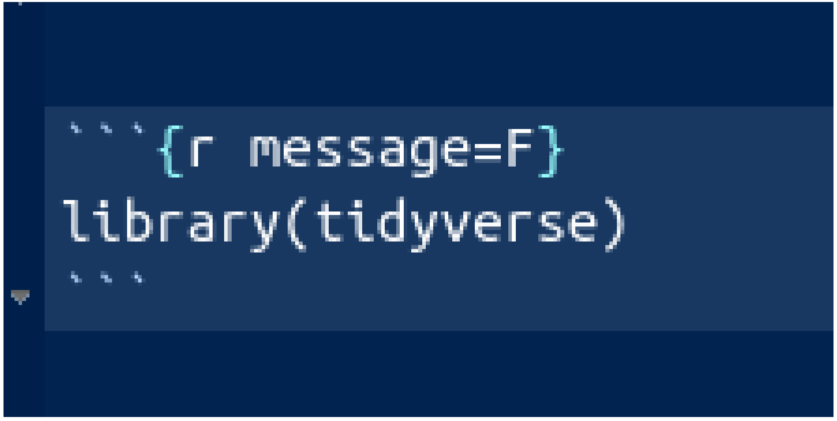
My complete R Notebook is at `http://www.utsc.utoronto.ca/~butler/c32/a0-notebook-1.Rmd`. Take a look at it. I added one extra thing: my variable names have "backticks" around them. You'll see the effect of this in a moment. Backtick is on the key to the left of 1 and below Esc on your keyboard, along with a "squiggle" symbol that we'll be using later in the course.

(i) Save your notebook (the usual way with File and Save). This saves it *on the R Studio Cloud servers* (and not on your computer). This means that when you come back to R Studio Cloud later, even from another device, this notebook will still be available to you. Now click Preview. This produces a pretty HTML version of your notebook.

Solution

Note that the HTML document only contains output from the chunks you've run in the notebook, so it's up to you to run them there first.

My HTML document is at `http://www.utsc.utoronto.ca/~butler/c32/a0-notebook-1.nb.html`. Here's where you see the effect of the backticks: all the variable names are in `typewriter font` so that you can see they are variable names and not something else. If you want to try this notebook out yourself, you have a couple of options: (i) make a new R Notebook on R Studio Cloud and copy-paste the contents of my file (it's just text), or (ii) download my R Notebook onto your computer, and then upload it to R Studio Cloud. Look in the Files pane bottom right, and next to New Folder you should see Upload. Upload the file from wherever it got saved to when you downloaded it. Extra: if you're feeling ambitious, click the arrow to the right of Preview and select Knit to Word. The button changes to Knit with a ball of wool beside it. Now, when you "knit" the notebook, you get a Word document directly — look for it in the Files pane. If you want to, you can hand this kind of thing in (on later assignments), but you'll have to do a little work first: first, find it in your Files list, then click the checkbox to the left of it, then click More (with the gear, on the same line as New Folder and Upload), then select Export (and click Download). This will put a copy in your downloads folder on your computer, and you can open it from there. If you're feeling extra-ambitious, you can try Knit to PDF. This produces something that looks as if it was written in LaTeX, but actually wasn't. To make this work, if you have a `library(tidyverse)` line somewhere, as you probably will, find the code chunk it's in, and make it look like this:



~~~
```{r message=F}
library(tidyverse)
```
~~~

Then it will work. Extra extra: if you like the keyboard better than the mouse, R Studio has a lot of keyboard shortcuts. Two that are useful now: control-alt-i inserts a code chunk where the cursor is, and control-shift-enter runs the code chunk that the cursor is in, if it is in one. (Mac users, "command" instead of "control" in both cases.) I use these two a lot.

(j) Optional extra: practice handing in your previewed R notebook, as if it were an assignment that was worth something. (It is good to get the practice in a low-stakes situation, so that you'll know what to do next week.)

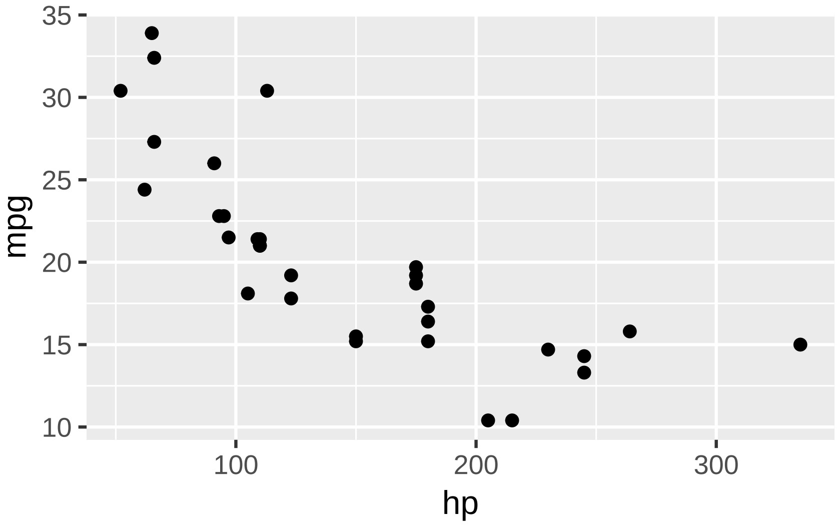
Solution

There are two steps: download the HTML file onto your computer, and then handing it in on Quercus. To download: find the HTML file that you want to download in the Files pane bottom right. There should be two files starting with the same thing, eg. `test1.Rmd`, which is the notebook you wrote, and `test1.nb.html`, which is the previewed version of it, and is the one you want to download. (The `test1` part is the name *you* chose when you saved it.) Click the checkbox to the left of the HTML file. Now click on More above the bottom-right pane. This pops up a menu from which you choose Export. This will pop up another window called Export Files, where you put the name that the file will have on your computer. (I usually leave the name the same.) Click Download. The file will go to your Downloads folder, or wherever things you download off the web go. Now, to hand it in. Open up Quercus at `q.utoronto.ca`, log in and navigate to this course. Click Assignments. Click (the title of) Assignment 0. There is a big blue Submit Assignment button top right. Click it. You'll get a File Upload at the bottom of the screen. Click Choose File and find the HTML file that you downloaded. Click Open (or equivalent on your system). The name of the file should appear next to Choose File. Click Submit Assignment. You'll see Submitted at the top right. If you want to try this again, you can Resubmit Assignment as many times as you like. (For the real thing, you can use this if you realize you made a mistake in something you submitted. The graders' instructions, for the real thing, are to grade the *last* file submitted, so in that case you need to make sure that the last thing submitted includes *everything* that you want graded. Here, though, it doesn't matter.)

(k) Optional extra. Something more ambitious: make a scatterplot of gas mileage `mpg`, on the y axis, against horsepower, `hp`, on the x-axis.

Solution
That goes like this. I'll explain the steps below.

```
library(tidyverse)
ggplot(mtcars, aes(x = hp, y = mpg)) + geom_point()
```

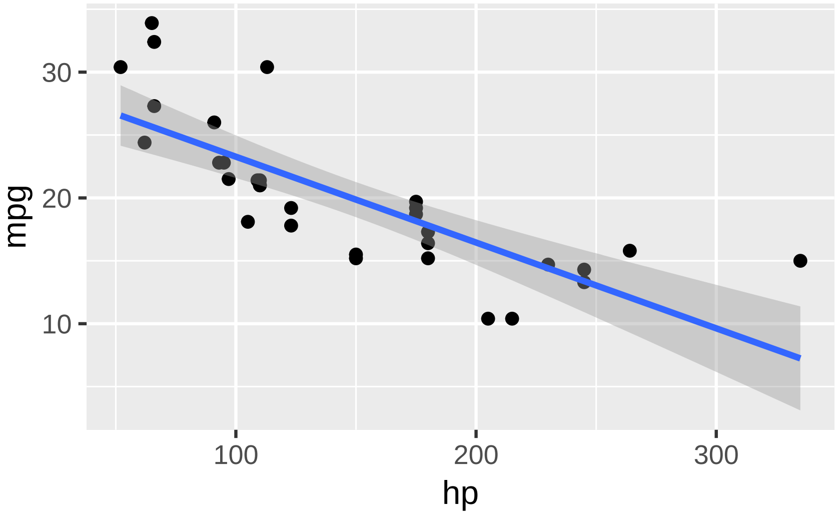


$ %$ %$

This shows a somewhat downward trend, which is what you'd expect, since a larger hp value means a more powerful engine, which will probably consume more gas and get *fewer* miles per gallon. As for the code: to make a ggplot plot, as we will shortly see in class, you first need a ggplot statement that says what to plot. The first thing in a ggplot is a data frame (mtcars here), and then the aes says that the plot will have hp on the x-axis and mpg on the y-axis, taken from the data frame that you specified. That's all of the what-to-plot. The last thing is how to plot it; geom_point() says to plot the data values as points.

You might like to add a regression line to the plot. That is a matter of adding this to the end of the plotting command:

```
ggplot(mtcars, aes(x = hp, y = mpg)) + geom_point() +
    geom_smooth(method = "lm")
```



The line definitely goes downhill. Decide for yourself how well you think a line fits these data.

2.3 *Reading data from a file*

In this question, we read a file from the web and do some descriptive statistics and a graph. This is very like what you will be doing on future assignments, so it's good to practice it now.

Take a look at the data file at https://www.utsc.utoronto.ca/~butler/c32/jumping.txt. These are measurements on 30 rats that were randomly made to do different amounts of jumping by group (we'll see the details later in the course). The control group did no jumping, and the other groups did "low jumping" and "high jumping". The first column says which jumping group each rat was in, and the second is the rat's bone density (the experimenters' supposition was that more jumping should go with higher bone density).

(a) What are the two columns of data separated by? (The fancy word is "delimited").

Solution
Exactly one space. This is true all the way down, as you can check.

(b) Make a new R Notebook. Leave the first four lines, but get rid of the rest of the template document. Start with a code chunk containing `library(tidyverse)`. Run it.

Solution
You will get either the same message as before or nothing. (I got nothing because I had already loaded the `tidyverse` in this session.)

(c) Put the URL of the data file in a variable called `my_url`. Then use `read_delim` to read in the file. (See solutions for how.) `read_delim` reads data files where the data values are always separated by the same single character, here a space. Save the data frame in a variable `rats`.

Solution
Like this:

```
my_url = "https://www.utsc.utoronto.ca/~butler/c32/jumping.txt"
rats = read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   group = col_character(),
##   density = col_integer()
## )
```

The second thing in `read_delim` is the thing that separates the data values. Often when you use `read_delim` it'll be a space.

(d) Take a look at your data frame, by making a new code chunk and putting the data frame's name in it (as we did with `mtcars`).

Solution

```
rats
```

```
## # A tibble: 30 x 2
##    group   density
##    <chr>     <int>
##  1 Control     611
##  2 Control     621
##  3 Control     614
##  4 Control     593
##  5 Control     593
##  6 Control     653
##  7 Control     600
##  8 Control     554
##  9 Control     603
## 10 Control     569
## # ... with 20 more rows
```

There are 30 rows and two columns, as there should be.

(e) Find the mean bone density for rats that did each amount of jumping.

Solution

This is something you'll see a lot: `group_by` followed by `summarize`. Reminder: to get that funny thing with the percent signs (called the "pipe symbol"), type control-shift-M (or equivalent on a Mac):

```
rats %>% group_by(group) %>% summarize(m = mean(density))
```

```
## # A tibble: 3 x 2
##   group        m
##   <chr>    <dbl>
## 1 Control   601.
## 2 Highjump  639.
## 3 Lowjump   612.
```

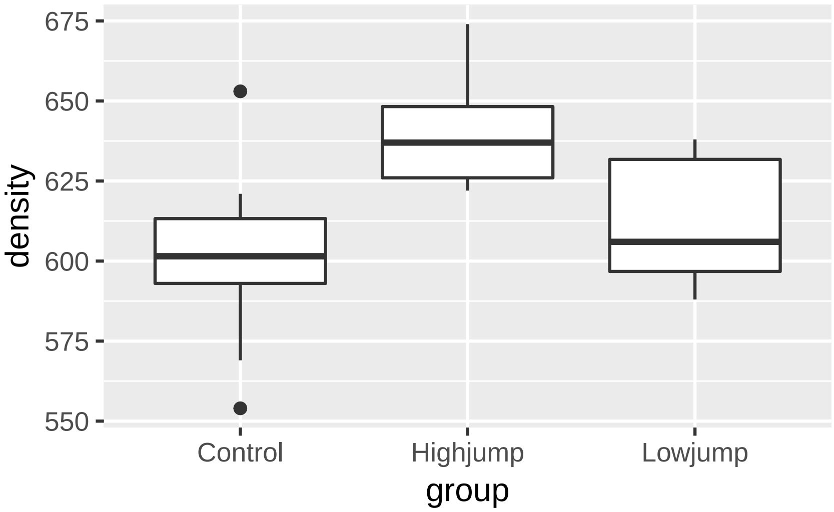
The mean bone density is clearly highest for the high jumping group, and not much different between the low-jumping and control groups.

(f) Make a boxplot of bone density for each jumping group.

Solution

On a boxplot, the groups go across and the values go up and down, so the right syntax is this:

```
ggplot(rats, aes(x = group, y = density)) + geom_boxplot()
```



Given the amount of variability, the control and low-jump groups are very similar (with the control group having a couple of outliers), but the high-jump group seems to have a consistently higher bone density than the others.

This is more or less in line with what the experimenters were guessing, but it seems that it has to be high jumping to make a difference.

You might recognize that this is the kind of data where we would use analysis of variance, which we will do later on in the course: we are comparing several (here three) groups.

3
Reading in data and drawing some graphs

3.1 Orange juice

The quality of orange juice produced by a manufacturer (identity unknown) is constantly being monitored. The manufacturer has developed a "sweetness index" for its orange juice, for which a higher value means sweeter juice. Is the sweetness index related to a chemical measure such as the amount of water-soluble pectin (parts per million) in the orange juice? Data were obtained from 24 production runs, and the sweetness and pectin content were measured for each run. The data are in link. Open that link up now. You can click on that link just above to open the file.

(a) The data values are separated by a space. Use the appropriate Tidyverse function to read the data directly from the course website into a "tibble".

Solution
Start with this (almost always):

```
library(tidyverse)
```

```
## -- Attaching packages ---- tidyverse 1.2.1 --
```

```
## v ggplot2 3.0.0     v purrr   0.2.5
## v tibble  1.4.2     v dplyr   0.7.6
## v tidyr   0.8.1     v stringr 1.3.1
## v readr   1.1.1     v forcats 0.3.0
```

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

The appropriate function, the data values being separated by a space, will be `read_delim`. Put the URL as the first thing in `read_delim`, or (better) define it into a variable first:

I say *better* because otherwise the read line gets rather long. This way you read it as *the URL is some long thing that I don't care about especially, and I what I need to do is to read the data from that URL, separated by spaces.*

```
url = "http://www.utsc.utoronto.ca/~butler/c32/ojuice.txt"
juice = read_delim(url, " ")

## Parsed with column specification:
## cols(
##   run = col_integer(),
##   sweetness = col_double(),
##   pectin = col_integer()
## )
```

read_delim (or read_csv or any of the others) tell you what variables were read in, and also tell you about any "parsing errors" where it couldn't work out what was what. Here, we have three variables, which is entirely consistent with the three columns of data values in the file.

read_delim can handle data values separated by *any* character, not just spaces, but the separating character, known as a "delimiter", does *not* have a default, so you have to say what it is, every time.

(b) Take a look at what got read in. Do you have data for all 24 runs?

Solution

Type the name of the data frame in a code chunk (a new one, or add it to the end of the previous one). Because this is actually a "tibble", which is what read_delim reads in, you'll only actually see the first 10 lines, but it will tell you how many lines there are altogether, and you can click on the appropriate thing to see the rest of it.

```
juice

## # A tibble: 24 x 3
##      run sweetness pectin
##    <int>     <dbl>  <int>
##  1     1       5.2    220
##  2     2       5.5    227
##  3     3       6      259
##  4     4       5.9    210
##  5     5       5.8    224
##  6     6       6      215
##  7     7       5.8    231
##  8     8       5.6    268
##  9     9       5.6    239
## 10    10       5.9    212
## # ... with 14 more rows
```

I appear to have all the data. If you want further convincing, click Next a couple of times (on yours) to be sure that the runs go down to number 24.

(c) In your data frame, where did the column (variable) names come from? How did R know where to get them from?

Solution

They came from the top line of the data file, so we didn't have to specify them. This is the default behaviour of all the read_ functions, so we don't have to ask for it specially. In fact, if the top line of your data file is *not* variable names, *that's* when you have to say something special. The read_ functions have an option col_names which can either be TRUE (the default), which means "read them in from the top line", FALSE ("they are not there, so make some up") or a list of column names to use. You might use the last alternative when the column names that are in the file are *not* the ones you want to use; in that case, you would also say skip=1 to skip the first line. For example, with file a.txt thus: timinput{.txt}

you could read the same data but call the columns x and y thus:

```
read_delim("a.txt", " ", col_names = c("x", "y"),
    skip = 1)
```

```
## Parsed with column specification:
## cols(
##   x = col_integer(),
##   y = col_integer()
## )
```

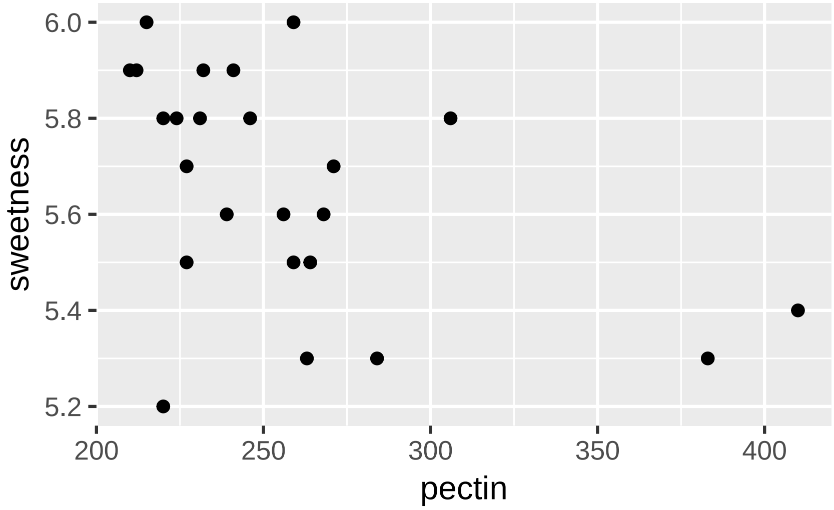
```
## # A tibble: 3 x 2
##       x     y
##   <int> <int>
## 1     1     2
## 2     3     4
## 3     5     6
```

(d) The juice manufacturer was interested in whether there was a relationship between sweetness and pectin. To assess this, draw a scatterplot. Does it look as if there is any kind of a relationship? (I think sweetness is the outcome variable and pectin is explanatory, so draw your scatterplot appropriately.)

Solution

This requires a ggplot plot. You can go back and look at the lecture notes to figure out how to make a scatterplot: the "what to plot" is the x-axis and y-axis variables, with the response on the y-axis (starting with a data frame to get the variables from), and the "how to plot" is `geom_point` to plot the points:

```
ggplot(juice, aes(x = pectin, y = sweetness)) +
    geom_point()
```

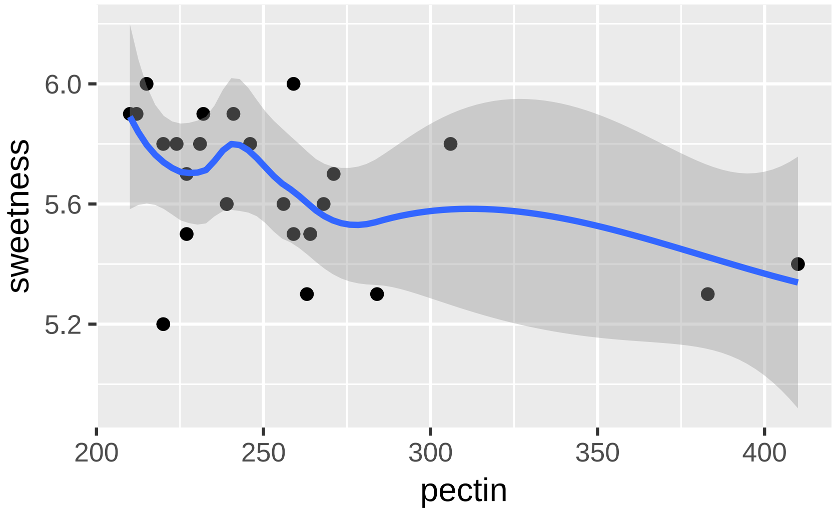


It looks to me as if there is a negative relationship: as pectin goes up, sweetness tends to go *down*. The trend appears to go top left to bottom right.

Having said that, I'm wondering how much of the apparent trend is caused by those two observations bottom right with pectin over 350. If you take those away, the trend seems to me to be a lot less convincing. As an extra, you could add a smooth trend to the plot:

```
ggplot(juice, aes(x = pectin, y = sweetness)) +
    geom_point() + geom_smooth()
```

```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



The smooth trend is kind of downhill, but not very convincing.

3.2 *Making soap*

A company operates two production lines in a factory for making soap bars. The production lines are labelled A and B. A production line that moves faster may produce more soap, but may possibly also produce more "scrap" (that is, bits of soap that can no longer be made into soap bars and will have to be thrown away).

The data are in link.

(a) Read the data into R. Display the data. There should be 27 rows. Are there?

Solution

Read directly from the URL, most easily:

```
url = "http://www.utsc.utoronto.ca/~butler/c32/soap.txt"
soap = read_delim(url, " ")
```

```
## Parsed with column specification:
## cols(
##   case = col_integer(),
##   scrap = col_integer(),
##   speed = col_integer(),
##   line = col_character()
## )
```

```
soap
```

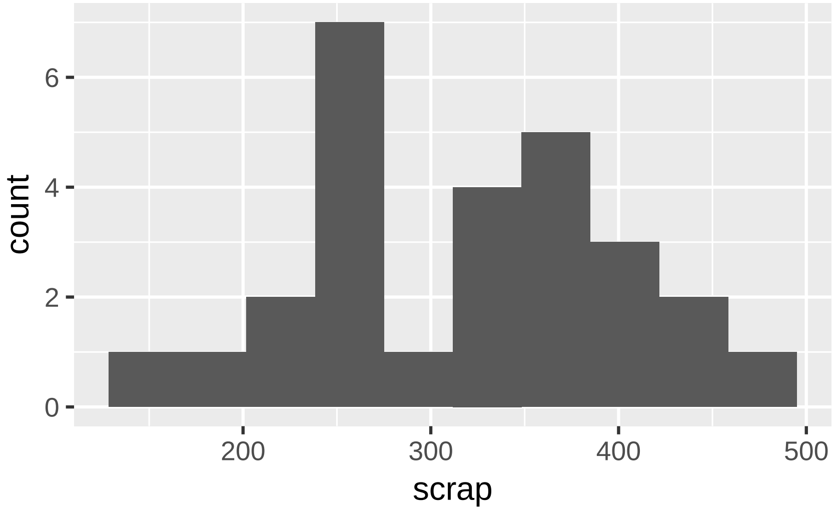
```
## # A tibble: 27 x 4
##     case scrap speed line
##    <int> <int> <int> <chr>
##  1     1   218   100 a
##  2     2   248   125 a
##  3     3   360   220 a
##  4     4   351   205 a
##  5     5   470   300 a
##  6     6   394   255 a
##  7     7   332   225 a
##  8     8   321   175 a
##  9     9   410   270 a
## 10    10   260   170 a
## # ... with 17 more rows
```

27 rows. `line`, which is either `a` or `b`, was correctly deduced to be text.

(b) Obtain a histogram of the `scrap` values, using 10 bins for your histogram.

Solution

```
ggplot(soap, aes(x = scrap)) + geom_histogram(bins = 10)
```

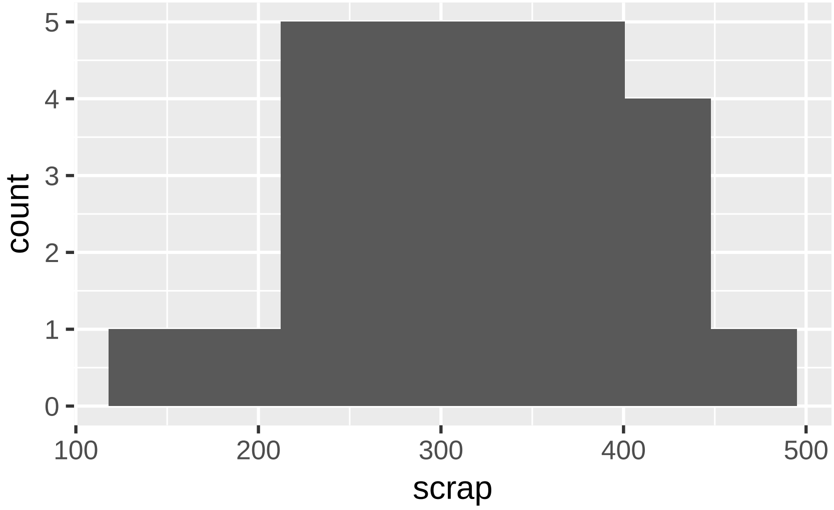


(c) Comment briefly on the shape of the histogram. Is it approximately symmetric, skewed to the left, skewed to the right or something else? (By "comment briefly" I mean "say in a few words why you gave the answer you did.")

Solution

I would call this "bimodal". There are two peaks to the histogram, one around 250 and one around 370, with a very small frequency in between (the bar around 300). Apart from the bimodality, there is no particular evidence for a long tail on either end, so I don't think you could otherwise call it anything other than symmetric. Having said that (this is going beyond the question), the way a histogram looks can depend on the bins you choose to draw it with. This is 8 bins rather than 10:

```
ggplot(soap, aes(x = scrap)) + geom_histogram(bins = 8)
```

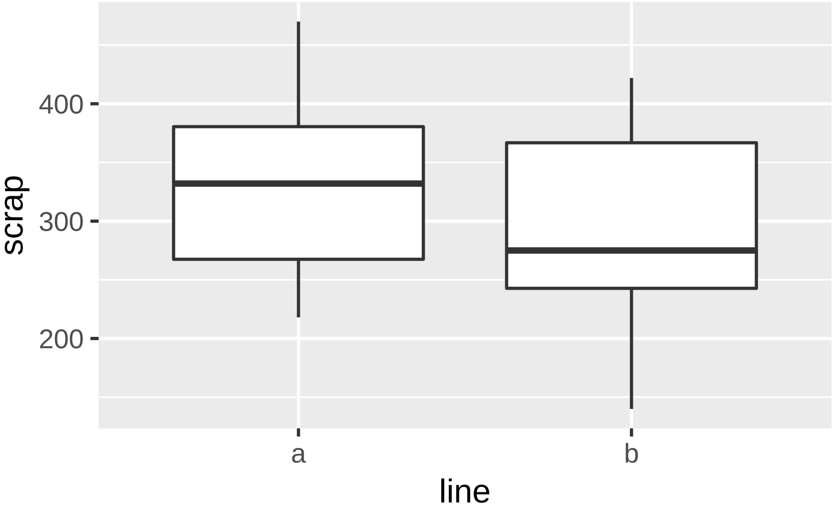


The middle low-frequency bin has gone, and this one just looks symmetric, with a kind of "flat top".

(d) Make side-by-side boxplots of scrap values for each production line.

Solution

```
ggplot(soap, aes(x = line, y = scrap)) + geom_boxplot()
```



One categorical, one quantitative variable, so boxplots make sense.

(e) Do you think your boxplot says that there are differences in the amount of scrap produced by the two production lines, or not? Explain briefly.

Solution

I would say that there *is* a difference between the two production lines, with line A producing an average (median) of about 330 and line B producing a median of about 275. But you could also make the case that, although the medians are rather different, there is a lot of variability and hence a lot of overlap between the two boxplots, and therefore that there is not a "substantial" difference. I would say that either of those answers are good *if you back them up with proper reasons*. This is going to be a common theme in this course: I am going to ask you to make a decision and support it, where the reasons you provide are often more important than the decision you make. You might be wondering whether the medians, or means, since there is no serious skewness here and definitely no outliers, are "significantly different". This is inference, which we will come to later, but a preview looks like this:

```
t.test(scrap ~ line, data = soap)
```

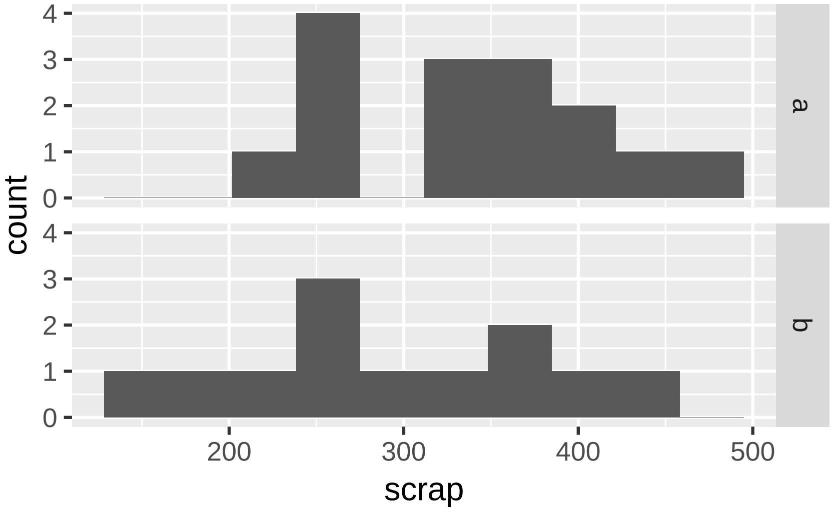
```
##
##  Welch Two Sample t-test
##
## data:  scrap by line
## t = 1.2493, df = 21.087, p-value =
## 0.2253
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -26.97888 108.21222
## sample estimates:
## mean in group a mean in group b
##        333.5333        292.9167
```

They are not: the P-value of 0.22 is not anywhere near as small as 0.05, so we can't reject the null hypothesis that the two lines have equal mean amount of scrap.

Rusty on this stuff? Don't worry; we're going to come back to it later in the course.

I was also wondering about something else: that bimodal histogram. Could that be explained by the scrap values being two different production lines being mixed together? One way to understand that is to have two separate histograms, one for each line, side by side, which is what facetting does. There is an extra wrinkle here that I explain afterwards:

```
ggplot(soap, aes(x = scrap)) + geom_histogram(bins = 10) +
    facet_grid(line ~ .)
```



I could have used `facet_wrap`, but that would have put the histograms side by side, and I wanted them one above the other (for ease of comparison, since they'll be on the same scale). `facet_grid` is like `facet_wrap`, but offers you more control over where the facets go: you can arrange them above and below by a variable, or left and right by a variable. Whatever is facetting the plots up and down (on the *y* axis) goes before the squiggle, and whatever facets them left and right goes after. If there is nothing separating the facets in one direction, here horizontally, the variable is replaced by a dot.

In some ways, `facet_grid` is also *less* flexible, because the facets have to be arranged up/down or left/right by a variable. That worked here, but if you think back to the Australian athletes, where there were ten different sports, it was `facet_wrap` that did the right thing, arranging the sports along rows *and* columns to produce a pleasing display.

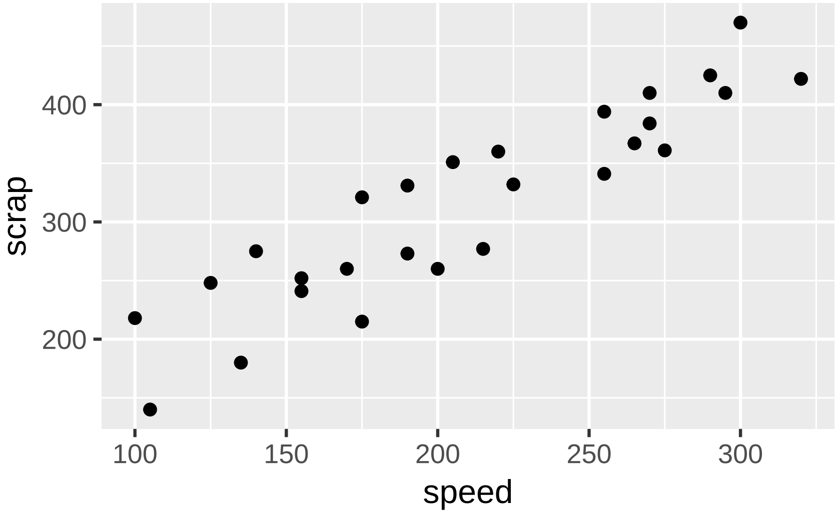
All right, that bimodality. I was expecting that the scrap values from one line would be centred about one value and the scrap values from the other line would be centred about a different value, with a gap in between. But that's not what happened at all: the line B values are all over the place, while it's the line A values that are actually bimodal all by themselves. I'm not sure whether that really means anything, since the data sets are pretty small, but it's kind of interesting.

(f) We started out with the suspicion that if the line was run faster, there would be more scrap. We haven't assessed this yet. Draw a scatter plot with `scrap` on the *y* axis and `speed` on the *x* axis.

Solution

Same mechanism as before:

```
ggplot(soap, aes(x = speed, y = scrap)) + geom_point()
```



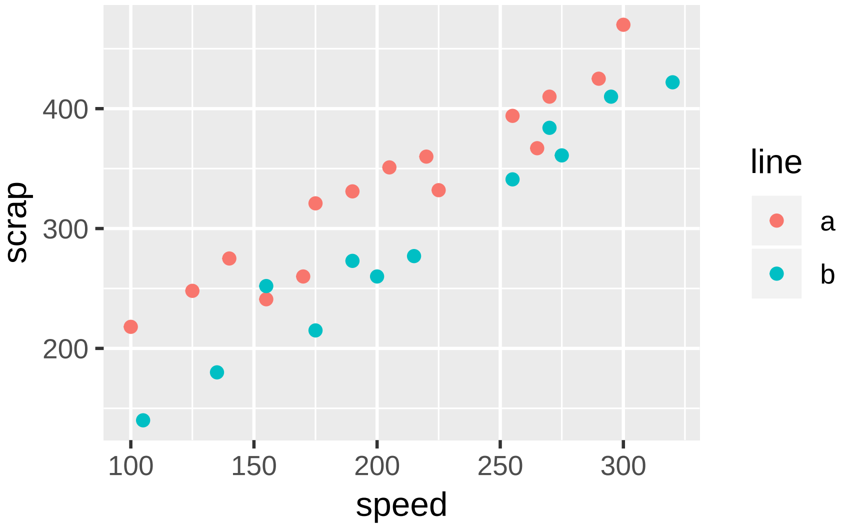
(g) What do you think is the most important conclusion from your plot of the previous part? Describe your conclusion in the context of the data.

Solution

There seems to be a pretty evident upward trend, apparently linear, which means that if the speed of the production line is higher, the amount of scrap produced is also higher. My last sentence was meant to remind you that "there is an upward trend" is *not a complete answer*: we are concerned with what that upward trend tells us about the data. This, in other words, confirms the suspicion expressed in the question, which was therefore a rather large clue: more speed tends to go with more scrap. That was as far as I wanted you to go: there seems to be an association with speed, and there might be an association with `line` that turned out not to be statistically significant. What we haven't done is to assess the relationship between speed and scrap for *each* production line. To do that, we want to plot the scrap-speed points distinguished for each production line. `ggplot` makes that easy: you add a `colour` to say what you want to distinguish by colour. This is two quantitative variables and one categorical variable, if you want to think of it that way:

If you are concerned about the spelling: the guy who wrote ggplot is from New Zealand, where they spell *colour* the same way we do. However, if you want to use *color*, that works too.

```
ggplot(soap, aes(x = speed, y = scrap, colour = line)) +
    geom_point()
```

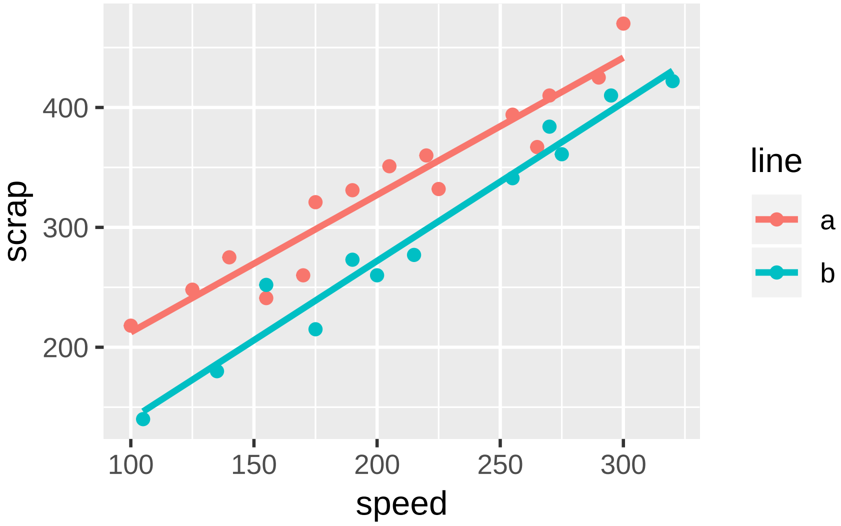


Notice that we get a legend, automatically.

What is interesting about this one is the red dots are mostly at the top (for any given speed), and the blue dots are mostly at the bottom. That seems to mean that *when we account for speed*, there is a difference between lines.

I want to show you one more embellishment, which is to put the regression lines on the plot for each group separately. This is where `ggplot` is so nice, since I just have to add one thing:

```
ggplot(soap, aes(x = speed, y = scrap, colour = line)) +
    geom_point() + geom_smooth(method = "lm",
    se = F)
```



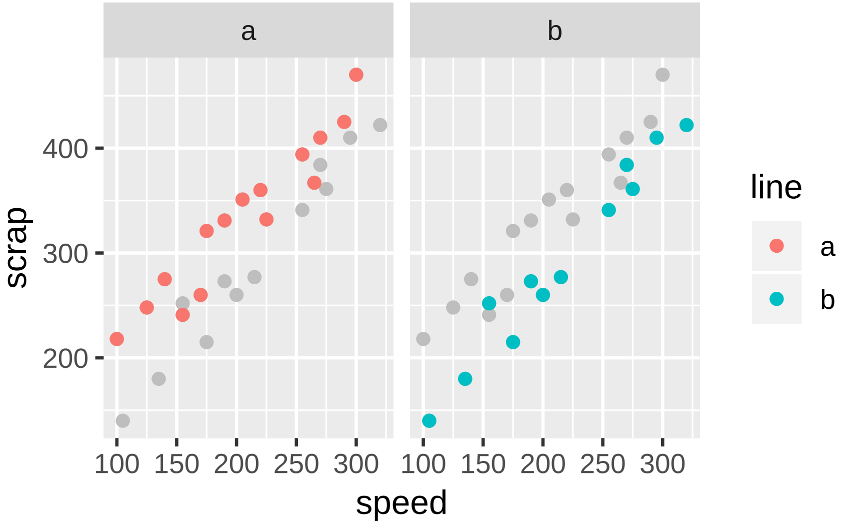
The points and lines have come out in different colours, without our having to think too hard.

Both lines show an upward trend, with about the same slope, which means that regardless of line, increasing the speed goes with increasing the scrap by the same amount. The fact that the red line is above the blue one, however, suggests that production line A produces more scrap at the same speed than production line B.

From a management point of view, there is an interesting dynamic at work: if you run the production line faster, you'll produce more bars of soap, but you'll produce more scrap as well. The crucial thing for the people in the supervisor's office is how much raw material is used per bar of soap, and if you make the soap bars faster, you might use more raw material, which will eat into your profits (from one angle), but you will also have more bars of soap to sell.

Here's another way to see the same thing. I'm *definitely* not expecting you to follow the code, but you can admire the result!

```
soap2 = soap %>% select(-line)
ggplot(soap, aes(x = speed, y = scrap)) + geom_point(data = soap2,
    colour = "grey") + geom_point(aes(colour = line)) +
    facet_wrap(~line)
```



$

The idea is that we plot all the points in grey (to "put them in the background") and then in each plot we plot the points again, *coloured, for the group we are looking at*: line A in the left, line B on the right. This is another way of seeing that line A has more scrap than line B, given the speed at which the line was being run. (I discovered this technique only yesterday. I think the code is remarkably concise for what it does.)

The logic of the code is:

- create a new data frame that contains everything in soap except for line

- make a scatter plot of all the points in this new data frame, coloured grey
- plot the points again (from the original data frame), coloured by which production line they're from
- produce a separate scatterplot for each production line.

The trick about creating the new data frame was to enable plotting of all points regardless of group on each subplot ("facet" in `ggplot` terminology), as well as the ones that come from that production line.

I don't expect you to be able to follow all the details of the code below, either, but I would like you to try and get the logic. What we do is a regression predicting `scrap` from *two* things: `speed` and production `line`. The results we get are these:

```
scrap.1 = lm(scrap ~ speed + line, data = soap)
summary(scrap.1)
```

```
##
## Call:
## lm(formula = scrap ~ speed + line, data = soap)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -39.557 -14.161  -0.121  17.518  33.953
##
## Coefficients:
##              Estimate Std. Error t value
## (Intercept)  80.41099   14.54379   5.529
## speed         1.23074    0.06555  18.775
## lineb       -53.12920    8.21003  -6.471
##             Pr(>|t|)
## (Intercept) 1.10e-05 ***
## speed       7.48e-16 ***
## lineb       1.08e-06 ***
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 21.13 on 24 degrees of freedom
## Multiple R-squared:  0.9402, Adjusted R-squared:  0.9352
## F-statistic: 188.6 on 2 and 24 DF,  p-value: 2.104e-15
```

The P-values for `speed` and `line` are the second and third things in the last column, 7×10^{-16} and 1×10^{-6} respectively. These are both very strongly significant, in contrast to the two-sample t-test where `line` was not significant.

So does production line make a difference or not?

The plot says that it does, and the meaning of model `scrap.1` just above is that *'speed' affects scrap when you account for 'line'*, and emph{`line` affects scrap when you account for speed}. (In the two-sample t-test above we didn't account for speed at all, since the various speeds were all mixed up.)

There is a moral to this story, which I would like you to get even if you don't get any of the statistics: if a variable makes a difference, it should be in your model and on your graph, because it enables you to get better (more precise) conclusions about your other variables. Here, there really is a difference between the production lines, but the t-test was too much of a blunt instrument to unearth it (because `speed` made a difference as well).

Meaning that the graph should contain all three variables, *speed*, *scrap* and *line*.

3.3 *Handling shipments*

A company called Global Electronics from time to time imports shipments of a certain large part used as a component in several of its products. The size of the shipment varies each time. Each shipment is sent to one of two warehouses (labelled A and B) for handling. The data in link show the `size` of each shipment (in thousands of parts) and the direct `cost` of handling it, in thousands of dollars. Also shown is the `warehouse` (A or B) that handled each shipment.

(a) Read the data into R and display your data frame. How many rows and columns does it have?

Solution

If you open the data file in your web browser, it will probably open as a spreadsheet, which is not really very helpful, since then it is not clear what to do with it. You could, I suppose, save it and upload it to R Studio Cloud, but it requires much less brainpower to open it directly from the URL:

```
url = "http://www.utsc.utoronto.ca/~butler/c32/global.csv"
shipments = read_csv(url)
```

```
## Parsed with column specification:
## cols(
##   warehouse = col_character(),
##   size = col_integer(),
##   cost = col_double()
## )
```

If you display your data frame and it looks like this, you are good (you can give the data frame any name):

```
shipments
```

```
## # A tibble: 10 x 3
##    warehouse  size  cost
##    <chr>     <int> <dbl>
##  1 A           225 12.0
##  2 B           350 14.1
##  3 A           150  8.93
##  4 A           200 11.0
##  5 A           175 10.0
##  6 A           180 10.1
##  7 B           325 13.8
##  8 B           290 13.3
##  9 B           400 15
## 10 A           125  7.97
```

It has 10 rows and 3 columns. *You need to say this to get the mark.*

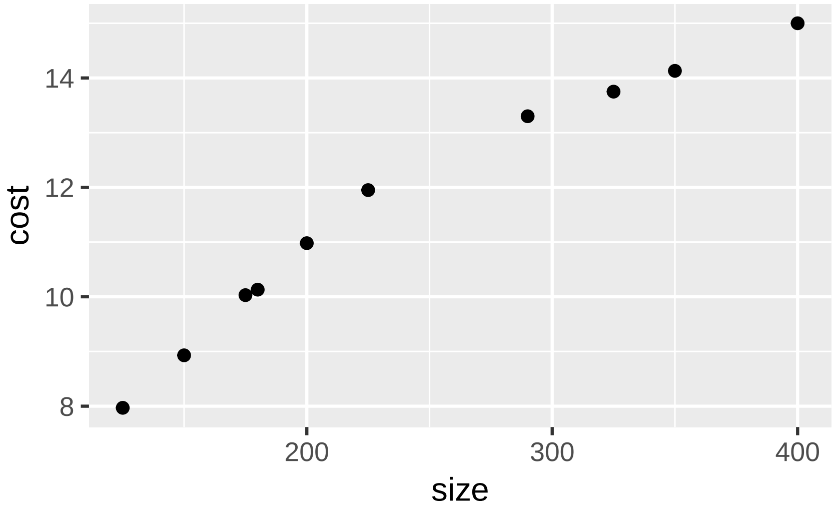
That is, there were 10 shipments recorded, and for each of them, 3 variables were noted: the size and cost of the shipment, and the warehouse it was handled at.

(b) Make a scatterplot of the cost of handling each shipment as it depends on the shipment's size.

Solution

The wording of the question says that cost is the response and so belongs on the y-axis. To make the plot, `ggplot` with an `x=` and a `y=` in the `aes` (the "what to plot" part), and a `geom_point()` after (the "how to plot it"):

```
ggplot(shipments, aes(x = size, y = cost)) + geom_point()
```



As a matter of coding, there are usually *two* brackets to close after the aes, the one that begins the ggplot and the one that begins the aes.

(c) What kind of relationship do you see on the scatterplot? Do you think a straight line would describe it appropriately? Explain briefly.

Solution

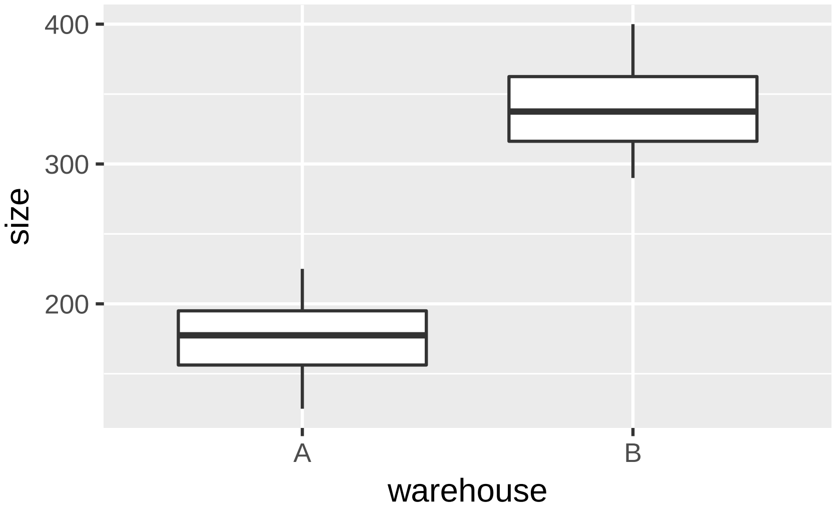
I see an upward trend: a shipment with larger size costs more to handle. If you look carefully at the scatterplot, you see that the cost of handling a small shipment goes up fairly steeply with its size, but the cost of handling a large shipment, while it still increases with size, does not increase so fast. Thus having one straight line to describe the whole relationship would not work so well. The relationship is actually two different straight lines joined end-to-end, which we will explore later, but if you think the relationship is curved, I'll accept that. The point is to get at the idea that the rate of increase is not constant.

(d) When a shipment comes in, the cost of handling it is not known. A decision is made about which warehouse to send it to, and then, after it is handled, the cost is recorded. What do you think determines which warehouse an incoming shipment goes to? Provide a graph to support your answer.

Solution

The veiled hint in the question is that the decision must depend on size, since it cannot depend on cost. So we have one quantitative variable size and one categorical variable warehouse, which suggests drawing boxplots:

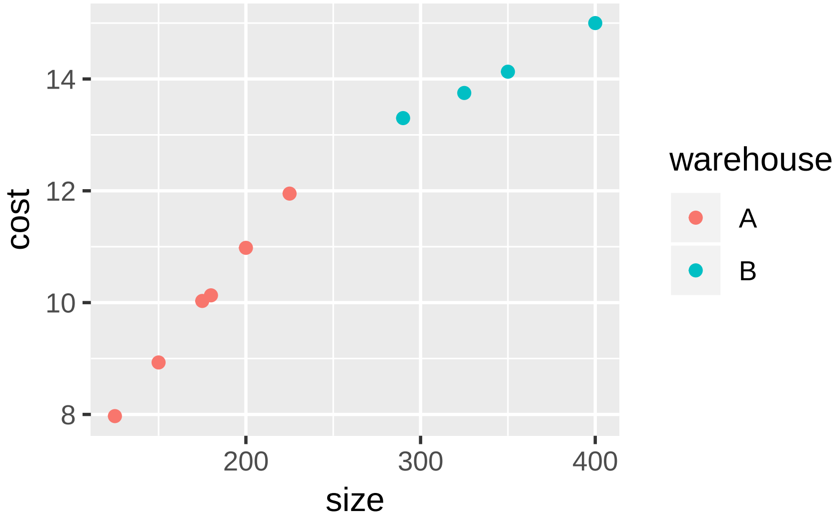
```
ggplot(shipments, aes(x = warehouse, y = size)) +
    geom_boxplot()
```



Well, there's the answer right there. When the shipment has small `size`, it goes to warehouse A, and when it's large, it goes to Warehouse B. We know this because *all* the shipments smaller than about 250 (thousand parts) went to A and *all* the shipments larger than that went to B. (If you want to provide a number to delineate "small" and "large", anything between the largest A, about 225, and the smallest B, about 290, will do.)

Another way to think about this is to add something to the scatterplot you drew before. The obvious thing is to make the two warehouses different colours:

```
ggplot(shipments, aes(x = size, y = cost, colour = warehouse)) +
    geom_point()
```



As a point of technique, you can split lines of code to make them fit on your screen. You can do this as long as *the code that ends the line must be incomplete*, so that R knows more is to come. Ending a line with a pipe symbol, or, as here, with one of the pluses in the middle of a `ggplot`, will work. If you put the plus on the start of the next line, you'll get a blank plot, because R thinks you're done plotting. Try it and see.

Anyway, this plot tells exactly the same story: the small shipments (in size or cost) go to Warehouse A and the large ones to Warehouse B. But we don't know cost when the decision is made about which warehouse to send a shipment to, so the decision must be based on `size`.

In the place where I got these data, it said "larger shipments are sent to Warehouse B, since this warehouse has specialized equipment that provides greater economies of scale for larger shipments". That is to say, very large shipments are more expensive to handle, but not as expensive as you might think. That makes sense with our scatterplot, because the *slope* for larger shipments is less than for smaller shipments.

This is the same idea that it costs more to ride the GO bus from UTSC to York U than it does to ride from UTSC to Scarborough Town, but if you work out how much it costs per kilometre, the longer journey costs less per km. As of when I'm writing this, $5.30 for the 7.2 km to Scarborough Town and 6.75$ for the 38 km to York. That's quite an economy of scale, isn't it?

When we get to regression later, we'll see what happens if we fit a straight line to data like these, and how to tell whether we really ought to be able to do better with a different form of relationship. There is also a trick to fit what is called a "piecewise linear regression", which has one slope for small shipment sizes, a different (smaller) slope for large ones, and joins up in the middle. But that's well beyond our scope now.

4
Data exploration

```
library(tidyverse)

## -- Attaching packages ---- tidyverse 1.2.1 --

## v ggplot2 3.0.0     v purrr   0.2.5
## v tibble  1.4.2     v dplyr   0.7.6
## v tidyr   0.8.1     v stringr 1.3.1
## v readr   1.1.1     v forcats 0.3.0

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

4.1 North Carolina births

The data in file link are about 500 randomly chosen births of babies in North Carolina. There is a lot of information: not just the weight at birth of the baby, but whether the baby was born prematurely, the ages of the parents, whether the parents are married, how long (in weeks) the pregnancy lasted (this is called the "gestation") and so on.

(a) Read in the data from the file into R, bearing in mind what type of file it is.

Solution

This is a .csv file (it came from a spreadsheet), so it needs reading in accordingly. Work directly from the URL (rather than downloading the file, unless you are working offline):

```
myurl = "http://www.utsc.utoronto.ca/~butler/c32/ncbirths.csv"
bw = read_csv(myurl)

## Parsed with column specification:
## cols(
##   ‘Father Age‘ = col_integer(),
##   ‘Mother Age‘ = col_integer(),
##   ‘Weeks Gestation‘ = col_integer(),
##   ‘Pre-natal Visits‘ = col_integer(),
##   ‘Marital Status‘ = col_integer(),
##   ‘Mother Weight Gained‘ = col_integer(),
##   ‘Low Birthweight?‘ = col_integer(),
##   ‘Weight (pounds)‘ = col_double(),
##   ‘Premie?‘ = col_integer(),
##   ‘Few Visits?‘ = col_integer()
## )
```

This shows you which variables the data set has (some of the names got a bit mangled), and it shows you that they are all integers except for the birth weight (a decimal number).

The easiest way to find out how many rows and columns there are is simply to list the data frame:

```
bw
```

```
## # A tibble: 500 x 10
##    ‘Father Age‘ ‘Mother Age‘ ‘Weeks Gestatio~
##           <int>        <int>            <int>
##  1           27           26               38
##  2           35           33               40
##  3           34           22               37
##  4           NA           16               38
##  5           35           33               39
##  6           32           24               36
##  7           33           33               38
##  8           38           35               38
##  9           28           29               40
## 10           NA           19               34
## # ... with 490 more rows, and 7 more
## #   variables: ‘Pre-natal Visits‘ <int>,
## #   ‘Marital Status‘ <int>, ‘Mother Weight
## #   Gained‘ <int>, ‘Low Birthweight?‘ <int>,
## #   ‘Weight (pounds)‘ <dbl>,
## #   ‘Premie?‘ <int>, ‘Few Visits?‘ <int>
```

or you can take a “glimpse” of it:

```
glimpse(bw)
```

```
## Observations: 500
## Variables: 10
## $ ‘Father Age‘           <int> 27, 35, 3...
## $ ‘Mother Age‘           <int> 26, 33, 2...
## $ ‘Weeks Gestation‘      <int> 38, 40, 3...
## $ ‘Pre-natal Visits‘     <int> 14, 11, 1...
## $ ‘Marital Status‘       <int> 1, 1, 2, ...
## $ ‘Mother Weight Gained‘ <int> 32, 23, 5...
## $ ‘Low Birthweight?‘     <int> 0, 0, 0, ...
## $ ‘Weight (pounds)‘      <dbl> 6.8750, 6...
## $ ‘Premie?‘              <int> 0, 0, 0, ...
## $ ‘Few Visits?‘          <int> 0, 0, 0, ...
```

Either of these displays show that there are 500 rows (observations, here births) and 10 columns (variables), and they both show what the variables are called. So they're both good as an answer to the question.

What you'll notice is that the variables have *spaces* in their names, which will require special handling later. These outputs show you what to do about those spaces in variable names: surround the variable name with "backticks". (On my keyboard, that's on the key to the left of number 1, where the squiggle is, that looks like a backwards apostrophe. Probably next to `Esc`, depending on the layout of your keyboard.)

Although almost all of the variables are stored as integers, the ones that have a question mark in their name are actually "logical", true or false, with 1 denoting true and 0 false. We could convert them later if we want to. (A question mark is not a traditional character to put in a variable name, so we have to surround these variables with backticks too.)

(b) From your output, verify that you have the right number of observations and that you have several variables. Which of your variables correspond to birthweight, prematureness and length of pregnancy? (You might have to make guesses based on the names of the variables.)

Solution

I do indeed have 500 observations on 10 variables ("several"). (If you don't have several variables, check to see that you didn't use `read_delim` or something by mistake.) After the "500 observations of 10 variables" line(s) in each case, you see all the variables by name, with what type of values they have, and the first few of the values.

The variable `Weight (pounds)` is the birthweight (in pounds), `Premie?` is 1 for a premature baby and 0 for a full-term baby, and `Weeks Gestation` is the number of weeks the pregnancy lasted. Don't forget to put backticks around each of those when you use them later.

these are mostly *int* or *integer*.

Other possible variable types are *num* for (real, decimal) numbers such as birth weight, *chr* for text, and *Factor* (with the number of levels) for factors/categorical variables. We don't have any of the last two here. There is also *lgl* for *logical*, things that were actually recorded as TRUE or FALSE. We have some variables that are actually logical ones, but they are recorded as integer values.

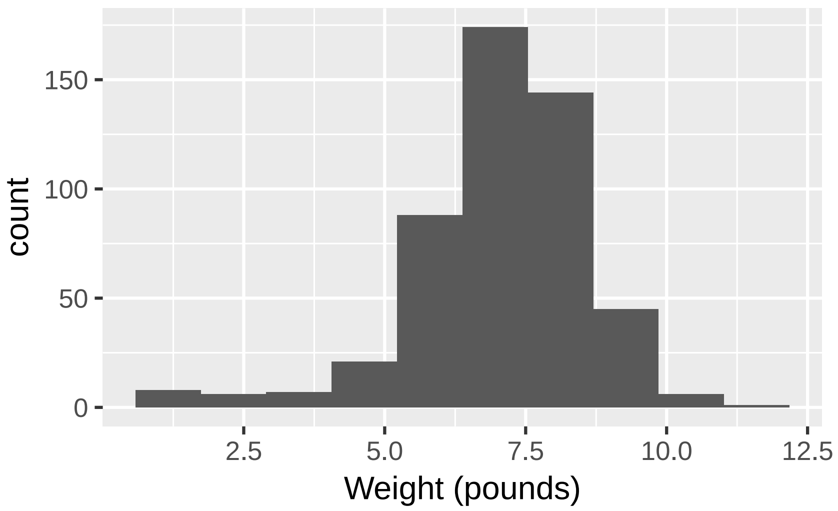
The backticks look different from each other for annoying technical reasons, but they're all backticks.

(c) The theory behind the *t*-test (which we do later) says that the distribution of birth weights should be (approximately) normally distributed. Obtain a histogram of the birth weights. Does it look approximately normal? Comment briefly. (You'll have to pick a number of bins for your histogram first. I don't mind very much what you pick, as long as it's not obviously too many or too few bins.)

Solution

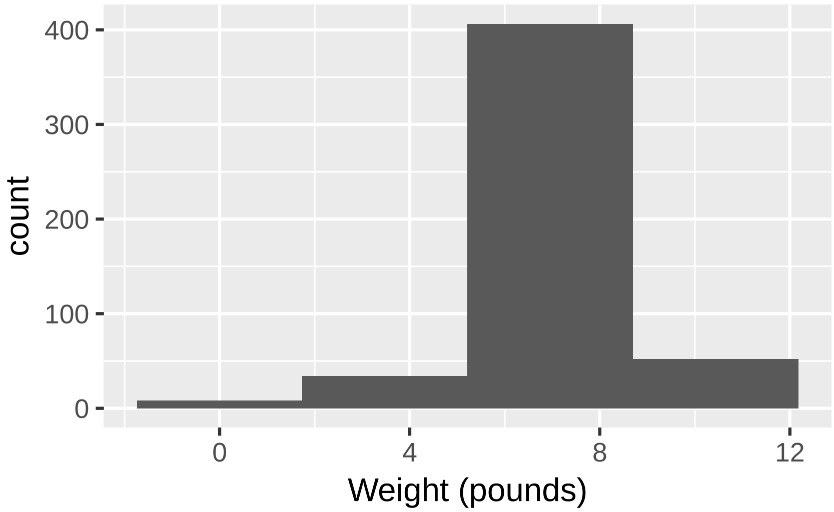
You'll have seen that I often start with 10 bins, or maybe not quite that many if I don't have much data, and this is a decent general principle. That would give

```
ggplot(bw, aes(x = `Weight (pounds)`)) + geom_histogram(bins = 10)
```



which is perfectly acceptable. You can try something a bit more or a bit less, and see how you like it in comparison. What you are looking for is a nice clear picture of *shape*. If you have too few bins, you'll lose the shape:

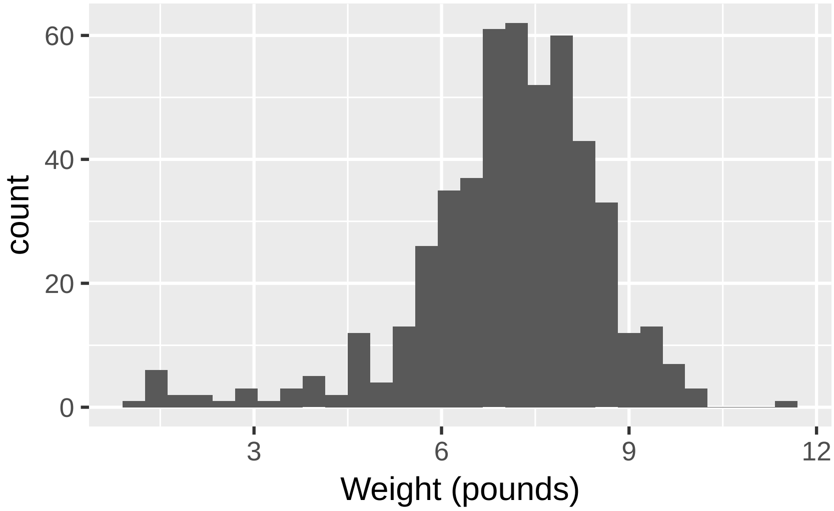
```
ggplot(bw, aes(x = `Weight (pounds)`)) + geom_histogram(bins = 4)
```



(is that leftmost bin an indication of skewness or some observations that happen to be smallish?)

And if you have too many, the shape will be there, but it will be hard to make out in all the noise, with frequencies going up and down:

```
ggplot(bw, aes(x = ‘Weight (pounds)‘)) + geom_histogram(bins = 30)
```



I generally am fairly relaxed about the number of bins you use, as long as it's not clearly too few or too many. You might have done exercises in the past that illustrate that the choice of number of bins (or the class intervals where you move from one bin to the next, which is another issue that I won't explore here) can make an appreciable difference to how a histogram looks. Extra: I had some thoughts about this issue that I put in a blog post, that you might like to read: link. The nice thing about Sturges' rule, mentioned there, is that you can almost get a number of bins for your histogram in your head (as long as you know the powers of 2, that is). What you do is to start with your sample size, here $n = 500$. You find the next power of 2 above that, which is here $512 = 2^9$. You then take that power and add 1, to get 10 bins. If you don't like that, you can get R to calculate it for you:

```
nclass.Sturges(bw$`Weight (pounds)`)
```

```
## [1] 10
```

The place where Sturges' rule comes from is an assumption of normal data (actually a binomial approximation to the normal, backwards though that sounds). If you have less than 30 observations, you'll get fewer than 6 bins, which won't do much of a job of showing the shape. Rob Hyndman wrote a critical note about Sturges' rule in which he asserts that it is just plain wrong (if you have taken B57, this note is very readable).

So what to use instead? Well, judgment is still better than something automatic, but if you want a place to start from, something with a better foundation than Sturges is the Freedman-Diaconis rule. This, in its original formulation, gives a bin width rather than a number of bins:

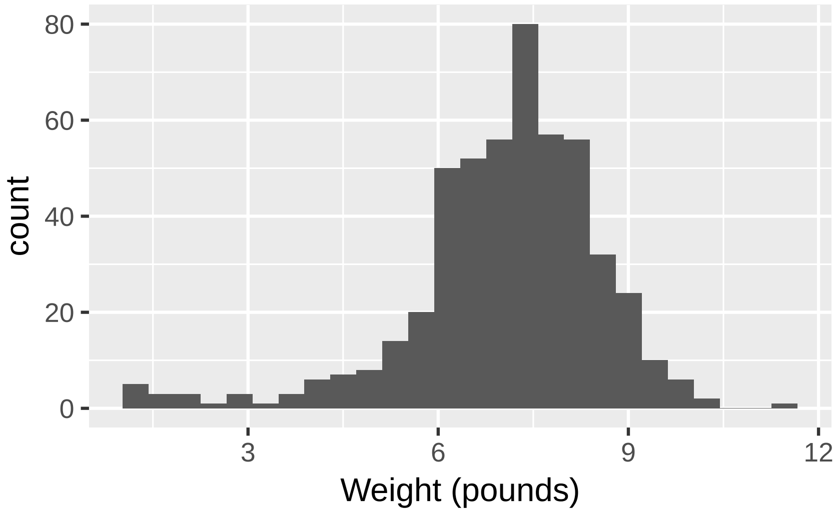
$$w = 2(IQR)n^{-1/3}$$

The nice thing about this is that it uses the interquartile range, so it won't be distorted by outliers. `geom_histogram` can take a bin width, so we can use it as follows:

```
w = 2 * IQR(bw$`Weight (pounds)`) * 500^(-1/3)
w
```

```
## [1] 0.4094743
```

```
ggplot(bw, aes(x = `Weight (pounds)`)) + geom_histogram(binwidth = w)
```



R also has

```
nc = nclass.FD(bw$‘Weight (pounds)‘)
nc
```

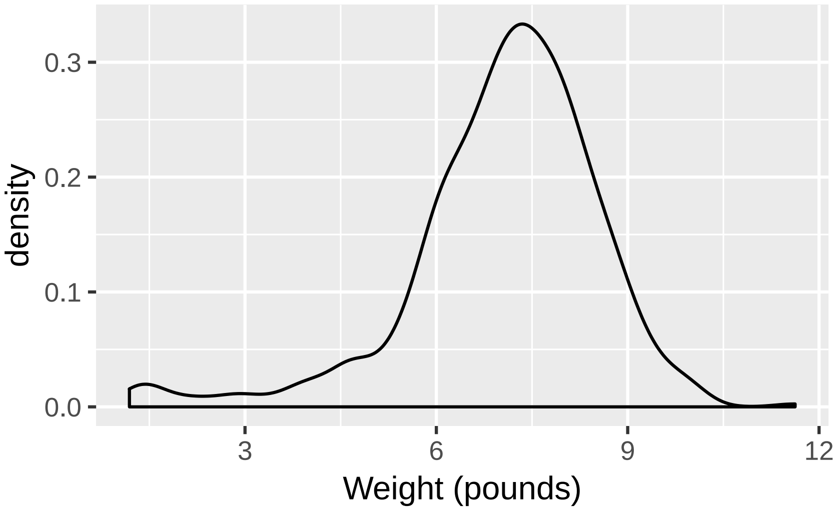
```
## [1] 26
```

which turns the Freedman-Diaconis rule into a number of bins rather than a binwidth; using that gives the same histogram as we got with `binwidth`.

In my opinion, Freedman-Diaconis tends to give too many bins (here there are 26 rather than the 10 of Sturges). But I put it out there for you to make your own call.

Another way to go is a “density plot”. This is a smoothed-out version of a histogram that is not obviously frequencies in bins, but which does have a theoretical basis. It goes something like this:

```
ggplot(bw, aes(x = ‘Weight (pounds)‘)) + geom_density()
```



geom_density has an optional parameter that controls how smooth or wiggly the picture is, but the default is usually good.

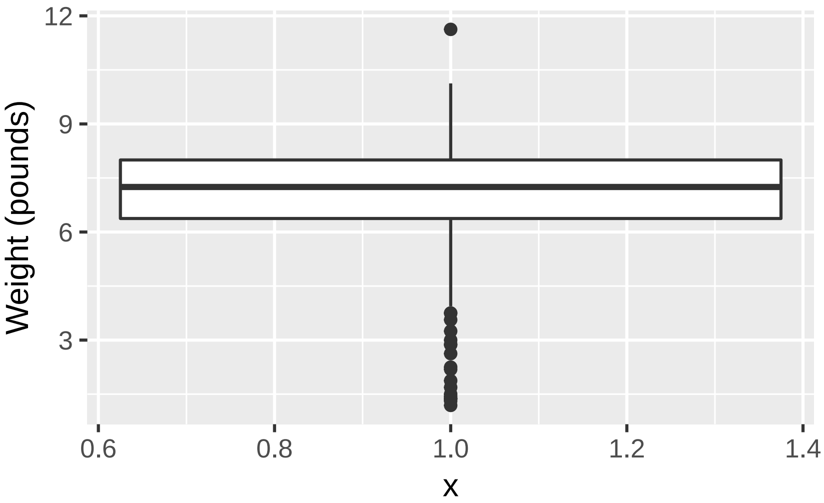
Alright, before we got distracted, we were assessing normality. What about that?

It is mostly normal-looking, but I am suspicious about those *very* low birth weights, the ones below about 4 pounds. There are a few too many of those, as I see it.

If you think this is approximately normal, you need to make some comment along the lines of "the shape is approximately symmetric with no outliers". I think my first answer is better, but this answer is worth something, since it is a not completely unreasonable interpretation of the histogram.

I have been making the distinction between a histogram (for one quantitative variable) and side-by-side boxplots (for one quantitative variable divided into groups by one categorical variable). When you learned the boxplot, you probably learned it in the context of one quantitative variable. You can draw a boxplot for that, too, but the ggplot boxplot has an x as well as a y. What you do to make a single boxplot is to set the x equal 1, which produces a weird *x*-axis (that you ignore):

```
ggplot(bw, aes(x = 1, y = `Weight (pounds)`)) +
    geom_boxplot()
```



The high weight is actually an outlier, but look at all those outliers at the bottom!

I think the reason for those extra very low values is that they are the premature births (that can result in *very* small babies). Which leads to the additional question coming up.

When Tukey, a name we will see again, invented the boxplot in the 1950s, 500 observations would have been considered a big data set. He designed the boxplot to produce a sensible number of outliers for the typical size of data set of his day, but a boxplot of a large data set tends to have a lot of outliers that are probably not really outliers at all.

4.2 More about the NC births

This is an exploration of some extra issues around the North Carolina births data set.

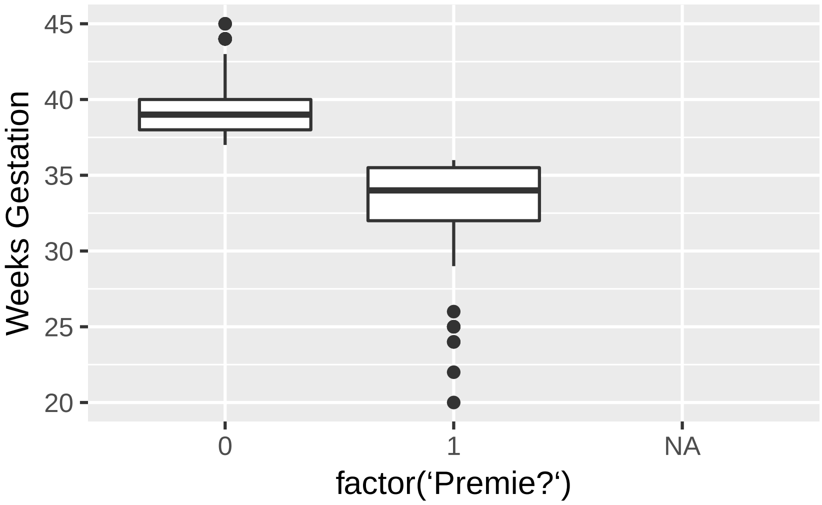
(a) How short does a pregnancy have to be, for the birth to be classified as "premature"? Deduce this from the data, by drawing a suitable graph or otherwise.

Solution

To figure it out from the data, we can see how `Weeks Gestation` depends on `Premie?`. Some possibilities are boxplots or a scatterplot. Either of the first two graphs would get full credit (for the graphing part: you still have to do the explanation) if this were being marked:

```
ggplot(bw, aes(x = factor(‘Premie?‘), y = ‘Weeks Gestation‘)) +
    geom_boxplot()
```

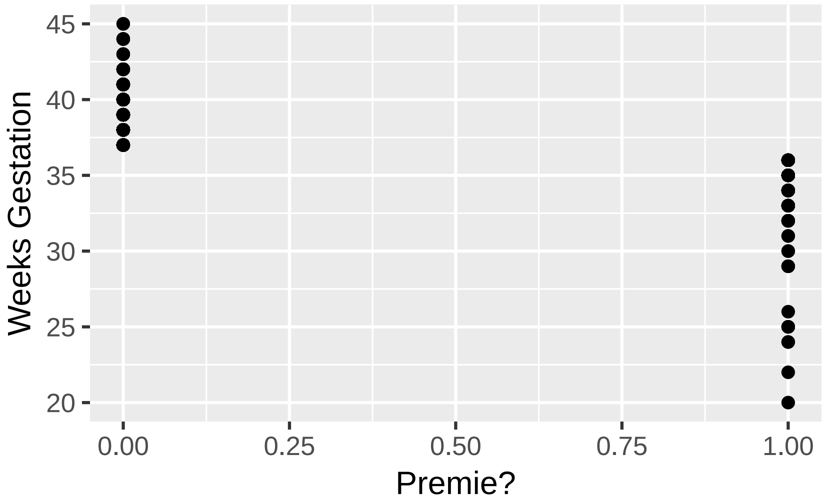
```
## Warning: Removed 1 rows containing non-finite
## values (stat_boxplot).
```



The warning is because the prematurity of one of the babies is not known. Or

```
ggplot(bw, aes(x = ‘Premie?‘, y = ‘Weeks Gestation‘)) +
    geom_point()
```

```
## Warning: Removed 1 rows containing missing values
## (geom_point).
```



The same warning again, for the same reason.

Notice how the graphs are similar in syntax, because the what-to-plot is the same (apart from the `factor` thing) and we just make a small change in how-to-plot-it. In the boxplot, the thing on the x-scale needs to be categorical, and `Premie?` is actually a number, so we'd better make it into a `factor`, which is R's version of a categorical variable. `Premie.` is actually a categorical variable ("premature" or "not premature") masquerading as a quantitative one (1 or 0). It is an "indicator variable", if you're familiar with that term.

It looks as if the breakpoint is 37 weeks: a pregnancy at least that long is considered normal, but a shorter one ends with a premature birth. Both plots show the same thing: the '`Premie?=1`' births all go with short pregnancies, shorter than 37 weeks. This is completely clear cut.

Another way to attack this is to use `summarize`, finding the max and min:

```
bw %>% summarize(n = n(), min = min(`Weeks Gestation`),
    max = max(`Weeks Gestation`))

## # A tibble: 1 x 3
##       n   min   max
##   <int> <dbl> <dbl>
## 1   500    NA    NA
```

only this is for *all* the babies, premature or not. So we want it by prematurity, which means a `group_by` first:

I explain the missing values below.

```
bw %>% group_by(`Premie?`) %>% summarize(n = n(),
    min = min(`Weeks Gestation`), max = max(`Weeks Gestation`))

## # A tibble: 3 x 4
##   ‘Premie?‘     n   min   max
##       <int> <int> <dbl> <dbl>
## 1         0   424    37    45
## 2         1    75    20    36
## 3        NA     1    NA    NA
```

group_by with a number works, even though using the number in Premie? in a boxplot didn't. group_by just uses the distinct values, whether they are numbers, text or factor levels.

Any of these graphs or summaries will help you answer the question, in the same way. The ultimate issue here is "something that will get the job done": it doesn't matter so much what.

In R, NA means "missing". When you try to compute something containing a missing value, the answer is usually missing (since you don't know what the missing value is). That's why the first summarize gave us missing values: there was one missing weeks of gestation in with all the ones for which we had values, so the max and min had to be missing as well. In the second summarize, the one by whether a baby was born prematurely or not, we learn a bit more about that missing Premie?: evidently its weeks of gestation was missing as well, since the min and max of that were missing.

If there had been a weeks of gestation, we could have figured out whether it was premature or not, according to whether the weeks of gestation was less than 37.

Here's that baby. I'm doing a bit of fiddling to show all the columns (as rows, since there's only one actual row). Don't worry about the second line of code below; we will investigate that later.

```
bw %>% filter(is.na(‘Premie?‘)) %>% gather(name,
    value, everything())
```

```
## # A tibble: 10 x 2
##    name                 value
##    <chr>                <dbl>
##  1 Father Age           33
##  2 Mother Age           32
##  3 Weeks Gestation      NA
##  4 Pre-natal Visits      9
##  5 Marital Status        1
##  6 Mother Weight Gained 25
##  7 Low Birthweight?      0
##  8 Weight (pounds)       7.19
##  9 Premie?              NA
## 10 Few Visits?           0
```

The *only* thing that was missing was its weeks of gestation, but that prevented anyone from figuring out whether it was premature or not.

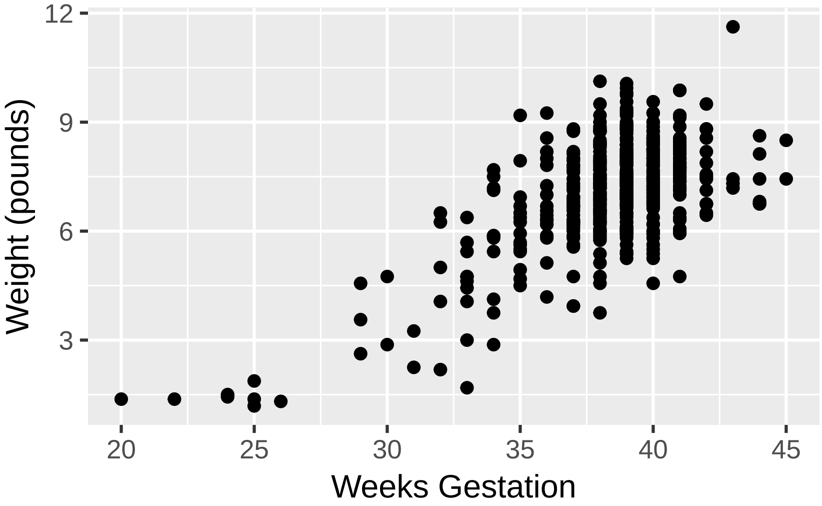
(b) Explore the relationship between birth weight and length of pregancy ("gestation") using a suitable graph. What do you see?

Solution

This needs to be a scatterplot because these are both quantitative variables:

```
ggplot(bw, aes(x = `Weeks Gestation`, y = `Weight (pounds)`)) +
    geom_point()
```

```
## Warning: Removed 1 rows containing missing values
## (geom_point).
```

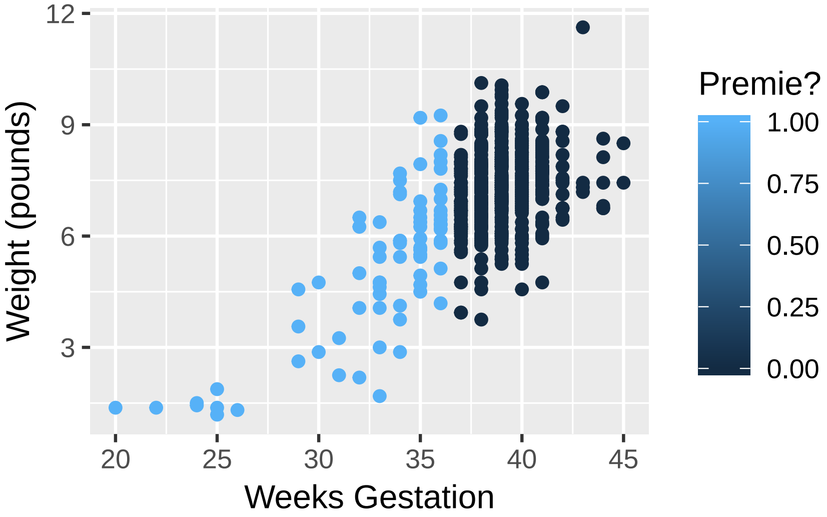


You see a rather clear upward trend. Those very underweight babies came from very short pregnancies, but the vast majority of pregnancies were of more or less normal length (40 weeks is normal) and resulted in babies of more or less normal birth weight.

I want to illustrate something else: how about *colouring* the births that were premature? Piece of cake with `ggplot`:

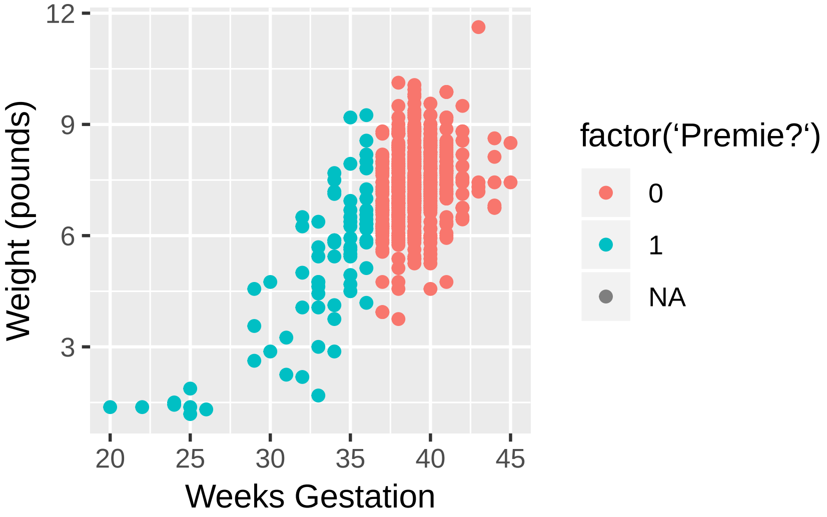
```
ggplot(bw, aes(x = `Weeks Gestation`, y = `Weight (pounds)`,
    colour = `Premie?`)) + geom_point()
```

```
## Warning: Removed 1 rows containing missing values
## (geom_point).
```



That was rather silly because `ggplot` treated prematureness as a *continuous* variable, and plotted the values on a dark blue-light blue scale. This is the same issue as on the boxplot above, and has the same solution:

```
ggplot(bw, aes(x = `Weeks Gestation`, y = `Weight (pounds)`,
    colour = factor(`Premie?`))) + geom_point()

## Warning: Removed 1 rows containing missing values
## (geom_point).
```



Better.

With the normal-length pregnancies (red), there seems to be no relationship between length of pregnancy and birth weight, just a random variation. But with the premature births, a shorter pregnancy typically goes with a *lower* birth weight. This would be why the birth weights for the premature births were more variable.

(c) Do a web search to find the standard (North American) definition of a premature birth. Does that correspond to what you saw in the data? Cite the website you used, for example by saying "according to URL, ldots", with URL replaced by the address of the website you found.

Solution

The website http://www.mayoclinic.org/diseases-conditions/premature-birth/basics/definition/con-20020050 says that "a premature birth is one that occurs before the start of the 37th week of pregnancy", which is exactly what we found. (Note that I am citing the webpage on which I found this, and I even made it into a link so that you can check it.) The Mayo Clinic is a famous hospital system with locations in several US states, so I think we can trust what its website says.

4.3 *Nenana, Alaska*

Nenana, Alaska, is about 50 miles west of Fairbanks. Every spring, there is a contest in Nenana. A wooden tripod is placed on the frozen river, and people try to guess the exact minute when the ice melts enough for the tripod to fall through the ice. The contest started in 1917 as an amusement for railway workers, and has taken place every year since. Now, hundreds of thousands of people enter their guesses on the Internet and the prize for the winner can be as much as $300,000.

Because so much money is at stake, and because the exact same tripod is placed at the exact same spot on the ice every year, the data are consistent and accurate. The data are in link.

(a) Read the data into R. Note that the values are separated by *tabs* rather than spaces, so you'll need an appropriate read_ to read it in.

Solution

These are "tab-separated values", so read_tsv is the thing, as for the Australian athletes:

```
myurl = "http://www.utsc.utoronto.ca/~butler/c32/nenana.txt"
nenana = read_tsv(myurl)
```

```
## Parsed with column specification:
## cols(
##   Year = col_integer(),
##   JulianDate = col_double(),
##   ‘Date&Time‘ = col_character()
## )
```

Use whatever name you like for the data frame. One that is different from any of the column headers is smart; then it is clear whether you mean the whole data frame or one of its columns. `ice` or `melt` or anything like that would also be good.

I haven't asked you to display or check the data (that's coming up), but if you look at it and find that it didn't work, you'll know to come back and try this part again. R usually gets it right or gives you an error.

If you look at the data, they do appear to be separated by spaces, but the text version of the date and time *also* have spaces in them, so things might go astray if you try and read the values in without recognizing that the actual separator is a tab:

```
x = read_delim(myurl, " ")
```

```
## Parsed with column specification:
## cols(
##   ‘Year  JulianDate  Date&Time‘ = col_character()
## )
```

```
## Warning in rbind(names(probs), probs_f):
## number of columns of result is not a multiple
## of vector length (arg 1)
```

```
## Warning: 87 parsing failures.
## row # A tibble: 5 x 5 col     row col   expected  actual file          expected   <int> <chr> <chr>
## ... ................. ... ............................................. ........ .......................
## See problems(...) for more details.
```

Ouch! A hint as to what went wrong comes from looking at the read-in data frame:

```
x
```

```
## # A tibble: 87 x 1
##    ‘Year\tJulianDate\tDate&Time‘
##    <chr>
##  1 "1917\t120.4795\tApril"
##  2 "1918\t131.3983\tMay"
##  3 "1919\t123.6066\tMay"
##  4 "1920\t132.4490\tMay"
##  5 "1921\t131.2795\tMay"
##  6 "1922\t132.5559\tMay"
##  7 "1923\t129.0837\tMay"
##  8 "1924\t132.6323\tMay"
##  9 "1925\t127.7726\tMay"
## 10 "1926\t116.6691\tApril"
## # ... with 77 more rows
```

Those t symbols mean “tab character”, which is our hint that the values were separated by tabs rather than spaces.

More detail (if you can bear to see it) is here:

```
problems(x)
```

```
## # A tibble: 87 x 5
##      row col   expected  actual file
##    <int> <chr> <chr>     <chr>  <chr>
##  1     1 <NA>  1 columns 5 col~ 'http://www~
##  2     2 <NA>  1 columns 5 col~ 'http://www~
##  3     3 <NA>  1 columns 5 col~ 'http://www~
##  4     4 <NA>  1 columns 5 col~ 'http://www~
##  5     5 <NA>  1 columns 5 col~ 'http://www~
##  6     6 <NA>  1 columns 5 col~ 'http://www~
##  7     7 <NA>  1 columns 5 col~ 'http://www~
##  8     8 <NA>  1 columns 5 col~ 'http://www~
##  9     9 <NA>  1 columns 5 col~ 'http://www~
## 10    10 <NA>  1 columns 5 col~ 'http://www~
## # ... with 77 more rows
```

The first line of the data file (with the variable names in it) had no spaces, only tabs, so read_delim thinks there is *one* column with a very long name, but in the actual data, there are *five* space-separated columns. The text date-times are of the form “April 30 at 11:30 AM”, which, if you think it’s all separated by spaces, is actually 5 things: April, 30, at and so on. These are the only things that are separated by spaces, so, from that point of view, there are five columns.

(b) Find a way of displaying how many rows and columns your data frame has, and some of the values. Describe the first and last of the variables that you appear to have.

Solution

The easiest is just to display the tibble:

```
nenana
```

```
## # A tibble: 87 x 3
##     Year JulianDate 'Date&Time'
##    <int>      <dbl> <chr>
##  1  1917       120. April 30 at 11:30 AM
##  2  1918       131. May 11 at 9:33 AM
##  3  1919       124. May 3 at 2:33 PM
##  4  1920       132. May 11 at 10:46 AM
##  5  1921       131. May 11 at 6:42 AM
##  6  1922       133. May 12 at 1:20 PM
##  7  1923       129. May 9 at 2:00 AM
##  8  1924       133. May 11 at 3:10 PM
##  9  1925       128. May 7 at 6:32 PM
## 10  1926       117. April 26 at 4:03 PM
## # ... with 77 more rows
```

Alternatively, you can take a `glimpse` of it:

```
glimpse(nenana)
```

```
## Observations: 87
## Variables: 3
## $ Year        <int> 1917, 1918, 1919, 19...
## $ JulianDate  <dbl> 120.4795, 131.3983, ...
## $ ‘Date&Time‘ <chr> "April 30 at 11:30 A...
```

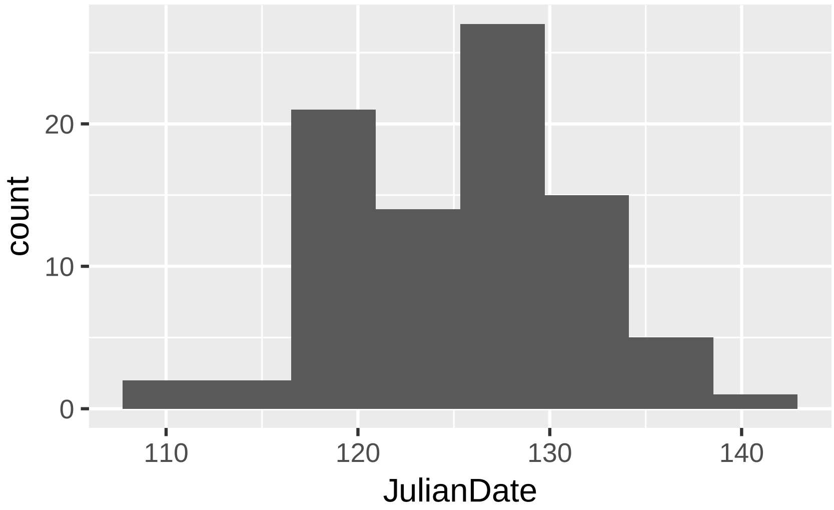
There are 87 years, and 3 columns (variables). The first column is year, and the last column is the date and time that the tripod fell into the river, written as a piece of text. I explain the second column in a moment.

(c) Dates and times are awkward to handle with software. (We see more ways later in the course.) The column `JulianDate` expresses the time that the tripod fell through the ice as a fractional number of days since December 31. This enables the time (as a fraction of the way through the day) to be recorded as well, the whole thing being an ordinary number. Make a histogram of the Julian dates. Comment briefly on its shape.

Solution

With a `ggplot` histogram, we need a number of bins first. I can do Sturges' rule in my head: the next power of 2 up from 87 (our n) is 128, which is 2^7, so the base 2 log of 87 rounds up to 7. That plus one is 8, so we need 8 bins. For you, any not-insane number of bins will do, or any not-insane bin width, if you want to go that way:

```
ggplot(nenana, aes(x = JulianDate)) + geom_histogram(bins = 8)
```

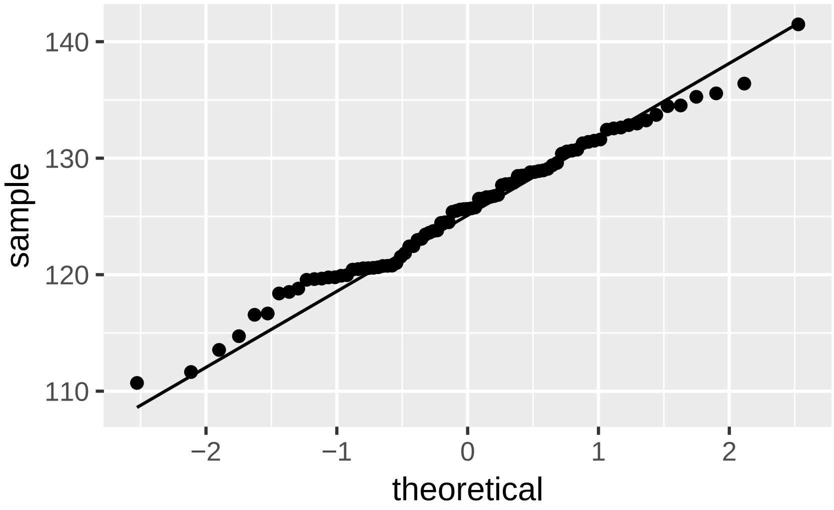


Note that you need to type `JulianDate` exactly as it appears, capital letters and all. R is case-sensitive.

This histogram looks more or less symmetric (and, indeed, normal). I really don't think you can justify an answer other than "symmetric" here. (Or "approximately normal": that's good too.) If your histogram is different, say so. I think that "hole" in the middle is not especially important.

We haven't done normal quantile plots yet, but looking ahead:

```
ggplot(nenana, aes(sample = JulianDate)) + stat_qq() +
    stat_qq_line()
```



That hugs the line pretty well, so I would call it close to normally-distributed. It bulges away from the line because there are more values just below 120 than you would expect for a normal. This corresponds to the histogram bar centred just below 120 being taller than you would have expected.

That is to say, the principal deviation from normality is not the hole on the histogram, the bar centred around 123 being too short, but that the bar centred just below 120 is too *tall*.

Extra: looking *way* ahead (to almost the end of the R stuff), this is how you handle the dates and times:

```
library(lubridate)
```

```
##
## Attaching package: 'lubridate'
```

```
## The following object is masked from 'package:base':
##
##     date
```

```
nenana %>% mutate(longdt = str_c(Year, " ", ‘Date&Time‘)) %>%
    mutate(datetime = ymd_hm(longdt, tz = "America/Anchorage"))
```

```
## # A tibble: 87 x 5
##     Year JulianDate ‘Date&Time‘ longdt
##    <int>      <dbl> <chr>       <chr>
##  1  1917       120. April 30 a~ 1917 ~
##  2  1918       131. May 11 at ~ 1918 ~
##  3  1919       124. May 3 at 2~ 1919 ~
##  4  1920       132. May 11 at ~ 1920 ~
##  5  1921       131. May 11 at ~ 1921 ~
##  6  1922       133. May 12 at ~ 1922 ~
##  7  1923       129. May 9 at 2~ 1923 ~
##  8  1924       133. May 11 at ~ 1924 ~
##  9  1925       128. May 7 at 6~ 1925 ~
## 10  1926       117. April 26 a~ 1926 ~
## # ... with 77 more rows, and 1 more
## #   variable: datetime <dttm>
```

I am not doing any further analysis with these, so just displaying them is good.

I have to do a preliminary step to get the date-times *with* their year in one place. `str_c` glues pieces of text together: in this case, the year, a space, and then the rest of the `Date&Time`. I stored this in `longdt`. The second `mutate` is the business end of it: `ymd_hm` takes a piece of text containing a year, month (by name or number), day, hours, minutes *in that order*, and extracts those things from it, storing the whole thing as an R date-time. Note that the AM/PM was handled properly. The benefit of doing that is we can extract anything from the dates, such as the month or day of week, or take differences between the dates. Or even check that the Julian dates were calculated correctly (the `lubridate` function is called `yday` for "day of year"):

```
nenana2 <- nenana %>% mutate(longdt = str_c(Year,
    " ", ‘Date&Time‘)) %>% mutate(datetime = ymd_hm(longdt,
    tz = "America/Anchorage")) %>% mutate(jd = yday(datetime))
nenana2 %>% select(JulianDate, jd, datetime)
```

```
## # A tibble: 87 x 3
##    JulianDate    jd datetime
##         <dbl> <dbl> <dttm>
##  1       120.   120 1917-04-30 11:30:00
##  2       131.   131 1918-05-11 09:33:00
##  3       124.   123 1919-05-03 14:33:00
##  4       132.   132 1920-05-11 10:46:00
##  5       131.   131 1921-05-11 06:42:00
##  6       133.   132 1922-05-12 13:20:00
##  7       129.   129 1923-05-09 02:00:00
##  8       133.   132 1924-05-11 15:10:00
##  9       128.   127 1925-05-07 18:32:00
## 10       117.   116 1926-04-26 16:03:00
## # ... with 77 more rows
```

Hmm, some of those are off by one. What do the off-by-one ones have in common? Let's look at more of them. `round` rounds off to the nearest integer (since these are actually decimal numbers):

```
nenana2 %>% filter(round(JulianDate) != round(jd)) %>%
    select(JulianDate, jd, datetime)
```

```
## # A tibble: 61 x 3
##    JulianDate    jd datetime
##         <dbl> <dbl> <dttm>
##  1       124.   123 1919-05-03 14:33:00
##  2       133.   132 1922-05-12 13:20:00
##  3       133.   132 1924-05-11 15:10:00
##  4       128.   127 1925-05-07 18:32:00
##  5       117.   116 1926-04-26 16:03:00
##  6       128.   127 1928-05-06 16:25:00
##  7       126.   125 1929-05-05 15:41:00
##  8       129.   128 1930-05-08 19:03:00
##  9       129.   128 1933-05-08 19:30:00
## 10       121.   120 1934-04-30 14:07:00
## # ... with 51 more rows
```

The ones shown here are all *after noon*, and the Julian date in the data file appears as one more than the one calculated by `lubridate`. What has actually happened is a quirk of how tibbles are displayed: they show 3 significant digits, *rounded*. The Julian dates given by `yday` are the whole-number part, so the ones in the data value are that plus more than 0.5, which will round *up*. The first line of code below displays 6 significant digits rather than only three:

```
options(pillar.sigfig = 6)
nenana2 %>% filter(round(JulianDate) != round(jd)) %>%
    select(JulianDate, jd, datetime)
```

```
## # A tibble: 61 x 3
##    JulianDate    jd datetime
##         <dbl> <dbl> <dttm>
##  1    123.607   123 1919-05-03 14:33:00
##  2    132.556   132 1922-05-12 13:20:00
##  3    132.632   132 1924-05-11 15:10:00
##  4    127.773   127 1925-05-07 18:32:00
##  5    116.669   116 1926-04-26 16:03:00
##  6    127.684   127 1928-05-06 16:25:00
##  7    125.654   125 1929-05-05 15:41:00
##  8    128.794   128 1930-05-08 19:03:00
##  9    128.813   128 1933-05-08 19:30:00
## 10    120.588   120 1934-04-30 14:07:00
## # ... with 51 more rows
```

Displaying more decimals shows that I was right: `jd` is (to this accuracy) a whole number, but `JulianDate` is a decimal with fractional part greater than 0.50.

Now I have to turn the extra signficant digits off:

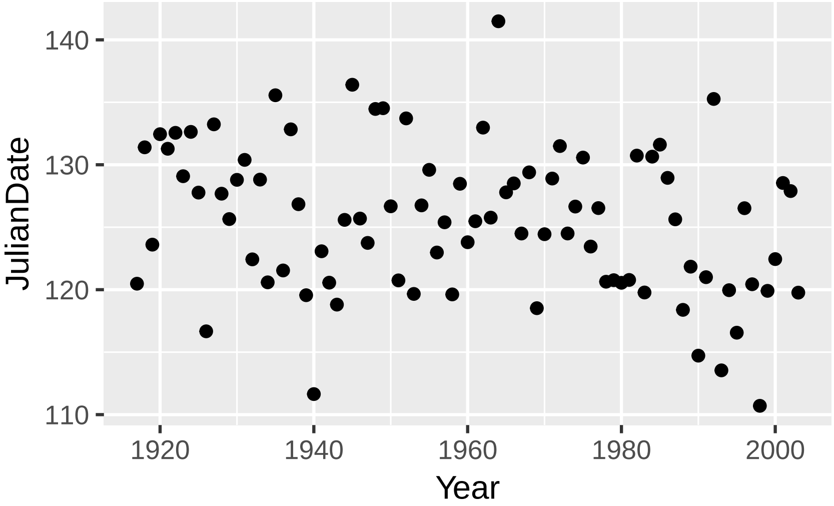
```
options(pillar.sigfig = 3)
```

(d) Plot `JulianDate` against `Year` on a scatterplot. What recent trends, if any, do you see? Comment briefly.

Solution

`geom_point`:

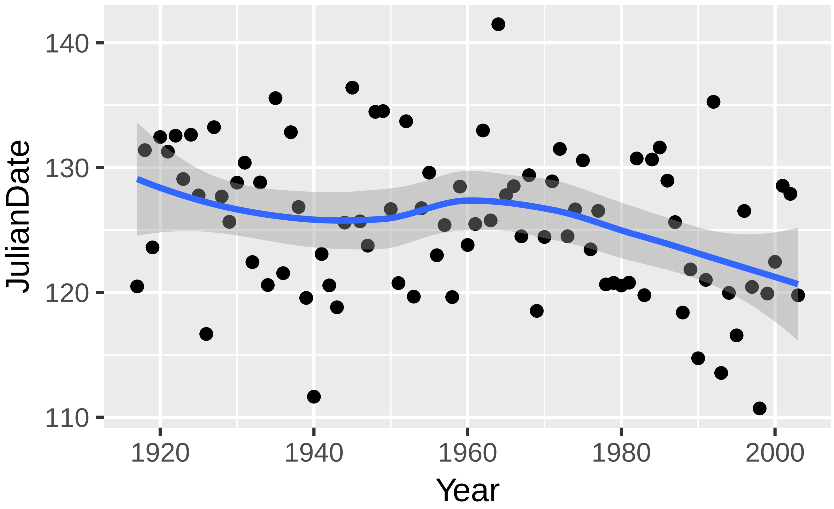
```
ggplot(nenana, aes(x = Year, y = JulianDate)) +
    geom_point()
```



This is actually a small-but-real downward trend, especially since about 1960, but the large amount of variability makes it hard to see, so I'm good with either "no trend" or "weak downward trend" or anything roughly like that. There is definitely not much trend before 1960, but most of the really early break-ups (less than about 118) have been since about 1990.

You can even add to the `ggplot`, by putting a smooth trend on it:

```
ggplot(nenana, aes(x = Year, y = JulianDate)) +
    geom_point() + geom_smooth()

## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



This is R's version of a trend that is not constrained to be linear (so that it "lets the data speak for itself").

Now there is something obvious to see: after about 1960, there is a clear downward trend: the ice is breaking up earlier on average every year. Even though there is a lot of variability, the overall trend, viewed this way, is clear.

What does this mean, in practice? This notion of the ice melting earlier than it used to is consistent all over the Arctic, and is one more indication of climate change. Precisely, it is an indication that climate change is happening, but we would have to delve further to make any statements about the *cause* of that climate change.

4.4 *Computerized accounting*

Beginning accounting students need to learn to learn to audit in a computerized environment. A sample of beginning accounting students took each of two tests: the Computer Attitude Scale (CAS) and the Computer Anxiety Rating Scale (CARS). A higher score in each indicates greater anxiety around computers. The test scores are scaled to be between 0 and 5. Also noted was each student's gender. The data are in `http://www.utsc.utoronto.ca/~butler/c32/compatt.txt`. The data values are separated by spaces.

(a) Read the data into R. Do you have what you expected? Explain briefly.

Solution

Read in and display the data. This, I think, is the easiest way.

```
url = "http://www.utsc.utoronto.ca/~butler/c32/compatt.txt"
anxiety = read_delim(url, " ")
```

```
## Parsed with column specification:
## cols(
##   gender = col_character(),
##   CAS = col_double(),
##   CARS = col_double()
## )
```

```
anxiety
```

```
## # A tibble: 35 x 3
##    gender   CAS  CARS
##    <chr>  <dbl> <dbl>
##  1 female  2.85  2.9
##  2 male    2.6   2.32
##  3 female  2.2   1
##  4 male    2.65  2.58
##  5 male    2.6   2.58
##  6 male    3.2   3.05
##  7 male    3.65  3.74
##  8 female  2.55  1.9
##  9 male    3.15  3.32
## 10 male    2.8   2.74
## # ... with 25 more rows
```

There is a total of 35 students with a CAS score, a CARS score and a gender recorded for each. This is in line with what I was expecting. (You can also note that the genders appear to be a mixture of males and females.)

(b) How many males and females were there in the sample?

Solution

Most easily `count`:

```
anxiety %>% count(gender)
```

```
## # A tibble: 2 x 2
##   gender     n
##   <chr>  <int>
## 1 female    15
## 2 male      20
```

This also works (and is therefore good):

```
anxiety %>% group_by(gender) %>% summarize(count = n())
```

```
## # A tibble: 2 x 2
##   gender count
##   <chr>  <int>
## 1 female    15
## 2 male      20
```

I want you to use R to do the counting (that is, don't just list out the whole data set with `print(n=Inf)` and count the males and females yourself). This is because you might have thousands of data values and you need to learn how to get R (or, later, SAS) to count them for you.

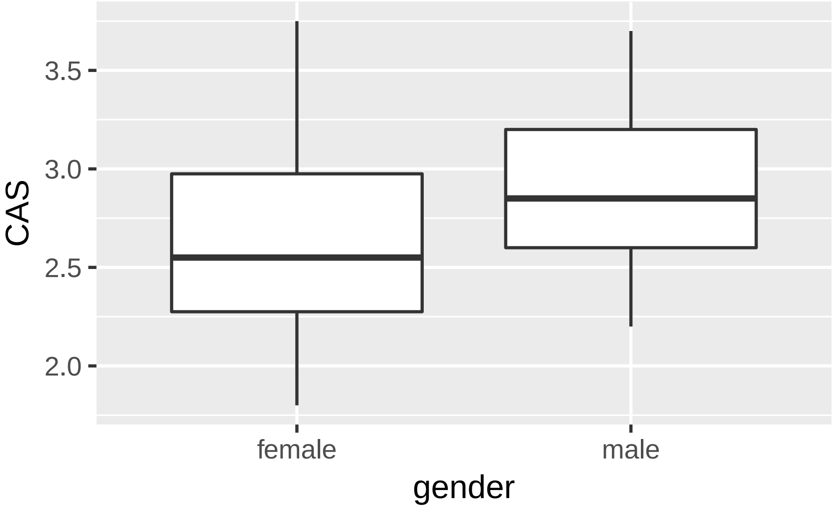
15 females and 20 males, *which you should say*. I made a point of *not* saying that it is enough to get the output with the answers on it, so you need to tell me what the answer is.

(c) Do the CAS scores tend to be higher for females or for males? Draw a suitable graph to help you decide, and come to a conclusion.

Solution

Gender is categorical and CAS score is quantitative, so a boxplot would appear to be the thing:

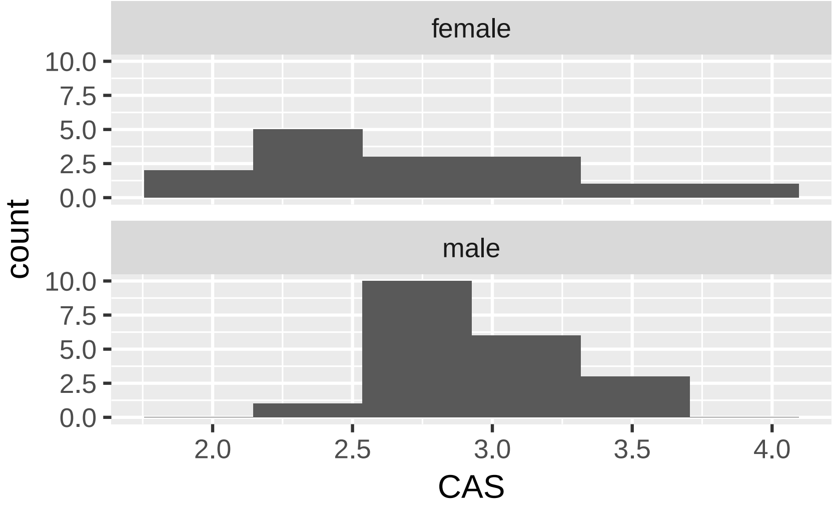
```
ggplot(anxiety, aes(x = gender, y = CAS)) + geom_boxplot()
```



The median for males is slightly higher, so male accountants are more anxious around computers than female accountants are.

If you wish, side-by-side (or, better, above-and-below) histograms would also work:

```
ggplot(anxiety, aes(x = CAS)) + geom_histogram(bins = 6) +
    facet_wrap(~gender, ncol = 1)
```



If you go this way, you have to make a call about where the centres of the histograms are. I guess the male one is slightly further to the right, but it's not so easy to tell. (Make a call.)

(d) Find the median CAS scores for each gender. Does this support what you saw on your plot? Explain briefly.

Solution

Group-by and summarize:

```
anxiety %>% group_by(gender) %>% summarize(med = median(CAS))
```

```
## # A tibble: 2 x 2
##   gender   med
##   <chr>  <dbl>
## 1 female  2.55
## 2 male    2.85
```

The median is a bit higher for males, which is what I got on my boxplot (and is apparently the same thing as is on the histograms, but it's harder to be sure there).

(e) Find the mean and standard deviation of both CAS and CARS scores (for all the students combined, ie. not separated by gender) *without* naming those columns explicitly.

Solution

Without naming them explicitly means using some other way to pick them out of the data frame, either `summarize\_if` or `summarize\_at`. To do it the first way, ask what these two columns have in common: they are the only two numeric (quantitative) columns:

```
anxiety %>% summarize_if(is.numeric, funs(mean,
    sd))
```

```
## # A tibble: 1 x 4
##   CAS_mean CARS_mean CAS_sd CARS_sd
##      <dbl>     <dbl>  <dbl>   <dbl>
## 1     2.82      2.77  0.484   0.671
```

Or the second way, asking yourself what the *names* of those columns have in common: they start with C and the gender column doesn't:

```
anxiety %>% summarize_at(vars(starts_with("C")),
    funs(mean, sd))
```

```
## # A tibble: 1 x 4
##   CAS_mean CARS_mean CAS_sd CARS_sd
##      <dbl>     <dbl>  <dbl>   <dbl>
## 1     2.82      2.77  0.484   0.671
```

Either of these is good, or anything equivalent (like noting that the two anxiety scales both `ends\_with` S):

```
anxiety %>% summarize_at(vars(ends_with("S")),
    funs(mean, sd))
```

```
## # A tibble: 1 x 4
##   CAS_mean CARS_mean CAS_sd CARS_sd
##      <dbl>     <dbl>  <dbl>   <dbl>
## 1     2.82      2.77  0.484   0.671
```

Because I didn't say otherwise, you should tell me what the means and SDs are, rounding off suitably: the CAS scores have mean 2.82 and SD 0.48, and the CARS scores have mean 2.77 and SD 0.67.

Yet another way to do it is to select the columns you want first (which you can do by number so as not to name them), and then find the mean and SD of all of them. This uses two tools that we haven't seen yet:

```
anxiety %>% select(2:3) %>% summarize_all(funs(mean,
    sd))
```

```
## # A tibble: 1 x 4
##   CAS_mean CARS_mean CAS_sd CARS_sd
##      <dbl>     <dbl>  <dbl>   <dbl>
## 1     2.82      2.77  0.484   0.671
```

This doesn't work:

```
summary(anxiety)
```

```
##     gender               CAS
##  Length:35          Min.   :1.800
##  Class :character   1st Qu.:2.575
##  Mode  :character   Median :2.800
##                     Mean   :2.816
##                     3rd Qu.:3.150
##                     Max.   :3.750
##       CARS
##  Min.   :1.000
##  1st Qu.:2.445
##  Median :2.790
##  Mean   :2.771
##  3rd Qu.:3.290
##  Max.   :4.000
```

because, although it gets the means, it does not get the standard deviations. (I added the SD to the original question to make you find a way other than this.)

In summary, find a way to get those answers without naming those columns in your code, and I'm good.

In case you were wondering about how to do this separately by gender, well, put the `group\_by` in like you did before:

```
anxiety %>% group_by(gender) %>% summarize_if(is.numeric,
    funs(mean, sd))
```

```
## # A tibble: 2 x 5
##   gender CAS_mean CARS_mean CAS_sd CARS_sd
##   <chr>     <dbl>     <dbl>  <dbl>   <dbl>
## 1 female     2.64      2.51  0.554   0.773
## 2 male       2.94      2.96  0.390   0.525
```

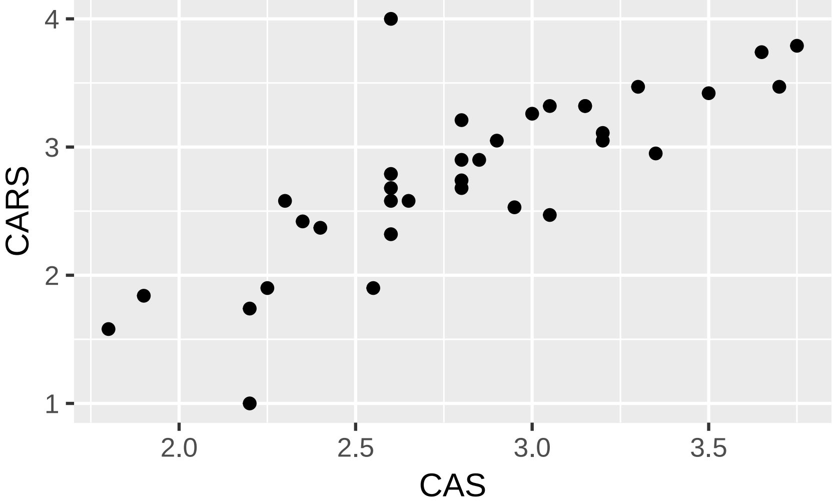
or

```
anxiety %>% group_by(gender) %>% summarize_at(vars(starts_with("C")),
    funs(mean, sd))
```

```
## # A tibble: 2 x 5
##   gender CAS_mean CARS_mean CAS_sd CARS_sd
##   <chr>     <dbl>     <dbl>  <dbl>   <dbl>
## 1 female     2.64      2.51  0.554   0.773
## 2 male       2.94      2.96  0.390   0.525
```

The male means are slightly higher on both tests, but the male standard deviations are a little smaller. You might be wondering whether the test scores are related. They are both quantitative, so the obvious way to find out is a scatterplot:

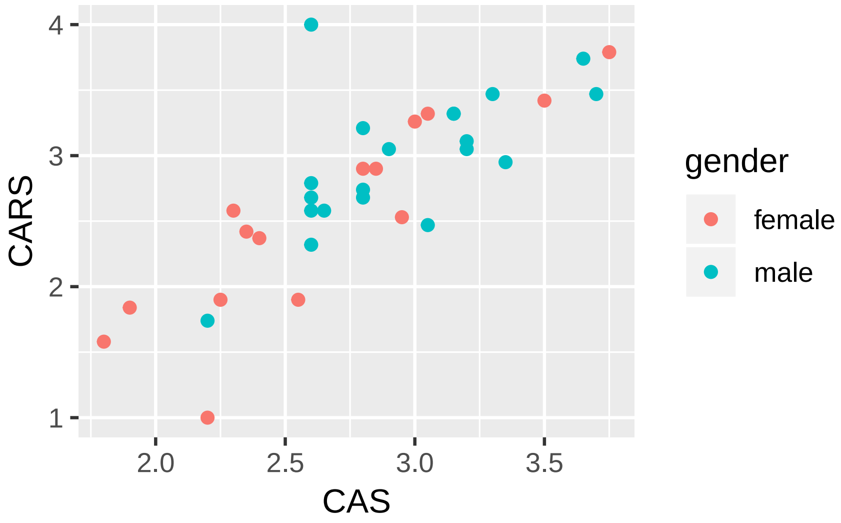
```
ggplot(anxiety, aes(x = CAS, y = CARS)) + geom_point()
```



The two variables can be on either axis, since there is no obvious response or explanatory variable. A higher score on one scale goes with a higher score on the other, suggesting that the two scales are measuring the same thing.

This plot mixes up the males and females, so you might like to distinguish them, which goes like this:

```
ggplot(anxiety, aes(x = CAS, y = CARS, colour = gender)) +
    geom_point()
```



There is a slight (but only slight) tendency for the males to be up and to the right, and for the females to be down and to the left. This is about what you would expect, given that the male means are slightly bigger on both scores, but the difference in means is not that big compared to the SD.

5
One-sample inference

```
library(tidyverse)
```

```
## -- Attaching packages ---- tidyverse 1.2.1 --

## v ggplot2 3.0.0     v purrr   0.2.5
## v tibble  1.4.2     v dplyr   0.7.6
## v tidyr   0.8.1     v stringr 1.3.1
## v readr   1.1.1     v forcats 0.3.0

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

5.1 Hunter-gatherers in Australia

A hunter-gatherer society is one where people get their food by hunting, fishing or foraging rather than by agriculture or by raising animals. Such societies tend to move from place to place. Anthropologists have studied hunter-gatherer societies in forest ecosystems across the world. The average population density of these societies is 7.38 people per 100 km^2. Hunter-gatherer societies on different continents might have different population densities, possibly because of large-scale ecological constraints (such as resource availability), or because of other factors, possibly social and/or historic, determining population density.

Some hunter-gatherer societies in Australia were studied, and the population density per 100 km^2 recorded for each. The data are in `http://www.utsc.utoronto.ca/~butler/c32/hg.txt`.

(a) Read the data into R. Do you have the correct variables? How many hunter-gatherer societies in Australia were studied? Explain briefly.

Solution

The data values are separated by (single) spaces, so read_delim is the thing:

```
url = "http://www.utsc.utoronto.ca/~butler/c32/hg.txt"
societies = read_delim(url, " ")
```

```
## Parsed with column specification:
## cols(
##   name = col_character(),
##   density = col_double()
## )
```

I like to put the URL in a variable first, because if I don't, the read_delim line can be rather long. But if you want to do it in one step, that's fine, as long as it's clear that you are doing the right thing.

Let's look at the data frame:

```
societies
```

```
## # A tibble: 13 x 2
##    name       density
##    <chr>        <dbl>
##  1 jeidji       17
##  2 kuku         50
##  3 mamu         45
##  4 ngatjan      59.8
##  5 undanbi      21.7
##  6 jinibarra    16
##  7 ualaria       9
##  8 barkindji    15.4
##  9 wongaibon     5.12
## 10 jaralde      40
## 11 tjapwurong   35
## 12 tasmanians   13.4
## 13 badjalang    13.4
```

I have the name of each society and its population density, as promised (so that is correct). There were 13 societies that were studied. For me, they were all displayed. For you, you'll probably see only the first ten, and you'll have to click Next to see the last three.

(b) The question of interest is whether these Australian hunter-gatherer societies are like the rest of the world in terms of mean population density. State suitable null and alternative hypotheses. *Define any symbols you use*: that is, if you use a symbol, you also have to say what it means.

Solution

The mean for the world as a whole ("average", as stated earlier) is 7.38. Let μ denote the population mean for Australia (of which these societies are a sample). Then our hypotheses are:

$$H_0 : \mu = 7.38$$

and

$$H_a : \mu \neq 7.38.$$

There is no reason for a one-sided alternative here, since all we are interested in is whether Australia is different from the rest of the world. *Expect to lose a point* if you use the symbol μ without saying what it means.

(c) Test your hypotheses using a suitable test. What do you conclude, in the context of the data?

Solution

A t-test, since we are testing a mean:

```
t.test(societies$density, mu = 7.38)
```

```
##
##  One Sample t-test
##
## data:  societies$density
## t = 3.8627, df = 12, p-value = 0.002257
## alternative hypothesis: true mean is not equal to 7.38
## 95 percent confidence interval:
##  15.59244 36.84449
## sample estimates:
## mean of x
##  26.21846
```

The P-value is 0.0023, less than the usual α of 0.05, so we *reject* the null hypothesis and conclude that the mean population density is not equal to 7.38. That is to say, Australia is different from the rest of the world in this sense.

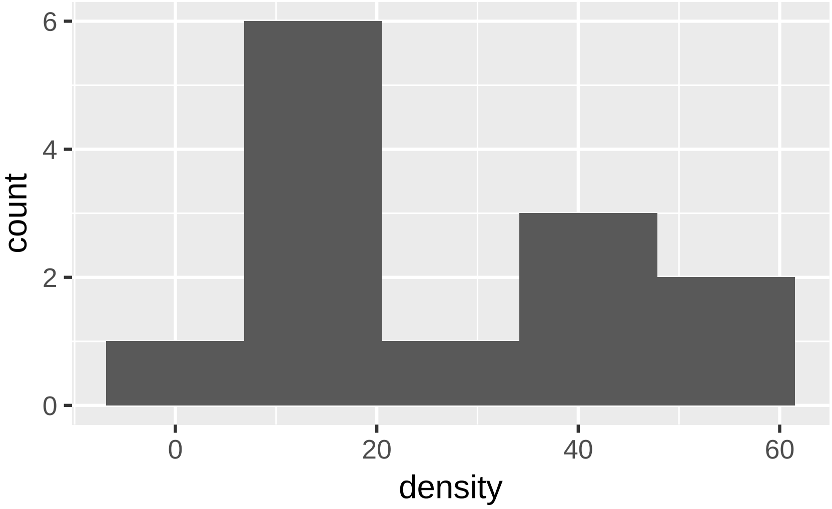
As you know, "reject the null hypothesis" is only part of the answer, so gets only part of the marks.

(d) Do you have any doubts about the validity of your test? Explain briefly, using a suitable graph to support your explanation.

Solution

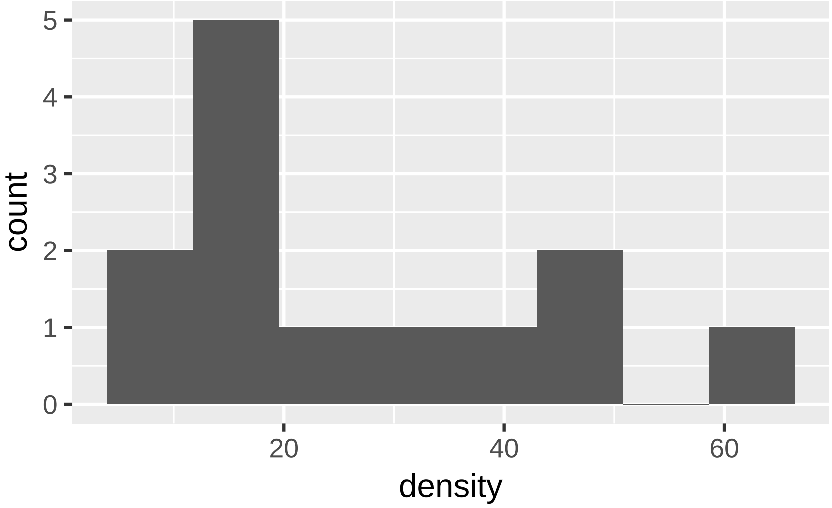
The assumption behind the t-test is that the data are approximately normal. We can assess that in several ways, but the simplest (which is perfectly acceptable at this point) is a histogram. You'll need to pick a suitable number of bins. This one comes from Sturges' rule:

```
ggplot(societies, aes(x = density)) + geom_histogram(bins = 5)
```



Your conclusion might depend on how many bins you chose for your histogram. Here's 8 bins (which is really too many with only 13 observations, but it actually shows the shape well):

```
ggplot(societies, aes(x = density)) + geom_histogram(bins = 8)
```



or you can get a number of bins from one of the built-in functions, such as:

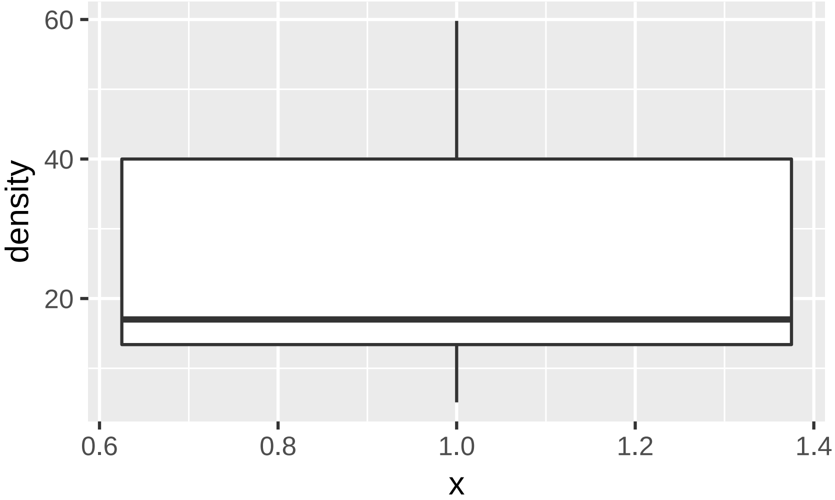
```
mybins = nclass.FD(societies$density)
mybins
```

```
## [1] 3
```

This one is small. The interquartile range is large and n is small, so the binwidth will be large and therefore the number of bins will be small.

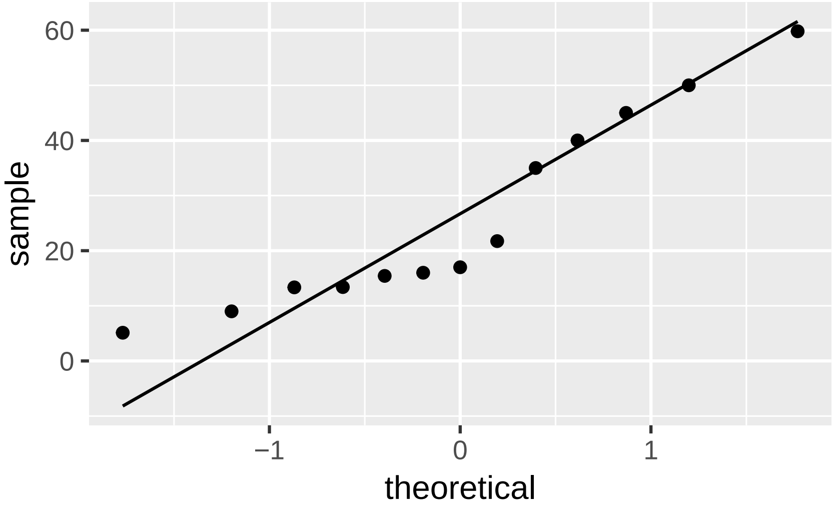
Other choices: a one-group boxplot:

```
ggplot(societies, aes(x = 1, y = density)) + geom_boxplot()
```



This isn't the best for assessing normality as such, but it will tell you about lack of symmetry and outliers, which are the most important threats to the t-test, so it's fine here. Or, a normal quantile plot:

```
ggplot(societies, aes(sample = density)) + stat_qq() +
    stat_qq_line()
```



This is actually the best way to assess normality, but I'm not expecting you to use this plot here, because we may not have gotten to it in class yet. (If you have read ahead and successfully use the plot, it's fine.)

After you have drawn your chosen plot (you need *one* plot), you need to say something about normality and thus whether you have any doubts about the validity of your t-test. This will depend on the graph you drew: if you think your graph is symmetric and outlier-free, you should have no doubts about your t-test; if you think it has something wrong with it, you should say what it is and express your doubts. My guess is that you will think this distribution is skewed to the right. Most of my plots are saying that.

On the website where I got these data, they were using the data as an example for another test, precisely *because* they thought the distribution was right-skewed. Later on, we'll learn about the sign test for the median, which I think is actually a better test here.

The normal quantile plot is rather interesting: it says that the uppermost values are approximately normal, but the *smallest* eight or so values are too bunched up to be normal. That is, normality fails not because of the long tail on the right, but the bunching on the left. Still right-skewed, though.

5.2 *Length of gestation in North Carolina*

The data in file link are about 500 randomly chosen births of babies in North Carolina. There is a lot of information: not just the weight at birth of the baby, but whether the baby was born prematurely, the ages of the parents, whether the parents are married, how long (in weeks) the pregnancy lasted (this is called the "gestation") and so on. We have seen these data before.

(a) Read in the data from the file into R, bearing in mind what type of file it is.

Solution

This is a .csv file (it came from a spreadsheet), so it needs reading in accordingly. Work directly from the URL (rather than downloading the file, unless you are working offline):

```
myurl = "http://www.utsc.utoronto.ca/~butler/c32/ncbirths.csv"
bw = read_csv(myurl)
```

```
## Parsed with column specification:
## cols(
##   ‘Father Age‘ = col_integer(),
##   ‘Mother Age‘ = col_integer(),
##   ‘Weeks Gestation‘ = col_integer(),
##   ‘Pre-natal Visits‘ = col_integer(),
##   ‘Marital Status‘ = col_integer(),
##   ‘Mother Weight Gained‘ = col_integer(),
##   ‘Low Birthweight?‘ = col_integer(),
##   ‘Weight (pounds)‘ = col_double(),
##   ‘Premie?‘ = col_integer(),
##   ‘Few Visits?‘ = col_integer()
## )
```

(b) Find a 95% confidence interval for the mean birth weight of all babies born in North Carolina (of which these babies are a sample). At the end, you should state what the confidence interval is. Giving some output is necessary, but *not* enough by itself.

If your variable name has a space or other special character (like a question mark) in it, remember that you have to surround its name with backticks, as discussed the first time we looked at these data.

Solution

This:

```
t.test(bw$‘Weight (pounds)‘)

##
##  One Sample t-test
##
## data:  bw$‘Weight (pounds)‘
## t = 104.94, df = 499, p-value < 2.2e-16
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  6.936407 7.201093
## sample estimates:
## mean of x
##   7.06875
```

or (the same, but remember to match your brackets):

```
with(bw, t.test(‘Weight (pounds)‘))

##
##  One Sample t-test
##
## data:  Weight (pounds)
## t = 104.94, df = 499, p-value < 2.2e-16
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  6.936407 7.201093
## sample estimates:
## mean of x
##   7.06875
```

The confidence interval goes from 6.94 to 7.20 pounds.

There is an annoyance about `t.test`. Sometimes you can use `data=` with it, and sometimes not. When we do a two-sample *t*-test later, there is a "model formula" with a squiggle in it, and there we can use `data=`, but here not, so you have to use the dollar sign or the `with` to say which data frame to get things from. The distinction seems to be that *if you are using a model formula*, you can use `data=`, and if not, not.

This is one of those things that is a consequence of R's history. The original `t.test` was without the model formula and thus without the `data=`, but the model formula got "retro-fitted" to it later. Since the model formula comes from things like regression, where `data=` is legit, that had to be retro-fitted as well. Or, at least, that's my understanding.

(c) Birth weights of babies born in the United States have a mean of 7.3 pounds. Is there any evidence that babies born in North Carolina are less heavy on average? State appropriate hypotheses, do your test, obtain a P-value and state your conclusion, in terms of the original data.

Solution

Let μ be the population mean (the mean weight of all babies born in North Carolina). Null hypothesis is $H_0 : \mu = 7.3$ pounds, and the alternative is that the mean is less: $H_a : \mu < 7.3$ pounds.

Note that I defined μ first before I used it.

This is a one-sided alternative, which we need to feed into `t.test`:

```
t.test(bw$‘Weight (pounds)‘, mu = 7.3, alternative = "less")

##
##  One Sample t-test
##
## data:  bw$‘Weight (pounds)‘
## t = -3.4331, df = 499, p-value =
## 0.0003232
## alternative hypothesis: true mean is less than 7.3
## 95 percent confidence interval:
##      -Inf 7.179752
## sample estimates:
## mean of x
##   7.06875
```

$ %$

Or with `with`. If you see what I mean.

The P-value is 0.0003, which is *less* than any α we might have chosen: we *reject* the null hypothesis in favour of the alternative, and thus we conclude that the mean birth weight of babies in North Carolina is indeed less than 7.3 pounds.

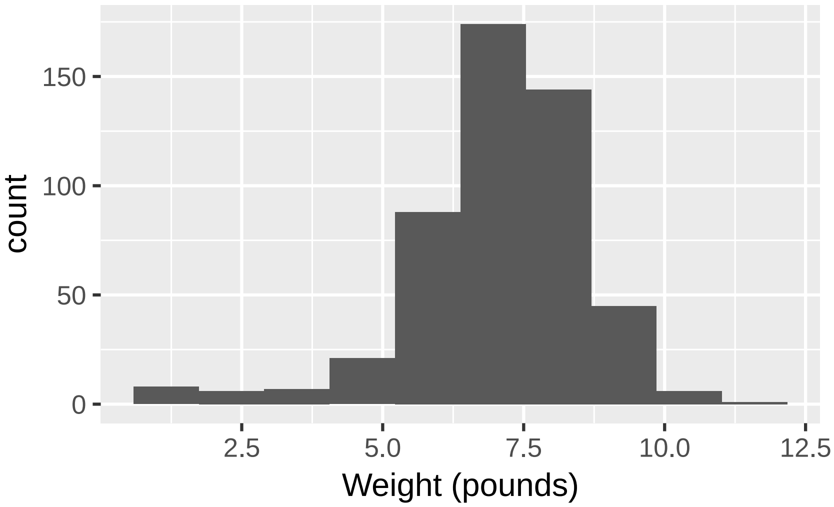
"Reject the null hypothesis" is *not* a complete answer. You need to say something about what rejecting the null hypothesis means *in* *this case*: that is, you must make a statement about birth weights of babies.

(d) The theory behind the t-test says that the distribution of birth weights should be (approximately) normally distributed. Obtain a histogram of the birth weights. Does it look approximately normal? Comment briefly. (You'll have to pick a number of bins for your histogram first. I don't mind very much what you pick, as long as it's not obviously too many or too few bins.)

Solution

We did this before (and discussed the number of bins before), so I'll just reproduce my 10-bin histogram (which is what I preferred, but this is a matter of taste):

```
ggplot(bw, aes(x = ‘Weight (pounds)‘)) + geom_histogram(bins = 10)
```



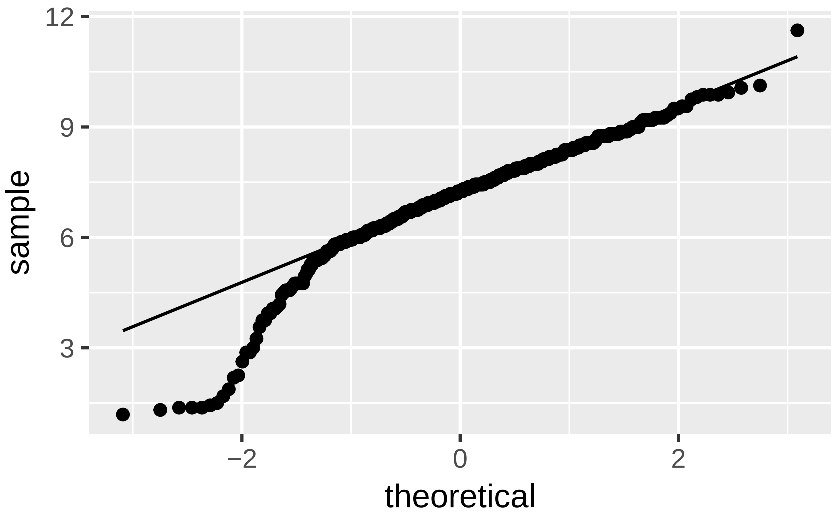
So, we were assessing normality. What about that?

It is mostly normal-looking, but I am suspicious about those *very* low birth weights, the ones below about 4 pounds. There are too many of those, as I see it.

If you think this is approximately normal, you need to make some comment along the lines of "the shape is approximately symmetric with no outliers". I think my first answer is better, but this answer is worth something, since it is a not completely unreasonable interpretation of the histogram.

A normal quantile plot is better for assessing normality than a histogram is, but I won't make you do one until we have seen the idea in class. Here's the normal quantile plot for these data:

```
ggplot(bw, aes(sample = ‘Weight (pounds)‘)) +
    stat_qq() + stat_qq_line()
```



This is rather striking: the lowest birthweights (the ones below 5 pounds or so) are *way* too low for a normal distribution to apply. The top end is fine (except perhaps for that one very heavy baby), but there are too many low birthweights for a normal distribution to be believable. Note how much clearer this story is than on the histogram.

Having said that, the *t*-test, especially with a sample size as big as this (500), behaves *very* well when the data are somewhat non-normal (because it takes advantage of the Central Limit Theorem: that is, it's the *sampling distribution of the sample mean* whose shape matters). So, even though the data are definitely not normal, I wouldn't be too worried about our test.

This perhaps gives some insight as to why Freedman-Diaconis said we should use so many bins for our histogram. We have a lot of low-end outliers, so that the IQR is actually *small* compared to the overall spread of the data (as measured, say, by the SD or the range) and so FD thinks we need a lot of bins to describe the shape. Sturges is based on data being approximately normal, so it will tend to produce a small number of bins for data that have outliers.

5.3 Inferring ice break-up in Nenana

Nenana, Alaska, is about 50 miles west of Fairbanks. Every spring, there is a contest in Nenana. A wooden tripod is placed on the frozen river, and people try to guess the exact minute when the ice melts enough for the tripod to fall through the ice. The contest started in 1917 as an amusement for railway workers, and has taken place every year since. Now, hundreds of thousands of people enter their guesses on the Internet and the prize for the winner can be as much as $300,000.

Because so much money is at stake, and because the exact same tripod is placed at the exact same spot on the ice every year, the data are consistent and accurate. The data are in link.

Yes, we saw these data before.

(a) Read the data into R, as before, or use the data frame that you read in before. Note that the values are separated by *tabs* rather than spaces, so you'll need an appropriate `read_` to read it in.

Solution

These are "tab-separated values", so `read_tsv` is the thing, as for the Australian athletes:

```
myurl = "http://www.utsc.utoronto.ca/~butler/c32/nenana.txt"
nenana = read_tsv(myurl)

## Parsed with column specification:
## cols(
##   Year = col_integer(),
##   JulianDate = col_double(),
##   ‘Date&Time‘ = col_character()
## )
```

Use whatever name you like for the data frame. One that is different from any of the column headers is smart; then it is clear whether you mean the whole data frame or one of its columns. `ice` or `melt` or anything like that would also be good.

(b) Obtain a 90% confidence interval for the mean `JulianDate`. What interval do you get? Looking back at your histogram, do you have any doubts about the validity of what you have just done?

Solution

This is a matter of using `t.test` and pulling out the interval. Since we are looking for a non-standard interval, we have to remember `conf.level` as the way to get the confidence level that we want. I'm going with `with` this time, though the dollar-sign thing is equally as good:

```
with(nenana, t.test(JulianDate, conf.level = 0.9))

##
##  One Sample t-test
##
## data:  JulianDate
## t = 197.41, df = 86, p-value < 2.2e-16
## alternative hypothesis: true mean is not equal to 0
## 90 percent confidence interval:
##  124.4869 126.6018
## sample estimates:
## mean of x
##  125.5443
```

Between 124.5 and 126.6 days into the year. Converting that into something we can understand (because I want to), there are $31 + 28 + 31 + 30 = 120$ days in January through April (in a non-leap year), so this says that the mean breakup date is between about May 4 and May 6.

The *t*-test is based on an assumption of data coming from a normal distribution. The histogram we made earlier looks pretty much normal, so there are no doubts about normality and thus no doubts about the validity of what we have done, on the evidence we have seen so far. (I have some doubts on different grounds, based on another of the plots we did earlier, which I'll explain later, but all I'm expecting you to do is to look at the histogram and say "Yep, that's normal enough". Bear in mind that the sample size is 87, which is large enough for the Central Limit Theorem to be pretty helpful, so that we don't need the data to be more than "approximately normal" for the sampling distribution of the sample mean to be very close to *t* with the right df.)

(c) An old-timer in Nenana strokes his grey beard and says "When I were young, I remember the tripod used to fall into the water around May 10". In a non-leap year, May 10 is Julian day 130. Test the null hypothesis that the mean `JulianDay` is 130, against the alternative that it is less. What do you conclude? What practical implication does that have (assuming that the old-timer has a good memory)?

Solution

The test is `t.test` again, but this time we have to specify a null mean and a direction of alternative:

```
with(nenana, t.test(JulianDate, mu = 130, alternative = "less"))
```

```
##
##  One Sample t-test
##
## data:  JulianDate
## t = -7.0063, df = 86, p-value =
## 2.575e-10
## alternative hypothesis: true mean is less than 130
## 95 percent confidence interval:
```

```
##      -Inf 126.6018
## sample estimates:
## mean of x
##  125.5443
```

For a test, look first at the P-value, which is 0.0000000002575: that is to say, the P-value is very small, definitely smaller than 0.05 (or any other α you might have chosen). So we *reject* the null hypothesis, and conclude that the mean `JulianDate` is actually *less* than 130.

Now, this is the date on which the ice breaks up on average, and we have concluded that it is *earlier* than it used to be, since we are assuming the old-timer's memory is correct.

This is evidence in favour of global warming; a small piece of evidence, to be sure, but the ice is melting earlier than it used to all over the Arctic, so it's not just in Nenana that it is happening. You don't need to get to the "global warming" part, but I *do* want you to observe that the ice is breaking up earlier than it used to.

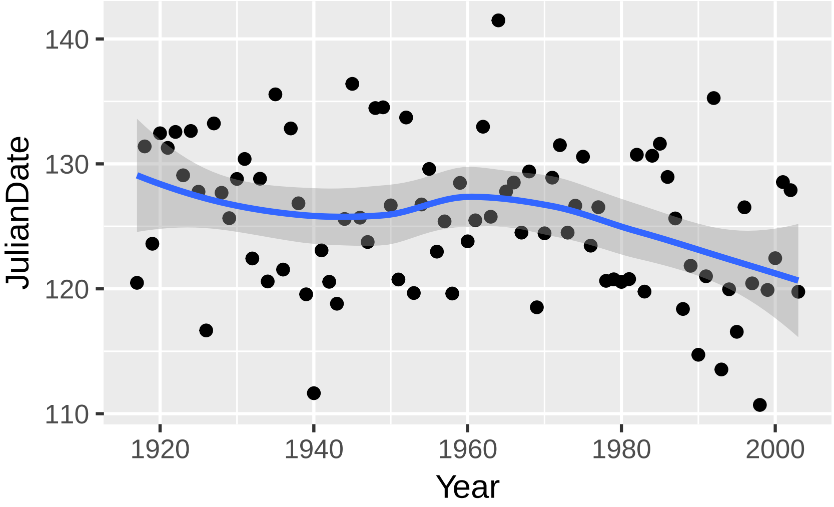
(d) Plot `JulianDate` against `Year` on a scatterplot. What recent trends, if any, do you see? Comment briefly. (You did this before, but I have some extra comments on the graph this time, so feel free to just read this part.)

Solution

I liked the `ggplot` with a smooth trend on it:

```
ggplot(nenana, aes(x = Year, y = JulianDate)) +
    geom_point() + geom_smooth()
```

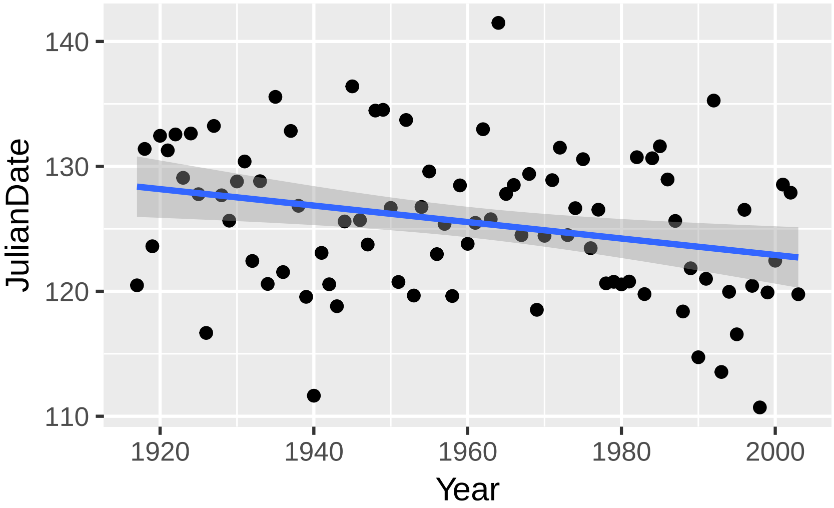
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



There was something obvious to see: after about 1960, there is a clear downward trend: the ice is breaking up earlier on average every year. Even though there is a lot of variability, the overall trend, viewed this way, is clear (and consistent with the test we did earlier). Note that the old-timer's value of 130 is the kind of `JulianDate` we would typically observe around 1920, which would make the old-timer over 90 years old.

All right, why did I say I had some doubts earlier? Well, because of this downward trend, the mean is not actually the same all the way through, so it doesn't make all that much sense to estimate it, which is what we were doing earlier by doing a confidence interval or a hypothesis test. What would actually make more sense is to estimate the mean `JulianDate` *for a particular year*. This could be done by a regression: predict `JulianDate` from `Year`, and then get a "confidence interval for the mean response" (as you would have seen in B27 or will see in C67). The trend isn't really linear, but is not that far off. I can modify the previous picture to give you an idea. Putting in `method="lm"` fits a line; as we see later, `lm` does regressions in R:

```
ggplot(nenana, aes(x = Year, y = JulianDate)) +
    geom_point() + geom_smooth(method = "lm")
```



Compare the confidence interval for the mean `JulianDate` in 1920: 126 to 131 (the shaded area on the graph), with 2000: 121 to 125. A change of about 5 days over 80 years. And with the recent trend that we saw above, it's probably changing faster than that now. Sobering indeed.

6
Two-sample inference

```
library(tidyverse)

## -- Attaching packages ---- tidyverse 1.2.1 --

## v ggplot2 3.0.0     v purrr   0.2.5
## v tibble  1.4.2     v dplyr   0.7.6
## v tidyr   0.8.1     v stringr 1.3.1
## v readr   1.1.1     v forcats 0.3.0

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

6.1 *Children and electronic devices*

Do children (aged 8–17) spend more time on electronic devices now than they did 10 years ago? Samples of 15 children aged 8–17 were taken in each of two years, 1999 and 2009, and the children (with their parents' help) were asked to keep a diary of the number of hours they spent using electronic devices on a certain day. The data are in the file `http://www.utsc.utoronto.ca/~butler/c32/pluggedin.txt`.

(a) Read in the data and verify that you have 30 rows of data from two different years.

Solution
I see this:

```
myurl = "http://www.utsc.utoronto.ca/~butler/c32/pluggedin.txt"
plugged = read_delim(myurl, " ")

## Parsed with column specification:
## cols(
##   year = col_integer(),
##   hours = col_integer()
## )
```

```
plugged
```

```
## # A tibble: 30 x 2
##     year hours
##    <int> <int>
##  1  1999     4
##  2  1999     5
##  3  1999     7
##  4  1999     7
##  5  1999     5
##  6  1999     7
##  7  1999     5
##  8  1999     6
##  9  1999     5
## 10  1999     6
## # ... with 20 more rows
```

I see only the first ten rows (with an indication that there are 20 more, so 30 altogether). In your notebook, it'll look a bit different: again, you'll see the first 10 rows, but you'll see exactly how many rows and columns there are, and there will be buttons "Next" and "Previous" to see earlier and later rows, and a little right-arrow to see more columns to the right (to which is added a little left-arrow if there are previous columns to scroll back to). If you want to check for yourself that there are 30 rows, you can click Next a couple of times to get down to row 30, and then see that the Next button cannot be clicked again, and therefore that 30 rows is how many there are.

Or, you can summarize the years by counting how many there are of each:

```
plugged %>% count(year)
```

```
## # A tibble: 2 x 2
##    year     n
##   <int> <int>
## 1  1999    15
## 2  2009    15
```

or the more verbose form of the same thing:

```
plugged %>% group_by(year) %>% summarize(rows = n())
```

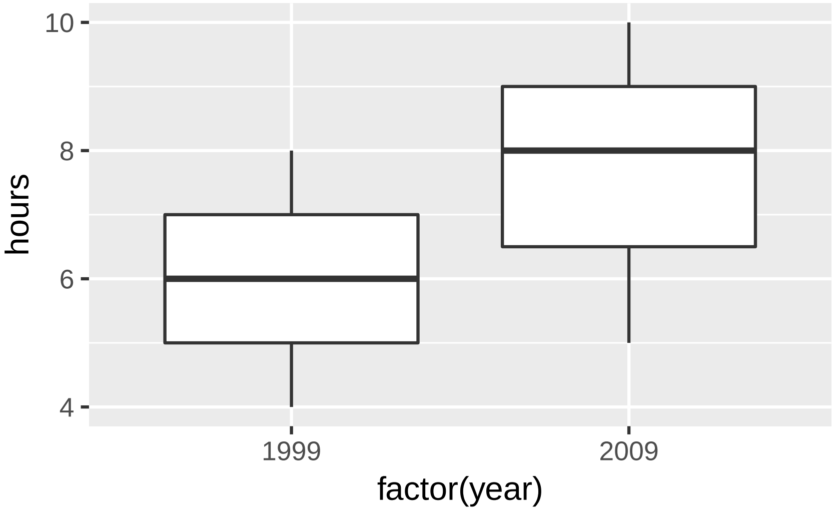
```
## # A tibble: 2 x 2
##    year  rows
##   <int> <int>
## 1  1999    15
## 2  2009    15
```

Any of those says that it looks good. 30 rows, 1999 and 2009, 15 measurements for each.

(b) Draw side-by-side boxplots of the number of hours for each year. `year` is a numeric variable that we want to treat as a factor, so we need to *make* it into a factor.

Solution

```
ggplot(plugged, aes(x = factor(year), y = hours)) +
    geom_boxplot()
```



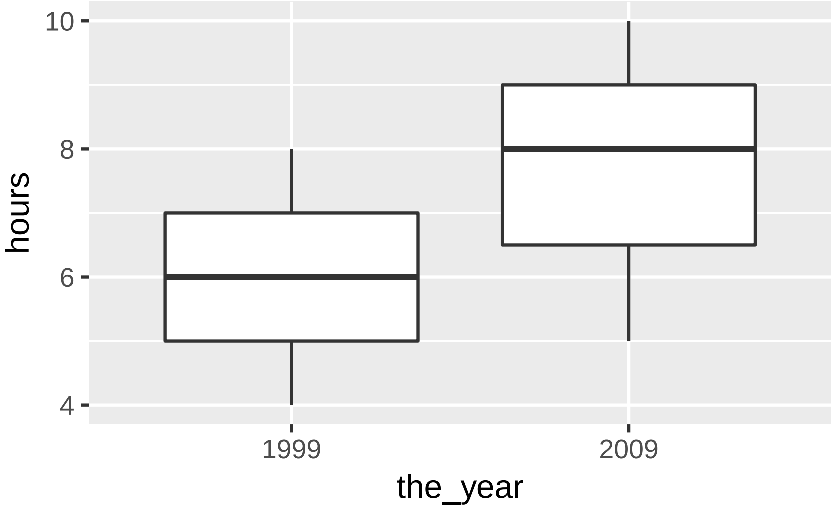
The `fct_inorder` trick from assignment 1 will also work, since the years are in the data in the order we want them to be displayed.

The median for 2009 is noticeably higher, and there is no skewness or outliers worth worrying about.

The measurements for the two years have a very similar spread, so there would be no problem running the pooled test here.

You might be bothered by the `factor(year)` on the *x*-axis. To get around that, you can define year-as-factor *first*, using `mutate`, then feed your new column into the boxplot. That goes like this. There is a wrinkle that I explain afterwards:

```
plugged %>% mutate(the_year = factor(year)) %>%
    ggplot(aes(x = the_year, y = hours)) + geom_boxplot()
```



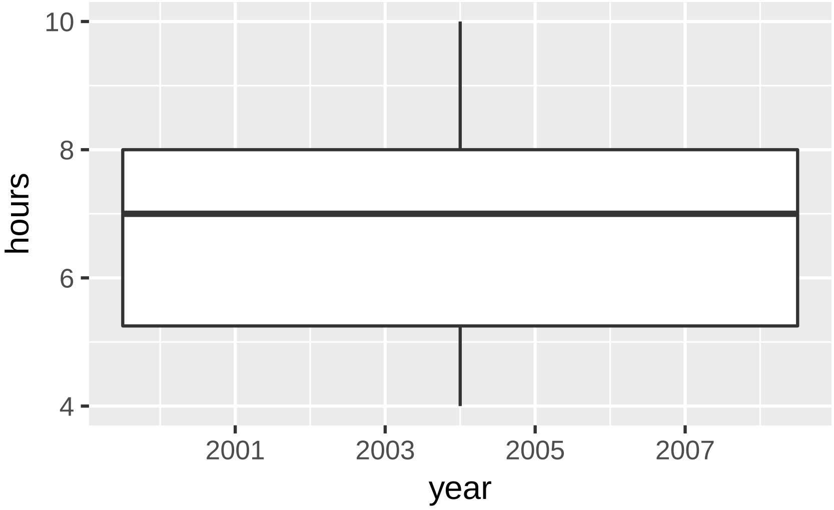
You could even redefine `year` to be the factor version of itself (if you don't need the year-as-number anywhere else). The wrinkle I mentioned above is that in the `ggplot` you *do not* name the data frame first; the data frame used is the (nameless) data frame that came out of the previous step, not `plugged` but `plugged` with a new column `the_year`.

Note how the *x*-axis now has the name of the new variable.

If you forget to make `year` into a factor, this happens:

```
ggplot(plugged, aes(x = year, y = hours)) + geom_boxplot()
```

```
## Warning: Continuous x aesthetic -- did you
## forget aes(group=...)?
```



You get *one* boxplot, for all the hours, without distinguishing by year, and a warning message that tries (and fails) to read our mind: yes, we have a continuous, quantitative `x`, but `geom_boxplot` doesn't take a `group`.

(c) Test whether the mean number of hours has *increased* since

1999. Which test did R do?

Solution

The hard part to remember is how you specify a one-sided test in R; it's `alternative="less"` (rather than "greater") because 1999 is "before" 2009:

```
t.test(hours ~ year, data = plugged, alternative = "less")
```

```
##
##  Welch Two Sample t-test
##
## data:  hours by year
## t = -3.3323, df = 24.861, p-value =
## 0.001348
## alternative hypothesis: true difference in means is less than 0
## 95 percent confidence interval:
##        -Inf -0.8121415
## sample estimates:
## mean in group 1999 mean in group 2009
##           5.933333           7.600000
```

The P-value is 0.0013. R does the Welch-Satterthwaite test by default (the unequal-variances one). Since we didn't change that, that's what we got. (The pooled test is below.)

This is the cleanest way to do it, because this version of `t.test`, with a "model formula" (the thing with the squiggle) allows a `data=` to say which data frame to get things from. The other ways, using (for example) `with`, also work:

```
with(plugged, t.test(hours ~ year, alternative = "less"))
```

```
##
##  Welch Two Sample t-test
##
## data:  hours by year
## t = -3.3323, df = 24.861, p-value =
## 0.001348
## alternative hypothesis: true difference in means is less than 0
## 95 percent confidence interval:
##        -Inf -0.8121415
## sample estimates:
## mean in group 1999 mean in group 2009
##           5.933333           7.600000
```

This also works, but is *ugly*:

```
t.test(plugged$hours ~ plugged$year, alternative = "less")
```

```
##
##  Welch Two Sample t-test
##
## data:  plugged$hours by plugged$year
## t = -3.3323, df = 24.861, p-value =
## 0.001348
## alternative hypothesis: true difference in means is less than 0
## 95 percent confidence interval:
##        -Inf -0.8121415
## sample estimates:
## mean in group 1999 mean in group 2009
##           5.933333           7.600000
```

Ugly because you've just typed the name of the data frame and the dollar sign *twice* for no reason. As a general principle, if you as a programmer are repeating yourself, you should stop and ask yourself how you can avoid the repeat.

If you want the pooled test in R, you have to ask for it:

```
t.test(hours ~ year, alternative = "less", data = plugged,
    var.equal = T)
```

```
##
##  Two Sample t-test
##
## data:  hours by year
## t = -3.3323, df = 28, p-value =
## 0.001216
## alternative hypothesis: true difference in means is less than 0
## 95 percent confidence interval:
##        -Inf -0.8158312
## sample estimates:
## mean in group 1999 mean in group 2009
##           5.933333           7.600000
```

As is often the case, the P-values for the pooled and Welch-Satterthwaite tests are very similar, so from that point of view it doesn't matter much which one you use. If you remember back to the boxplots, the number of hours had about the same spread for the two years, so if you used the pooled test instead of the Welch-Satterthwaite test, that would have been just fine.

There is a school of thought that says we should learn the Welch-Satterthwaite test and use that always. This is because W-S (i) works when the populations from which the groups are sampled have different SDs and (ii) is pretty good even when those SDs are the same.

The pooled test can go badly wrong if the groups have very different SDs. The story is this: if the larger sample is from the population with the larger SD, the probability of a type I error will be smaller than α, and if the larger sample is from the population with the *smaller* SD, the probability of a type I error will be larger than α. This is why you see S-W in STAB22. You see the pooled test in STAB57 because the logic of its derivation is so much clearer, not because it's really the better test in practice. The theory says that if your data are normal in both groups with the same variance, then the pooled test is best, but it says *nothing* about the quality of the pooled test if any of that goes wrong. The usual approach to assessing things like this is via simulation, as we do for estimating power (later): generate some random data eg. from normal distributions with the same means, SDs 10 and 20 and sample sizes 15 and 30, run the pooled t-test, see if you reject, then repeat lots of times and see whether you reject about 5% of the time. Then do the same thing again with the sample sizes switched around. Or, do the same thing with Welch-Satterthwaite.

I return to this issue when we look at the same data in SAS later.

(d) Obtain a 99% confidence interval for the difference in means.

Solution

Take off the thing that made it one-sided, and put in a thing that gets the right CI:

```
t.test(hours ~ year, data = plugged, conf.level = 0.99)
```

```
##
##  Welch Two Sample t-test
##
## data:  hours by year
## t = -3.3323, df = 24.861, p-value =
## 0.002696
## alternative hypothesis: true difference in means is not equal to 0
## 99 percent confidence interval:
##  -3.0614628 -0.2718705
## sample estimates:
## mean in group 1999 mean in group 2009
##           5.933333           7.600000
```

-3.06 to -0.27. The interval contains only negative values, which is consistent with our having rejected a null hypothesis of no difference in means.

6.2 *Parking close to the curb*

In 2009, the Toronto Star commissioned a survey to address the issue of who is better at parking a car: men or women. The researchers recorded 93 drivers who were parallel-parking their car in downtown Toronto, and for each driver, recorded the distance between the car and the curb, in inches, when the driver was finished parking their car. The data are in an Excel spreadsheet, link. (Let me know if you cannot handle this format.) Click on the link. The data will probably download automatically. Check the folder on your computer where things get downloaded. If the spreadsheet is just displayed and not downloaded, save it somewhere on your computer.

Mine is rather prosaically called *Downloads*.

(a) There are two sheets in this spreadsheet workbook. They are of the same data in two different formats. Take a look at Sheet 1 and Sheet 2. Describe the format of the data in each case. Which will be the most suitable data layout, bearing in mind that one of the first things we do is to make side-by-side boxplots of parking distances for males and females? Explain briefly.

Solution

The data in Sheet 1 has one column of parking distances for males, and another for females. This is often how you see data of this sort laid out. Sheet 2 has *one* column of parking distances, all combined together, and a second column indicating the gender of the driver whose distance is in the first column. If you look back at the kind of data we've used to make side-by-side boxplots, it's always been in the format of Sheet 2: one column containing all the values of the variable we're interested in, with a second column indicating which group each observation belongs to ("group" here being "gender of driver"). So we need to use the data in Sheet 2, because the data in Sheet 1 are not easy to handle with R. The layout of Sheet 2 is the way R likes to do most things: so-called "long format" with a lot of rows and not many columns. This is true for descriptive stuff: side-by-side boxplots or histograms or means by group, as well as modelling such as (here) a two-sample *t*-test, or (in other circumstances, as with several groups) a one-way analysis of variance. Hadley Wickham, the guy behind the `tidyverse`, likes to talk about "tidy data" (like Sheet 2), with each column containing a variable, and "untidy data" (like Sheet 1), where the two columns are the same thing (distances), but under different circumstances (genders). As we'll see later, it is possible to convert from one format to the other. Usually you want to make untidy data tidy (the function for this is called `gather`).

(b) Read your preferred sheet directly into R, *without* using a `.csv` file. (There is a clue in the lecture notes, in the section about reading in files.) If you get stuck, make a .csv file and read that in.

Solution

The direct way is to use the package readxl. This has a read_excel that works the same way as any of the other read_ functions. You'll have to make sure that you read in sheet 2, since that's the one you want. There is some setup first. There are a couple of ways you can do that:

- Download the spreadsheet to your computer, and upload it to your project on R Studio Cloud (or, if you are running R Studio on your computer, use something like file.choose to get the file from wherever it got downloaded to).

- Use the function download.file to get the file from the URL and store it in your project folder directly. This also works in R Studio Cloud, and completely by-passes the download-upload steps that you would have to do otherwise. (I am grateful to Rose Gao for this idea.) Here is how you can use download.file here:

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/parking.xlsx"
local = "parking.xlsx"
download.file(my_url, local, mode = "wb")
```

When you've gotten the spreadsheet into your project folder via one of those two ways, you go ahead and do this:

```
library(readxl)
parking = read_excel("parking.xlsx", sheet = 2)
parking
```

```
## # A tibble: 93 x 2
##    distance gender
##       <dbl> <chr>
##  1      0.5 male
##  2      1   male
##  3      1.5 male
##  4      1.5 male
##  5      1.5 male
##  6      3   male
##  7      3.5 male
##  8      5   male
##  9      6   male
## 10      6   male
## # ... with 83 more rows
```

You have to do it this way, using the version of the spreadsheet on your computer, since read_excel won't take a URL, or if it does, I can't make it work. I put the spreadsheet in R Studio's current folder, so I could read it in by name, or you can do the f=file.choose() thing, find it, then read it in. The sheet= thing can take either a number (as here: the second sheet in the workbook), or a name (whatever name the sheet has on its tab in the workbook).

Let me know if you have more success than I did.

Extra: Rose actually came up with a better idea, which I will show you and explain:

```
tf = tempfile()
download.file(my_url, tf, mode = "wb")
p = read_excel(tf, sheet = 2)
```

What tempfile() does is to create a temporary file to hold the spreadsheet that you are about to download. After downloading the spreadsheet to the temporary file, you then use read_excel to read *from the temporary file* into the data frame.

The advantage of this approach is that the temporary file disappears as soon as you close R, and so you don't have a copy of the spreadsheet lying around that you don't need (once you have created the data frame that I called parking, anyway).

If you are wondering about that mode thing on download.file: files are of two different types, "text" (like the text of an email, that you can open and look at in something like Notepad), and "binary" that you can't look at directly, but for which you need special software like Word or Excel to decode it for you.

A Word or Excel document has all kinds of formatting information hidden in the file as well as the text that you see on the screen.

The first character in mode is either w for "write a new file", which is what we want here, or a for "append", which would mean adding to the end of a file that already exists. Thus mode="wb" means "create a new binary file". End of Extra. If you can't make any of this work, then do it in two steps: save the appropriate sheet as a .csv file, and then read the .csv file using read_csv. If you experiment, you'll find that saving a spreadsheet workbook as .csv only saves the sheet you're looking at, so make sure you are looking at sheet 2 before you Save As .csv. I did that, and called my saved .csv parking2.csv (because it was from sheet 2, but you can use any name you like). Then I read this into R thus:

```
parking2 = read_csv("parking2.csv")
```

```
## Parsed with column specification:
## cols(
##   distance = col_double(),
##   gender = col_character()
## )
```

```
parking2
```

```
## # A tibble: 93 x 2
##    distance gender
##       <dbl> <chr>
##  1      0.5 male
##  2      1   male
##  3      1.5 male
##  4      1.5 male
##  5      1.5 male
##  6      3   male
##  7      3.5 male
##  8      5   male
##  9      6   male
## 10      6   male
## # ... with 83 more rows
```

The read-in data frame `parking` has 93 rows ($47 + 46 = 93$ drivers) and two columns: the distance from the curb that the driver ended up at, and the gender of the driver. This is as the spreadsheet Sheet 2 was, and the first few distances match the ones in the spreadsheet.

If I were grading this, you'd get some credit for the `.csv` route, but I really wanted you to figure out how to read the Excel spreadsheet directly, so that's what would be worth full marks.

You might want to check that you have some males and some females, and how many of each, which you could do this way:

```
parking %>% count(gender)
```

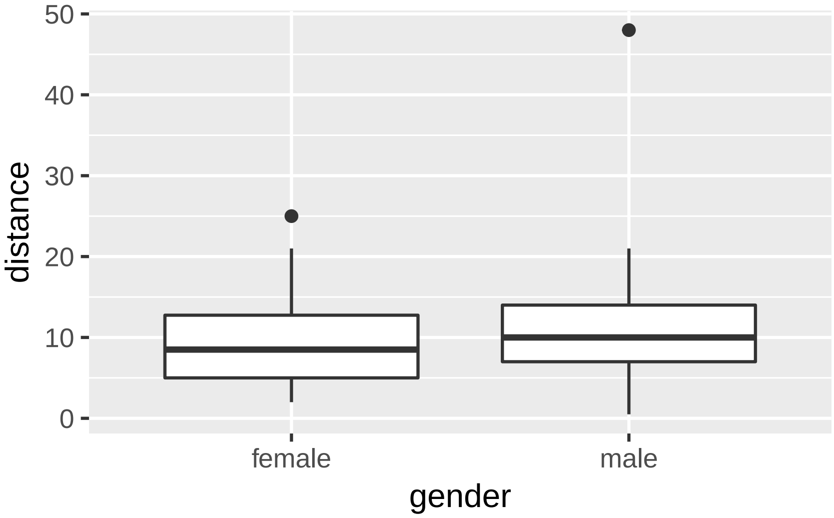
```
## # A tibble: 2 x 2
##   gender     n
##   <chr>  <int>
## 1 female    47
## 2 male      46
```

(c) Obtain side-by-side boxplots of parking distances for males and females. Does one gender seem to be better at parking than the other? Explain briefly.

Solution

With the right data set, this is a piece of cake:

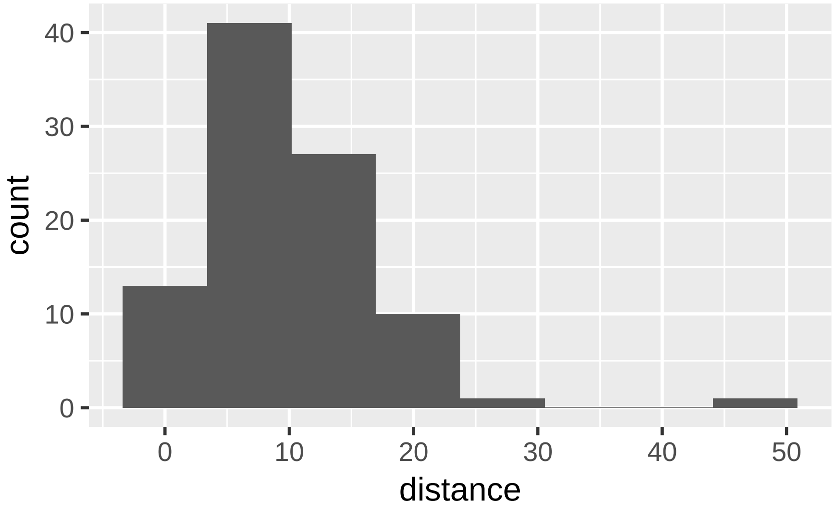
```
ggplot(parking, aes(x = gender, y = distance)) +
    geom_boxplot()
```



The outcome variable is distance from the curb, so smaller should be better (more accurate parking). With that in mind, the median for females is a little smaller than for males (about 8.5 vs. about 10), so it seems that on average females are more accurate parkers than males are. The difference is small, however (and so you might be wondering at this point whether it's a statistically significant difference — don't worry, that's coming up).

Before I leave this one, I want to show you something else: above-and-below histograms, as another way of comparing males and females (two or more groups, in general). First, we make a histogram of all the distances, without distinguishing by gender:

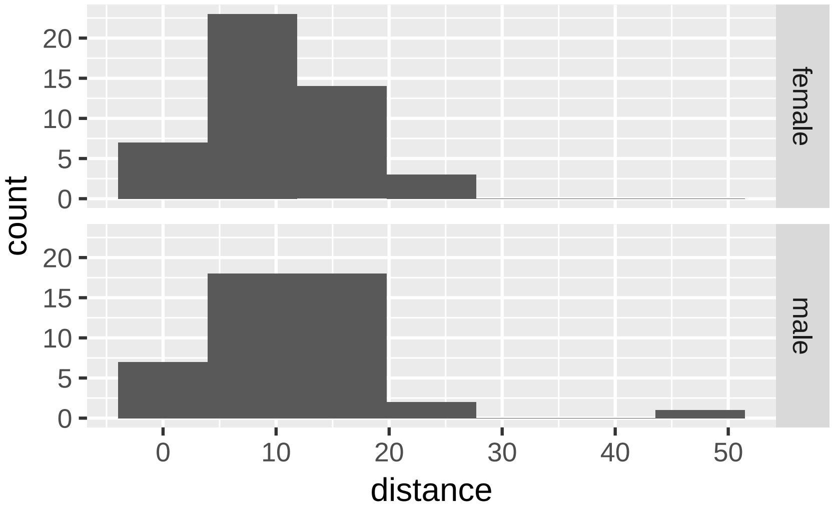
```
ggplot(parking, aes(x = distance)) + geom_histogram(bins = 8)
```



That big outlier is the very inaccurate male driver.

Now, how do we get a *separate* histogram for each `gender`? In `ggplot`, separate plots for each "something" are called **facets**, and the way to get facets arranged as you want them is called `facet_grid`. Let me show you the code first, and then explain how it works:

```
ggplot(parking, aes(x = distance)) + geom_histogram(bins = 7) +
    facet_grid(gender ~ .)
```

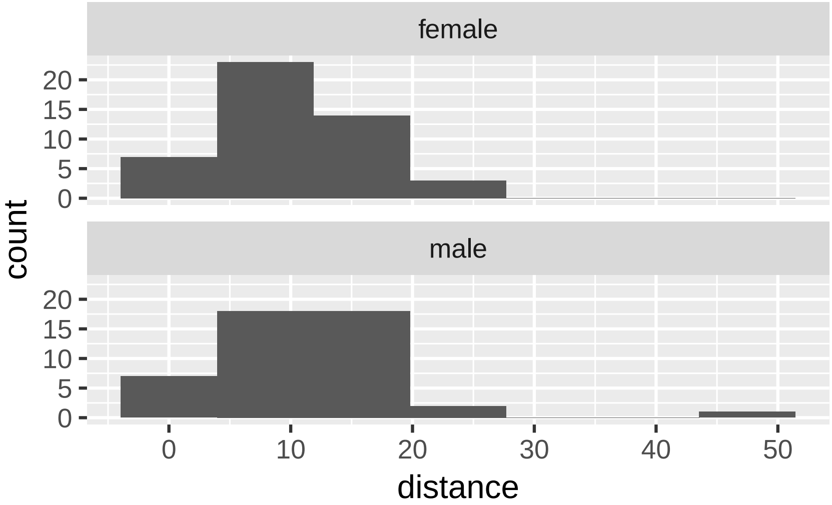


`facet_grid` takes a "model formula" with a squiggle, with y on the left and x on the right. We want to compare our two histograms, one for males and one for females, and I think the best way to compare histograms is to have one on top of the other. Note that the same `distance` scale is used for both histograms, so that it is a fair comparison. The above-and-below is accomplished by having `gender` as the y in the arrangement of the facets, so it goes before the squiggle. We don't have any x in the arrangement of the facets, and we tell `ggplot` this by putting a dot where the x would be.

You might have a second categorical variable by which you want to arrange the facets left and right, and that would go where the dot is.

You can also use `facet_wrap` for this, but you have to be more careful since you don't have any control over how the histograms come out (you probably get them side by side, which is not so helpful for comparing distributions). You can make it work by using `ncol=1` to arrange "all" the histograms in one column:

```
ggplot(parking, aes(x = distance)) + geom_histogram(bins = 7) +
    facet_wrap(~gender, ncol = 1)
```



The centres of both histograms are somewhere around 10, so it's hard to see any real difference between males and females here. Maybe this is further evidence that the small difference we saw between the boxplots is really not worth getting excited about.

You might be concerned about how you know what to put with the squiggle-thing in `facet_grid` and `facet_wrap`. The answer is that `facet_wrap` *only* has something to the right of the squiggle (which `ggplot` then decides how to arrange), but `facet_grid` *must* have something on *both* sides of the squiggle (how to arrange in the y direction on the left, how to arrange in the x direction on the right), and if you don't have anything else to put there, you put a dot. Here's my `facet_grid` code from above, again:

```
ggplot(parking, aes(x = distance)) + geom_histogram(bins = 7) +
    facet_grid(gender ~ .)
```

We wanted gender to go up and down, and we had nothing to go left and right, hence the dot. Contrast that with my `facet_wrap` code:

I took out the *ncol* since that confuses the explanation here.

```
ggplot(parking, aes(x = distance)) + geom_histogram(bins = 7) +
    facet_wrap(~gender)
```

This says "make a separate facet for each gender", but it doesn't say anything about how to arrange them. The choice of bins for my histogram(s) came from Sturges' rule: with n being the number of observations, you use k bins where $k = \log_2(n) + 1$, rounded up. If we were to make a histogram of all the parking distances combined together, we would have $n = 47 + 48 = 95$ observations, so we should use this many bins:

```
sturges = log(95, 2) + 1
sturges
```

```
## [1] 7.569856
```

Round this up to 8. (The second thing in `log` is the base of the logs, if you specify it, otherwise it defaults to e and gives you "natural" logs.) I seem to have the powers of 2 in my head, so I can do it mentally by saying "the next power of 2 is 128, which is 2^7, so I need $7 + 1 = 8$ bins."

Or:

```
with(parking, nclass.Sturges(distance))
```

```
## [1] 8
```

Sturges' rule tends to produce not enough bins if n is small, so be prepared to increase it a bit if you don't have much data. I think that gives a fairly bare-bones picture of the shape: skewed to the right with outlier.

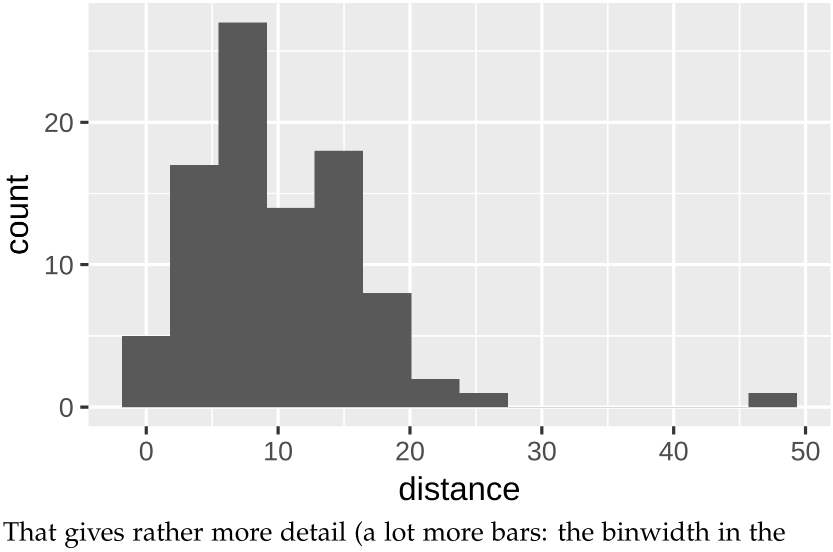
The other rule we saw was Freedman-Diaconis:

```
with(parking, nclass.FD(distance))
```

```
## [1] 14
```

and that leads to this histogram:

```
ggplot(parking, aes(x = distance)) + geom_histogram(bins = 14)
```



That gives rather more detail (a lot more bars: the binwidth in the Sturges-rule histogram is about 7, or twice what you see here), but in this case the overall story is about the same.

In the case of faceted histograms, you would want to apply a rule that uses the number of observations in *each* histogram. The facets might have quite different numbers of observations, but you can only use one `binwidth` (or `bins`), so you may have to compromise. For example, using Sturges' rule based on 47 observations (the number of males; the number of females is one more):

```
log(47, 2) + 1
```

```
## [1] 6.554589
```

and so each facet should have that many bins, rounded up. That's where I got my 7 for the facetted histogram from. This one doesn't work immediately with `nclass.Sturges`, because we do not have *one* column whose length is the number of observations we want: we have one column of distances that are males and females mixed up. To do *that*, `filter` one of the genders first:

```
parking %>% filter(gender == "female") %>% with(.,
    nclass.Sturges(distance))
```

```
## [1] 7
```

I used the "dot" trick again, which you can read as "it": "from `parking`, take only the rows for the females, and with it, give me the number of bins for a histogram by Sturges' rule."

(d) Explain briefly why this is two independent samples rather than matched pairs.

Solution

There is no way to pair any male with a corresponding female, because they are unrelated people. You might also notice that there are not even the *same number* of males and females, so there can be no way of pairing them up without leaving one over. (In general, if the two samples are paired, there must be the same number of observations in each; if there are different numbers in each, as here, they cannot be paired.) If you want that more mathematically, let n_1 and n_2 be the two sample sizes; then:

$$\text{Paired} \Longrightarrow n_1 = n_2$$

from which it follows logically (the "contrapositive") that

$$n_1 \neq n_2 \Longrightarrow \text{not paired}$$

You'll note from the logic that if the two sample sizes are the same, that tells you *nothing* about whether it's paired or independent samples: it could be either, and in that case you have to look at the description of the data to decide between them.

Here, anything that gets at why the males and females cannot be paired up is good.

(e) Run a suitable *t*-test for comparing parking distances for males and females. What do you conclude, in the context of the data?

Solution

A two-sample *t*-test. I think either the Welch or the pooled one can be justified (and I would expect them to give similar answers). You can do the Welch one either without comment or by asserting that the boxplots show different spreads; if you are going to do the pooled one, you need to say that the spreads are "about equal", by comparing the heights of the boxes on the boxplots:

```
t.test(distance ~ gender, data = parking)

##
##  Welch Two Sample t-test
##
## data:  distance by gender
## t = -1.3238, df = 79.446, p-value =
## 0.1894
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -4.5884103  0.9228228
## sample estimates:
## mean in group female   mean in group male
##             9.308511            11.141304
```

This is the Welch-Satterthwaite version of the test, the one that does not assume equal SDs in the two groups. The P-value of 0.1894 is not small, so there is no evidence of any difference in parking accuracy between males and females.

Or, this being the pooled one:

```
t.test(distance ~ gender, data = parking, var.equal = T)

##
##  Two Sample t-test
##
## data:  distance by gender
## t = -1.329, df = 91, p-value = 0.1872
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -4.5722381  0.9066506
## sample estimates:
## mean in group female   mean in group male
##             9.308511            11.141304
```

You might have thought, looking at the boxplots, that the groups had about the same SD (based, for example, on noting that the two boxes were about the same height, so the IQRs were about the same). In that case, you might run a pooled *t*-test, which here gives an almost identical P-value of 0.1872, and the exact same conclusion.

(f) Why might you have some doubts about the *t*-test that you just did? Explain briefly.

Solution

The two-sample *t*-test is based on an assumption of normally-distributed data within each group. If you go back and look at the boxplots, you'll see either (depending on your point of view) that both groups are right-skewed, or that both groups have outliers, neither of which fits a normal distribution. The outlier in the male group is particularly egregious. So I think we are entitled to question whether a two-sample *t*-test is the right thing to do. Having said that, we should go back and remember that the *t*-tests are "robust to departures from normality" (since we are working with the Central Limit Theorem here), and therefore that this test might be quite good even though the data are not normal, because the sample sizes of 40-plus are large (by the standards of what typically makes the Central Limit Theorem work for us). So it may not be as bad as it seems. A common competitor for the two-sample *t*-test is the Mann-Whitney test. This doesn't assume normality, but it *does* assume symmetric distributions, which it's not clear that we have here. I like a test called Mood's Median Test, which is kind of the two-sample equivalent of the sign test (which we will also see later). It goes like this: Work out the overall median of all the distances, regardless of gender:

Google defines this as meaning *outstandingly bad, shocking*.

```
parking %>% summarize(med = median(distance))
```

```
## # A tibble: 1 x 1
##     med
##   <dbl>
## 1     9
```

The overall median is 9.

Count up how many distances of each gender were above or below the overall median. (Strictly, I'm supposed to throw away any values that are exactly equal to the overall median, but I won't here for clarity of exposition.)

```
tab = with(parking, table(gender, distance < 9))
tab
```

```
##
## gender   FALSE TRUE
##   female    23   24
##   male      27   19
```

For example, 19 of the male drivers had a distance (strictly) less than 9. Both genders are pretty close to 50–50 above and below the overall median, which suggests that the males and females have about the same median. This can be tested (it's a chi-squared test for independence, if you know that):

```
chisq.test(tab, correct = F)
```

```
##
##  Pearson's Chi-squared test
##
## data:  tab
## X-squared = 0.89075, df = 1, p-value =
## 0.3453
```

This is even less significant (P-value 0.3453) than the two-sample *t*-test, and so is consistent with our conclusion from before that there is actually no difference between males and females in terms of average parking distance. The Mood's median test is believable because it is not affected by outliers or distribution shape.

(g) The Toronto Star in its report said that females are more accurate at parking their cars. Why do you think they concluded that, and do you think they were right to do so? Explain briefly.

Solution

The conclusion from the boxplots was that the female median distance was less than the males, slightly, in this sample. That is probably what the Star seized on. Were they right? Well, that was why we did the test of significance. We were trying to see whether this observed difference between males and females was "real" (would hold up if you looked at "all" male and female drivers) or "reproducible" (you would expect to see it again if you did another study like this one). The large, non-significant P-values in all our tests tell us that the difference observed here was nothing more than chance. So it was not reasonable to conclude that females generally are more accurate at parallel-parking than males are.

7
Power and sample size

```
library(tidyverse)
```

```
## -- Attaching packages ---- tidyverse 1.2.1 --

## v ggplot2 3.0.0     v purrr   0.2.5
## v tibble  1.4.2     v dplyr   0.7.6
## v tidyr   0.8.1     v stringr 1.3.1
## v readr   1.1.1     v forcats 0.3.0

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

7.1 Simulating power

This question investigates power by simulation.

(a) Use `rnorm` to generate 10 random values from a normal distribution with mean 20 and SD 2. Do your values look reasonable? Explain briefly. (You don't need to draw a graph.)

Solution
`rnorm` with the number of values first, then the mean, then the SD:

```
x = rnorm(10, 20, 2)
x
```

```
##  [1] 21.59476 18.64044 21.83231 18.76556
##  [5] 18.64861 21.81889 21.62614 20.18249
##  [9] 16.91266 20.63490
```

95% of the sampled values should be within 2 SDs of the mean, that is, between 16 and 24 (or 99.7% should be within 3 SDs of the mean, between 14 and 26). None of my values are even outside the interval 16 to 24, though yours may be different.

I saved mine in a variable and then displayed them, which you don't need to do. I did because there's another way of assessing them for reasonableness: turn the sample into *z*-scores and see whether the values you get look like *z*-scores (that is, most of them are between -2 and 2, for example):

```
(x - 20)/2
```

```
##  [1]  0.79738130 -0.67977910  0.91615386
##  [4] -0.61722168 -0.67569291  0.90944266
##  [7]  0.81307163  0.09124563 -1.54367207
## [10]  0.31744905
```

These ones look very much like *z*-scores. This, if you think about it, is really the flip-side of 68–95–99.7, so it's another way of implementing the same idea.

You might also think of finding the *sample* mean and SD, and demonstrating that they are close to the right answers. Mine are:

```
mean(x)
```

```
## [1] 20.06568
```

```
sd(x)
```

```
## [1] 1.731305
```

The sample SD is more variable than the sample mean, so it can get further away from the population SD than the sample mean does from the population mean.

The downside to this idea is that it doesn't get at assessing the normality, which looking at *z*-scores or equivalent does. Maybe coupling the above with a boxplot would have helped, had I not said “no graphs”, since then you'd (hopefully) see no outliers and a roughly symmetric shape.

This is old-fashioned “base R” technology; you could do it with a data frame like this:

```
d = tibble(x = rnorm(10, 20, 2))
d
```

```
## # A tibble: 10 x 1
##        x
##    <dbl>
##  1  20.6
##  2  19.3
##  3  20.2
##  4  18.7
##  5  21.3
##  6  17.8
##  7  19.8
##  8  20.9
##  9  21.7
## 10  20.6
```

```
d %>% summarize(m = mean(x), s = sd(x))
```

```
## # A tibble: 1 x 2
##       m     s
##   <dbl> <dbl>
## 1  20.1  1.21
```

These are different random numbers, but are about equally what you'd expect. (These ones are a bit less variable than you'd expect, but with only ten values, don't expect perfection.)

Some discussion about the kind of values you should get, and whether or not you get them, is what is called for here. I want you to say something convincing about how the values you get come from a normal distribution with mean 20 *and* SD 2. "Close to 20" is not the whole answer here, because that doesn't get at "how close to 20?": that is, it talks about the mean but not about the SD.

(b) Estimate by simulation the power of a *t*-test to reject a null hypothesis of 20 when the true mean is also 20, the population SD is 2, and the sample size is 10, against a (default) two-sided alternative. Remember the steps: (i) generate a lot of random samples from the true distribution, (ii) run the *t*-test with the required null mean, (iii) pull out the P-values, (iv) count how many of them are 0.05 or less.

Solution

Once you get the hang of these, they all look almost the same. This one is easier than some because we don't have to do anything special to get a two-sided alternative hypothesis:

```
pvals <- rerun(1000, rnorm(10, 20, 2)) %>% map(~t.test(.,
    mu = 20)) %>% map_dbl("p.value")
tibble(pvals) %>% count(pvals <= 0.05)
```

```
## # A tibble: 2 x 2
##   `pvals <= 0.05`     n
##   <lgl>           <int>
## 1 FALSE             958
## 2 TRUE               42
```

The power is about 4.2%. This seems depressingly small, but see the next part.

(c) In the simulation you just did, was the null hypothesis true or false? Do you want to reject the null hypothesis or not? Explain briefly why the simulation results you got were (or were not) about what you would expect.

Solution

The null mean and the true mean were both 20: that is, the null hypothesis was correct, and rejecting it would be a mistake, to be precise a type I error. We were doing the test at $\alpha = 0.05$ (by comparing our collection of simulated P-values with 0.05), so we should be making a type I error 5% of the time. This is entirely in line with the 4.2% of (wrong) rejections that I had. Your estimation is likely to be different from mine, but you should be rejecting about 5% of the time. If your result is very different from 5%, that's an invitation to go back and check your code. On the other hand, if it *is* about 5%, that ought to give you confidence to go on and use the same ideas for the next part.

(d) By copying, pasting and editing your code from the previous part, estimate the power of the test of $H_0 : \mu = 20$ (against a two-sided alternative) when the true population mean is 22 (rather than 20).

Solution

Here's the code we just used:

```
pvals <- rerun(1000, rnorm(10, 20, 2)) %>% map(~t.test(.,
    mu = 20)) %>% map_dbl("p.value")
tibble(pvals) %>% count(pvals <= 0.05)
```

One of those 20s needs to become 22. Not the one in the `t.test`, since the hypotheses have not changed. So we need to change the 20 in the `rnorm` line to 22, since that's where we're generating data from the true distribution. The rest of it stays the same:

```
pvals <- rerun(1000, rnorm(10, 22, 2)) %>% map(~t.test(.,
    mu = 20)) %>% map_dbl("p.value")
tibble(pvals) %>% count(pvals <= 0.05)
```

```
## # A tibble: 2 x 2
##   ‘pvals <= 0.05‘     n
##   <lgl>           <int>
## 1 FALSE             202
## 2 TRUE              798
```

This time, we *want* to reject, since the null hypothesis is false. So look at the TRUE count of 798: the power is about 798/1000 $\simeq$ 80%. We are very likely to correctly reject a null of 20 when the mean is actually 22.

Another way to reason that the power should be fairly large is to think about what kind of sample you are likely to get from the true distribution: one with a mean around 22 and an SD around 2. Thus the t-statistic should be somewhere around this (we have a sample size of 10):

```
t_stat = (22 - 20)/(2/sqrt(10))
t_stat
```

```
## [1] 3.162278
```

and the two-sided P-value should be about

```
2 * (1 - pt(t_stat, 10 - 1))
```

```
## [1] 0.01150799
```

Of course, with your actual data, you will sometimes be less lucky than this (a sample mean nearer 20 or a larger sample SD), but sometimes you will be luckier. But the suggestion is that most of the time, the P-value will be pretty small and you will end up correctly rejecting.

The quantity t_stat above, 3.16, is known to some people as an "effect size", and summarizes how far apart the null and true means are, relative to the amount of variability present (in the sampling distribution of the sample mean). As effect sizes go, this one is pretty large.

(e) Use R to calculate this power exactly (without simulation). Compare the exact result with your simulation.

Solution

This is power.t.test. The quantity delta is the difference between true and null means:

```
power.t.test(n = 10, delta = 22 - 20, sd = 2,
    type = "one.sample", alternative = "two.sided")
```

```
##
##      One-sample t test power calculation
##
##               n = 10
##           delta = 2
##              sd = 2
##       sig.level = 0.05
##           power = 0.8030962
##     alternative = two.sided
```

This, 0.803, is very close to the 0.798 I got from my simulation. Which makes me think I did them both right. This is not a watertight proof, though: for example, I might have made a mistake and gotten lucky somewhere. But it does at least give me confidence. Extra: when you estimate power by simulation, what you are doing is rejecting or not with a certain probability (which is the same for all simulations). So the number of times you actually *do* reject has a binomial distribution with n equal to the number of simulated P-values you got (1000 in my case; you could do more) and a p that the simulation is trying to estimate. This is inference for a proportion, exactly what `prop.test` does.

Recall that `prop.test` has as input:

- a number of "successes" (rejections of the null in our case)
- the number of trials (simulated tests)
- the null-hypothesis value of `p` (optional if you only want a CI)
- (optional) a confidence level `conf.level`.

In part (b), we knew that the probability of (incorrectly) rejecting should have been 0.05 and we rejected 42 times out of 1000:

```
prop.test(42, 1000, 0.05)
```

```
##
##  1-sample proportions test with
##  continuity correction
##
## data:  42 out of 1000, null probability 0.05
## X-squared = 1.1842, df = 1, p-value =
## 0.2765
## alternative hypothesis: true p is not equal to 0.05
## 95 percent confidence interval:
##  0.03079269 0.05685194
## sample estimates:
##     p
## 0.042
```

Looking at the P-value, we definitely fail to reject that the probability of (incorrectly) rejecting is the 0.05 that it should be. Ouch. That's true, but unnecessarily confusing. Look at the confidence interval instead, 0.031 to 0.057. The right answer is 0.05, which is inside that interval, so good.

In part (c), we didn't know what the power was going to be (not until we calculated it with `power.t.test`, anyway), so we go straight for a confidence interval; the default 95% confidence level is fine. We (correctly) rejected 798 times out of 1000:

```
prop.test(798, 1000)
```

```
##
##  1-sample proportions test with
##  continuity correction
##
## data:  798 out of 1000, null probability 0.5
## X-squared = 354.02, df = 1, p-value <
## 2.2e-16
## alternative hypothesis: true p is not equal to 0.5
## 95 percent confidence interval:
##  0.7714759 0.8221976
## sample estimates:
##     p
## 0.798
```

I left out the 3rd input since we're not doing a test, and ignore the P-value that comes out. (The default null proportion is 0.5, which often makes sense, but not here.)

According to the confidence interval, the estimated power is between 0.771 and 0.822. This interval definitely includes what we now know is the right answer of 0.803.

This might be an accurate enough assessment of the power for you, but if not, you can do more simulations, say 10,000:

```
pvals <- rerun(10000, rnorm(10, 22, 2)) %>% map(~t.test(.,
    mu = 20)) %>% map_dbl("p.value")
tibble(pvals) %>% count(pvals <= 0.05)
```

```
## # A tibble: 2 x 2
##   `pvals <= 0.05`     n
##   <lgl>           <int>
## 1 FALSE            2004
## 2 TRUE             7996
```

I copied and pasted my code again, which means that I'm dangerously close to turning it into a function, but anyway.

The confidence interval for the power is then

```
prop.test(7996, 10000)
```

```
##
##  1-sample proportions test with
##  continuity correction
##
## data:  7996 out of 10000, null probability 0.5
## X-squared = 3589.2, df = 1, p-value <
## 2.2e-16
## alternative hypothesis: true p is not equal to 0.5
## 95 percent confidence interval:
##  0.7915892 0.8073793
## sample estimates:
##      p
## 0.7996
```

that is, from 0.792 to 0.807, which once again includes the right answer of 0.803. The first interval, based on 1,000 simulations, has length 0.051, while this interval has length 0.015. The first interval is more than three times as long as the second, which is about what you'd expect since the first one is based on 10 times fewer simulations, and thus ought to be a factor of $\sqrt{10} \simeq 3.16$ times longer.

This means that you can estimate power as accurately as you like by doing a large enough number of simulations. Provided, that is, that you are prepared to wait a possibly long time for it to finish working!

7.2 *Calculating power and sample size for estimating mean*

We are planning a study to estimate a population mean. The population standard deviation is believed to be 20, and the population distribution is believed to be approximately normal. We will be testing the null hypothesis that the population mean is 100. Suppose the population mean is actually 110, and we want to determine how likely we are to (correctly) reject the null hypothesis in this case, using a two-sided (but one-sample) test with $\alpha = 0.05$.

(a) We will take a sample of size $n = 30$. Calculate the power of this test.

Solution

`power.t.test`. Fill in: sample size `n`, difference in means `delta` ($10 = 110 - 100$), population SD `sd`, type of test `type` (`one.sample`) and kind of alternative hypothesis `alternative` (`two.sided`). Leave out `power` since that's what we want:

```
power.t.test(n = 30, delta = 10, sd = 20, type = "one.sample",
    alternative = "two.sided")
```

```
##
##      One-sample t test power calculation
##
##               n = 30
##           delta = 10
##              sd = 20
##       sig.level = 0.05
##           power = 0.7539627
##     alternative = two.sided
```

I meant "calculate" exactly rather than "estimate" (by simulation). Though if you want to, you can do that as well, thus:

```
pvals <- rerun(1000, rnorm(30, 110, 20)) %>% map(~t.test(.,
    mu = 100)) %>% map_dbl("p.value")
tibble(pvals) %>% count(pvals <= 0.05)
```

```
## # A tibble: 2 x 2
##   ‘pvals <= 0.05‘     n
##   <lgl>           <int>
## 1 FALSE             257
## 2 TRUE              743
```

That came out alarmingly close to the exact answer.

(b) Find the sample size necessary to obtain a power of at least 0.80 under these conditions. What sample size do you need? Explain briefly how your answer is consistent with (a).

Solution

Again, the implication is "by calculation". This time, in `power.t.test`, put in 0.80 for `power` and leave out `n`. The order of things doesn't matter (since I have named everything that's going into `power.t.test`):

```
power.t.test(delta = 10, power = 0.8, sd = 20,
    type = "one.sample", alternative = "two.sided")
```

```
##
##      One-sample t test power calculation
##
##               n = 33.3672
##           delta = 10
##              sd = 20
##       sig.level = 0.05
##           power = 0.8
##     alternative = two.sided
```

To get sample size for power at least 0.80, we have to round 33.36 *up* to the next whole number, ie. $n = 34$ is needed. (A sample of size 33 wouldn't quite have enough power.)

This answer is consistent with (a) because a sample size of 30 gave a power a bit less than 0.80, and so to increase the power by a little (0.75 to 0.80), we had to increase the sample size by a little (30 to 34).

Estimating sample sizes by simulation is tricky, because the sample size has to be input to the simulation. That means your only strategy is to try different sample sizes until you find one that gives the right power.

In this case, we know that a sample of size 30 doesn't give quite enough power, so we have to up the sample size a bit. How about we try 40? I copied and pasted my code from above and changed 30 to 40:

```
pvals <- rerun(1000, rnorm(40, 110, 20)) %>% map(~t.test(.,
    mu = 100)) %>% map_dbl("p.value")
tibble(pvals) %>% count(pvals <= 0.05)
```

```
## # A tibble: 2 x 2
##   ‘pvals <= 0.05‘     n
##   <lgl>           <int>
## 1 FALSE             130
## 2 TRUE              870
```

Now the power is a bit too big, so we don't need a sample size quite as big as 40. So probably our next guess would be 35. But before we copy and paste again, we should be thinking about making a function of it first, with the sample size as input. Copy-paste once more and edit:

```
sim_power = function(n) {
    pvals <- rerun(1000, rnorm(30, 110, 20)) %>%
        map(~t.test(., mu = 100)) %>% map_dbl("p.value")
    tibble(pvals) %>% count(pvals <= 0.05)
}
```

In the grand scheme of things, we might want to have the null and true means, population SD and α be inputs to the function as well, so that we have a more general tool, but this will do for now.

Let's run it with a sample size of 35:

```
sim_power(35)
```

```
## # A tibble: 2 x 2
##   ‘pvals <= 0.05‘     n
##   <lgl>           <int>
## 1 FALSE             238
## 2 TRUE              762
```

and I'm going to call that good. (Because there is randomness in the estimation of the power, don't expect to get *too* close to the right answer. This one came out a fair bit less than the right answer; the power for $n = 35$ should be a bit *more* than 0.80.)

Now that you have the software to do it, you can see that figuring out a sample size like this, at least roughly, won't take very long: each one of these simulations takes maybe seconds to run, and all you have to do is copy and paste the previous one, and edit it to contain the new sample size before running it again. You're making the computer work hard while you lazily sip your coffee, but there's no harm in that: programmer's brain cells are more valuable than computer CPU cycles, and you might as well save your brain cells for when you really need them.

7.3 *Simulating power for proportions*

In opinion surveys (and other places), we are testing for a proportion p (for example, the proportion of people agreeing with some statement). Often, we want to know whether the proportion is "really" greater than 0.5.

That would mean assessing whether an observed proportion could be greater than 0.5 just by chance, or whether it is bigger enough than 0.5 to reject chance as a plausible explanation.

That would entail testing a null $H_0 : p = 0.5$ against an alternative $H_a : p > 0.5$. This is usually done by calculating the test statistic

$$z = \frac{\hat{p} - 0.5}{\sqrt{0.25/n}},$$

where $\hat{p}$ is the observed proportion in the sample, and getting a P-value from the upper tail of a standard normal distribution. (The 0.25 is $p(1-p)$ where $p = 0.5$.) This is what `prop.test` does, as we investigate shortly.

(a) Use `rbinom` to generate a random value from a binomial distribution with $n = 100$ and $p = 0.6$. There are three inputs to `rbinom`: the first one should be the number 1, and the second and third are the n and p of the binomial distribution.

Solution

I am doing some preparatory work that you don't need to do:

```r
set.seed(457299)
```

By setting the "seed" for the random number generator, I guarantee that I will get the same answers every time I run my code below (and therefore I can talk about my answers without worrying that they will change). Up to you whether you do this. You can "seed" the random number generator with any number you like. A lot of people use 1. Mahinda seems to like 123. Mine is an old phone number.

And so to work:

```
rbinom(1, 100, 0.6)
```

```
## [1] 60
```

I got exactly 60% successes this time. You probably won't get exactly 60, but you should get somewhere close. (If you use my random number seed and use the random number generator exactly the same way I did, you should get the same values I did.)

For fun, you can see what happens if you change the 1:

```
rbinom(3, 100, 0.6)
```

```
## [1] 58 57 55
```

Three random binomials, that happened to come out just below 60. We're going to leave the first input as 1, though, and let `rerun` handle "lots of sampled values" later.

(b) Using the random binomial that you generated just above, use `prop.test` to test whether it could reasonably have come from a binomial population with $n = 100$ and $p = 0.5$, or whether p is actually bigger than 0.5. (Of course, you know it actually did not come from a population with $p = 0.5$.) `prop.test` has, for us, four inputs, thus:

- the observed number of successes
- the `n` of the binomial distribution
- the null-hypothesis `p` of the binomial distribution
- the alternative hypothesis, here "greater"

Solution

I got exactly 60 successes, so I do this:

```
prop.test(60, 100, 0.5, alternative = "greater")
```

```
##
##  1-sample proportions test with
##  continuity correction
##
```

```
## data:  60 out of 100, null probability 0.5
## X-squared = 3.61, df = 1, p-value =
## 0.02872
## alternative hypothesis: true p is greater than 0.5
## 95 percent confidence interval:
##  0.5127842 1.0000000
## sample estimates:
##   p
## 0.6
```

The P-value should at least be fairly small, since 60 is a bit bigger than 50. (Think about tossing a coin 100 times; would 60 heads make you doubt the coin's fairness? The above says it should.)

(c) Run `prop.test` again, just as you did before, but this time save the result, and extract the piece of it called `p.value`. Is that the P-value from your test?

Solution
Copying and pasting:

```
p_test = prop.test(60, 100, 0.5, alternative = "greater")
p_test$p.value
```

```
## [1] 0.02871656
```

Yep, the same.

(d) Use `rerun` to estimate the power of a test of $H_0 : p = 0.5$ against $H_a : p > 0.5$ when $n = 500$ and $p = 0.56$, using $\alpha = 0.05$. There are three steps:

- use `rerun` to generate random samples from binomial distributions with $n = 500$ and $p = 0.56$, repeated "many" times (something like 1000 or 10,000 is good)
- use `map` to run `prop.test` on each of those random samples
- use `map_dbl` to extract the P-value for each test and save the results (in a vector called, perhaps, `pvals`).

So I lied: the fourth and final step is to count how many of those P-values are 0.05 or less.

Solution
The previous parts, using `rbinom` and `prop.test`, were meant to provide you with the ingredients for this part. The first step is to use `rbinom`. The first input is 1 since we only want one random binomial each time (the `rerun` will handle the fact that you actually want lots

of them). The second step runs `prop.test`; the first input to that is each one of the numbers of successes from the first step. (This is an implied for-each, with each of the simulated binomials playing the role of "it", in turn.). The last part is to pull out all the P-values and make a table of them, just like the example in class.

```
pvals <- rerun(10000, rbinom(1, 500, 0.56)) %>%
    map(~prop.test(., 500, 0.5, alternative = "greater")) %>%
    map_dbl("p.value")
tibble(pvals) %>% count(pvals <= 0.05)
```

```
## # A tibble: 2 x 2
##   ‘pvals <= 0.05‘     n
##   <lgl>           <int>
## 1 FALSE            1491
## 2 TRUE             8509
```

The estimated power is about 85%. That is, if p is actually 0.56 and we have a sample of size 500, we have a good chance of (correctly) rejecting that $p = 0.5$.

Extra: It turns out that SAS can work out this power by calculation (using `proc power`). SAS says our power is also about 85%, as our simulation said. I was actually pleased that my simulation came out so close to the right answer.

In contrast to `power.t.test`, SAS's `proc power` handles power analyses for a lot of things, including analysis of variance, correlation and (multiple) regression. What these have in common is some normal-based theory that allows you (under assumptions of sufficiently normal-shaped populations) to calculate the exact answer (that is, the distribution of the test statistic when the *alternative* hypothesis is true). The case we looked at is one of those because of the normal approximation to the binomial: once n gets big, particularly if p is somewhere near 0.5, the binomial is very well approximated by a normal with the right mean and SD.

The moral of this story is that when you have a decently large sample, $n = 500$ in this case, p doesn't have to get very far away from 0.5 before you can correctly reject 0.5. Bear in mind that sample sizes for estimating proportions need to be larger than those for estimating means, so $n = 500$ is large without being huge. The practical upshot is that if you design a survey and give it to 500 (or more) randomly chosen people, the proportion of people in favour doesn't have to be much above 50% for you to correctly infer that it *is* above 50%, most of the time.

8
The sign test and Mood's median test

```
library(tidyverse)

## -- Attaching packages ---- tidyverse 1.2.1 --

## v ggplot2 3.0.0     v purrr   0.2.5
## v tibble  1.4.2     v dplyr   0.7.6
## v tidyr   0.8.1     v stringr 1.3.1
## v readr   1.1.1     v forcats 0.3.0

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

library(smmr)
```

8.1 Running a maze

A researcher is trying to design a maze that can be run by rats in about 60 seconds. One particular maze was run by a sample of 21 rats, with the times shown in link.

(a) Read the data into R. What (if anything) are the data values delimited by?

Solution

Take a look at the data file first. There is only one column of data, so you can treat it as being delimited by anything you like: a space, or a comma (the file can also be treated as a `.csv`), etc.:

```
myurl = "http://www.utsc.utoronto.ca/~butler/c32/maze.txt"
times = read_delim(myurl, " ")

## Parsed with column specification:
## cols(
##   time = col_double()
## )
```

```
times
```

```
## # A tibble: 21 x 1
##     time
##    <dbl>
##  1  38.4
##  2  46.2
##  3  62.5
##  4  38
##  5  62.8
##  6  33.9
##  7  50.4
##  8  35
##  9  52.8
## 10  60.1
## # ... with 11 more rows
```

(b) Run a sign test, doing it yourself as we did in class: count the number of values above and below 60, take the *smaller* of those, and find the probability of a value of that or smaller still on a binomial distribution with $n = 21$ and $p = 0.5$ (we have 21 data points), doubling the answer because the test is two-sided.

Solution
Count how many values are above and below 60:

```
times %>% count(time > 60)
```

```
## # A tibble: 2 x 2
##   ‘time > 60‘     n
##   <lgl>       <int>
## 1 FALSE          16
## 2 TRUE            5
```

5 above and 16 below. Then find out how likely it is that a binomial with $n = 21, p = 0.5$ would produce 5 or fewer successes:

```
p = sum(dbinom(0:5, 21, 0.5))
p
```

```
## [1] 0.01330185
```

or if you prefer count upwards from 16:

```
sum(dbinom(16:21, 21, 0.5))
```

```
## [1] 0.01330185
```

and double it to get a two-sided P-value:

```
2 * p
```

```
## [1] 0.0266037
```

We'll compare this with smmr in a moment.

(c) Install my package smmr, if you haven't already. To do this, you first need to install the package devtools (if you haven't already), by going to the console and typing

```
install.packages("devtools")
```

When that's all done, install smmr thus:

```
library(devtools)
install_github("nxskok/smmr")
```

That all needs to be done only once. Then, each R Studio session where you want to use smmr needs this:

```
library(smmr)
```

As usual, only the library thing only needs to be done every time.

When you have smmr installed, use sign_test from that package to re-run your sign test. Do you get the same P-value?

Solution

The sign test function takes a data frame, an (unquoted) column name from that data frame of data to test the median of, and a null median (which defaults to 0 if you omit it):

```
library(smmr)
sign_test(times, time, 60)
```

```
## $above_below
## below above
##    16     5
##
## $p_values
##   alternative    p_value
## 1       lower 0.01330185
## 2       upper 0.99640131
## 3   two-sided 0.02660370
```

This shows you two things: a count of the values below and above the null median, and then the P-values according to the various alternative hypotheses you might have.

In our case, we see again the 16 maze-running times below 60 seconds and 5 above (one of which was a long way above, but we don't care about that here). We were testing whether the median was different from 60, so we look at the two-sided P-value of 0.0266, which is exactly what we had before.

If `sign_test` doesn't work for you (perhaps because it needs a function `enquo` that you don't have), there is an alternative function `sign_test0` that doesn't use it. It requires as input a *column* of values (extracted from the data frame) and a null median, thus:

```
with(times, sign_test0(time, 60))
```

```
## $above_below
## below above
##    16     5
##
## $p_values
##   alternative    p_value
## 1       lower 0.01330185
## 2       upper 0.99640131
## 3   two-sided 0.02660370
```

The output should be, and here is, identical.

(d) Package `smmr` also has a function `pval_sign`, which has the same input as `sign_test`, but with the null median *first*. Run it on your data and see what it gives.

Solution

Try it and see:

```
pval_sign(60, times, time)
```

```
## [1] 0.0266037
```

The two-sided P-value, and that is all. We'll be using this in a minute.

Alternatively, there is also this, which needs a null median and a *column* as input:

```
with(times, pval_sign0(60, time))
```

```
## [1] 0.0266037
```

(e) Obtain a 95% confidence interval for the median based on these data. Do this two ways. First, use the trial and error way from class (either the try-lots-of-values way or the bisection way; either is good). Second, use `ci_median` from `smmr`. The latter takes as input a data frame, a column name (unquoted) and optionally a `conf.level` that defaults to 0.95.

Solution

The reason for showing you pval_sign in the previous part is that this is a building block for the confidence interval. What we do is to try various null medians and find out which ones give P-values less than 0.05 (outside the interval) and which ones bigger (inside). We know that the value 60 is outside the 95% CI, and the sample median is close to 50 (which we expect to be inside), so sensible values to try for the upper end of the interval would be between 50 and 60:

```
pval_sign(58, times, time)
```

```
## [1] 0.0266037
```

```
pval_sign(55, times, time)
```

```
## [1] 0.6636238
```

So, 55 is inside the interval and 58 is outside. I could investigate further in similar fashion, but I thought I would try a whole bunch of null medians all at once. That goes like this:

```
meds = seq(55, 58, 0.25)
meds
```

```
##  [1] 55.00 55.25 55.50 55.75 56.00 56.25
##  [7] 56.50 56.75 57.00 57.25 57.50 57.75
## [13] 58.00
```

```
pvals = map_dbl(meds, pval_sign, times, time)
data.frame(meds, pvals)
```

```
##     meds      pvals
## 1  55.00 0.66362381
## 2  55.25 0.38331032
## 3  55.50 0.26317596
## 4  55.75 0.18924713
## 5  56.00 0.18924713
## 6  56.25 0.18924713
## 7  56.50 0.07835388
## 8  56.75 0.07835388
## 9  57.00 0.07835388
## 10 57.25 0.07835388
## 11 57.50 0.07835388
## 12 57.75 0.02660370
## 13 58.00 0.02660370
```

So values for the median all the way up to and including 57.5 are in the confidence interval.

What map_dbl does is to take a vector of values, here the ones in meds (55 through 58 in steps of 0.25), feed them into a function, here pval_sign, one by one and gather together the results. pval_sign has two other inputs, times and time, which are added to map_dbl at the end. (They are the same no matter what median we are testing.) So, putting the calculated P-values side by side with the null medians they belong to shows you which medians are inside the confidence interval and which are outside.

The function is called map_dbl because *my* function called pval_sign that is called repeatedly returns a single decimal number (a dbl). There is also, for example, map_chr for repeatedly calling a function that returns a single piece of text, and plain map that is used when the repeatedly-called function returns a data frame.

Since you don't know about map_dbl, I didn't want to confuse things more than necessary, but now that you *do* know what it does, you might be in a better position to understand this more Tidyverse-flavoured code, with the map_dbl inside a mutate and the data frame created as we go:

```
tibble(meds = seq(55, 58, 0.25)) %>% mutate(pvals = map_dbl(meds,
    pval_sign, times, time))
```

```
## # A tibble: 13 x 2
##     meds  pvals
##    <dbl>  <dbl>
##  1  55   0.664
##  2  55.2 0.383
##  3  55.5 0.263
##  4  55.8 0.189
##  5  56   0.189
##  6  56.2 0.189
##  7  56.5 0.0784
##  8  56.8 0.0784
##  9  57   0.0784
## 10  57.2 0.0784
## 11  57.5 0.0784
## 12  57.8 0.0266
## 13  58   0.0266
```

Now for the other end of the interval. I'm going to do this a different way: more efficient, but less transparent. The first thing I need is a pair of values for the median: one inside the interval and one outside. Let's try 40 and 50:

```
pval_sign(40, times, time)
```

```
## [1] 0.00719738
```

```
pval_sign(50, times, time)
```

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

OK, so 40 is outside and 50 is inside. So what do I guess for the next value to try? I could do something clever like assuming that the relationship between hypothesized median and P-value is *linear*, and then guessing where that line crosses 0.05. But I'm going to assume *nothing* about the relationship except that it goes uphill, and therefore crosses 0.05 somewhere. So my next guess is halfway between the two values I tried before:

```
pval_sign(45, times, time)
```

```
## [1] 0.07835388
```

So, 45 is inside the interval, and my (slightly) improved guess at the bottom end of the interval is that it's between 40 and 45. So next, I try halfway between *those*:

```
pval_sign(42.5, times, time)
```

```
## [1] 0.0266037
```

42.5 is outside, so the bottom end of the interval is between 42.5 and 45.

What we are doing is narrowing down where the interval's bottom end is. We started by knowing it to within 10, and now we know it to within 2.5. So if we keep going, we'll know it as accurately as we wish.

This is called a "bisection" method, because at each step, we're dividing our interval by 2.

There is one piece of decision-making at each step: if the P-value for the median you try is greater than 0.05, that becomes the top end of your interval (as when we tried 45); if it is less, it becomes the bottom end (when we tried 42.5).

This all begs to be automated into a loop. It's not a `for`-type loop, because we don't know how many times we'll be going around. It's a `while` loop: keep going while something is true. Here's how it goes:

```
lo = 40
hi = 50
while (abs(hi - lo) > 0.1) {
    try = (hi + lo)/2
    ptry = pval_sign(try, times, time)
    print(c(try, ptry))
    if (ptry < 0.05) {
        lo = try
    } else {
        hi = try
    }
}

## [1] 45.00000000  0.07835388
## [1] 42.5000000  0.0266037
## [1] 43.7500000  0.0266037
## [1] 44.37500000  0.07835388
## [1] 44.0625000  0.0266037
## [1] 44.2187500  0.0266037
## [1] 44.2968750  0.0266037
```

```
lo

## [1] 44.29688
```

```
pval_sign(lo, times, time)

## [1] 0.0266037
```

```
hi

## [1] 44.375
```

```
pval_sign(hi, times, time)

## [1] 0.07835388
```

The loop stopped because 44.297 and 44.375 are less than 0.1 apart. The first of those is outside the interval and the second is inside. So the bottom end of our interval is 44.375, to this accuracy. If you want it more accurately, change 0.1 in the `while` line to something smaller (but then you'll be waiting longer for the answer).

I put the `print` statement in the loop so that you could see what values were being tried, and what P-values they were producing. What happens with these is that the P-value jumps at each data value, so you won't get a P-value exactly 0.05; you'll get one above and one below.

Likewise, you can use the function with a zero on its name and feed it a column rather than a data frame and a column name:

```
meds = seq(55, 58, 0.25)
meds
```

```
##  [1] 55.00 55.25 55.50 55.75 56.00 56.25
##  [7] 56.50 56.75 57.00 57.25 57.50 57.75
## [13] 58.00
```

```
pvals = map_dbl(meds, ~with(times, pval_sign0(.,
    time)))
data.frame(meds, pvals)
```

```
##     meds      pvals
## 1  55.00 0.66362381
## 2  55.25 0.38331032
## 3  55.50 0.26317596
## 4  55.75 0.18924713
## 5  56.00 0.18924713
## 6  56.25 0.18924713
## 7  56.50 0.07835388
## 8  56.75 0.07835388
## 9  57.00 0.07835388
## 10 57.25 0.07835388
## 11 57.50 0.07835388
## 12 57.75 0.02660370
## 13 58.00 0.02660370
```

Or adapt the idea I had above for bisection. All that was a lot of work, but I wanted you to see it all once, so that you know where the confidence interval is coming from. `smmr` also has a function `ci_median` that does all of the above without you having to do it. As I first wrote it, it was using the trial and error thing with `map_dbl`, but I chose to rewrite it with the bisection idea, because I thought that would be more accurate.

```
ci_median(times, time)
```

```
## [1] 44.30747 57.59766
```

This is a more accurate interval than we got above. (The `while` loop for the bisection keeps going until the two guesses at the appropriate end of the interval are less than 0.01 apart, by default.)

You can change this by adding something like *tol=1e-4* to the end of your *ci-median*.

If you want some other confidence level, you add `conf.level` on the end, as you would for `t.test`:

```
ci_median(times, time, conf.level = 0.75)
```

```
## [1] 46.20444 55.49473
```

A 75% CI, just for fun. This is a shorter interval than the 95% one, as it should be.

Likewise there is a `ci_median0` that takes a column and an optional confidence level:

```
with(times, ci_median0(time))
```

```
## [1] 44.30747 57.59766
```

```
with(times, ci_median0(time, conf.level = 0.75))
```

```
## [1] 46.20444 55.49473
```

with the same results. Try `ci_median` first, and if it doesn't work, try `ci_median0`.

8.2 Chocolate chips

A famous cookie manufacturer claims that their bags of chocolate chip cookies contain "more than 1100 chocolate chips on average". A diligent group of students buys 16 bags of these cookies and counts the number of chocolate chips in each bag. The results are in `http://www.utsc.utoronto.ca/~butler/c32/chips.txt`.

(a) Read in and display (some of) the data.

Solution

I'll pretend it's a `.csv` this time, just for fun. Give the data frame a name different from `chips`, so that you don't get confused:

```
bags = read_csv("chips.txt")
```

```
## Parsed with column specification:
## cols(
##   chips = col_integer()
## )
```

```
bags
```

```
## # A tibble: 16 x 1
##    chips
##    <int>
##  1  1219
##  2  1214
##  3  1087
##  4  1200
##  5  1419
##  6  1121
##  7  1325
##  8  1345
##  9  1244
## 10  1258
## 11  1356
## 12  1132
## 13  1191
## 14  1270
## 15  1295
## 16  1135
```

That looks sensible.

(b) Build your own sign test in R for testing that the median is 1100 chocolate chips, against the alternative that it is greater. (Do this as in class: count the appropriate thing, compare it with an appropriate binomial distribution, and obtain a P-value.

Solution

The null median is 1100, so we count the number of values above and below:

```
bags %>% count(chips < 1100)
```

```
## # A tibble: 2 x 2
##   'chips < 1100'     n
##   <lgl>          <int>
## 1 FALSE             15
## 2 TRUE               1
```

The un-standard thing there is that we can put a logical condition directly into the `count`. If you don't think of that, you can also do this, which creates a new variable `less` that is `TRUE` or `FALSE` for each bag appropriately:

```
bags %>% mutate(less = (chips < 1100)) %>% count(less)
```

```
## # A tibble: 2 x 2
##   less      n
##   <lgl> <int>
## 1 FALSE    15
## 2 TRUE      1
```

or the more verbose

```
bags %>% mutate(less = (chips < 1100)) %>% group_by(less) %>%
    summarize(howmany = n())
```

```
## # A tibble: 2 x 2
##   less  howmany
##   <lgl>   <int>
## 1 FALSE      15
## 2 TRUE        1
```

Just one value below, with all the rest above. Getting the right P-value, properly, requires some careful thought (but you will probably get the right answer anyway). If the alternative hypothesis is true, and the median is actually bigger than 1100 (say, 1200), you would expect half the data values to be bigger than 1200 and half smaller. So *more* than half the data values would be bigger than *1100*, and fewer than half of them would be less than 1100. So, if we are going to reject the null (as it looks as if we will), that small number of values below 1100 is what we want.

The P-value is the probability of a value 1 or less in a binomial distribution with $n = 16, p = 0.5$:

```
sum(dbinom(0:1, 16, 0.5))

## [1] 0.0002593994
```

Or, equivalently, count *up* from 15:

```
sum(dbinom(15:16, 16, 0.5))

## [1] 0.0002593994
```

This is correctly one-sided, so we don't have to do anything with it.

(c) Use my R package `smmr` to reproduce your sign test above, and verify that you get consistent results. (See the maze-design question for instructions on installing this, if you haven't yet.)

Solution

This will mean reading the output carefully:

```
library(smmr)
sign_test(bags, chips, 1100)

## $above_below
## below above
##     1    15
##
## $p_values
##   alternative      p_value
## 1       lower 0.9999847412
## 2       upper 0.0002593994
## 3   two-sided 0.0005187988
```

This time, we're doing a one-sided test, specifically an *upper-tail* test, since we are looking for evidence that the median is *greater than* 1100. The results are exactly what we got "by hand": 15 values above and one below, and a P-value (look along the `upper` line) of 0.00026. The two-sided P-value of 0.00052 rounds to the same 0.0005 as SAS got.

Alternatively, you can do this:

```
sign_test0(bags$chips, 1100)
```

```
## $above_below
## below above
##     1    15
##
## $p_values
##   alternative      p_value
## 1       lower 0.9999847412
## 2       upper 0.0002593994
## 3   two-sided 0.0005187988
```

with the same result (but only go this way if you need to).

(d) Use `smmr` to obtain a 95% confidence interval for the median number of chocolate chips per bag of cookies.

Solution

Once everything is in place, this is simplicity itself:

```
ci_median(bags, chips)
```

```
## [1] 1135.003 1324.996
```

1135 to 1325. I would round these off to whole numbers, since the data values are all whole numbers. These values are all above 1100, which supports the conclusion we got above that the median is above 1100. This is as it should be, because the CI is “all those medians that would *not* be rejected by the sign test”.

Or,

```
ci_median0(bags$chips)
```

```
## [1] 1135.003 1324.996
```

8.3 The power of the sign test

I’ve mentioned several times that the sign test has less power than the t-test. Let’s investigate this with a specific example.

Let’s suppose we are testing $H_0 : \mu = 40$ against $H_a : \mu \neq 40$, where μ is the population mean (and median, as we shall see). Our population actually has a normal distribution with mean 50 and SD

15, so that the null hypothesis is *wrong* and we want to reject it most of the time. On the other hand, the population actually *is* normally-distributed and so the t-test is the right one to use.

(This is an old question, so I tackle the simulated power differently than I did it in class this time. But see if you can follow what I do here.)

(a) Use `power.t.test` to find the probability that a t-test correctly rejects the null hypothesis using a sample size of $n = 10$.

Solution

```
power.t.test(delta = 50 - 40, n = 10, sd = 15,
    type = "one.sample", alternative = "two.sided")
```

```
##
##      One-sample t test power calculation
##
##               n = 10
##           delta = 10
##              sd = 15
##       sig.level = 0.05
##           power = 0.4691805
##     alternative = two.sided
```

The power is 0.469. Not great, but we'll see how this stacks up against the sign test.

(b) What code in R would draw a random sample of size 10 from the *true* population distribution and save the sample in a variable?

Solution

The data actually have a normal distribution with mean 50 and SD 15, so we use `rnorm` with this mean and SD, obtaining 10 values:

```
x = rnorm(10, 50, 15)
x
```

```
##  [1] 71.040478 30.347205 56.347831 41.262454
##  [5] 39.338762 42.598468 27.782193 63.671833
##  [9]  7.328107 45.130755
```

(c) What code would count how many of the sampled values are less than 40 and how many are greater (or equal)?

Solution

The way we know this is to put x into a data frame first:

```
tibble(x) %>% count(x < 40)
```

```
## # A tibble: 2 x 2
##   ‘x < 40‘     n
##   <lgl>    <int>
## 1 FALSE        6
## 2 TRUE         4
```

2 values less (and 8 greater-or-equal).

(d) It turns out the sign test would reject $H_0 : M = 40$ against $H_a : M \neq 40$ at $\alpha = 0.05$ if the smaller of the numbers in the last part is 1 or less. (M is the population median.) Add to your pipeline to obtain `TRUE` if you should reject the null for your data and `FALSE` otherwise.

Solution

This is actually easier than you might think. The output from `count` is a data frame with a column called `n`, whose minimum value you want. I add to my pipeline:

```
tibble(x) %>% count(x < 40) %>% summarize(the_min = min(n)) %>%
    mutate(is_rejected = (the_min <= 1))
```

```
## # A tibble: 1 x 2
##   the_min is_rejected
##     <dbl> <lgl>
## 1       4 FALSE
```

This will fail sometimes. If all 10 of your sample values are greater than 40, which they might turn out to be, you'll get a table with only one line, `FALSE` and 10; the minimum of the `n` values is 10 (since there is only one), and it will falsely say that you should not reject. The fix is

```
tibble(x) %>% count(x < 40) %>% summarize(the_min = min(n)) %>%
    mutate(is_rejected = (the_min <= 1 | the_min ==
        10))
```

```
## # A tibble: 1 x 2
##   the_min is_rejected
##     <dbl> <lgl>
## 1       4 FALSE
```

The above is almost the right thing, but not quite: we only want that value that I called `is_rejected`, rather than the whole data frame, so a `pull` will grab it:

```
tibble(x) %>% count(x < 40) %>% summarize(the_min = min(n)) %>%
    mutate(is_rejected = (the_min <= 1 | the_min ==
        10)) %>% pull(is_rejected)
```

```
## [1] FALSE
```

You might be wondering where the "1 or less" came from. Getting a P-value for the sign test involves the binomial distribution: if the null is correct, each data value is independently either above or below 40, with probability 0.5 of each, so the number of values below 40 (say) is binomial with $n = 10$ and $p = 0.5$. The P-value for 1 observed value below 40 and the rest above is

```
2 * pbinom(1, 10, 0.5)
```

```
## [1] 0.02148438
```

which is less than 0.05; the P-value for 2 values below 40 and the rest above is

```
2 * pbinom(2, 10, 0.5)
```

```
## [1] 0.109375
```

which is bigger than 0.05.

You might have encountered the term "critical region" for a test. This is the values of your test statistic that you would reject the null hypothesis for. In this case, the critical region is 1 and 0 observations below 40, along with 1 and 0 observations above 40.

When you're thinking about power, I think it's easiest to think in terms of the critical region (rather than directly in terms of P-values) since you have a certain α in mind all the way through, 0.05 in the power examples that I've done. The steps are then:

- Work out the critical region for your test, the values of the test statistic (or sample mean or sample count) that would lead to rejecting the null hypothesis.
- Under your particular alternative hypothesis, find the probability of falling into your critical region.

When I say "work out", I mean either calculating (along the lines of STAB57), or simulating, as we have done here.

(e) Use `rerun` to simulate the above process 1000 times: drawing a random sample from a normal distribution with mean 50 and SD 15, counting the number of values below and above 40, rejecting if the minimum of those is 1 or less, then counting the number of rejections out of 1000.

Solution

The way we've used rerun is to use it to select the random samples, and then we use map ideas to do what we want to do with each random sample, along the lines of what we did with the one random sample above. This is liable to go wrong the first few times, so make sure that each line works before you go on to the next. (rerun will produce you a list of random samples, with each of which you want to do something.) While you're debugging, try it with a small number of random samples like 5. I start with setting the random number seed, so it comes out the same each time. I discuss the results below and the code below that.

```
set.seed(457299)
rerun(1000, rnorm(10, 50, 15)) %>% map(~tibble(x = .)) %>%
    map(~count(., x < 40)) %>% map(~summarize(.,
    the_min = min(n))) %>% map(~mutate(., is_rejected = (the_min <=
    1 | the_min == 10))) %>% map_lgl(~pull(.,
    is_rejected)) %>% tibble(was_true = .) %>%
    count(was_true)
```

```
## # A tibble: 2 x 2
##   was_true     n
##   <lgl>    <int>
## 1 FALSE      757
## 2 TRUE       243
```

The estimated power of the sign test is 0.243, since that was the number of times a simulated sample gave us 0 or 1 values above or below 40 (and the rest on the other side).

All right, that code is seriously scary. Let me try to take you through it.

- The rerun line is the same kind of thing we had before: generate 1000 different random samples of size 10 from a normal distribution with mean 50 and SD 15.

- The output from the previous step is a list of vectors. But we like data frames to count things in, so for each vector we turn it into a data frame, filling a column called x with whatever was in each vector (that random sample). So now we have 1000 data frames each containing a column called x.

- Next, in each of those data frames, count up how many of the x values are less than 40. This will produce a data frame each time containing a column n that is the frequencies. Here and below, the . is used to denote "it": that is, each of the elements of the list created originally by `rerun` that we are doing something with. Also, at the moment, the output for each element of the list is a data frame, so we stick with `map` for the time being.

- Next, for each of those tables of frequencies, find the smallest one and call it `the_min`. (As discussed above, all the values might be bigger than 40, in which case `the_min` will be 10 rather than 0, which we handle next.)

- Next, we create a new column called `is_rejected` which says that we should reject a median of 40 if the minimum value we just calculated is 1 or less, or if it happens to be 10, in which case that would have been the only entry in the frequency table, so that the missing one would have been zero.

- Next, we pull out only the true-or-false value in `is_rejected`. At last, the answer here is not a data frame but a simple logical value; `map_lgl` is like `map_dbl` except that the thing we are doing returns a `TRUE` or a `FALSE` rather than a number.

- At this point we have a vector of 1000 true-or-false. We want to count them, so we put them into a data frame (with a column called `was_true`), and in the last line, count them up. There are 243 (correct) rejections and 757 (incorrect) non-rejections.

You may now breathe again.

I'm now thinking a better way to do this is to write a function that takes a sample (in a vector) and returns a TRUE or FALSE according to whether or not a median of 40 would be rejected for that sample:

```
is_reject = function(x) {
    tibble(x = x) %>% count(x < 40) %>% summarize(the_min = min(n)) %>%
        mutate(is_rejected = the_min <= 1 | the_min ==
            10) %>% pull(is_rejected)
}
```

Now, we have to use that. This function will be "mapped" over for each of the random samples that come out of `rerun`, but now there will be only one `map` because the complication of the multiple `maps` has been subsumed into this one function. I'll set my random number seed so that I get the same results as before:

```
set.seed(457299)
rerun(1000, rnorm(10, 50, 15)) %>% map_lgl(~is_reject(.)) %>%
    tibble(rejected = .) %>% count(rejected)
```

```
## # A tibble: 2 x 2
##   rejected     n
##   <lgl>    <int>
## 1 FALSE      757
## 2 TRUE       243
```

Same results, and yeah, I like that a lot better.

(f) Which is more powerful in this case, the sign test or the *t*-test? How do you know?

Solution

The power of the sign test is estimated as 0.243, which is quite a bit less than the power of the *t*-test, which we found back in (a) to be 0.469. So the *t*-test, in this situation where it is valid, is the right test to use: it is (i) valid and (ii) more powerful. So the *t*-test is more powerful. One way to think about how *much* more powerful is to ask "how much smaller of a sample size would be needed for the *t*-test to have the same power as this sign test?" The power of my sign test was 0.243, so in `power.t.test` we set `power` equal to that and omit the sample size `n`:

```
power.t.test(delta = 50 - 40, power = 0.243, sd = 15,
    type = "one.sample", alternative = "two.sided")
```

```
##
##      One-sample t test power calculation
##
##               n = 5.599293
##           delta = 10
##              sd = 15
##       sig.level = 0.05
##           power = 0.243
##     alternative = two.sided
```

A sample of size 6 gives the same power for the *t*-test that a sample of size 10 does for the sign test. The ratio of these two sample sizes is called the *relative efficiency* of the two tests: in this case, the *t*-test is $10/6 = 1.67$ times more efficient. The data that you have are being used "more efficiently" by the *t*-test. It is possible to derive

the limiting relative efficiency of the *t* test relative to the sign test when the data are actually normal, as the sample size gets larger. This turns out not to depend on how far wrong the null is (as long as it is the same for both the *t*-test and the sign test). This "asymptotic relative efficiency" is $\pi/2 = 1.57$. Our relative efficiency for power 0.243, namely 1.67, was pretty close to this, even though our sample sizes 10 and 6 are not especially close to infinity. This says that, if your data are actually from a normal distribution, you do a lot better

Meaning, I forget how to do it. But it has something to do with looking at alternatives that are very close to the null.

to use the *t*-test than the sign test, because the sign test is wasteful of data (it only uses above/below rather than the actual values). If your data are *not* from a normal distribution, then the story can be very different. Of course you knew I would investigate this. There is a distribution called the "Laplace" or "double exponential" distribution, that has very long tails. The distribution is not in base R, but there is a package called `smoothmest` that contains a function `rdoublex` to generate random values from this distribution. So we're going to do a simulation investigation of the power of the sign test for Laplace data, by the same simulation technique that we did above. Like the normal, the Laplace distribution is symmetric, so its mean and median are the same (which makes our life easier).

If you've ever run into the exponential distribution, you'll recall that this is right skewed with a very long tail. The Laplace distribution looks like two of these glued back to back.

This is about the *only* way in which the normal and Laplace distributions are alike.

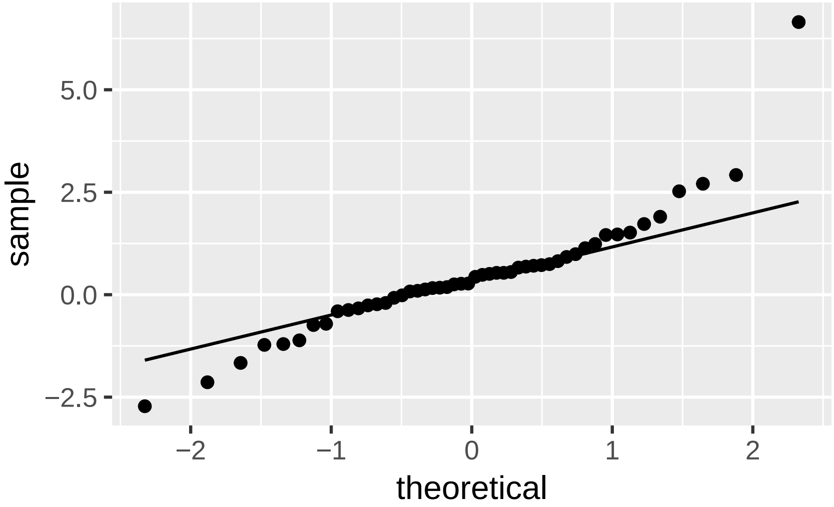
Let's test the hypothesis that the median is zero. We'll suppose that the true median is 0.5 (this is called `mu` in `rdoublex`). The first problem we run into is that we can't use `power.t.test` because they assume normal data, which we are far from having. So we have to do two simulations: one to simulate the power of the *t* test, and one to simulate the power of the sign test.

To simulate the *t* test, we first have to generate some Laplace data with the true mean of 0.5. We'll use a sample size of 50 throughout these simulations.

```
library(smoothmest)

## Loading required package: MASS

##
## Attaching package: 'MASS'

## The following object is masked from 'package:dplyr':
##
##     select

rl = rdoublex(50, mu = 0.5)
rl

##  [1] -0.33323285  0.70569291 -1.22513053
##  [4]  0.68517708  0.12778518  0.50749949
##  [7]  0.26700527  1.90236874  0.53288312
## [10] -0.37374732  0.27256566  0.53365929
## [13]  0.43581431 -0.01545866  0.18594908
## [16] -0.40403202  1.13540289  0.16137306
## [19] -0.23360644 -0.74050354  2.92089551
## [22] -2.72173880  0.48428815  1.23636045
## [25]  0.17078618  1.72456334  0.07903058
## [28]  0.25210411  0.09512810  2.52310082
## [31] -2.13629814  0.81851434  0.74615575
## [34] -0.26068744  2.70683355  1.46981530
## [37]  1.45646489 -0.20232517  6.65249860
## [40]  1.51575026 -0.07606399 -1.11338640
## [43] -1.20427995 -0.70986104 -1.66466321
## [46]  0.55346854  0.66091469  0.72100677
## [49]  0.92025176  0.98922656
```

This seems to have some unusual values, far away from zero:

```
tibble(rl) %>% ggplot(aes(sample = rl)) + stat_qq() +
    stat_qq_line()
```



You see the long tails compared to the normal.

Now, we feed these values into t.test and see whether we reject a null median of zero (at $\alpha = 0.05$):

```
tt = t.test(rl)
tt
```

```
##
##  One Sample t-test
##
## data:  rl
## t = 2.2556, df = 49, p-value = 0.0286
## alternative hypothesis: true mean is not equal to 0
## 95 percent confidence interval:
##  0.04959344 0.85981931
## sample estimates:
## mean of x
## 0.4547064
```

Or we can just pull out the P-value and even compare it to 0.05:

```
pval = tt$p.value
pval

## [1] 0.02859596

is.reject = (pval <= 0.05)
is.reject

## [1] TRUE
```

$

This one has a small P-value and so the null median of 0 should be (correctly) rejected.

We'll use these ideas to simulate the power of the *t*-test for these data, testing a mean of 0. This uses the same ideas as for any power simulation; the difference here is the true distribution:

```
pvals <- rerun(1000, rdoublex(50, mu = 0.5)) %>%
    map(~t.test(., mu = 0)) %>% map_dbl("p.value")
```

and then count them:

```
tibble(pvals) %>% count(pvals <= 0.05)

## # A tibble: 2 x 2
##   `pvals <= 0.05`     n
##   <lgl>           <int>
## 1 FALSE             304
## 2 TRUE              696
```

And now we simulate the sign test. Since what we want is a P-value from a vector, the easiest way to do this is to use `pval_sign0` from `smmr`, which returns exactly the two-sided P-value that we want, so that the procedure is a step simpler:

```
pvals_sign <- rerun(1000, rdoublex(50, mu = 0.5)) %>%
    map_dbl(~pval_sign0(0, .))
```

and then

```
tibble(pvals_sign) %>% count(pvals_sign <= 0.05)

## # A tibble: 2 x 2
##   `pvals_sign <= 0.05`     n
##   <lgl>                <int>
## 1 FALSE                  239
## 2 TRUE                   761
```

For data from this Laplace distribution, the power of this *t*-test is 0.696, but the power of the sign test on the same data is 0.761, *bigger*. For Laplace-distributed data, the sign test is *more* powerful than the *t*-test.

This is not to say that you will ever run into data that comes from the Laplace distribution. But the moral of the story is that the sign test *can* be more powerful than the *t*-test, under the right circumstances (and the above simulation is the "proof" of that statement). So a blanket statement like "the sign test is not very powerful" needs to be qualified a bit: when your data come from a sufficiently long-tailed distribution, the sign test can be more powerful relative to the *t*-test than you would think.

I finish by "unloading" the two packages that got loaded:

```
detach(package:smoothmest, unload = T)
detach(package:MASS, unload = T)
```

8.4 *Sugar in breakfast cereals*

The data for this question are in `http://www.utsc.utoronto.ca/~butler/c32/cereal-sugar.txt`. The story here is whether breakfast cereals marketed to children have a lot of sugar in them; in particular, whether they have more sugar on average than cereals marketed to adults.

(a) Read in the data (to R) and display the data set. Do you have a variable that distinguishes the children's cereals from the adults' cereals, and another that contains the amount of sugar?

Solution

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/cereal-sugar.txt"
cereals = read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   who = col_character(),
##   sugar = col_double()
## )
```

```
cereals
```

```
## # A tibble: 40 x 2
##    who      sugar
##    <chr>    <dbl>
##  1 children  40.3
##  2 children  55
##  3 children  45.7
##  4 children  43.3
##  5 children  50.3
##  6 children  45.9
##  7 children  53.5
##  8 children  43
##  9 children  44.2
## 10 children  44
## # ... with 30 more rows
```

The variable who is a categorical variable saying who the cereal is intended for, and the variable sugar says how much sugar each cereal has.

(b) Calculate the mean sugar content for each group of cereals (the adults' ones and the children's ones). Do they look similar or different?

Solution
group_by and summarize:

```
cereals %>% group_by(who) %>% summarize(sugar_mean = mean(sugar))
```

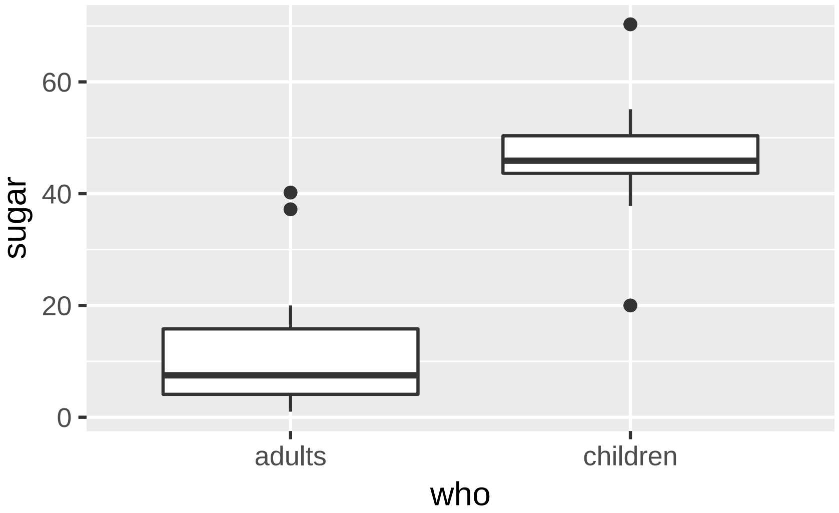
```
## # A tibble: 2 x 2
##   who      sugar_mean
##   <chr>         <dbl>
## 1 adults         10.9
## 2 children       46.6
```

These means look very different, though it would be better to look at a boxplot (coming up in a moment).

(c) Make side-by-side boxplots of the sugar contents of the two types of cereal. What do you see that is out of the ordinary?

Solution
The usual:

```
ggplot(cereals, aes(x = who, y = sugar)) + geom_boxplot()
```



I see outliers: two high ones on the adults' cereals, and one high and one low on the children's cereals.

My thought above about the means being very different is definitely supported by the medians being very different on the boxplots. We should have no trouble declaring that the "typical" amounts of sugar in the adults' and children's cereals are different.

(d) Explain briefly why you would not trust a two-sample *t*-test with these data. (That is, say what the problem is, and why it's a problem.)

Solution

The problem is the outliers (which is rather a giveaway), but the reason it's a problem is that the two-sample *t*-test assumes (approximately) normal data, and a normal distribution doesn't have outliers. Not only do you need to note the outliers, but you also need to say why the outliers cause a problem *in this case*. Anything less than that is not a complete answer.

(e) Run a suitable test to see whether the "typical" amount of sugar differs between adult's and children's cereals. Justify the test that you run. (You can use the version of your test that lives in a package, if that is easier for you.) What do you conclude, in the context of the data?

Solution

Having ruled out the two-sample *t*-test, we are left with Mood's median test. I didn't need you to build it yourself, so you can use package `smmr` to run it with:

```
library(smmr)
median_test(cereals, sugar, who)
```

```
## $table
##           above
## group      above below
##   adults       2    19
##   children    18     1
##
## $test
##        what        value
## 1 statistic 2.897243e+01
## 2        df 1.000000e+00
## 3   P-value 7.341573e-08
```

We conclude that there *is* a difference between the median amounts of sugar between the two groups of cereals, the P-value of 0.00000007 being extremely small.

Why did it come out so small? Because the amount of sugar was smaller than the overall median for almost all the adult cereals, and larger than the overall median for almost all the children's ones. That is, the children's cereals really do have more sugar.

Mood's median test doesn't come with a confidence interval (for the difference in population medians), because whether or not a certain difference in medians is rejected depends on what those medians actually are, and the idea of the duality of the test and CI doesn't carry over as we would like.

My daughter likes chocolate Cheerios, but she also likes Shredded Wheat and *Bran Flakes*. Go figure. (Her current favourite is Raisin Bran, even though she doesn't like raisins by themselves.)

Mood's median test is the test we should trust, but you might be curious about how the *t*-test stacks up here:

```
t.test(sugar ~ who, data = cereals)
```

```
##
##  Welch Two Sample t-test
##
## data:  sugar by who
## t = -11.002, df = 37.968, p-value =
## 2.278e-13
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -42.28180 -29.13925
## sample estimates:
##   mean in group adults
##               10.90000
## mean in group children
##               46.61053
```

The P-value is *even smaller*, and we have the advantage of getting a confidence interval for the difference in means: from about 30 to about 40 units less sugar in the adult cereals. Whatever the units were.

8.5 *Fear of math*

Two new short courses have been proposed for helping students who suffer from severe math phobia. The courses are labelled A and B. Ten students were randomly allocated to one of these two courses, and each student's score on a math phobia test was recorded after they completed their course. The math phobia test produces whole-number scores between 0 and 10, with a higher score indicating a greater fear of mathematics. The data can be found in link. We start with R for this question.

(a) Read in the data and check, however you like, that you have 10 observations, 5 from each course.

Solution

This doesn't need much comment:

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/mathphobia.txt"
math = read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   course = col_character(),
##   phobia = col_integer()
## )
```

```
math
```

```
## # A tibble: 10 x 2
##    course phobia
##    <chr>   <int>
##  1 a           8
##  2 a           7
##  3 a           7
##  4 a           6
##  5 a           6
##  6 b           9
##  7 b           8
##  8 b           7
##  9 b           2
## 10 b           1
```

This will do, counting the `a` and `b`. Or, to save yourself that trouble:

```
math %>% count(course)
```

```
## # A tibble: 2 x 2
##   course     n
##   <chr>  <int>
## 1 a          5
## 2 b          5
```

Five each. The story is to get the computer to do the grunt work for you, if you can make it do so. Other ways:

```
math %>% group_by(course) %>% summarize(count = n())
```

```
## # A tibble: 2 x 2
##   course count
##   <chr>  <int>
## 1 a          5
## 2 b          5
```

and this:

```
with(math, table(course))
```

```
## course
## a b
## 5 5
```

giving the same answer. Lots of ways.

Extra: there is an experimental design issue here. You might have noticed that each student did only *one* of the courses. Couldn't students do both, in a matched-pairs kind of way? Well, it's a bit like the kids learning to read in that if the first of the courses reduces a student's anxiety, the second course won't appear to do much good (even if it actually would have been helpful had the student done that one first). This is the same idea as the kids learning to read: once you've learned to read, you've learned to read, and learning to read a second way won't help much. The place where matched pairs scores is when you can "wipe out" the effect of one treatment before a subject gets the other one. We have an example of kids throwing baseballs and softballs that is like that: if you throw one kind of ball, that won't affect how far you can throw the other kind.

(b) Do a two-sample t-test to assess whether there is a difference in mean phobia scores after the students have taken the two courses. What do you conclude? (You have no *a priori* reason to suppose that a particular one of the tests will produce a higher mean than the other, so do a two-sided test.)

That is, before looking at the data. This is Latin. It's also the place that the Bayesian *prior distribution* comes from. The *posterior distribution* comes from the Latin *a posteriori*, which means *afterwards*, that is, after you have looked at the data.

Solution

A two-sided test is the default, so there is not much to do here:

```
t.test(phobia ~ course, data = math)

##
##  Welch Two Sample t-test
##
## data:  phobia by course
## t = 0.83666, df = 4.4199, p-value =
## 0.4456
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -3.076889  5.876889
## sample estimates:
## mean in group a mean in group b
##             6.8             5.4
```

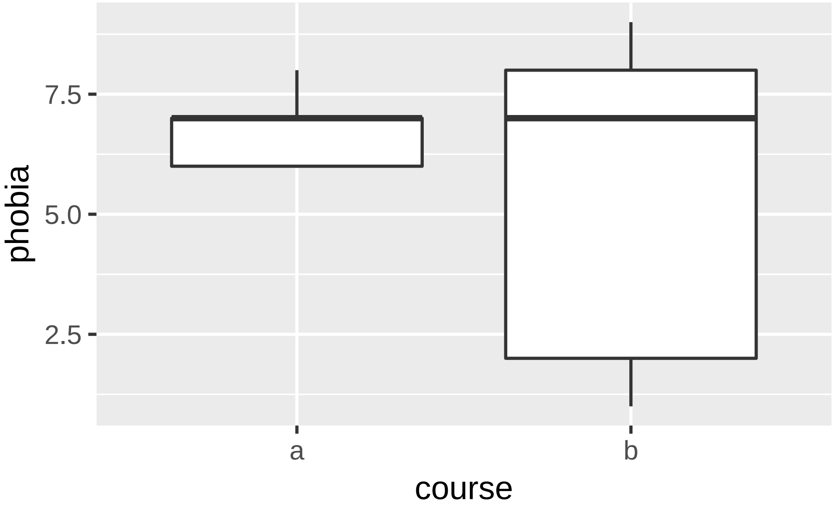
The P-value of 0.4456 is nowhere near less than 0.05, so there is no evidence at all that the

mean math phobia scores are different between the two courses.

(c) Draw boxplots of the math phobia scores for each group (one line of code). What is the most striking thing that you notice?

Solution

```
ggplot(math, aes(x = course, y = phobia)) + geom_boxplot()
```



Boxplot a is just weird. The bar across the middle is actually at the top, and it has no bottom. (Noting something sensible like this is enough.) Boxplot b is hugely spread out.

The two groups have very different spreads, but that is not a problem as long as we remember to do the Welch-Satterthwaite test that does not assume equal spreads. This is the default in R, so we are good, at least with that.

By way of explanation: the course a scores have a number of values equal so that the 3rd quartile and the median are the name, and also that the first quartile and the minimum value are the same:

```
tmp = math %>% filter(course == "a")
tmp %>% count(phobia)
```

```
## # A tibble: 3 x 2
##   phobia     n
##    <int> <int>
## 1      6     2
## 2      7     2
## 3      8     1
```

```
summary(tmp)
```

```
##     course              phobia
##  Length:5           Min.   :6.0
##  Class :character   1st Qu.:6.0
##  Mode  :character   Median :7.0
##                     Mean   :6.8
##                     3rd Qu.:7.0
##                     Max.   :8.0
```

The phobia scores from course A are two 6's, two 7's and an 8. The median and third quartile are both 7, and the first quartile is the same as the lowest value, 6.

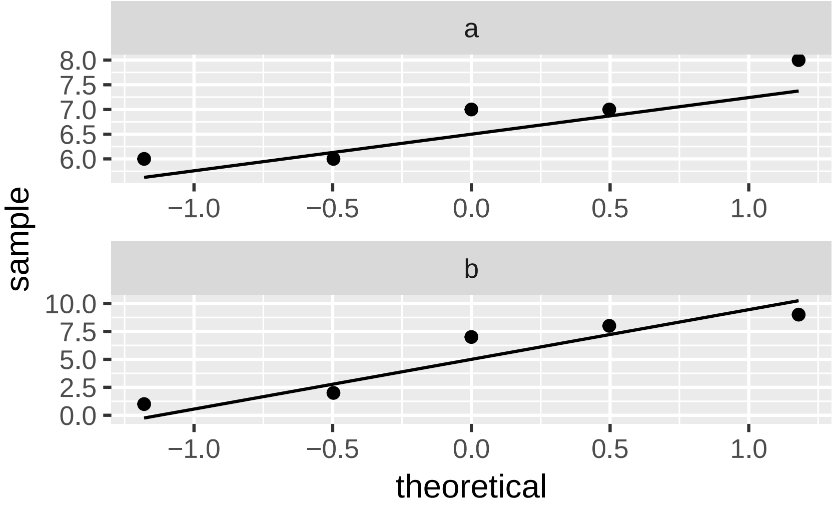
Technique note: I wanted to do two things with the phobia scores from course A: count up how many of each score, and show you what the five-number summary looks like. One pipe won't do this (the pipe "branches"), so I saved what I needed to use, before it branched, into a data frame tmp and then used tmp twice. Pipes are powerful, but not *all*-powerful.

(d) Explain briefly why a *t*-test would not be good for these data. (There are two things that you need to say.)

Solution

The easiest way to structure this is to ask yourself first what the *t*-test needs, and second whether you have it. The *t*-test assumes (approximately) normal data. The boxplot for group a doesn't even look symmetric, and the one for group b has an oddly asymmetric box. So I think the normality is in question here, and therefore another test would be better. (This is perhaps a bit glib of an answer, since there are only 5 values in each group, and so they can certainly look non-normal even if they actually are normal, but these values are all integers, so it is perhaps wise to be cautious.) We have the machinery to assess the normality for these, in one shot:

```
ggplot(math, aes(sample = phobia)) + stat_qq() +
    stat_qq_line() + facet_wrap(~course, ncol = 1,
    scales = "free")
```



I don't know what *you* make of those, but they both look pretty straight to me (and there are only five observations, so it's hard to judge). Course `b` maybe has a "hole" in it (three large values and two small ones). Maybe. I dunno. What I would *really* be worried about is outliers, and at least we don't have those. I mentioned in class that the t-tests are robust to non-normality. I ought to have expanded on that a bit: what really makes the t-test still behave itself with non-normality is when you have *large* samples, that is, when the Central Limit Theorem has had a chance to take hold. (That's what drives the normality not really being necessary in most cases.) But, even with small samples, exact normality doesn't matter so much. Here, we have two tiny samples, and so we have to insist a bit more, but only a bit more, on a more-or-less normal shape in each group. (It's kind of a double jeopardy in that the situation where normality matters most, namely with small samples, is where it's the hardest to judge, because samples of size 5 even from a normal distribution can look very non-normal.) But, the biggest threats to the t-test are big-time skewness and outliers, and we are not suffering too badly from those.

(e) Run a suitable test to compare the "typical" scores for the two courses. (You can use the version from a package rather than building your own.) What do you conclude?

Solution

This is an invite to use `smmr`:

```
library(smmr)
median_test(math, phobia, course)
```

```
## $table
##      above
## group above below
##     a     1     2
##     b     2     2
##
## $test
##        what     value
## 1 statistic 0.1944444
## 2        df 1.0000000
## 3   P-value 0.6592430
```

We are nowhere near rejecting equal medians; in fact, both courses are very close to 50–50 above and below the overall median.

If you look at the frequency table, you might be confused by something: there were 10 observations, but there are only $1+2+2+2=7$ in the table. This is because three of the observations were equal to the overall median, and had to be thrown away:

```
math %>% summarize(med = median(phobia))
```

```
## # A tibble: 1 x 1
##     med
##   <dbl>
## 1     7
```

```
math %>% count(phobia)
```

```
## # A tibble: 6 x 2
##   phobia     n
##    <int> <int>
## 1      1     1
## 2      2     1
## 3      6     2
## 4      7     3
## 5      8     2
## 6      9     1
```

The overall median was 7. Because the actual data were really discrete (the phobia scores could only be whole numbers), we risked losing a lot of our data when we did this test (and we didn't have much to begin with). The other thing to say is that with small sample sizes, the frequencies in the table have to be *very* lopsided for you to have a chance of rejecting the null. Something like this is what you'd need:

```
x = c(1, 1, 2, 6, 6, 6, 7, 8, 9, 10)
g = c(1, 1, 1, 1, 1, 2, 2, 2, 2, 2)
d = tibble(x, g)
median_test(d, x, g)
```

```
## $table
##      above
## group above below
##     1     0     3
##     2     4     0
##
## $test
##        what       value
## 1 statistic 7.000000000
## 2        df 1.000000000
## 3   P-value 0.008150972
```

I faked it up so that we had 10 observations, three of which were equal to the overall median. Of the rest, all the small ones were in group 1 and all the large ones were in group 2. This is lopsided enough to reject with, though, because of the small frequencies, there actually was a warning about "chi-squared approximation may be inaccurate".

There *was*, in the *chisq.test* inside *median-test*, but in *smmr* I didn't pass that warning back to the outside world.

8.6 Medical instructions

Do people understand medical instructions better at certain times of the day? In a study, students in a grade 12 class are randomly divided into two groups, A and B. All students see a video describing how to use an infant forehead thermometer. The students in Group A see the video at 8:30 am, while the students in Group B see the same video at 3:00 pm (on the same day). The next day, all the students are given a test on the material in the video (graded out of 100). The observed scores are in link (values separated by spaces).

(a) Read the data into R and display the (first ten) values.

Solution

Separated by spaces, so read_delim:

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/forehead.txt"
instr = read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   group = col_character(),
##   score = col_integer()
## )
```

```
instr
```

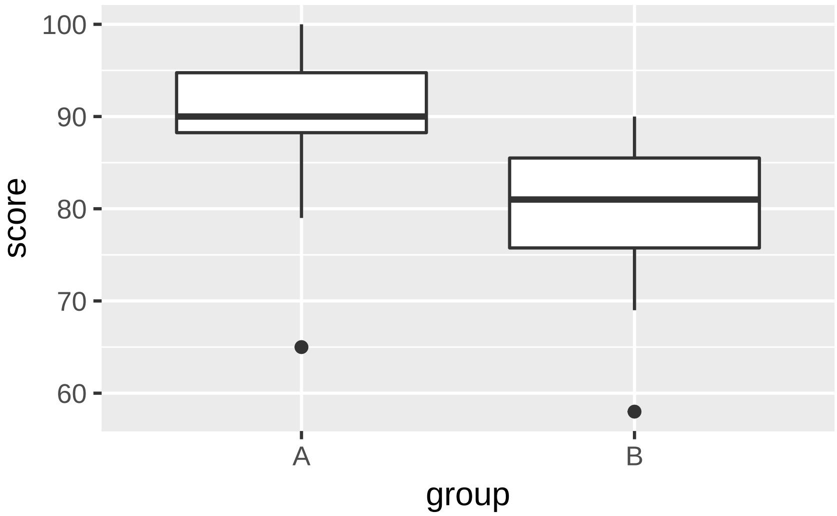
```
## # A tibble: 18 x 2
##    group score
##    <chr> <int>
##  1 A        88
##  2 A        89
##  3 A        79
##  4 A       100
##  5 A        98
##  6 A        89
##  7 A        65
##  8 A        94
##  9 A        95
## 10 A        91
## 11 B        87
## 12 B        69
## 13 B        78
## 14 B        79
## 15 B        83
## 16 B        90
## 17 B        85
## 18 B        58
```

(b) Obtain a suitable plot that will enable you to assess the assumptions for a two-sample *t*-test.

Solution

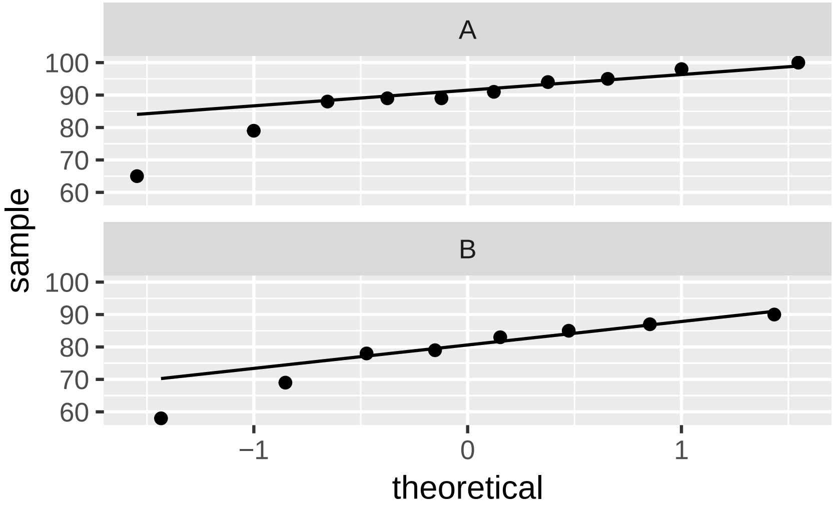
We need the values in each group to be approximately normally distributed. Side-by-side boxplots will do it:

```
ggplot(instr, aes(x = group, y = score)) + geom_boxplot()
```



or, if you like, separate (facetted) normal quantile plots, which I would do this way:

```
ggplot(instr, aes(sample = score)) + stat_qq() +
    stat_qq_line() + facet_wrap(~group, ncol = 1)
```



(c) Why might you have doubts about using a two-sample *t*-test here?

Solution

We are looking for non-normality in at least one of the groups. Here, both groups have an outlier at the low end that would be expected to pull the mean downward. I don't think there is left-skewness here, since there is no particular evidence of the high-end values being bunched up: the problem in both cases with normality is at the low end. One way or another, I'm expecting you to have noticed the outliers. Extra: last year, when I first drew the normal quantile plots, there was no `stat_qq_line`, so you had to imagine where the line went if you did it this way. Without the line, these plots look somewhat curved, which would have pointed to left-skewness, but now we see that the lowest observation is too low, and maybe the second-lowest one as well, while the other observations are just fine.

(d) Run Mood's median test as in class (*without* using smmr). What do you conclude, in the context of the data? What recommendation would you make about the time of day to see the video? (You might get a warning about "chisquared approximation being incorrect", which you can ignore here.)

Solution
The overall median first:

```
instr %>% summarize(med = median(score))
```

```
## # A tibble: 1 x 1
##     med
##   <dbl>
## 1  87.5
```

87.5, which is not equal to any of the data values (they are all integers). This will avoid any issues with values-equal-to-median later.

Then, create and save a table of the value by group and above/below median. You can count either above or below (it comes out equivalently either way):

```
tab = with(instr, table(group, score > 87.5))
tab
```

```
##
## group FALSE TRUE
##     A     2    8
##     B     7    1
```

Then, chi-squared test for independence (the null) or association of some kind (the alternative). The correct=F is saying not to do Yates's correction, so that it would come out the same if you were doing it by hand ("observed minus expected, squared, divided by expected" and all that stuff).

```
chisq.test(tab, correct = F)
```

```
## Warning in chisq.test(tab, correct = F): Chi-
## squared approximation may be incorrect
```

```
##
##  Pearson's Chi-squared test
##
## data:  tab
## X-squared = 8.1, df = 1, p-value =
## 0.004427
```

The P-value is 0.0044, which is (much) smaller than 0.05, and therefore you can reject independence and conclude association: that is, whether a student scores above or below the median depends on which group they are in, or, that the median scores are different for the two groups.

The warning is because the expected frequencies are on the small side (if you have done this kind of problem by hand, you might remember something about "expected frequencies less than 5". This is that.) Here, the P-value is so small that we can afford to have it be inaccurate by a bit and still not affect the conclusion, so I think we are safe.

As for which group is better, well, the easiest way is to go back to your boxplots and see that the median for group A (8:30 am) is substantially higher than for group B (3:00pm). But you can also see it from your frequency table, if you displayed it:

```
tab
```

```
##
## group FALSE TRUE
##     A     2    8
##     B     7    1
```

Most of the people in the 8:30 am group scored above the median, and most of the people in the 3:00 pm group scored below the median. So the scores at 8:30 am were better overall.

As I write this, it is just after 3:00 pm and I am about to make myself a pot of tea!

Extra: about that `correct=F` thing. There was a point of view for a long time that when you are dealing with a 2 × 2 table, you can get better P-values by, before squaring "observed minus expected", taking 0.5 away from the absolute value of the difference. This is called Yates's correction. It is in the same spirit as the "continuity correction" that you might have encountered in the normal approximation to the binomial, where in the binomial you have to have a whole number of successes, but the normal allows fractional values as well. In about the 1960s, the usefulness of Yates's correction was shot down, for general contingency tables. There is, however, one case where it *is* useful, and that is the case where the row totals and column totals are *fixed*.

What do I mean by that? Well, first let's look at a case where the totals are *not* all fixed. Consider a survey in which you want to see whether males and females agree or disagree on some burning issue of the day. You collect random samples of, say, 500 males and 500 females, and you count how many of them say Yes or No to your statement. You might get results like this:

To simplify things, we'll assume that everyone gave a Yes or a No answer, though you could add a column like *No answer* if you wanted to make it more realistic.

```
Yes  No  Total
Males    197 303   500
Females  343 157   500
Total    540 460  1000
```

In this table, the row totals must be 500, because you asked this many males and this many females, and each one must have answered something. The column totals, however, are not fixed: you didn't know, ahead of time, that 540 people would answer "yes". That was just the way the data turned out, and if you did another survey with the same design, you'd probably get a different number of people saying "yes".

For another example, let's go back to Fisher (yes, *that* Fisher). A "lady" of his acquaintance claimed to be able, by drinking a cup of tea with milk and sugar in it, whether the milk or the sugar had been added first. Fisher, or, more likely, his housekeeper, prepared 8 cups of tea, 4 with milk first and 4 with sugar first. The lady knew that four of the cups had milk first, and her job was to say which four. The results might have been like this:

```
Actual
Milk first  sugar first  Total
Lady   Milk first       3            1         4
says   sugar first      1            3         4
Total             4            4         8
```

This time, all of the row totals and all of the column totals must be 4, regardless of what the lady thinks. Even if she thinks 5 of the cups of tea actually had milk first, she is going to pick 4 of them to say that they have milk first, since she knows there are only 4. In this case, all of the row and column totals are fixed at 4, and the right analysis is called Fisher's Exact Test, based on the hypergeometric distribution. In a 2×2 table like this one, there is only one "degree of freedom", since as soon as you specify one of the frequencies, say the number of cups where the lady said milk first and they actually were milk first, you can work out the others. But, leaving that aside, the usual chi-squared analysis is a perfectly good approximation, especially if the frequencies are large, and especially if you use Yates's correction.

It is clear that Fisher must have been English, since he was able to get a publication out of drinking tea.

How does that apply to Mood's median test? Well, let's remind ourselves of the table we had:

```
tab
```

```
##
## group FALSE TRUE
##     A     2    8
##     B     7    1
```

We know how many students were in each group: 10 in group A and 8 in B. So the row totals are fixed. What about the columns? These are whether each observation was above or below the overall median. There were 18 observations altogether, so there *must* be 9 above and 9 below. So the column totals are fixed as well. All totals fixed, so we should be using Yates's correction. I didn't, because I wanted to keep things simple, but I should have done.

Except in the case of the previous problem, where there were multiple observations equal to the overall median. Which we ignore for the moment.

R's `chisq.test` by default *always* uses Yates's correction, and if you don't want it, you have to say `correct=F`. Which is why I have been doing so all through.

(e) Run Mood's median test on these data using my `smmr` package, and verify that you get the same answer.

Solution

Not much to it, since the data is already read in:

```
library(smmr)
median_test(instr, score, group)
```

```
## $table
##      above
## group above below
##     A     8     2
##     B     1     7
##
## $test
##        what       value
## 1 statistic 8.100000000
## 2        df 1.000000000
## 3   P-value 0.004426526
```

Identical, test statistic, degrees of freedom and P-value. The table of frequencies is also the same, just with columns rearranged. (In `smmr` I counted the number of values below the overall median, whereas in my build-it-yourself I counted the number of values above.)

9
Matched pairs t and sign test

```
library(tidyverse)

## -- Attaching packages ---- tidyverse 1.2.1 --

## v ggplot2 3.0.0     v purrr   0.2.5
## v tibble  1.4.2     v dplyr   0.7.6
## v tidyr   0.8.1     v stringr 1.3.1
## v readr   1.1.1     v forcats 0.3.0

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

library(smmr)
```

9.1 Measuring body fat

Athletes are concerned with measuring their body fat percentage. Two different methods are available: one using ultrasound, and the other using X-ray technology. We are interested in whether there is a difference in the mean body fat percentage as measured by these two methods, and if so, how big that difference is. Data on 16 athletes are at link.

(a) Explain briefly why a matched pairs analysis is more suitable for these data than a two-independent-samples analysis (using a two-sample *t*-test). You might find that looking at the data (clicking on the link) helps you figure this out.

Solution

The data file looks like this: `timinput{bodyft.txt}` The data are two measurements for each of the 16 athletes: that is, each athlete had their body fat percentage measured using *both* of the two methods. Extra: a two-sample *t* approach would be reasonable if one set of

16 athletes had been measured by X-ray and *another different* set of 16 athletes had been measured by ultrasound. (That is, if there had been 32 athletes in total, with each one randomly assigned to *one* of the measurement methods.) But that's not what happened. It is easy to measure one athlete's body fat percentage using both of the two methods, so a matched pairs design is easy to implement (as well as being better). If you use two independent samples (each athlete doing only one measurement method), you introduce an extra source of variability: athletes differ one from another in body fat, as well as differing possibly by measurement method. If you use a matched-pairs design, you remove the athlete-to-athlete differences, leaving only the differences due to measurement method.

(b) Read in the data and check that you have a sensible number of rows and columns.

Solution

This kind of thing. Since you looked at the data (didn't you?), you'll know that the values are separated by single spaces:

```
myurl = "http://www.utsc.utoronto.ca/~butler/c32/bodyfat.txt"
bodyfat = read_delim(myurl, " ")
```

```
## Parsed with column specification:
## cols(
##   athlete = col_integer(),
##   xray = col_double(),
##   ultrasound = col_double()
## )
```

```
bodyfat
```

```
## # A tibble: 16 x 3
##    athlete  xray ultrasound
##      <int> <dbl>      <dbl>
##  1       1  5          4.75
##  2       2  7          3.75
##  3       3  9.25       9
##  4       4 12         11.8
##  5       5 17.2       17
##  6       6 29.5       27.5
##  7       7  5.5        6.5
##  8       8  6          6.75
##  9       9  8          8.75
## 10      10  8.5        9.5
## 11      11  9.25       9.5
## 12      12 11          12
## 13      13 12          12.2
## 14      14 14          15.5
## 15      15 17          18
## 16      16 18          18.2
```

16 rows (athletes) and 3 columns, one for each measurement method and one labelling the athletes. All good.

Since 16 is not too much bigger than 10, I got the whole data frame here. (At least, I think that's the reason I got more than 10 rows.) In an R Notebook, you'll see the first ten rows as normal, with a button to click to see the other six.

(c) Carry out a suitable test to determine whether the means are the same or different. (At this point, obtain the R output including a P-value.)

Solution

Feed the two columns into `t.test` along with `paired=T`. This is a two-sided test, so we don't have to take any special steps for that. Note that we're back to the "old-fashioned" version of `t.test` that *does not* allow `data=`, so we have to go the `with` way:

```
with(bodyfat, t.test(xray, ultrasound, paired = T))
```

```
##
##  Paired t-test
##
## data:  xray and ultrasound
## t = -0.30801, df = 15, p-value = 0.7623
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.7425068  0.5550068
## sample estimates:
## mean of the differences
##                -0.09375
```

(d) What do you conclude from the test?

Solution

The P-value of 0.7623 is not at all small, so there is no way we can reject the null hypothesis. There is no evidence of a difference in means; we can act as if the two methods produce the same mean body fat percentage. That is to say, on this evidence we can use either method, whichever one is cheaper or more convenient. Extra: an informal way of seeing whether this is reasonable is to see how often

My hat stays on my head.

the first value of the pair is larger, and how often the second. If the null hypothesis is true, there should be about a 50–50 split, but if false, there should be a very uneven split. Here that would go like this:

```
with(bodyfat, table(xray > ultrasound))
```

```
##
## FALSE  TRUE
##    10     6
```

or like this:

```
bodyfat %>% count(xray > ultrasound)
```

```
## # A tibble: 2 x 2
##   ‘xray > ultrasound‘     n
##   <lgl>               <int>
## 1 FALSE                  10
## 2 TRUE                    6
```

6 times the X-ray value was bigger, and 10 times the ultrasound value was. A pretty even split, so it’s not surprising that we failed to reject the null. (You might recognize this as an informal version of the sign test.)

(e) Obtain a 95% confidence interval for the population mean difference. How is the interval consistent with your test?

Solution

You don’t even need to do any more coding: the test was two-sided, so just pick the confidence interval off the output above: -0.74 to 0.56. The interval includes both positive and negative values (or, 0 is inside the interval), so the difference could go either way. This is entirely consistent with not being able to reject the null.

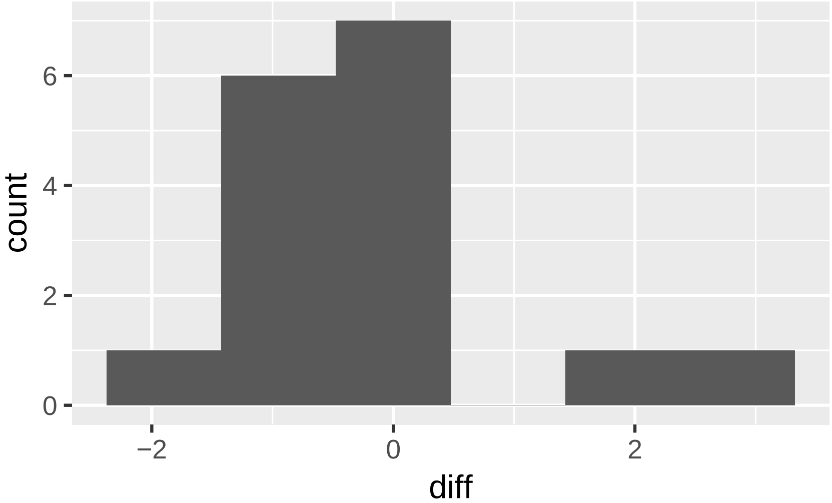
(f) Calculate the differences, and make a normal quantile plot of them. Is there any evidence that normality of differences fails? Explain briefly. (If we haven’t gotten to normal quantile plots in class when you read this, make a different plot to assess this issue.)

Solution

The smoothest way to do this is to use a pipeline: use a `mutate` to create the column of differences, and then pipe that into `ggplot`, omitting the data frame that would normally go first (the input data frame here is the new one with the differences in it, which doesn’t have a name). I’ll make a normal quantile plot in a moment, but if we haven’t talked about that yet, the plot to make is a histogram:

I learned yesterday that the Welsh word for *ironing* is *smwddio*, which seems weird until you say it out loud: it sounds like *smoothio*.

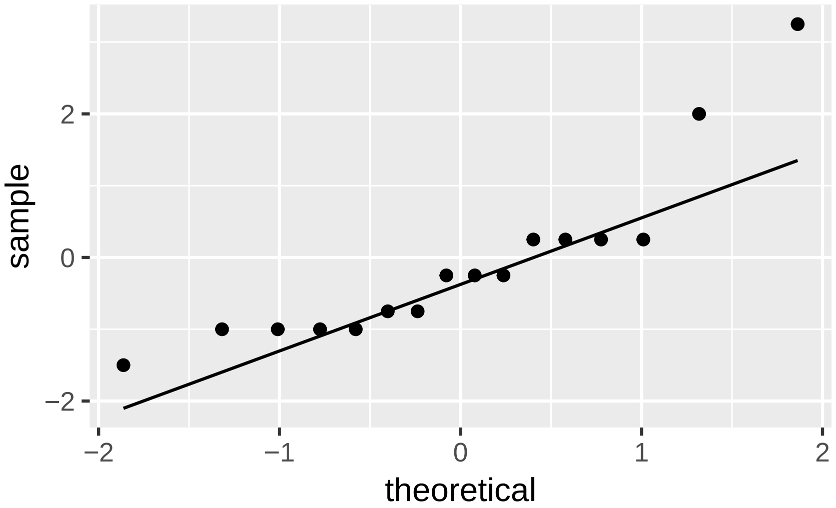
```
bodyfat %>% mutate(diff = xray - ultrasound) %>%
    ggplot(aes(x = diff)) + geom_histogram(bins = 6)
```



I don't know whether you'd call that "approximately normal" or not. We are in kind of a double-bind with this one: the sample size is small, so normality matters, but with a small sample, the data might not look very normal. It's kind of skewed right, but most of the evidence for the skewness is contained in those two observations with difference 2 and above, which is pretty flimsy evidence for anything. (In the normal quantile plot below, the suggestion is that those two observations really are a bit too large. It's easier to tell there.)

Below, I'm repeating the calculation of the differences, which is inefficient. If I'm going to draw two graphs of the differences, the right way is to calculate the differences *and save the data frame*, then use that new data frame twice. But you're probably only going to draw either the histogram or the normal quantile plot, not both, so you can use the appropriate one of my two bits of code. The normal quantile plot:

```
bodyfat %>% mutate(diff = xray - ultrasound) %>%
    ggplot(aes(sample = diff)) + stat_qq() + stat_qq_line()
```



This is showing a little evidence of skewness or outliers (depending on your point of view: either is good). The lowest and highest values are both too high, and the pattern of points on the plot is kind of curved (which would be evidence of skewness). Or you could say that the two highest values are too high, with the other values being more or less in line (that would be evidence of outliers at the upper end). I like outliers better than skewness, since those bottom-end points are not far off the line. I would also accept "no substantial problems", if you can make the case that those two highest points are not too far off the line. With only 16 observations as we have here, even truly normal data would stray off the line a bit.

As ever, your explanation is more important than your conclusion. Can you justify what you think?

If you took your differences the other way around, as `ultrasound` minus `xray`, your plot will also be the other way around, with the "outliers" at the bottom. That's good too.

Where this is going (which I didn't ask you) is whether or not we trust the result of the matched pairs test. I would say that the test is so far from being significant, and the failure of normality is not gross, that it is hard to imagine *any* alternative test coming up with a significant result. So I would be happy to trust this paired t-test.

9.2 *Throwing baseballs and softballs*

Can students throw a baseball farther than a softball? A statistics class, containing 24 students, went out to a football field to try to answer this question. Each student warmed up and then threw each type of ball as far as they could. The order of ball types was randomized: some students threw the baseball first, and some threw the softball first. (A softball is bigger than a baseball, so we might expect that a softball would be harder to throw a long way than a baseball.) The data are in `http://www.utsc.utoronto.ca/~butler/c32/throw.txt` in three columns: the first is a number identifying the student, the second is the distance thrown with the baseball (in yards) and the third is the distance thrown with the softball (also in yards).

(a) Read the data into R. You'll need to supply some names to the columns.

Solution

This kind of thing:

```
myurl = "http://www.utsc.utoronto.ca/~butler/c32/throw.txt"
throws = read_delim(myurl, " ", col_names = c("student",
    "baseball", "softball"))
```

```
## Parsed with column specification:
## cols(
##   student = col_integer(),
##   baseball = col_integer(),
##   softball = col_integer()
## )
```

```
throws
```

```
## # A tibble: 24 x 3
##    student baseball softball
##      <int>    <int>    <int>
##  1       1       65       57
##  2       2       90       58
##  3       3       75       66
##  4       4       73       61
##  5       5       79       65
##  6       6       68       56
##  7       7       58       53
##  8       8       41       41
##  9       9       56       44
## 10      10       70       65
## # ... with 14 more rows
```

This is one of those times where we have to tell R what names to give the columns. Or you can put `col_names=F` and leave the columns called `X1, X2, X3` or whatever they end up as.

(b) Calculate a column of differences, baseball minus softball, *in* the data frame.

Solution

Add it to the data frame using mutate. Use the right-arrow assignment to create what I called throws2 below, or put something like throws2= on the beginning of the line. Your choice.

```
throws2 <- throws %>% mutate(diff = baseball -
    softball)
```

(c) Carry out a sign test in R, testing the null hypothesis that the median difference is zero, against the alternative that it is greater than zero. Obtain a P-value. Your option whether you use smmr or not.

Solution

I think using smmr is way easier, so I'll do that first. There is even a shortcut in that the null median defaults to zero, which is exactly what we want here:

```
library(smmr)
sign_test(throws2, diff)
```

```
## $above_below
## below above
##     2    21
##
## $p_values
##   alternative      p_value
## 1       lower 9.999971e-01
## 2       upper 3.302097e-05
## 3   two-sided 6.604195e-05
```

We want, this time, the upper-tailed one-sided test, since we want to prove that students can throw a baseball a *longer* distance than a softball. Thus the P-value we want is 0.000033.

To build it yourself, you know the steps by now. First step is to count how many differences are greater and less than zero:

```
table(throws2$diff > 0)
```

```
##
## FALSE  TRUE
##     3    21
```

or

```
table(throws2$diff < 0)
```

```
##
## FALSE  TRUE
##    22     2
```

or, since we have things in a data frame,

```
throws2 %>% count(diff > 0)
```

```
## # A tibble: 2 x 2
##   ‘diff > 0‘     n
##   <lgl>      <int>
## 1 FALSE          3
## 2 TRUE          21
```

or count those less than zero. I'd take any of those.

Note that these are *not all the same*. One of the differences is in fact exactly zero. The technically right thing to do with the zero difference is to throw it away (leaving 23 differences with 2 negative and 21 positive). I would take that, or 2 or 3 negative differences out of 24 (depending on whether you count "greater than zero" or "less than zero"). We hope that this won't make a material difference to the P-value; it'll make some difference, but won't (we hope) change the conclusion about whether to reject.

Second step is to get a P-value for whichever one of those you got, from the appropriate binomial distribution.

The P-value is the probability of getting 21 (or 22) positive differences out of 24 (or 23) or more, since this is the end of the distribution we should be at if the alternative hypothesis is correct. Thus any of these will get you a defensible P-value:

```
sum(dbinom(21:23, 23, 0.5))
```

```
## [1] 3.302097e-05
```

```
sum(dbinom(22:24, 24, 0.5))
```

```
## [1] 1.7941e-05
```

```
sum(dbinom(21:24, 24, 0.5))
```

```
## [1] 0.0001385808
```

```
sum(dbinom(0:2, 23, 0.5))
```

```
## [1] 3.302097e-05
```

```
sum(dbinom(0:2, 24, 0.5))
```

```
## [1] 1.7941e-05
```

```
sum(dbinom(0:3, 24, 0.5))
```

```
## [1] 0.0001385808
```

The first and fourth of those are the same as smmr (throwing away the exactly-median value).

As we hoped, there is no *material* difference here: there is no doubt with any of these possibilities that we will reject a median difference of zero in favour of a median difference greater than zero.

9.3 *Throwing baseballs and softballs, again*

Previously, you carried out a sign test to determine whether students could throw a baseball farther than a softball. This time, we will calculate a confidence interval for the median difference baseball minus softball, using the results of sign tests.

(a) Read the data into R from link, giving appropriate names to the columns, and add a column of differences.

Solution

I did it this way, combining the reading of the data with the calculation of the differences in *one* pipe:

```
myurl = "http://www.utsc.utoronto.ca/~butler/c32/throw.txt"
throws = read_delim(myurl, " ", col_names = c("student",
    "baseball", "softball")) %>% mutate(diff = baseball -
    softball)
```

```
## Parsed with column specification:
## cols(
##   student = col_integer(),
##   baseball = col_integer(),
##   softball = col_integer()
## )
```

```
throws
```

```
## # A tibble: 24 x 4
##    student baseball softball  diff
##      <int>    <int>    <int> <int>
##  1       1       65       57     8
##  2       2       90       58    32
##  3       3       75       66     9
##  4       4       73       61    12
##  5       5       79       65    14
##  6       6       68       56    12
##  7       7       58       53     5
##  8       8       41       41     0
##  9       9       56       44    12
## 10      10       70       65     5
## # ... with 14 more rows
```

(b) Use smmr to find a 95% confidence interval for the median difference.

Solution
ci_median, with 95% being the default confidence level:

```
ci_median(throws, diff)
```

```
## [1] 2.002930 8.999023
```

2 to 9. The ends of a CI for the median will be data values, which are all whole numbers, so round off that 8.999.

(c) What function in smmr will run a two-sided sign test and return only the P-value? Check that it works by testing whether the median difference for your data is zero or different from zero.

Solution
The rest of the way, we are trying to reproduce that confidence interval by finding it ourselves. The function is called pval_sign. If you haven't run into it before, in R Studio click on Packages, find smmr, and click on its name. This will bring up package help, which includes a list of all the functions in the package, along with a brief description of what each one does. (Clicking on a function name brings up the help for that function.) Let's check that it works properly by repeating the previous sign_test and verifying that pval_sign gives the same thing:

```
sign_test(throws, diff, 0)
```

```
## $above_below
## below above
##     2    21
##
## $p_values
##   alternative      p_value
## 1       lower 9.999971e-01
## 2       upper 3.302097e-05
## 3   two-sided 6.604195e-05
```

```
pval_sign(0, throws, diff)
```

```
## [1] 6.604195e-05
```

The P-values are the same (for the two-sided test) and both small, so the median difference is not zero.

(d) Based on your P-value, do you think 0 is inside the confidence interval or not? Explain briefly.

Solution

Absolutely not. The median difference is definitely not zero, so zero cannot be in the confidence interval. Our suspicion, from the one-sided test from earlier, is that the differences were mostly positive (people could throw a baseball farther than a softball, in most cases). So the confidence interval ought to contain only positive values. I ask this because it drives what happens below.

(e) Obtain a 95% confidence interval for the population median difference, baseball minus softball, using a trial-and-error procedure that determines whether a number of possible medians are inside or outside the CI.

Solution

I've given you a fair bit of freedom to tackle this as you wish. Anything that makes sense is good: whatever mixture of mindlessness, guesswork and cleverness that you want to employ. The most mindless way to try some values one at a time and see what you get, eg.:

```
pval_sign(1, throws, diff)
```

```
## [1] 0.001489639
```

```
pval_sign(5, throws, diff)
```

```
## [1] 1.168188
```

So median 1 is outside and median 5 is inside the 95% interval. Keep trying values until you've figured out where the lower and upper ends of the interval are: where the P-values cross from below 0.05 to above, or vice versa.

Something more intelligent is to make a long list of potential medians, and get the P-value for each of them, eg.:

```
d = tibble(my.med = seq(0, 20, 2))
d %>% mutate(pvals = map_dbl(my.med, ~pval_sign(.,
    throws, diff)))
```

```
## # A tibble: 11 x 2
##    my.med      pvals
##     <dbl>      <dbl>
##  1      0 0.0000660
##  2      2 0.0525
##  3      4 0.839
##  4      6 0.678
##  5      8 0.210
##  6     10 0.0227
##  7     12 0.00149
##  8     14 0.0000660
##  9     16 0.0000359
## 10     18 0.00000572
## 11     20 0.00000298
```

2 is just inside the interval, 8 is also inside, and 10 is outside. Some closer investigation:

```
d = tibble(my.med = seq(0, 2, 0.5))
d %>% mutate(pvals = map_dbl(my.med, ~pval_sign(.,
    throws, diff)))
```

```
## # A tibble: 5 x 2
##   my.med     pvals
##    <dbl>     <dbl>
## 1    0   0.0000660
## 2    0.5 0.000277
## 3    1   0.00149
## 4    1.5 0.0227
## 5    2   0.0525
```

The bottom end of the interval actually is 2, since 2 is inside and 1.5 is outside.

```
d = tibble(my.med = seq(8, 10, 0.5))
d %>% mutate(pvals = map_dbl(my.med, ~pval_sign(.,
    throws, diff)))
```

```
## # A tibble: 5 x 2
##   my.med  pvals
##    <dbl>  <dbl>
## 1    8   0.210
## 2    8.5 0.152
## 3    9   0.0525
## 4    9.5 0.0227
## 5   10   0.0227
```

The top end is 9, 9 being inside and 9.5 outside.

Since the data values are all whole numbers, I think this is accurate enough. The most sophisticated way is the "bisection" idea we saw before. We already have a kickoff for this, since we found, mindlessly, that 1 is outside the interval on the low end and 5 is inside, so the lower limit has to be between 1 and 5. Let's try halfway between, ie. 3:

```
pval_sign(3, throws, diff)
```

```
## [1] 0.3833103
```

Inside, so lower limit is between 1 and 3. This can be automated, thus:

```
lo = 1
hi = 3
while (abs(hi - lo) > 0.1) {
    try = (lo + hi)/2
    ptry = pval_sign(try, throws, diff)
    if (ptry > 0.05) {
        hi = try
    } else {
        lo = try
    }
}
c(lo, hi)
```

```
## [1] 1.9375 2.0000
```

The difficult bit is to decide whether the value `try` becomes the new `lo` or the new `hi`. If the P-value for the median of `try` is greater than 0.05, `try` is inside the interval, and it becomes the new `hi`; otherwise it's outside and becomes the new `lo`. Whatever the values are, `lo` is always outside the interval and `hi` is always inside, and they move closer and closer to each other.

At the other end of the interval, `lo` is inside and `hi` is outside, so there is a little switching around within the loop. For starting values, you can be fairly mindless: for example, we know that 5 is inside and something big like 20 must be outside:

```
lo = 5
hi = 20
while (abs(hi - lo) > 0.1) {
    try = (lo + hi)/2
    ptry = pval_sign(try, throws, diff)
    if (ptry > 0.05) {
        lo = try
    } else {
        hi = try
    }
}
c(lo, hi)
```

```
## [1] 8.984375 9.042969
```

The interval goes from 2 to (as calculated here) about 9. (This is apparently the same as `ci_median` in `smmr` got.) `ci_median` uses the bisection method with a smaller "tolerance" than we did, so its answer is more accurate. It looks as if the interval goes from 2 to 9: that is, students can throw a baseball on average between 2 and 9 feet further than they can throw a softball.

9.4 *Changes in salary*

A company is growing and would like to attract more employees. The company would like to advertise that salaries there are increasing. To do this, the company randomly samples 20 employees that have been working there since January 2016, and for each of these employees, records their salary in January 2016 and January 2017. The data, with salaries in thousands of dollars, are in link.

(a) Read the data into R and demonstrate that you have two salaries for each of 20 employees.

Solution

Looking at the file, we see that the values are separated by exactly one space:

```
my_url = "https://www.utsc.utoronto.ca/~butler/c32/salaryinc.txt"
salaries = read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   employee = col_character(),
##   jan2016 = col_double(),
##   jan2017 = col_double()
## )
```

```
salaries
```

```
## # A tibble: 20 x 3
##    employee jan2016 jan2017
##    <chr>      <dbl>   <dbl>
##  1 A           36      39.5
##  2 B           41.2    47
##  3 C           40      45
##  4 D           42.8    49
##  5 E           51      57.8
##  6 F           50.5    54
##  7 G           56      62
##  8 I           57.8    69.9
##  9 J           62      66.8
## 10 K           65.5    71
## 11 L           66      72
## 12 M           68.9    74
## 13 N           71      80
## 14 O           72.3    79
## 15 P           74.6    80
## 16 Q           77      83.1
## 17 R           79.9    82.5
## 18 S           81      92
## 19 T           83.2    85
## 20 U           90     101
```

There are 20 employees (rows), and two columns of salaries: for each employee in the data set, their salary in January 2016 and in January 2017 (thus, two salaries for each employee).

(b) To compare the salaries, explain briefly why a matched-pairs test would be better than a two-sample test.

Solution

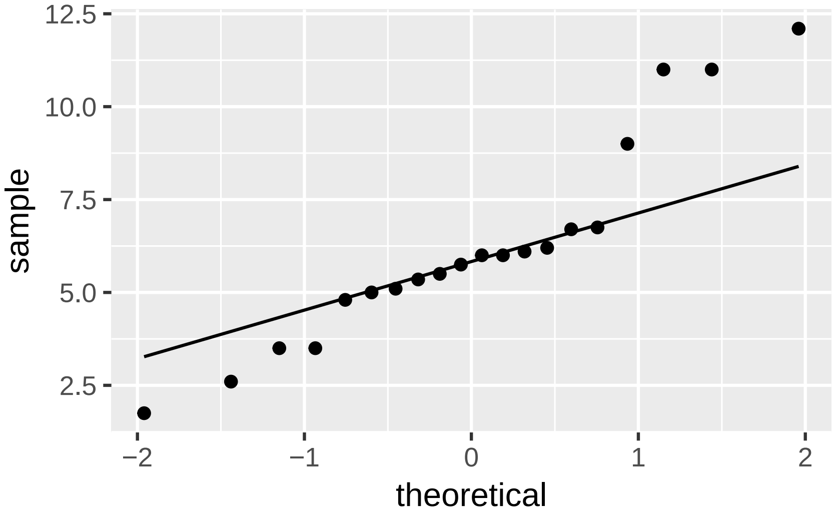
A matched-pairs test would be better because we have two observations (salaries) for each subject (employee). A two-sample test would be appropriate if we had two separate sets of employees, one set with their salaries recorded in 2016 and the other with their salaries recorded in 2017. That is not what we have here. You can go after this either way: why a matched-pairs approach is appropriate, or why a two-sample approach is not (or a bit of both).

(c) Make a suitable graph to assess the assumptions for a matched-pairs *t*-test. What does your graph tell you?

Solution

This requires thought first before you do any coding (and this is the reason for this one being four points). What has to be at least approximately normally distributed is the set of *differences*, salary at one time point minus the salary at the other, for each employee. The individual salaries don't have to be normally distributed at all. We don't have the differences here, so we have to calculate them first. The smoothest way is to make a pipeline:

```
salaries %>% mutate(diff = jan2017 - jan2016) %>%
    ggplot(aes(sample = diff)) + stat_qq() + stat_qq_line()
```



A couple of coding notes: (i) you can take the differences 2016 minus 2017 if you like (then they will tend to be negative), (ii) `ggplot` used in a pipeline like this does *not* have a data frame first (the data frame used is the nameless output from the `mutate`, with the differences in it).

Also, there's no problem doing the `mutate`, saving that, and then feeding the saved data frame into `ggplot`. If you find that clearer, go for it.

As for what I see: I think those points get a bit far from the line at the high and low ends: the high values are too high and the low values are too low, which is to say that we have outliers at both ends, or the distribution has long tails (either way of saying it is good).

The important conclusion here is whether these differences are normal *enough* to trust a matched pairs t-test here. We have a sample of size 20, so the central limit theorem will help us some, but you can reasonably say that these tails are too long and that we should not trust a matched-pairs t-test.

I actually wanted you to practice doing a matched-pairs t-test anyway, hence my comment in the next part, but the result is probably not *so* trustworthy.

(d) Carry out a suitable matched-pairs t-test on these data. (If you thought in the previous part that this was the wrong thing to do, do it anyway for the purposes of this assignment.) What do you conclude?

Solution

The company is trying to prove that salaries are *increasing* over time, so we need a one-sided alternative. Following through the procedure, even though you may not trust it much:

```
with(salaries, t.test(jan2016, jan2017, alternative = "less",
    paired = T))

##
##  Paired t-test
##
## data:  jan2016 and jan2017
## t = -10.092, df = 19, p-value =
## 2.271e-09
## alternative hypothesis: true difference in means is less than 0
## 95 percent confidence interval:
##       -Inf -5.125252
## sample estimates:
## mean of the differences
##                  -6.185
```

You could also have the years the other way around, in which case the alternative has to be the other way around as well:

```
with(salaries, t.test(jan2017, jan2016, alternative = "greater",
    paired = T))

##
##  Paired t-test
##
## data:  jan2017 and jan2016
## t = 10.092, df = 19, p-value =
## 2.271e-09
## alternative hypothesis: true difference in means is greater than 0
## 95 percent confidence interval:
##  5.125252      Inf
## sample estimates:
## mean of the differences
##                   6.185
```

Or, if you saved the data frame with the differences in it, do a one-sample test on those, again making sure that you get the `alternative` right. I didn't save it, so I'm calculating the differences again:

```
salaries %>% mutate(diff = jan2017 - jan2016) %>%
    with(., t.test(diff, mu = 0, alternative = "greater"))
```

```
##
##  One Sample t-test
##
## data:  diff
## t = 10.092, df = 19, p-value =
## 2.271e-09
## alternative hypothesis: true mean is greater than 0
## 95 percent confidence interval:
##  5.125252      Inf
## sample estimates:
## mean of x
##     6.185
```

Whichever way you do it, the P-value is the same 2.271×10^{-9}, which is a whole lot less than 0.05, so there is no doubt at all that salaries are increasing.

(Your intuition ought to have expected something like this, because everyone's 2017 salary appears to be greater than their 2016 salary.)

Extra: you might be feeling that we ought to be doing a matched-pairs sign test, which you could do this way:

```
library(smmr)
salaries %>% mutate(diff = jan2017 - jan2016) %>%
    sign_test(diff, 0)
```

```
## $above_below
## below above
##     0    20
##
## $p_values
##   alternative      p_value
## 1       lower 1.000000e+00
## 2       upper 9.536743e-07
## 3   two-sided 1.907349e-06
```

and then take the "upper" P-value, which is in the same ballpark as the one from the *t*-test. So the salaries really are increasing, whether you believe the *t*-test or not. And note that *every single employee's salary increased*.

(Again, the "missing" data frame in `sign_test` is the nameless one with the differences in it.)

(e) The company would like to estimate *how much* salaries are increasing, on average. Obtain some output that will enable the company to assess this, and tell the CEO which piece of the output they should look at.

Solution

A confidence interval. 95% is fine. As before, we have to run `t.test` again because we ran a one-sided test and a confidence interval for us is two-sided:

```
with(salaries, t.test(jan2017, jan2016, paired = T))
```

```
##
##  Paired t-test
##
## data:  jan2017 and jan2016
## t = 10.092, df = 19, p-value =
## 4.542e-09
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  4.902231 7.467769
## sample estimates:
## mean of the differences
##                   6.185
```

Between about $5,000 and about $7,500. This is what to tell the CEO.

9.5 *Body fat revisited*

Athletes are concerned with measuring their body fat percentage. Two different methods are available: one using ultrasound, and the other using X-ray technology. We are interested in whether there is a difference in the mean body fat percentage as measured by these two methods, and if so, how big that difference is. Data on 16 athletes are at link.

We saw this data set before.

(a) Read in the data again.

Solution

This kind of thing. Since you looked at the data (didn't you?), you'll know that the values are separated by single spaces:

```
myurl = "http://www.utsc.utoronto.ca/~butler/c32/bodyfat.txt"
bodyfat = read_delim(myurl, " ")
```

```
## Parsed with column specification:
## cols(
##   athlete = col_integer(),
##   xray = col_double(),
##   ultrasound = col_double()
## )
```

```
bodyfat
```

```
## # A tibble: 16 x 3
##    athlete  xray ultrasound
##      <int> <dbl>      <dbl>
##  1       1  5          4.75
##  2       2  7          3.75
##  3       3  9.25       9
##  4       4 12         11.8
##  5       5 17.2       17
##  6       6 29.5       27.5
##  7       7  5.5        6.5
##  8       8  6          6.75
##  9       9  8          8.75
## 10      10  8.5        9.5
## 11      11  9.25       9.5
## 12      12 11         12
## 13      13 12         12.2
## 14      14 14         15.5
## 15      15 17         18
## 16      16 18         18.2
```

(b) Calculate the differences, and make a normal quantile plot of them. Is there any evidence that normality of differences fails? Explain briefly.

Solution

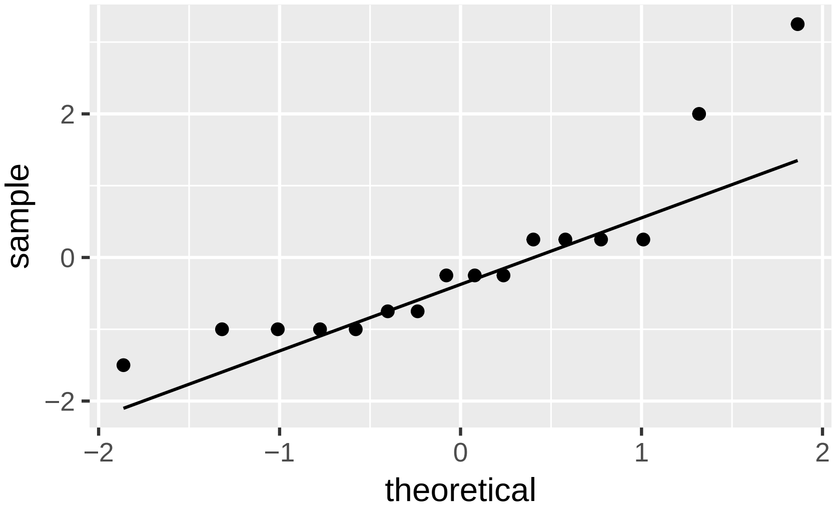
This is a good place to look ahead. We'll need the differences in two places, most likely: first for the normal quantile plot, and second for the matched-pairs sign test. So we should calculate and save them first:

```
bodyfat2 <- bodyfat %>% mutate(diff = xray - ultrasound)
```

I seem to be using a 2 on the end to name my dataframe-with-differences, but you can use whatever name you like.

Then, not forgetting to use the data frame that we just made:

```
ggplot(bodyfat2, aes(sample = diff)) + stat_qq() +
    stat_qq_line()
```



This is showing a little evidence of skewness or outliers (depending on your point of view: either is good). The lowest and highest values are both too high, and the pattern of points on the plot is kind of curved (which would be evidence of skewness). Or you could say that the two highest values are too high, with the other values being more or less in line (that would be evidence of outliers at the upper end). I like outliers better than skewness, since those bottom-end points are not far off the line. I would also accept "no substantial problems", if you can make the case that those two highest points are not too far off the line. With only 16 observations as we have here, even truly normal data would stray off the line a bit.

As ever, your explanation is more important than your conclusion. Can you justify what you think?

If you took your differences the other way around, as `ultrasound` minus `xray`, your plot will also be the other way around, with the "outliers" at the bottom. That's good too.

(c) Previously, we did a matched-pairs *t*-test for these data. In the light of your normal quantile plot, do you think that was a good idea? Explain briefly.

Solution

We are looking for the differences to be approximately normal, bearing in mind that we have a sample of size 16, which is not that large. Say what you think here; the points, if I were giving any here, would be for the way in which you support it. The comment I made before when we did a matched-pairs *t*-test was that the P-value was so large and non-significant that it was hard to imagine any other test giving a significant result. Another way of saying that is that I considered these differences to be "normal enough", given the circumstances. You might very well take a different view. You could say that these differences are clearly not normal, and that the sample size of 16 is not large enough to get any substantial help from the Central Limit Theorem. From that point of view, running the *t*-test is clearly not advisable.

(d) Use the sign test appropriately to compare the two methods for measuring body fat. (Use `smmr` if you wish.) What do you conclude, as ever in the context of the data?

Solution

That means using a sign test to test the null hypothesis that the median difference is zero, against the alternative that it is not zero. (I don't see anything here to indicate that we are looking only for positive or only for negative differences, so I think two-sided is right. You need some reason to do a one-sided test, and there isn't one here.)

Remembering again to use the data frame that has the differences in it:

```
sign_test(bodyfat2, diff, 0)
```

```
## $above_below
## below above
##    10     6
##
## $p_values
##   alternative   p_value
## 1       lower 0.2272491
## 2       upper 0.8949432
## 3   two-sided 0.4544983
```

The two-sided P-value is 0.4545, so we are nowhere near rejecting the null hypothesis that the median difference is zero. There is no evidence that the two methods for measuring body fat show any difference on average.

The table of aboves and belows says that there were 6 positive differences and 10 negative ones. This is not far from an even split, so the lack of significance is entirely what we would expect.

Extra: this is the same conclusion that we drew the last time we looked at these data (with a matched-pairs *t*-test). That supports what I said then, which is that the *t*-test was so far from being significant, that it could be very wrong without changing the conclusion. That is what seems to have happened.

10
Normal quantile plots

```
library(tidyverse)
```

```
## -- Attaching packages ---- tidyverse 1.2.1 --
```

```
## v ggplot2 3.0.0     v purrr   0.2.5
## v tibble  1.4.2     v dplyr   0.7.6
## v tidyr   0.8.1     v stringr 1.3.1
## v readr   1.1.1     v forcats 0.3.0
```

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

10.1 Lengths of heliconia flowers

The tropical flower *Heliconia* is fertilized by hummingbirds, a different species for each variety of Heliconia. Over time, the lengths of the flowers and the form of the hummingbirds' beaks have evolved to match each other. The length of the Heliconia flower is therefore an important measurement. Does it have a normal distribution for each variety?

The data set at `http://www.utsc.utoronto.ca/~butler/c32/heliconia.csv` contains the lengths (in millimetres) of samples of flowers from each of three varieties of Heliconia: *bihai*, *caribaea* red, and *caribaea* yellow.

(a) Read the data into R. There are different numbers of length measurements for each variety. How does this show up in the data frame? (Look at all the rows, not just the first ten.)

Solution

The usual `read_csv`:

```
heliconia = read_csv("heliconia.csv")
```

```
## Parsed with column specification:
## cols(
##   bihai = col_double(),
##   caribaea_red = col_double(),
##   caribaea_yellow = col_double()
## )
```

I suggested to look at *all* the rows. Here's why:

```
heliconia %>% print(n = Inf)
```

```
## # A tibble: 23 x 3
##    bihai caribaea_red caribaea_yellow
##    <dbl>        <dbl>           <dbl>
##  1  47.1         41.9            36.8
##  2  46.8         42.0            37.0
##  3  46.8         41.9            36.5
##  4  47.1         43.1            36.1
##  5  46.7         41.5            36.0
##  6  47.4         41.7            35.4
##  7  46.4         39.8            38.1
##  8  46.6         40.6            37.1
##  9  48.1         39.6            35.2
## 10  48.3         42.2            36.8
## 11  48.2         40.7            36.7
## 12  50.3         37.9            35.7
## 13  50.1         39.2            36.0
## 14  46.3         37.4            34.6
## 15  46.9         38.2            34.6
## 16  48.4         38.1            NA
## 17  NA           38.1            NA
## 18  NA           38.0            NA
## 19  NA           38.8            NA
## 20  NA           38.2            NA
## 21  NA           38.9            NA
## 22  NA           37.8            NA
## 23  NA           38.0            NA
```

The varieties with fewer values have missings (NAs) attached to the end. This is because all the columns in a data frame have to have the same number of values. (The missings won't impact what we do below — we get a warning but not an error, and the plots are the same as they would be without the missings — but you might be aesthetically offended by them, in which case you can read what I do later on.)

(b) Make a normal quantile plot for the variety *bihai*.

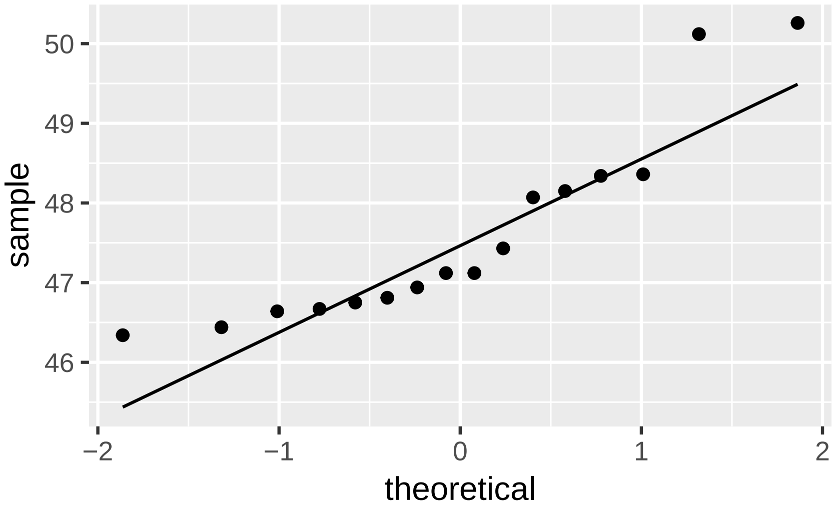
Solution

There's a certain amount of repetitiveness here (that we work around later):

```
ggplot(heliconia, aes(sample = bihai)) + stat_qq() +
    stat_qq_line()
```

```
## Warning: Removed 7 rows containing non-finite
## values (stat_qq).
```

```
## Warning: Removed 7 rows containing non-finite
## values (stat_qq_line).
```



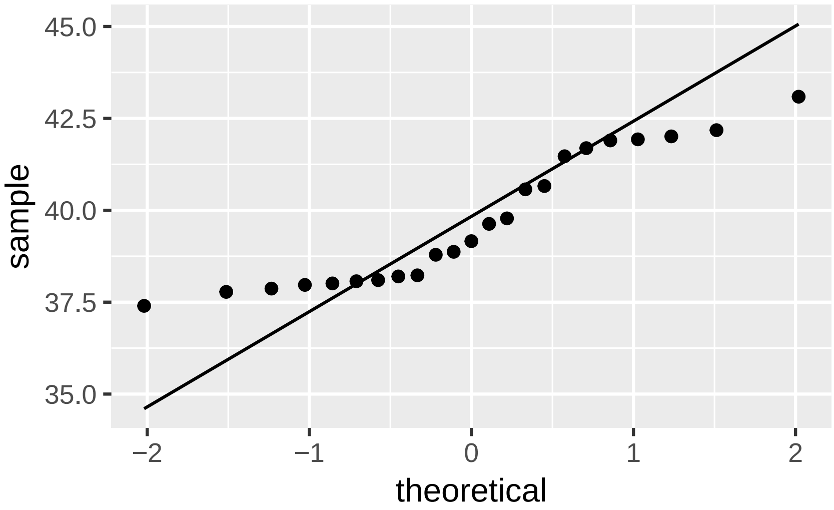
I'm saving the comments until we've seen all three.

(c) Make a normal quantile plot for the variety *Caribaea* red (note that the variable name in the data frame has an underscore in it).

Solution

Same idea again:

```
ggplot(heliconia, aes(sample = caribaea_red)) +
    stat_qq() + stat_qq_line()
```



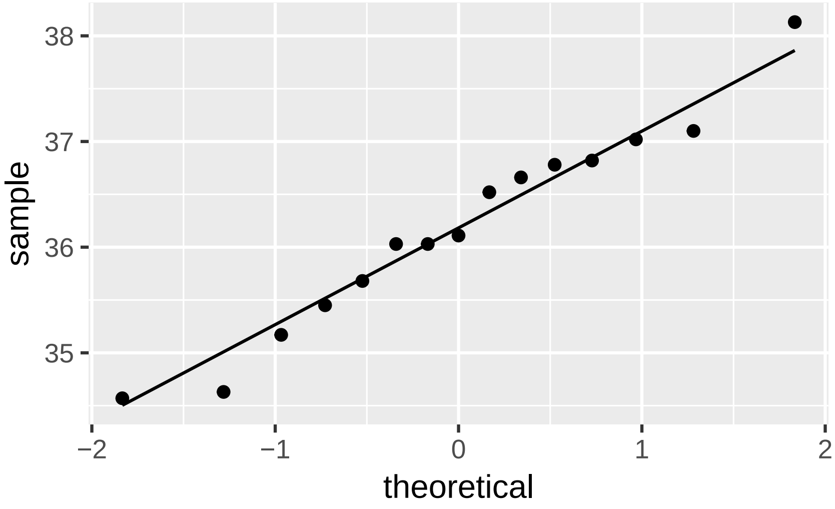
(d) Make a normal quantile plot for the variety *Caribaea* yellow (this also has an underscore in it).

Solution
And, one more time:

```
ggplot(heliconia, aes(sample = caribaea_yellow)) +
    stat_qq() + stat_qq_line()
```

```
## Warning: Removed 8 rows containing non-finite
## values (stat_qq).
```

```
## Warning: Removed 8 rows containing non-finite
## values (stat_qq_line).
```



I did a lot of copying and pasting there.

(e) Which of the three varieties is closest to having a normal distribution? Explain (very) briefly.

Solution

Look at the three plots, and see which one stays closest to the line. To my mind, this is clearly the last one, *Caribaea* yellow. So your answer ought to be "*Caribaea* yellow, because the points are closest to the line". This, I would say, is acceptably close to normal, so using a t-test here would be fine. The answer "the last one" is not quite complete, because I asked you which *variety*, so your answer needs to name a variety.

(f) For each of the two other varieties, apart from the one you mentioned in the last part, describe briefly how their distributions fail to be normal.

Solution

Let's look at *bihai* first. I see this one as an almost classic curve: the points are above the line, then below, then above again. If you look at the data scale (y-axis), the points are too bunched up to be normal at the bottom, and too spread out at the top: that is, skewed to the *right*. You might also (reasonably) take the view that the points at the bottom are close to the line (not sure about the very smallest one, though), but the points at the top are farther away, so that what we have here is two outliers at the top. I'm OK with that. It's often difficult to distinguish between skewness and outliers (at the end of the long tail). What you conclude can often depend on how you look. We also had to look at the second plot, *caribaea* red. This is a rather strange one: the points veer away from the line at the ends, but look carefully: it is *not* outliers at both ends, but rather the points are *too bunched up* to be normal at both ends: that is, the distribution has *short tails* compared to the normal. It is something more like a uniform distribution, which has no tails at all, than a normal distribution, which won't have outliers but it *does* have some kind of tails. So, "short tails". Extra: that's all you needed, but I mentioned above that you might have been offended aesthetically by those missing values that were not really missing. Let's see if we can do this aesthetically. As you might expect, it uses several of the tools from the "tidyverse". First, tidy the data. The three columns of the data frame are all lengths, just lengths of different things, which need to be labelled. This is `gather` from `tidyr`.

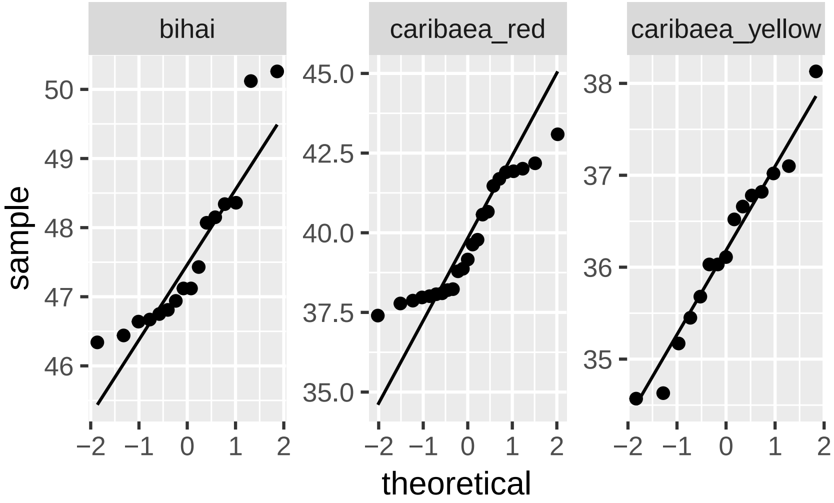
```
heliconia.long = heliconia %>% gather(variety,
    length, bihai:caribaea_yellow, na.rm = T)
heliconia.long
```

```
## # A tibble: 54 x 2
##    variety length
##  * <chr>    <dbl>
##  1 bihai     47.1
##  2 bihai     46.8
##  3 bihai     46.8
##  4 bihai     47.1
##  5 bihai     46.7
##  6 bihai     47.4
##  7 bihai     46.4
##  8 bihai     46.6
##  9 bihai     48.1
## 10 bihai     48.3
## # ... with 44 more rows
```

This is now aesthetic as well as tidy: all those NA lines have gone (you can check that there are now $16 + 23 + 15 = 54$ rows of actual data, as there should be).

Now, how to get a normal quantile plot for each variety? This is facet_wrap on the end of the ggplot again.

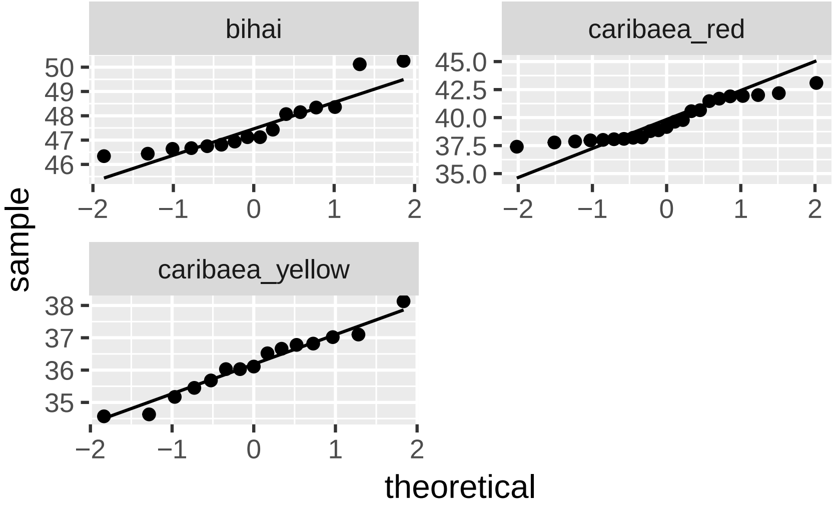
```
ggplot(heliconia.long, aes(sample = length)) +
    stat_qq() + stat_qq_line() + facet_wrap(~variety,
    scale = "free")
```



These are a bit elongated vertically. The scale="free" allows a different vertical scale for each plot (otherwise there would be one vertical scale for all three plots); I decided that was best here since the typical lengths for the three varieties are different. *Caribaea* yellow is more or less straight, *bihai* has outliers (and may also be curved), *caribaea* red has that peculiar S-bend shape.

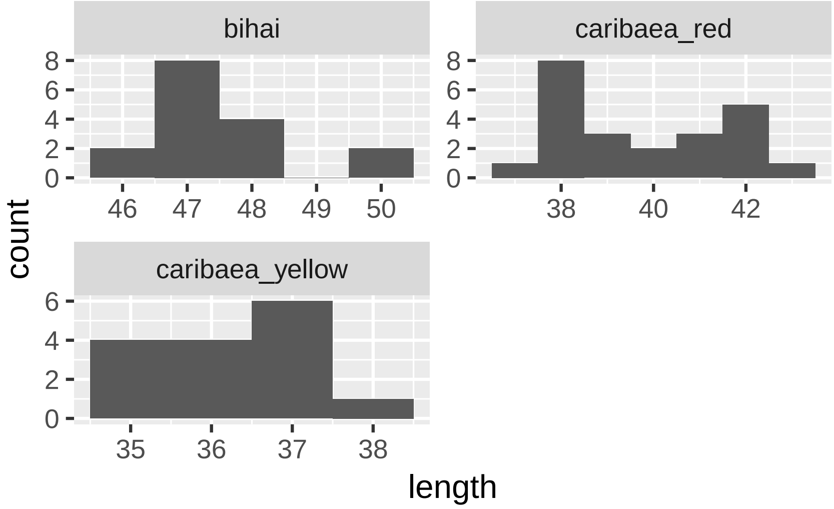
I didn't really like the vertical elongation. I'd rather have the plots be almost square, which they would be if we put them in three cells of a 2×2 grid. facet_wrap has nrow and ncol which you can use one or both of to make this happen. This creates an array of plots with two columns and as many rows as needed:

```
ggplot(heliconia.long, aes(sample = length)) +
    stat_qq() + stat_qq_line() + facet_wrap(~variety,
    scale = "free", ncol = 2)
```



I think the square plots make it easier to see the shape of these: curved, S-bend, straightish. Almost the same code will get a histogram for each variety, which I'll also make squarish:

```
ggplot(heliconia.long, aes(x = length)) + geom_histogram(binwidth = 1) +
    facet_wrap(~variety, scale = "free", ncol = 2)
```



bihai has those two outliers, *caribaea* red has no tails to speak of (or you might say "it's bimodal", which would be another explanation of the pattern on the normal quantile plot), and *caribaea* yellow is shoulder-shruggingly normal (I looked at that and said, "well, I *guess*

If you have studied a thing called kurtosis, the fourth moment about the mean, you'll know that this measures *both* tail length *and* peakedness, so a short-tailed distribution also has a strong peak. Or, maybe, in this case, two strong peaks.

it's normal".) After you've looked at the normal quantile plots, you see what a crude tool a histogram is for assessing normality.

10.2 *Ferritin and normality*

In the lecture notes, we looked at some data on different athletes from the Australian Institute of Sport. This data set can be found at `http://www.utsc.utoronto.ca/~butler/c32/ais.txt`. Recall that the values are separated by *tabs*. In this question, we will assess one of the variables in the data set for normality.

(a)[1] Read the data set into R. (Only one point since you can copy from the lecture notes.)

Solution

`read_tsv` is the right thing:

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/ais.txt"
athletes = read_tsv(my_url)
```

```
## Parsed with column specification:
## cols(
##   Sex = col_character(),
##   Sport = col_character(),
##   RCC = col_double(),
##   WCC = col_double(),
##   Hc = col_double(),
##   Hg = col_double(),
##   Ferr = col_integer(),
##   BMI = col_double(),
##   SSF = col_double(),
##   ‘%Bfat‘ = col_double(),
##   LBM = col_double(),
##   Ht = col_double(),
##   Wt = col_double()
## )
```

```
athletes
```

```
## # A tibble: 202 x 13
##    Sex   Sport   RCC   WCC    Hc    Hg  Ferr
##    <chr> <chr> <dbl> <dbl> <dbl> <dbl> <int>
##  1 fema~ Netb~  4.56  13.3  42.2  13.6    20
##  2 fema~ Netb~  4.15   6    38    12.7    59
##  3 fema~ Netb~  4.16   7.6  37.5  12.3    22
##  4 fema~ Netb~  4.32   6.4  37.7  12.3    30
##  5 fema~ Netb~  4.06   5.8  38.7  12.8    78
##  6 fema~ Netb~  4.12   6.1  36.6  11.8    21
##  7 fema~ Netb~  4.17   5    37.4  12.7   109
##  8 fema~ Netb~  3.8    6.6  36.5  12.4   102
##  9 fema~ Netb~  3.96   5.5  36.3  12.4    71
## 10 fema~ Netb~  4.44   9.7  41.4  14.1    64
## # ... with 192 more rows, and 6 more
## #   variables: BMI <dbl>, SSF <dbl>,
## #   ‘%Bfat‘ <dbl>, LBM <dbl>, Ht <dbl>,
## #   Wt <dbl>
```

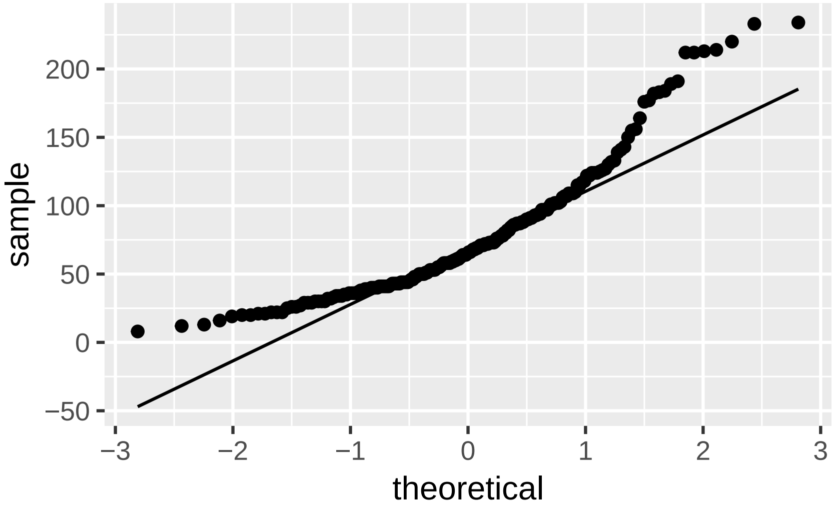
I listed the data to check that I had it right, but I didn't ask you to. (If you didn't have it right, that will show up soon enough.)

(b)[3] One of the variables, `Ferr`, is a measurement of Ferritin for each athlete. Obtain a normal quantile plot of the Ferritin values, for all the athletes together. What do you conclude about the shape of the distribution? Explain briefly.

Solution

As you would expect:

```
ggplot(athletes, aes(sample = Ferr)) + stat_qq() +
    stat_qq_line()
```



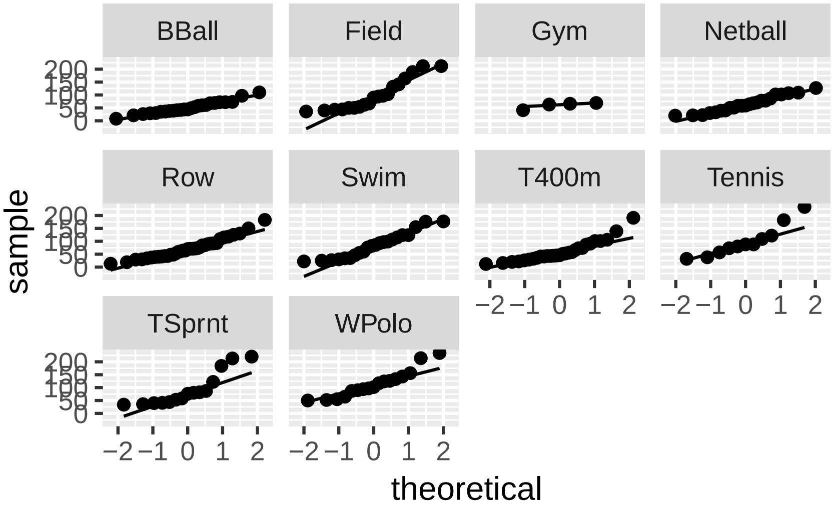
This is almost a classic right skew: the values are too bunched up at the bottom and too spread out at the top. The curved shape should be making you think "skewed" and then you can work out which way it's skewed.

(c)[3] It is possible that the shape you found in the previous part is because the athletes from all the different sports were mixed together. Use `ggplot` to obtain one normal quantile plot for each sport, collected together on one plot.

Solution

Your previous plot had all the sports mixed together. To that you add something that will put each sport in its own facet:

```
ggplot(athletes, aes(sample = Ferr)) + stat_qq() +
    stat_qq_line() + facet_wrap(~Sport)
```



(d)[2] Looking at the plots in the previous part, would you say that the Ferritin values for each sport individually have a more normal shape than they do for all the sports together? Explain briefly.

Solution

There are a couple of ways you can go, and as ever I'm looking mostly for consistency of argument. The two major directions you can go are (i) most of these plots are still curved the same way as the previous one, and (ii) they are mostly straighter than they were before. Possible lines of argument include that pretty much all of these plots are right-skewed still, with the same upward-opening curve. Pretty much the only one that doesn't is Gymnastics, for which there are only four observations, so you can't really tell. So, by this argument, Ferritin just *does* have a right-skewed distribution, and breaking things out by sport doesn't make much difference to that. Or, you could go another way and say that the plot of all the data together was *very* curved, and these plots are much less curved, that is to say, much less skewed. Some of them, such as basketball and netball, are almost straight, and they are almost normally distributed. Some of the distributions, such as track sprinting (`TSprnt`), are definitely still right-skewed, but not as seriously so as before. Decide what you think and then discuss how you see it.

11
Analysis of variance

```
library(tidyverse)
```

```
## -- Attaching packages ---- tidyverse 1.2.1 --
```

```
## v ggplot2 3.0.0     v purrr   0.2.5
## v tibble  1.4.2     v dplyr   0.7.6
## v tidyr   0.8.1     v stringr 1.3.1
## v readr   1.1.1     v forcats 0.3.0
```

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

11.1 *Movie ratings and lengths*

Before a movie is shown in theatres, it receives a "rating" that says what kind of material it contains. link explains the categories, from G (suitable for children) to R (anyone under 17 must be accompanied by parent/guardian). In 2011, two students collected data on the length (in minutes) and the rating category, for 15 movies of each rating category, randomly chosen from all the movies released that year. The data are at link.

(a) Read the data into R, and display (some of) what you read in.

Solution

`read_csv`:

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/movie-lengths.csv"
movies = read_csv(my_url)
```

```
## Parsed with column specification:
## cols(
##   length = col_integer(),
##   rating = col_character()
## )
```

```
movies
```

```
## # A tibble: 60 x 2
##    length rating
##     <int> <chr>
##  1     25 G
##  2     75 G
##  3     88 G
##  4     63 G
##  5     76 G
##  6     97 G
##  7     68 G
##  8     82 G
##  9     98 G
## 10     74 G
## # ... with 50 more rows
```

Something that looks like a length in minutes, and a rating.

(b) Count how many movies there are of each rating.

Solution

```
movies %>% count(rating)
```

```
## # A tibble: 4 x 2
##   rating     n
##   <chr>  <int>
## 1 G         15
## 2 PG        15
## 3 PG-13     15
## 4 R         15
```

Fifteen of each rating. (It's common to have the same number of observations in each group, but not necessary for a one-way ANOVA.)

(c) Carry out an ANOVA and a Tukey analysis (if warranted).

Solution

ANOVA first:

```
length.1 = aov(length ~ rating, data = movies)
summary(length.1)
```

```
##             Df Sum Sq Mean Sq F value
## rating       3  14624    4875   11.72
## Residuals   56  23295     416
##               Pr(>F)
## rating      4.59e-06 ***
## Residuals
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
```

This P-value is 0.00000459, which is way less than 0.05.

Having rejected the null (which said "all means equal"), we now need to do Tukey, thus:

```
TukeyHSD(length.1)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = length ~ rating, data = movies)
##
## $rating
##                diff        lwr       upr
## PG-G      26.333333   6.613562 46.053104
## PG-13-G   42.800000  23.080229 62.519771
## R-G       30.600000  10.880229 50.319771
## PG-13-PG  16.466667  -3.253104 36.186438
## R-PG       4.266667 -15.453104 23.986438
## R-PG-13  -12.200000 -31.919771  7.519771
##              p adj
## PG-G     0.0044541
## PG-13-G  0.0000023
## R-G      0.0007379
## PG-13-PG 0.1327466
## R-PG     0.9397550
## R-PG-13  0.3660019
```

Cast your eye down the `p adj` column and look for the ones that are significant, here the first three. These are all comparisons with the G ("general") movies, which are shorter on average than the others (which are not significantly different from each other).

If you like, you can make a table of means to verify that:

```
movies %>% group_by(rating) %>% summarize(mean = mean(length))
```

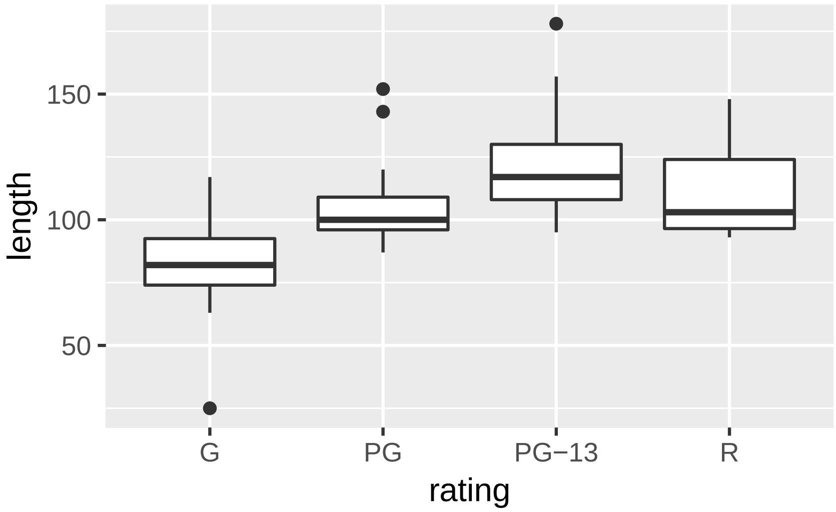
```
## # A tibble: 4 x 2
##   rating  mean
##   <chr>  <dbl>
## 1 G       80.6
## 2 PG      107.
## 3 PG-13   123.
## 4 R       111.
```

When we do this problem in SAS, you'll see the Tukey get handled a different way, one that you might find more appealing.

(d) Make a graph to assess whether this ANOVA is trustworthy. Discuss your graph and its implications briefly.

Solution
The obvious graph is a boxplot:

```
ggplot(movies, aes(x = rating, y = length)) +
    geom_boxplot()
```



For ANOVA, we are looking for approximately normal distributions within each group and approximately equal spreads. Without the outliers, I would be more or less happy with that, but the G movies have a low outlier that would pull the mean down and the PG and PG-13 movies have outliers that would pull the mean up. So a comparison of means might make the differences look more significant than they should. Having said that, you could also say that the ANOVA is *very* significant, so even considering the effect of the outliers, the differences between G and the others are still likely to be significant.

Extra: the way to go if you don't trust the ANOVA is (as for the two-sample t) the Mood's median test. This applies to any number of groups, and works in the same way as before:

```
library(smmr)
median_test(movies, length, rating)
```

```
## $table
##        above
## group   above below
##   G         2    13
##   PG        7     7
##   PG-13    12     3
##   R         8     6
##
## $test
##        what        value
## 1 statistic 13.752380952
## 2        df  3.000000000
## 3   P-value  0.003262334
```

Still significant, though not quite as small a P-value as before (which echoes our thoughts about what the outliers might do to the means). If you look at the table above the test results, you see that the G movies are mostly shorter than the overall median, but now the PG-13 movies are mostly *longer*. So the picture is a little different.

Mood's median test does not naturally come with something like Tukey. What you can do is to do all the pairwise Mood's median tests, between each pair of groups, and then adjust to allow for your having done several tests at once. I thought this was generally useful enough that I put it into smmr under the name pairwise_median_test:

```
pairwise_median_test(movies, length, rating)
```

```
## # A tibble: 6 x 4
##   g1    g2      p_value adj_p_value
##   <chr> <chr>     <dbl>       <dbl>
## 1 G     PG    0.00799      0.0479
## 2 G     PG-13 0.0000590    0.000354
## 3 G     R     0.0106       0.0635
## 4 PG    PG-13 0.0106       0.0635
## 5 PG    R     0.715        4.29
## 6 PG-13 R     0.273        1.64
```

You can ignore those (adjusted) P-values rather stupidly bigger than 1. These are not significant.

There are two significant differences in median length: between G movies and the two flavours of PG movies. The G movies are significantly shorter (as you can tell from the boxplot), but the difference between G and R movies is no longer significant (a change from the regular ANOVA).

You may be puzzled by something in the boxplot: how is it that the G movies are significantly shorter than the PG movies, but not significantly shorter than the R movies, *when the difference in medians between G and R movies is bigger*? In Tukey, if the difference in means is bigger, the P-value is smaller. The resolution to this puzzle, such as it is, is that Mood's median test is not directly comparing the medians of the groups (despite its name); it's counting values above and below a *joint* median, which might be a different story.

Actually, this doesn't always work if the sample sizes in each group are different. If you're comparing two small groups, it takes a *very large* difference in means to get a small P-value. But in this case the sample sizes are all the same.

11.2 Deer and how much they eat

Do adult deer eat different amounts of food at different times of the year? The data in link are the weights of food (in kilograms) consumed by randomly selected adult deer observed at different times of the year (in February, May, August and November). We will assume that these were different deer observed in the different months. (If the same animals had been observed at different times, we would have been in the domain of "repeated measures", which would require a different analysis, beyond the scope of this course.)

(a) Read the data into R, and calculate numbers of observations and the median amounts of food eaten each month.

Solution
The usual stuff for data values separated by spaces:

```
myurl = "http://www.utsc.utoronto.ca/~butler/c32/deer.txt"
deer = read_delim(myurl, " ")
```

```
## Parsed with column specification:
## cols(
##   month = col_character(),
##   food = col_double()
## )
```

and then, recalling that `n()` is the handy way of getting the number of observations in each group:

```
deer %>% group_by(month) %>% summarize(n = n(),
    med = median(food))
```

```
## # A tibble: 4 x 3
##   month     n   med
##   <chr> <int> <dbl>
## 1 Aug       6  4.7
## 2 Feb       5  4.8
## 3 May       6  4.35
## 4 Nov       5  5.2
```

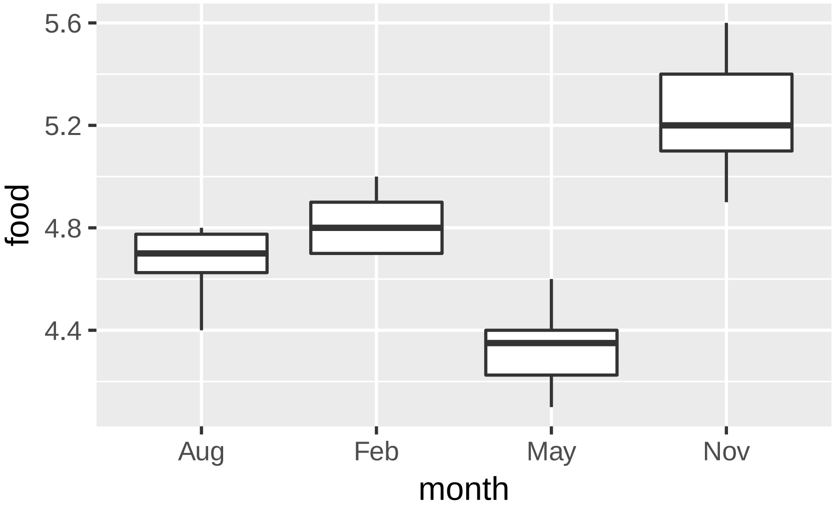
When you want the number of observations *plus* some other summaries, as here, the group-by and summarize idea is the way, using `n()` to get the number of observations in each group. `count` counts the number of observations per group when you *only* have grouping variables.

The medians differ a bit, but it's hard to judge without a sense of spread, which the boxplots (next) provide. November is a bit higher and May a bit lower.

(b) Make side-by-side boxplots of the amount of food eaten each month. Comment briefly on what you see.

Solution

```
ggplot(deer, aes(x = month, y = food)) + geom_boxplot()
```

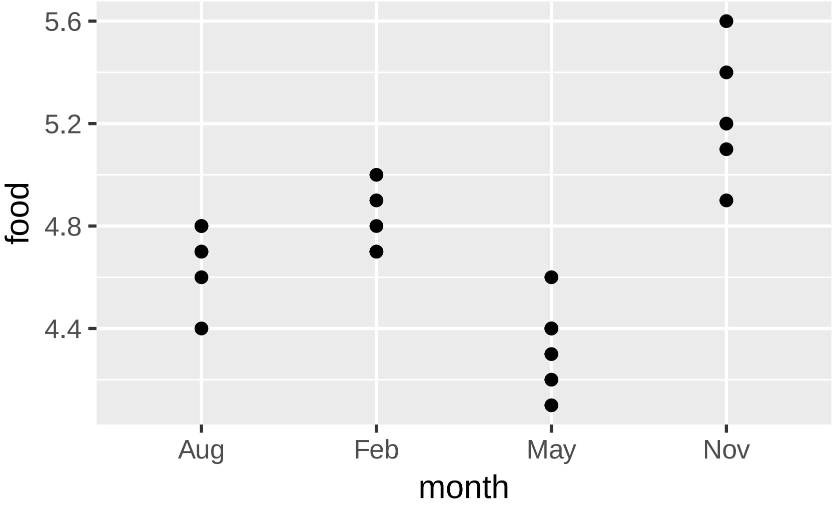


This offers the suggestion that maybe November will be significantly higher than the rest and May significantly lower, or at least they will be significantly different from each other.

This is perhaps getting ahead of the game: we should be thinking about spread and shape. Bear in mind that there are only 5 or 6 observations in each group, so you won't be able to say much about normality. In any case, we are going to be doing a Mood's median test, so any lack of normality doesn't matter (eg. perhaps that 4.4 observation in August). Given the small sample sizes, I actually think the spreads are quite similar.

Another way of looking at the data, especially with these small sample sizes, is a "dot plot": instead of making a boxplot for each month, we plot the actual points for each month as if we were making a scatterplot:

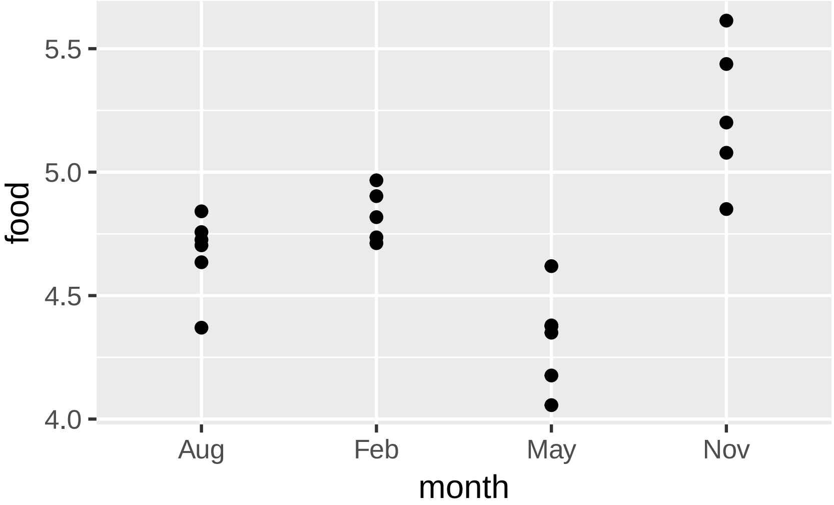
```
ggplot(deer, aes(x = month, y = food)) + geom_point()
```



Wait a minute. There were five deer in February and six in August. Where did they go?

The problem is *overplotting*: more than one of the deer plotted in the same place on the plot, because the amounts of food eaten were only given to one decimal place and there were some duplicated values. One way to solve this is to randomly move the points around so that no two of them plot in the same place. This is called *jittering*, and is done like this:

```
ggplot(deer, aes(x = month, y = food)) + geom_jitter(width = 0,
    height = 0.05)
```



Now you see all the deer, and you can see that two pairs of points in August and one pair of points in February are close enough on the jittered plot that they would have been the same to one decimal place.

I wanted to keep the points above the months they belong to, so I only allowed vertical jitter (that's the `width` and `height` in the geom_jitter; the width is zero so there is no horizontal jittering). If you like, you can colour the months; it's up to you whether you think that's making the plot easier to read, or is overkill (see my point on the facetted plots on the 2017 midterm).

This way you see the whole distribution for each month. Normally it's nicer to see the summary made by the boxplots, but here there are not very many points. The value of 4.4 in August does look quite a bit lower than the rest, but the other months look believably normal given the small sample sizes. I don't know about equal spreads (November looks more spread out), but normality looks believable. Maybe this is the kind of situation in which Welch's ANOVA is a good idea. (If you believe that the normality-with-unequal-spreads is a reasonable assumption to make, then the Welch ANOVA will be more powerful than the Mood's median test, and so should be preferred.)

(c) Run a Mood's median test as in lecture (ie. not using smmr). What do you conclude, in the context of the data?

Solution

To give you some practice with the mechanics, first find the overall median:

```
deer %>% summarize(med = median(food))
```

```
## # A tibble: 1 x 1
##     med
##   <dbl>
## 1   4.7
```

or

```
median(deer$food)
```

```
## [1] 4.7
```

I like the first way because it's the same idea as we did before, just not differentiating by month. I think there are some observations exactly equal to the median, which will mess things up later:

```
deer %>% filter(food == 4.7)
```

```
## # A tibble: 4 x 2
##   month  food
##   <chr> <dbl>
## 1 Feb     4.7
## 2 Feb     4.7
## 3 Aug     4.7
## 4 Aug     4.7
```

There are, two in February and two in August.

Next, make (and save) a table of the observations within each month that are above and below this median:

```
tab1 = with(deer, table(month, food < 4.7))
tab1
```

```
##
## month FALSE TRUE
##   Aug     4    2
##   Feb     5    0
##   May     0    6
##   Nov     5    0
```

or

```
tab2 = with(deer, table(month, food > 4.7))
tab2
```

```
##
## month FALSE TRUE
##   Aug     4    2
##   Feb     2    3
##   May     6    0
##   Nov     0    5
```

Either of these is good, but note that they are different. Two of the February observations (the ones that were exactly 4.7) have "switched sides", and (look carefully) two of the August ones also. Hence the test results will be different, and `smmr` (later) will give different results again:

```
chisq.test(tab1, correct = F)
```

```
## Warning in chisq.test(tab1, correct = F):
## Chi-squared approximation may be incorrect
```

```
##
##  Pearson's Chi-squared test
##
## data:  tab1
## X-squared = 16.238, df = 3, p-value =
## 0.001013
```

```
chisq.test(tab2, correct = F)
```

```
## Warning in chisq.test(tab2, correct = F):
## Chi-squared approximation may be incorrect
```

```
##
##  Pearson's Chi-squared test
##
## data:  tab2
## X-squared = 11.782, df = 3, p-value =
## 0.008168
```

The warnings are because of the small frequencies. If you've done these by hand before (which you will have if you took PSYC08), you'll remember that thing about "expected frequencies less than 5". This is that. It means "don't take those P-values *too* seriously."

The P-values are different, but they are both clearly significant, so the median amounts of food eaten in the different months are not all the same. (This is the same "there are differences" that you get from an ANOVA, which you would follow up with Tukey.) Despite the injunction not to take the P-values too seriously, I think these are small enough that they could be off by a bit without affecting the conclusion.

The first table came out with a smaller P-value because it looked more extreme: all of the February measurements were taken as higher than the overall median (since we were counting "strictly less" and "the rest"). In the second table, the February measurements look more evenly split, so the overall P-value is not quite so small.

You can make a guess as to what `smmr` will come out with (next), since it throws away any data values exactly equal to the median.

(d) Run a Mood's median test using `smmr`, and compare the results with the previous part.

Solution

Off we go:

```
library(smmr)
median_test(deer, food, month)
```

```
## $table
##      above
## group above below
##   Aug     2     2
##   Feb     3     0
##   May     0     6
##   Nov     5     0
##
## $test
##        what        value
## 1 statistic 13.950000000
## 2        df  3.000000000
## 3   P-value  0.002974007
```

The P-value came out in between the other two, but the conclusion is the same all three ways: the months are not all the same in terms of median food eaten. The researchers can then go ahead and try to figure out *why* the animals eat different amounts in the different months.

You might be wondering how you could get rid of the equal-to-median values in the build-it-yourself way. This is `filter` from `dplyr`, which you use first:

```
deer2 = deer %>% filter(food != 4.7)
tab3 = with(deer2, table(month, food < 4.7))
tab3
```

```
##
## month FALSE TRUE
##   Aug     2    2
##   Feb     3    0
##   May     0    6
##   Nov     5    0
```

```
chisq.test(tab3)
```

```
## Warning in chisq.test(tab3): Chi-squared
## approximation may be incorrect

##
##  Pearson's Chi-squared test
##
## data:  tab3
## X-squared = 13.95, df = 3, p-value =
## 0.002974
```

which is exactly what smmr does, so the answer is identical. How would an ANOVA come out here? My guess is, very similarly:

The computer scientists among you will note that I should not use equals or not-equals to compare a decimal floating-point number, since decimal numbers are not represented exactly in the computer. R, however, is ahead of us here, since when you try to do food not equal to 4.7, it tests whether food is more than a small distance away from 4.7, which is the right way to do it. In R, therefore, code like my *food != 4.7* does exactly what I want, but in something like C, it *does not*, and you have to be more careful: *abs(food-4.7)>1e-8*, or something like that. The small number *1e-8* is typically equal to **machine epsilon**, the smallest number on a computer that is distinguishable from zero.

```
deer.1 = aov(food ~ month, data = deer)
summary(deer.1)
```

```
##             Df Sum Sq Mean Sq F value
## month        3 2.3065  0.7688   22.08
## Residuals   18 0.6267  0.0348
##               Pr(>F)
## month       2.94e-06 ***
## Residuals
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
```

```
TukeyHSD(deer.1)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = food ~ month, data = deer)
##
## $month
##               diff         lwr        upr
## Feb-Aug  0.1533333 -0.16599282  0.4726595
## May-Aug -0.3333333 -0.63779887 -0.0288678
## Nov-Aug  0.5733333  0.25400718  0.8926595
## May-Feb -0.4866667 -0.80599282 -0.1673405
## Nov-Feb  0.4200000  0.08647471  0.7535253
## Nov-May  0.9066667  0.58734052  1.2259928
##             p adj
## Feb-Aug 0.5405724
## May-Aug 0.0290758
## Nov-Aug 0.0004209
## May-Feb 0.0021859
## Nov-Feb 0.0109631
## Nov-May 0.0000013
```

The conclusion is the same, but the P-value on the *F*-test is much smaller. I think this is because the *F*-test uses the actual values, rather than just whether they are bigger or smaller than 4.7. The Tukey says that all the months are different in terms of (now) mean, except for February and August, which were those two very similar ones on the boxplot.

(e) How is it that Mood's median test does not completely answer the question you really want to answer? How might you get an answer to the question you *really* want answered? Explain briefly, and obtain the answer you *really* want, discussing your results briefly.

Solution

That's rather a lot, so let's take those things one at a time.

Most of these parts are old from assignment questions that I actually asked a previous class to do, but not this part. I added it later.

Mood's median test is really like the *F*-test in ANOVA: it's testing the null hypothesis that the groups (months) all have the same median (of food eaten), against the alternative that the null is not true. We rejected this null, but we don't know which months differ significantly from which. To resolve this in ANOVA, we do Tukey (or Games-Howell if we did the Welch ANOVA). The corresponding thing here is to do all the possible two-group Mood tests on all the pairs of groups, and, after adjusting for doing (here) six tests at once, look at the adjusted P-values to see how the months differ in terms of food eaten.

This is accomplished in `smmr` via `pairwise_median_test`, thus:

```
pairwise_median_test(deer, food, month)

## # A tibble: 6 x 4
##   g1    g2    p_value adj_p_value
##   <chr> <chr>   <dbl>       <dbl>
## 1 Aug   Feb   0.147       0.884
## 2 Aug   May   0.0209      0.126
## 3 Aug   Nov   0.00270     0.0162
## 4 Feb   May   0.00157     0.00939
## 5 Feb   Nov   0.0578      0.347
## 6 May   Nov   0.00157     0.00939
```

This compares each month with each other month. Looking at the last column, there are only three significant differences: August-November, February-May and May-November. Going back to the table of medians we made in (a), November is significantly higher (in terms of median food eaten) than August and May (but not February), and February is significantly higher than May. The other differences are not big enough to be significant.

Extra: Pairwise median tests done this way are not likely to be very sensitive (that is, powerful), for a couple of reasons: (i) the usual one that the median tests don't use the data very efficiently, and (ii) the way I go from the unadjusted to the adjusted P-values is via Bonferroni (here, multiply the P-values by 6), which is known to be safe but conservative. This is why the Tukey produced more significant differences among the months than the pairwise median tests did.

11.3 Movie ratings again

??q:movies-b?? This question again uses the movie rating data at link.

(a) Read the data into R and obtain the number of movies of each rating and the *median* length of movies of each rating.

Solution

Reading in is as in the other question using these data (just copy your code, or mine). No credit for that, since you've done it before.

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/movie-lengths.csv"
movies = read_csv(my_url)
```

```
## Parsed with column specification:
## cols(
##   length = col_integer(),
##   rating = col_character()
## )
```

```
movies
```

```
## # A tibble: 60 x 2
##     length rating
##      <int> <chr>
##  1     25 G
##  2     75 G
##  3     88 G
##  4     63 G
##  5     76 G
##  6     97 G
##  7     68 G
##  8     82 G
##  9     98 G
## 10     74 G
## # ... with 50 more rows
```

Now, the actual for-credit part, which is a `group_by` and `summarize`:

```
movies %>% group_by(rating) %>% summarize(count = n(),
    med = median(length))
```

```
## # A tibble: 4 x 3
##   rating count   med
##   <chr>  <int> <int>
## 1 G         15    82
## 2 PG        15   100
## 3 PG-13     15   117
## 4 R         15   103
```

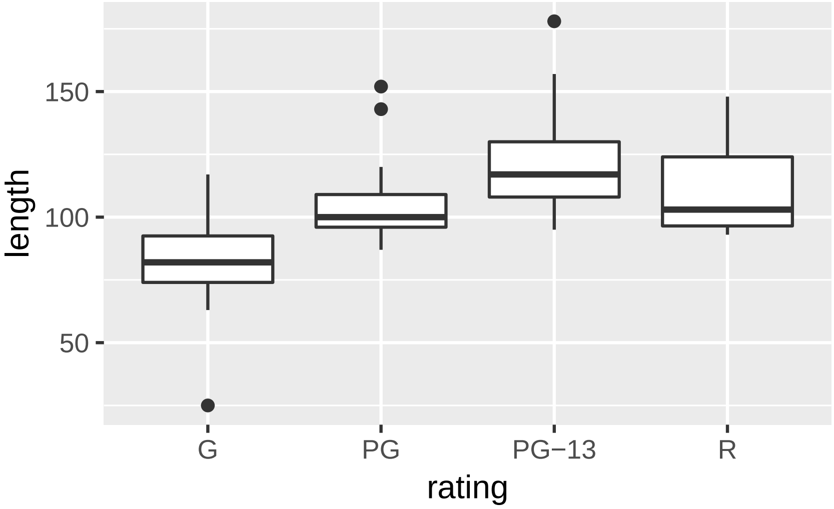
The G movies have a smaller median than the others, but also the PG-13 movies seem to be longer on average (not what we found before).

(b) Obtain a suitable graph that assesses the assumptions for ANOVA. Why do you think it is not reasonable to run ANOVA here? Explain briefly.

Solution

The graph would seem to be a boxplot, side by side for each group:

```
ggplot(movies, aes(x = rating, y = length)) +
    geom_boxplot()
```



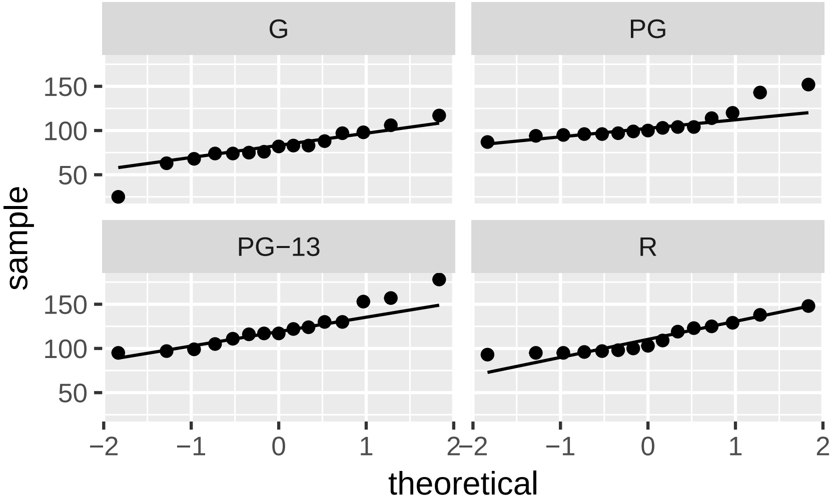
We are looking for approximate normal distributions with approximately equal spreads, which I don't think we have: there are outliers, at the low end for G movies, and at the high end for PG and PG-13 movies. Also, you might observe that the distribution of lengths for R movies is skewed to the right. (Noting either the outliers or skewness as a reason for not believing normality is enough, since all we need is *one* way that normality fails.)

I think the spreads (as measured by the interquartile ranges) are acceptably similar, but since we have rejected normality, it is a bit late for that.

So I think it is far from reasonable to run an ANOVA here. In my opinion 15 observations in each group is not enough to gain much from the Central Limit Theorem either.

Extra: since part of the assumption for ANOVA is (approximate) normality, it would also be entirely reasonable to make normal quantile plots, one for each movie type, facetted. Remember the process: you pretend that you are making a normal quantile plot for all the data together, regardless of group, and then at the last minute, you throw in a `facet_wrap`. I've written the code out on three lines, so that you can see the pieces: the "what to plot", then the normal quantile plot part, then the facetting:

```
ggplot(movies, aes(sample = length)) + stat_qq() +
    stat_qq_line() + facet_wrap(~rating)
```



Since there are four movie ratings, `facet_wrap` has arranged them into a 2 × 2 grid, which satisfyingly means that each normal quantile plot is more or less square and thus easy to interpret.

The principal problem unveiled by these plots is outliers. It looks as if the G movies have one low outlier, the PG movies have two high outliers, the PG-13 movies have one or maybe three high outliers (depending on how you count them), and the R movies have none. Another way to look at the last two is you could call them curved, with too much bunching up at the bottom and (on PG-13) too much spread-out-ness at the top, indicating right-skewed distributions. The distribution of lengths of the R-rated movies is too bunched up at the bottom, but as you would expect for a normal at the top. The R movies show the right-skewedness in an odd way: usually this skewness shows up by having too many high values, but this time it's having too *few low* values.

The assumption for ANOVA is that all four of these are at least approximately normal (with the same spread). We found problems with the normality on at least three of them, so we definitely have doubts about trusting ANOVA here.

I could have used `scales=free` here to get a separate y-axis for each plot, but since the y-axis is movie length each time, and all four groups would be expected to have at least roughly similar movie lengths, I left it as it was. (The other advantage of leaving the scales the same is that you can compare spread by comparing the slopes of the lines on these graphs; since the lines connect the observed and theoretical quartiles, a steeper slope means a larger IQR. Here, the R line is steepest and the PG line is flattest. Compare this with the spreads of the boxplots.)

Extra extra: if you want, you can compare the normal quantile plots with the boxplots to see whether you get the same conclusion from both. For the G movies, the low outlier shows up both ways, and the rest of the distribution is at least more or less normal. For the PG movies, I'd say the distribution is basically normal except for the highest two values (on both plots). For the PG-13 movies, only the highest value shows up as an outlier, but the next two apparent outliers on the normal quantile plot are at the upper end of the long upper whisker, so the boxplot is saying "right-skewed with one upper outlier" rather than "three upper outliers". The distribution of the R movies is skewed right, with the bunching at the bottom showing up as the very small lower whisker.

The boxplots and the normal quantile plots are basically telling the same story in each case, but they are doing it in a slightly different way.

(c) Run a Mood's median test (use smmr if you like). What do you conclude, in the context of the data?

Solution

The smart way is to use smmr, since it is much easier:

```
library(smmr)
median_test(movies, length, rating)
```

```
## $table
##        above
## group   above below
##   G         2    13
##   PG        7     7
##   PG-13    12     3
##   R         8     6
##
## $test
##        what        value
## 1 statistic 13.752380952
## 2        df  3.000000000
## 3   P-value  0.003262334
```

The movies do not all have the same median length, or at least one of the rating types has movies of different median length from the others. Or something equivalent to that. It's the same conclusion as for ANOVA, only with medians instead of means.

You can speculate about why the test came out significant. My guess is that the G movies are shorter than average, and that the PG-13 movies are longer than average. (We had the first conclusion before, but not the second. This is where medians are different from means.)

The easiest way to see which movie types really differ in length from which is to do all the pairwise median tests, which is in smmr thus:

```
pairwise_median_test(movies, length, rating)
```

```
## # A tibble: 6 x 4
##   g1    g2      p_value adj_p_value
##   <chr> <chr>     <dbl>       <dbl>
## 1 G     PG    0.00799      0.0479
## 2 G     PG-13 0.0000590    0.000354
## 3 G     R     0.0106       0.0635
## 4 PG    PG-13 0.0106       0.0635
## 5 PG    R     0.715        4.29
## 6 PG-13 R     0.273        1.64
```

The inputs for this are the same ones in the same order as for median_test. (A design decision on my part, since otherwise *I* would never have been able to remember how to run these!) Only the first two of these are significant (look in the last column). We can remind ourselves of the sample medians:

```
movies %>% group_by(rating) %>% summarize(count = n(),
    med = median(length))
```

```
## # A tibble: 4 x 3
##   rating count   med
##   <chr>  <int> <int>
## 1 G         15    82
## 2 PG        15   100
## 3 PG-13     15   117
## 4 R         15   103
```

The G movies are significantly shorter than the PG and PG-13 movies, but not quite significantly different from the R movies. This is a little odd, since the difference in sample medians between G and PG, significant, is *less* than for G and R (not significant). There are several Extras here, which you can skip if you don't care about the background. First, we can do the median test by hand: This has about four steps: (i) find the median of all the data, (ii) make a table tabulating the number of values above and below the overall median for each group, (iii) test the table for association, (iv) draw a conclusion. Thus (i):

```
median(movies$length)
```

```
## [1] 100
```

or

```
movies %>% summarize(med = median(length))
```

```
## # A tibble: 1 x 1
##     med
##   <dbl>
## 1   100
```

or store it in a variable, and then (ii):

```
tab1 = with(movies, table(length < 100, rating))
tab1
```

```
##        rating
##          G PG PG-13  R
##   FALSE  2  8    12  9
##   TRUE  13  7     3  6
```

or

```
tab2 = with(movies, table(length > 100, rating))
tab2
```

```
##        rating
##          G PG PG-13  R
##   FALSE 13  8     3  7
##   TRUE   2  7    12  8
```

These differ because there are evidently some movies of length exactly 100 minutes, and it matters whether you count $<$ and $\geq$ (as in `tab1`) or $>$ and *le* (`tab2`). Either is good.

Was I right about movies of length exactly 100 minutes?

```
movies %>% filter(length == 100)
```

```
## # A tibble: 2 x 2
##   length rating
##    <int> <chr>
## 1    100 PG
## 2    100 R
```

One PG and one R. It makes a difference to the R movies, but if you look carefully, it makes a difference to the PG movies as well, because the False and True switch roles between `tab1` and `tab2` (compare the G movies, for instance). You need to store your table in a variable because it has to get passed on to `chisq.test` below, (iii):

```
chisq.test(tab1, correct = F)
```

```
##
##  Pearson's Chi-squared test
##
## data:  tab1
## X-squared = 14.082, df = 3, p-value =
## 0.002795
```

or

```
chisq.test(tab2, correct = F)
```

```
##
##  Pearson's Chi-squared test
##
## data:  tab2
## X-squared = 13.548, df = 3, p-value =
## 0.003589
```

Either is correct, or, actually, without the correct=F.

see discussion elsewhere about Yates' Correction and fixed margins.

The conclusion (iv) is the same either way: the null of no association is clearly rejected (with a P-value of 0.0028 or 0.0036 as appropriate), and therefore whether a movie is longer or shorter than median length depends on what rating it has: that is, the median lengths do differ among the ratings. The same conclusion, in other words, as the *F*-test gave, though with not quite such a small P-value.

Second, you might be curious about how we might do something like Tukey having found some significant differences (that is, what's lurking in the background of pairwise_median_test).

Let's first suppose we are comparing G and PG movies. We need to pull out just those, and then compare them using smmr. Because the first input to median_test is a data frame, it fits neatly into a pipe (with the data frame omitted):

```
movies %>% filter(rating == "G" | rating == "PG") %>%
    median_test(length, rating)
```

```
## $table
##      above
## group above below
##    G      4    11
##    PG    10     3
##
## $test
##        what       value
## 1 statistic 7.035897436
## 2        df 1.000000000
## 3   P-value 0.007989183
```

We're going to be doing this about six times — $\binom{4}{2} = 6$ choices of two rating groups to compare out of the four — so we should have a function to do it. I think the input to the function should be a data frame that has a column called `rating`, and two names of ratings to compare:

```
comp2 = function(rat_1, rat_2, d) {
    d %>% filter(rating == rat_1 | rating == rat_2) %>%
        median_test(length, rating)
}
```

The way I wrote this function is that you have to specify the movie ratings in quotes. It is *possible* to write it in such a way that you input them without quotes, `tidyverse` style, but that gets into "non-standard evaluation" and `enquo()` and `!!`, which (i) I have to look up every time I want to do it, and (ii) I am feeling that the effort involved in explaining it to you is going to exceed the benefit you will gain from it. I mastered it enough to make it work in `smmr` (note that you specify column names without quotes there). There are tutorials on this kind of thing if you're interested.

Anyway, testing:

```
comp2("G", "PG", movies)

## $table
##      above
## group above below
##    G      4    11
##    PG    10     3
##
## $test
##        what       value
## 1 statistic 7.035897436
## 2        df 1.000000000
## 3   P-value 0.007989183
```

That works, but I really only want to pick out the P-value, which is in the list item `test` in the column `value`, the third entry. So let's rewrite the function to return just that:

```
comp2 = function(rat_1, rat_2, d) {
    d %>% filter(rating == rat_1 | rating == rat_2) %>%
        median_test(length, rating) %>% pluck("test",
        "value", 3)
}
comp2("G", "PG", movies)
```

```
## [1] 0.007989183
```

Gosh.

What `median_test` returns is an R `list` that has two things in it, one called `table` and one called `test`. The thing called `test` is a data frame with a column called `value` that contains the P-values. The third of these is the two-sided P-value that we want.

You might not have seen `pluck` before. This is a way of getting things out of complicated data structures. This one takes the output from `median_test` and from it grabs the piece called `test`. This is a data frame. Next, we want the column called `value`, and from that we want the third row. These are specified one after the other to `pluck` and it pulls out the right thing.

So now our function returns just the P-value.

I have to say that it took me several goes and some playing around in R Studio to sort this one out. Once I thought I understood `pluck`, I wondered why my function was not returning a value. And then I realized that I was saving the value inside the function and not returning it. Ooops. The nice thing about `pluck` is that I can put it on the end of the pipeline and and it will pull out (and return) whatever I want it to.

Let's grab a hold of the different rating groups we have:

```
the_ratings = unique(movies$rating)
the_ratings
```

```
## [1] "G"     "PG-13" "PG"    "R"
```

The Pythonisti among you will know how to finish this off: do a loop-inside-a-loop over the rating groups, and get the P-value for each pair. You can do that in R, if you must. It's not pretty at all, but it works:

```
ii = character(0)
jj = character(0)
pp = numeric(0)
for (i in the_ratings) {
    for (j in the_ratings) {
        pval = comp2(i, j, movies)
        ii = c(ii, i)
        jj = c(jj, j)
        pp = c(pp, pval)
    }
}
tibble(ii, jj, pp)
```

```
## # A tibble: 16 x 3
##    ii    jj           pp
##    <chr> <chr>     <dbl>
##  1 G     G     1
##  2 G     PG-13 0.0000590
##  3 G     PG    0.00799
##  4 G     R     0.0106
##  5 PG-13 G     0.0000590
##  6 PG-13 PG-13 1
##  7 PG-13 PG    0.0106
##  8 PG-13 R     0.273
##  9 PG    G     0.00799
## 10 PG    PG-13 0.0106
## 11 PG    PG    1
## 12 PG    R     0.715
## 13 R     G     0.0106
## 14 R     PG-13 0.273
## 15 R     PG    0.715
## 16 R     R     1
```

This is a lot of fiddling about, since you have to initialize three vectors, and then update them every time through the loop. It's hard to read, because the actual business part of the loop is the calculation of the P-value, and that's almost hidden by all the book-keeping. (It's also slow and inefficient, though the slowness doesn't matter too much here since it's not a very big problem.)

Let's try another way:

```
crossing(first = the_ratings, second = the_ratings)
```

```
## # A tibble: 16 x 2
##    first second
##    <chr> <chr>
##  1 G     G
##  2 G     PG
##  3 G     PG-13
##  4 G     R
##  5 PG    G
##  6 PG    PG
##  7 PG    PG-13
##  8 PG    R
##  9 PG-13 G
## 10 PG-13 PG
## 11 PG-13 PG-13
## 12 PG-13 R
## 13 R     G
## 14 R     PG
## 15 R     PG-13
## 16 R     R
```

This does "all possible combinations" of one rating with another. We don't actually need all of that; we just need the ones where the first one is (alphabetically) strictly less than the second one. This is because we're never comparing a rating with itself, and each pair of ratings appears twice, once in alphabetical order, and once the other way around. The ones we need are these:

```
crossing(first = the_ratings, second = the_ratings) %>%
    filter(first < second)
```

```
## # A tibble: 6 x 2
##   first second
##   <chr> <chr>
## 1 G     PG
## 2 G     PG-13
## 3 G     R
## 4 PG    PG-13
## 5 PG    R
## 6 PG-13 R
```

A technique thing to note: instead of asking "how do I pick out the distinct pairs of ratings?", I use two simpler tools: first I make all the combinations of pairs of ratings, and then out of those, pick the ones that are alphabetically in ascending order, which we know how to do.

Now we want to call our function `comp2` for each of the things in `first` *and* each of the things in `second`, and make a new column called `pval` that contains exactly that. This (coming fresh from page 332 of the R book, this being the first time I've ever used it) is exactly what the texttt{map2} family of functions does. In our case, `comp2` returns a decimal number, a `dbl`, so `map2_dbl` does it. Thus:

This was a year ago when I first wrote this.

```
crossing(first = the_ratings, second = the_ratings) %>%
    filter(first < second) %>% mutate(pval = map2_dbl(first,
    second, ~comp2(.x, .y, movies)))
```

```
## # A tibble: 6 x 3
##   first second      pval
##   <chr> <chr>      <dbl>
## 1 G     PG     0.00799
## 2 G     PG-13  0.0000590
## 3 G     R      0.0106
## 4 PG    PG-13  0.0106
## 5 PG    R      0.715
## 6 PG-13 R      0.273
```

The logic of map2_dbl is "for each of the things in first, and each of the things in second, taken in parallel, call the function comp2 with those two inputs in that order, always with data frame movies". The .x and .y play the role of the . that we usually have inside a map, but now we're "mapping" over two things rather than just one, so that they cannot both be called ..

One more thing: we're doing 6 tests at once here, so we're giving ourselves 6 chances to reject a null (all medians equal) that might have been true. So the true probability of a type I error is no longer 0.05 but something bigger.

The easiest way around that is to do a so-called Bonferroni adjustment: instead of rejecting if the P-value is less than 0.05, we only reject if it is less than 0.05/6, since we are doing 6 tests. This is a fiddly calculation to do by hand, but it's easy to build in another mutate, thus:

```
crossing(first = the_ratings, second = the_ratings) %>%
    filter(first < second) %>% mutate(pval = map2_dbl(first,
    second, ~comp2(.x, .y, movies))) %>% mutate(reject = pval <
    0.05/6)
```

```
## # A tibble: 6 x 4
##   first second      pval reject
##   <chr> <chr>      <dbl> <lgl>
## 1 G     PG     0.00799   TRUE
## 2 G     PG-13  0.0000590 TRUE
## 3 G     R      0.0106    FALSE
## 4 PG    PG-13  0.0106    FALSE
## 5 PG    R      0.715     FALSE
## 6 PG-13 R      0.273     FALSE
```

In the pairwise median test in *smmr*, I did this backwards: rather than changing the alpha that you compare each P-value with from 0.05 to 0.05/6, I flip it around so that you adjust the P-values by *multiplying* them by 6, and then comparing the adjusted P-values with the usual 0.05. It comes to the same place in the end, except that this way you can get adjusted P-values that are greater than 1, which makes no sense. You read those as being definitely not significant.

And not a loop in sight.

This is how I coded it in pairwise_median_test. If you want to check it, it's on Github: link. The function median_test_pair is the same as comp2 above.

So the only significant differences are now G compared to PG and PG-13. There is not a significant difference in median movie length between G and R, though it is a close call. We thought the PG-13 movies might have a significantly different median from other rating groups beyond G, but they turn out not to have. (The third and fourth comparisons would have been significant had we not made the Bonferroni adjustment to compensate for doing six tests at once; with that adjustment, we only reject if the P-value is less than $0.05/6 = 0.0083$, and so 0.0106 is not quite small enough to reject with.)

Listing the rating groups sorted by median would give you an idea of how far different the medians have to be to be significantly different:

```
medians = movies %>% group_by(rating) %>% summarize(med = median(length)) %>%
    arrange(desc(med))
medians
```

```
## # A tibble: 4 x 2
##   rating   med
##   <chr>  <int>
## 1 PG-13    117
## 2 R        103
## 3 PG       100
## 4 G         82
```

Something rather interesting has happened: even though the comparison of G and PG (18 apart) is significant, the comparison of G and R (21 apart) is not significant. This seems very odd, but it happens because the Mood median test is not actually literally comparing the sample medians, but only assessing the splits of values above and below the median of the combined sample. A subtlety, rather than an error, I'd say.

Here's something extremely flashy to finish with:

```
crossing(first = the_ratings, second = the_ratings) %>%
    filter(first < second) %>% mutate(pval = map2_dbl(first,
    second, ~comp2(.x, .y, movies))) %>% mutate(reject = pval <
    0.05/6) %>% left_join(medians, by = c(first = "rating")) %>%
    left_join(medians, by = c(second = "rating"))
```

```
## # A tibble: 6 x 6
##   first second      pval reject med.x med.y
##   <chr> <chr>      <dbl> <lgl>  <int> <int>
## 1 G     PG     0.00799   TRUE      82   100
## 2 G     PG-13  0.0000590 TRUE      82   117
## 3 G     R      0.0106    FALSE     82   103
## 4 PG    PG-13  0.0106    FALSE    100   117
## 5 PG    R      0.715     FALSE    100   103
## 6 PG-13 R      0.273     FALSE    117   103
```

The additional two lines look up the medians of the rating groups in `first`, then `second`, so that you can see the actual medians of the groups being compared each time. You see that medians different by 30 are definitely different, ones differing by 15 or less are definitely not different, and ones differing by about 20 could go either way.

I think that's *quite* enough of that.

11.4 *Atomic weight of carbon*

??q:carbon?? The atomic weight of the chemical element carbon is 12. Two methods of measuring the atomic weight of samples of carbon were compared. The results are shown in link. The methods are labelled 1 and 2. The first task is to find out whether the two methods have different "typical" measures (mean or median, as appropriate) of the atomic weight of carbon.

For this question, compose a report in R Markdown. (R Markdown is what you use in an R Notebook, but you can also have a separate R Markdown document from which you can produce HTML, Word etc. output.) See part (a) for how to get this started.

Your report should read like an actual report, not just the answers to some questions that I set you. To help with that, write some text that links the parts of the report together smoothly, so that it reads as a coherent whole. The grader had 3 discretionary marks to award for the overall quality of your writing. The scale for this was:

- 3 points: excellent writing. The report flows smoothly, is easy to read, and contains everything it should (and nothing it shouldn't).
- 2 points: satisfactory writing. Not the easiest to read, but says what it should, and it looks at least somewhat like a report rather than a string of answers to questions.
- 1 point: writing that is hard to read or to understand. If you get this (or 0), you should consider what you need to do to improve when you write your project.
- 0 points: you answered the questions, but you did almost nothing to make it read like a report.

(a) Create a new R Markdown document. To do this, in R Studio, select File, New File, R Markdown. Type the report title and your name in the boxes, and leave the output on the default HTML. Click OK.

Solution

You'll see the title and your name in a section at the top of the document, and below that you'll see a template document, as you would for an R Notebook. The difference is that where you are used to seeing Preview, it now says "knit", but this has the same effect of producing the formatted version of your report.

(b) Write an introduction that explains the purpose of this study and the data collected in your own words.

Solution
Something like this:

> This study is intended to compare two different methods (labelled 1 and 2) for measuring the atomic weight of carbon (which is known in actual fact to be 12). Fifteen samples of carbon were used; ten of these were assessed using method 1 and the remaining five using method 2. The primary interest in this particular study is to see whether there is a difference in the mean or median atomic weight as measured by the two methods.

Before that, start a new section like this: `## Introduction`. Also, get used to expressing your understanding in your words, not mine. (Using my words, in this course, is likely to be worth very little.)

(c) Begin an appropriately-titled new section in your report, read the data into R and display the results.

Solution
Values separated by spaces:

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/carbon.txt"
carbon = read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   method = col_integer(),
##   weight = col_double()
## )
```

```
carbon
```

```
## # A tibble: 15 x 2
##    method weight
##     <int>  <dbl>
##  1      1   12.0
##  2      1   12.0
##  3      1   12.0
##  4      1   12.0
##  5      1   12.0
##  6      1   12.0
##  7      1   12.0
##  8      1   12.0
##  9      1   12.0
## 10      1   12.0
## 11      2   12.0
## 12      2   12.0
## 13      2   12.0
## 14      2   12.0
## 15      2   12.0
```

I would expect you to include, without being told to include it, some text in your report indicating that you have sensible data: two methods labelled 1 and 2 as promised, and a bunch of atomic weights close to the nominal figure of 12.

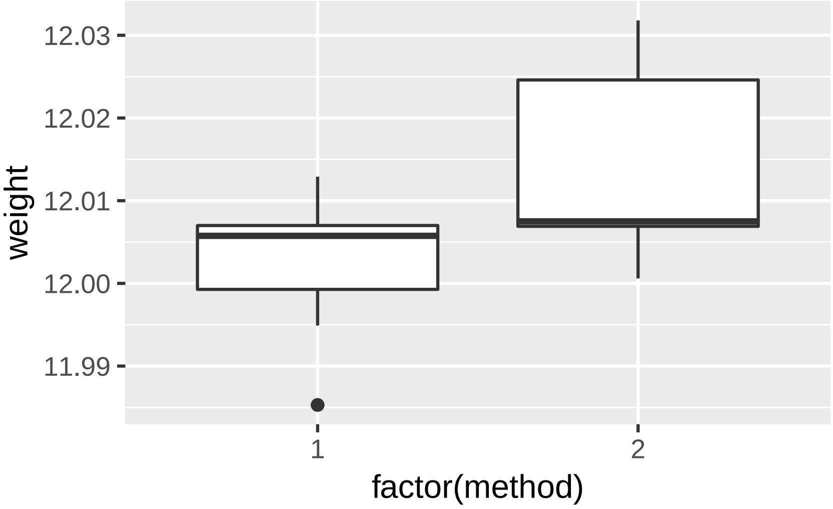
It's probably better in a report to use language a bit more formal than *a bunch*. Something like *a number* would be better.

(d) Make an appropriate plot to compare the measurements obtained by the two methods. You might need to do something about the two methods being given as numbers even though they are really only identifiers. (If you do, your report ought to say what you did and why.)

Solution

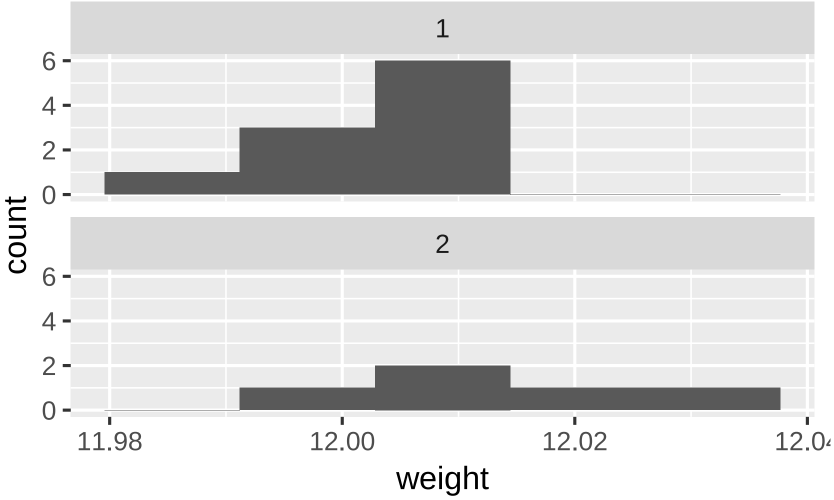
The appropriate plot, with a categorical method and quantitative weight, is something like a boxplot. If you're not careful, `method` will get treated as a quantitative variable, which you don't want; the easiest way around that, for a boxplot at least, is to turn it into a factor like this:

```
ggplot(carbon, aes(x = factor(method), y = weight)) +
    geom_boxplot()
```



If you insist, you could do a faceted histogram (above and below, for preference):

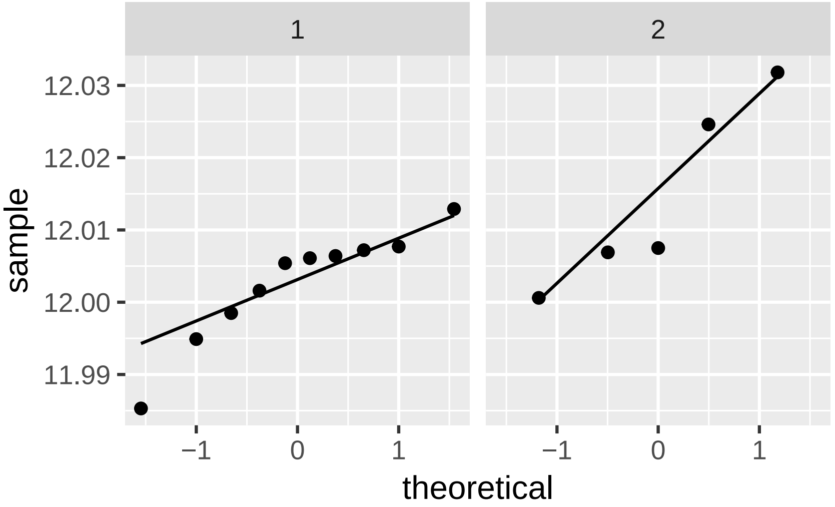
```
ggplot(carbon, aes(x = weight)) + geom_histogram(bins = 5) +
    facet_wrap(~method, ncol = 1)
```



There are really not enough data values for a histogram to be of much help, so I don't like this as much.

If you are thinking ahead (we are going to be doing a *t*-test), then you'll realize that normality is the kind of thing we're looking for, in which case normal quantile plots would be the thing. However, we might have to be rather forgiving for method 2 since there are only 5 observations:

```
ggplot(carbon, aes(sample = weight)) + stat_qq() +
    stat_qq_line() + facet_wrap(~method)
```



I don't mind these coming out side by side, though I would rather have them squarer.

I would say, boxplots are the best, normal quantile plots are also acceptable, but expect to lose something for histograms because they offer only a rather crude comparison in this case.

(e) Comment briefly on what you see in your plot.

Solution

In boxplots, if that's what you drew, there are several things that deserve comment: the medians, the spreads and the shapes. The median for method 1 is a little bit lower than for method 2 (the means are probably more different, given the shapes of the boxes). The spread for method 2 is a lot bigger. (Looking forward, that suggests a Welch-Satterthwaite rather than a pooled test.) As for shape, the method 2 measurements seem more or less symmetric (the whiskers are equal anyway, even if the position of the median in the box isn't), but the method 1 measurements have a low outlier. The histograms are hard to compare. Try to say something about centre and spread and shape. I think the method 2 histogram has a slightly higher centre and definitely bigger spread. On my histogram for method 1, the distribution looks skewed left. If you did normal quantile plots, say something sensible about normality for each of the two methods. For method 1, I would say the low value is an outlier and the rest of the values look pretty straight. Up to you whether you think there is a curve on the plot (which would indicate skewness, but then that highest value is too high: it would be bunched up with the other values below 12.01 if there were really skewness). For method 2, it's really hard to say anything since there are only five values. Given where the line goes, there isn't much you can say to doubt normality. Perhaps the best you can say here is that in a sample of size 5, it's difficult to assess normality at all.

(f) Carry out the most appropriate *t*-test. (You might like to begin another new section in your report here.)

Solution

This would be the Welch-Satterthwaite version of the two-sample *t*-test, since the two groups do appear to have different spreads:

```r
t.test(weight ~ method, data = carbon)
```

```
##
##  Welch Two Sample t-test
##
## data:  weight by method
## t = -1.817, df = 5.4808, p-value =
## 0.1238
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
```

```
##  -0.027777288  0.004417288
## sample estimates:
## mean in group 1 mean in group 2
##        12.00260        12.01428
```

Imagining that this is a report that would go to your boss, you ought to defend your choice of the Welch-Satterthwaite test (as I did above), and not just do the default *t*-test without comment.

If, in your discussion above, you thought the spreads were equal enough, then you should do the pooled *t*-test here, which goes like this:

```
t.test(weight ~ method, data = carbon, var.equal = T)
```

```
##
##  Two Sample t-test
##
## data:  weight by method
## t = -2.1616, df = 13, p-value = 0.04989
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -2.335341e-02 -6.588810e-06
## sample estimates:
## mean in group 1 mean in group 2
##        12.00260        12.01428
```

The point here is that you should do the right test based on your conclusion. Being consistent is the most important thing. (In this case, note that the P-values are very different. We'll get to that shortly.)

If we were doing this in SAS, as we see later, we'd get a test at the bottom of the output that compares the two variances. I feel that it's just as good to eyeball the spreads and make a call about whether they are "reasonably close". Or even, to always do the Welch-Satterthwaite test on the basis that it is pretty good even if the two populations have the same variance. (If this last point of view is one that you share, you ought to say something about that when you do your *t*-test.)

Extra: I guess this is a good place to say something about tests for comparing variances, given that you might be pondering that. There are several that I can think of, that R can do, of which I mention two.

The first is the *F*-test for variances that you might have learned in B57 (that is the basis for the ANOVA *F*-test):

```
var.test(weight ~ method, data = carbon)
```

```
##
##  F test to compare two variances
##
## data:  weight by method
## F = 0.35768, num df = 9, denom df = 4,
## p-value = 0.1845
## alternative hypothesis: true ratio of variances is not equal to 1
## 95 percent confidence interval:
##  0.04016811 1.68758230
## sample estimates:
## ratio of variances
##          0.3576842
```

This, unfortunately, is rather dependent on the data in the two groups being approximately normal. Since we are talking variances rather than means, there is no Central Limit Theorem to rescue us for large samples (quite aside from the fact that these samples are *not* large). Since the ANOVA *F*-test is based on the same theory, this is why normality is also more important in ANOVA than it is in a *t*-test.

The second is Levene's test. This doesn't depend on normality (at least, not nearly so much), so I like it better in general:

```
library(car)
```

```
## Loading required package: carData
```

```
##
## Attaching package: 'car'
```

```
## The following object is masked from 'package:dplyr':
##
##     recode
```

```
## The following object is masked from 'package:purrr':
##
##     some
```

```
leveneTest(weight ~ factor(method), data = carbon)
```

```
## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  1  0.9887 0.3382
##       13
```

Levene's test takes a different approach: first the absolute differences from the group medians are calculated, and then an ANOVA is run on the absolute differences. If, say, one of the groups has a larger spread than the other(s), its absolute differences from the median will tend to be bigger. As for what we conclude here, well, neither of the variance tests show any significance at all, so from that point of view there is no evidence against using the pooled *t*-test. Having said that, the samples are small, and so it would be difficult to *prove* that the two methods have different variance, even if they actually did.

The use of absolute differences, and the median, downplays the influence of outliers. The assumption here is that the absolute differences from the medians are approximately normal, which seems a less big assumption than assuming the actual data are approximately normal.

This is coming back to the *power* of something like Levene's test; the power of any test is not going to be very big if the sample sizes are small.

Things are never as clear-cut as you would like. In the end, it all comes down to making a call and defending it.

(g) Do the most appropriate test you know that does not assume normally-distributed data.

Solution

That would be Mood's median test. Since I didn't say anything about building it yourself, feel free to use `smmr`:

```
library(smmr)
median_test(carbon, weight, method)
```

```
## $table
##      above
## group above below
##     1     3     6
##     2     4     1
##
## $test
##        what      value
## 1 statistic 2.80000000
## 2        df 1.00000000
## 3   P-value 0.09426431
```

As an aside, if you have run into a non-parametric test such as Mann-Whitney or Kruskal-Wallis that applies in this situation, be careful about using it here, because they have additional assumptions that you may not want to trust. Mann-Whitney started life as a test for "equal distributions". This means that the null is equal location *and* equal spread, and if you reject the null, one of those has failed. But here, we suspect that equal spread will fail, so that the Mann-Whitney test may end up rejecting *whether or not* the medians are different, so it won't answer the question you want an answer to. Mood's median test doesn't have that problem; all it's saying if the null is true is that the medians are equal; the spreads could be anything at all.

The test goes back to the 1940s.

The same kind of issues apply to the signed-rank test vs. the sign test. In the case of the signed-rank test, the extra assumption is of a symmetric distribution — to my mind, if you don't believe normality, you probably don't have much confidence in symmetry either. That's why I like the sign test and Mood's median test: in the situation where you don't want to be dealing with assumptions, these tests don't make you worry about that.

Another comment that you don't need to make is based on the not-quite-significance of the Mood test. The P-value is less than 0.10 but not less than 0.05, so it doesn't quite reach significance by the usual standard. But if you look up at the table, the frequencies seem rather unbalanced: 6 out of the remaining 9 weights in group 1 are below the overall median, but 4 out of 5 weights in group 2 are above. This seems as if it ought to be significant, but bear in mind that the sample sizes are small, and thus Mood's median test needs *very* unbalanced frequencies, which we don't quite have here.

(h) Discuss the results of your tests and what they say about the two methods for measuring the atomic weight of carbon. If it seems appropriate, put the discussion into a section called Conclusions.

Solution

Begin by pulling out the P-values for your preferred test(s) and say what they mean. The P-value for the Welch-Satterthwaite t-test is 0.1238, which indicates no difference in mean atomic weights between the two methods. The Mood median test gives a similarly non-significant 0.0943, indicating no difference in the *median* weights. If you think both tests are plausible, then give both P-values and do a compare-and-contrast with them; if you think that one of the tests is clearly preferable, then say so (and why) and focus on that test's results. If you thought the pooled test was the right one, then you'll have a bit more discussion to do, since its P-value is 0.0499, and at $\alpha = 0.05$ this test disagrees with the others. If you are comparing this test with the Mood test, you ought to make some kind of reasoned recommendation about which test to believe. As ever, be consistent in your reasoning. This dataset, where I found it, was actually being used to illustrate a case where the pooled and the Welch-Satterthwaite tests disagreed. The authors of the original paper that used this dataset (a 1987 paper by Rayner and Best, [1]; the data come from 1924!) point out that the pooled t-test can be especially misleading when the smaller sample is also the one with the larger variance. This is what happened here. In the Rayner and Best paper, the Mood (or the Mann-Whitney) test was not being considered, but I think it's good practice to draw a picture and make a call about which test is appropriate. I loaded package `car` above; I'd better be tidy and unload it before I go on:

```
detach(package:car, unload = T)
```

[1]

12
Tidying and selecting data

```
library(tidyverse)
```

```
## -- Attaching packages ---- tidyverse 1.2.1 --
```

```
## v ggplot2 3.0.0     v purrr   0.2.5
## v tibble  1.4.2     v dplyr   0.7.6
## v tidyr   0.8.1     v stringr 1.3.1
## v readr   1.1.1     v forcats 0.3.0
```

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

12.1 Tidying the Jays data

This question is about the Blue Jays data set (that I used in class).

(a) The Blue Jays baseball data set is at link. Read it into R. Check that you have 25 rows and a bunch of variables.

Solution

Save the URL into a variable and then read from the URL, using `read_csv` because it's a `.csv` file:

```
myurl = "http://www.utsc.utoronto.ca/~butler/c32/jays15-home.csv"
jays = read_csv(myurl)
```

```
## Parsed with column specification:
## cols(
##   .default = col_character(),
##   row = col_integer(),
##   game = col_integer(),
##   runs = col_integer(),
##   Oppruns = col_integer(),
##   innings = col_integer(),
##   position = col_integer(),
##   ‘game time‘ = col_time(format = ""),
##   attendance = col_integer()
## )

## See spec(...) for full column specifications.
```

```
jays
```

```
## # A tibble: 25 x 21
##      row  game date  box   team  venue opp  
##    <int> <int> <chr> <chr> <chr> <chr> <chr>
##  1    82     7 Mond~ boxs~ TOR   <NA>  TBR  
##  2    83     8 Tues~ boxs~ TOR   <NA>  TBR  
##  3    84     9 Wedn~ boxs~ TOR   <NA>  TBR  
##  4    85    10 Thur~ boxs~ TOR   <NA>  TBR  
##  5    86    11 Frid~ boxs~ TOR   <NA>  ATL  
##  6    87    12 Satu~ boxs~ TOR   <NA>  ATL  
##  7    88    13 Sund~ boxs~ TOR   <NA>  ATL  
##  8    89    14 Tues~ boxs~ TOR   <NA>  BAL  
##  9    90    15 Wedn~ boxs~ TOR   <NA>  BAL  
## 10    91    16 Thur~ boxs~ TOR   <NA>  BAL  
## # ... with 15 more rows, and 14 more
## #   variables: result <chr>, runs <int>,
## #   Oppruns <int>, innings <int>, wl <chr>,
## #   position <int>, gb <chr>, winner <chr>,
## #   loser <chr>, save <chr>, ‘game
## #   time‘ <time>, Daynight <chr>,
## #   attendance <int>, streak <chr>
```

If you must, copy and paste the spreadsheet into R Studio, and read it in with `read_delim` (or possibly `read_tsv`), but this runs the risk of being defeated by spreadsheet cells that contain spaces. I don't think there are any here, but you might run into a pitcher whose name has more than one word, like (Andy) Van Hekken, who is in the Seattle Mariners farm system.

I found this by googling, after I had scrolled past all the pages of articles about the baseball pitcher who *lives* in a van.

Anyway, 25 rows and 21 columns. As usual, it's a tibble, so you see 10 rows and as many columns as will fit. This is often enough to see whether we have the right thing (as we appear to have, here). You can run through all the columns and check that they're the right kind of thing; most of them are text with a few numbers and one `time`, which is `game time`, the length of the game in hours and minutes, which is turned into an R `time` in hours, minutes and seconds.

With all those columns, `read_csv` doesn't tell you what column specification it inferred for all of them, but you can type

```
spec(jays)
```

```
## cols(
##   row = col_integer(),
##   game = col_integer(),
##   date = col_character(),
##   box = col_character(),
##   team = col_character(),
##   venue = col_character(),
##   opp = col_character(),
##   result = col_character(),
##   runs = col_integer(),
##   Oppruns = col_integer(),
##   innings = col_integer(),
##   wl = col_character(),
##   position = col_integer(),
##   gb = col_character(),
##   winner = col_character(),
##   loser = col_character(),
##   save = col_character(),
##   ‘game time‘ = col_time(format = ""),
##   Daynight = col_character(),
##   attendance = col_integer(),
##   streak = col_character()
## )
```

to find it all out.

(b) Pick out only the games that were against the New York Yankees (the variable opp is equal to NYY). Investigate all the columns. What do you notice about these games?

Solution
I get to do this:

```
jays %>% filter(opp == "NYY") %>% print(width = Inf)
```

```
## # A tibble: 3 x 21
##     row  game date              box      team
##   <int> <int> <chr>             <chr>    <chr>
## 1    92    27 Monday, May 4     boxscore TOR
## 2    93    28 Tuesday, May 5    boxscore TOR
## 3    94    29 Wednesday, May 6 boxscore TOR
##   venue opp   result  runs Oppruns innings
##   <chr> <chr> <chr>  <int>   <int>   <int>
## 1 <NA>  NYY   W          3       1      NA
## 2 <NA>  NYY   L          3       6      NA
## 3 <NA>  NYY   W          5       1      NA
##   wl    position gb    winner  loser
##   <chr>    <int> <chr> <chr>   <chr>
## 1 13-14        4 3.5   Dickey  Martin
## 2 13-15        5 4.5   Pineda  Estrada
## 3 14-15        3 3.5   Buehrle Sabathia
##   save   ‘game time‘ Daynight attendance
##   <chr>  <time>      <chr>         <int>
## 1 Cecil  02:18       N             19217
## 2 Miller 02:54       N             21519
## 3 <NA>   02:30       N             21312
##   streak
##   <chr>
## 1 +
## 2 -
## 3 +
```

but you will probably need to click the little right-arrow at the top to see more columns.

What I notice is that these games are all on consecutive nights (against the same team). This is quite common, and goes back to the far-off days when teams travelled by train: teams play several games on one visit, rather than coming back many times. You might have noticed something else; that's fine for this. For example, "each of the games lasted less than three hours", or "the attendances were all small" (since we looked at all the attendances in class). I just want you to notice something meaningful that seems to be interesting about these games.

Hockey is similar: teams go on road trips, playing several different teams before returning home. Hockey teams, though, tend to play each team only once on a road trip: for example, a west coast team like the Canucks might play a game in each of Toronto, Montreal, Boston and New York on a road trip. Well, maybe three games in the New York area: one each against the Rangers, Islanders and Devils.

You could also print all the columns in two or more goes, using `select`, for example:

```
jays %>% filter(opp == "NYY") %>% select(row:innings) %>%
    print(width = Inf)
```

```
## # A tibble: 3 x 11
##     row  game date              box      team
##   <int> <int> <chr>             <chr>    <chr>
## 1    92    27 Monday, May 4    boxscore TOR
## 2    93    28 Tuesday, May 5   boxscore TOR
## 3    94    29 Wednesday, May 6 boxscore TOR
##   venue opp   result  runs Oppruns innings
##   <chr> <chr> <chr>  <int>   <int>   <int>
## 1 <NA>  NYY   W          3       1      NA
## 2 <NA>  NYY   L          3       6      NA
## 3 <NA>  NYY   W          5       1      NA
```

```
jays %>% filter(opp == "NYY") %>% select(wl:streak) %>%
    print(width = Inf)
```

```
## # A tibble: 3 x 10
##   wl    position gb    winner  loser
##   <chr>    <int> <chr> <chr>   <chr>
## 1 13-14        4 3.5   Dickey  Martin
## 2 13-15        5 4.5   Pineda  Estrada
## 3 14-15        3 3.5   Buehrle Sabathia
##   save   ‘game time‘ Daynight attendance
##   <chr>  <time>      <chr>         <int>
## 1 Cecil  02:18       N             19217
## 2 Miller 02:54       N             21519
## 3 <NA>   02:30       N             21312
##   streak
##   <chr>
## 1 +
## 2 -
## 3 +
```

(c) From the whole data frame, pick out only the games where the attendance was more than 30,000, showing only the columns `attendance` and `Daynight`. How many of them are there (just count them)? How many are day games and how many night games (just count those too)?

Solution
Two steps, since we selecting rows *and* columns.

```
jays %>% filter(attendance > 30000) %>% select(c(attendance,
    Daynight))
```

```
## # A tibble: 8 x 2
##   attendance Daynight
##        <int> <chr>
## 1      48414 N
## 2      34743 D
## 3      44794 D
## 4      30430 N
## 5      42917 D
## 6      42419 D
## 7      33086 D
## 8      37929 D
```

Or this way, since we are selecting *consecutive* columns:

```
jays %>% filter(attendance > 30000) %>% select(c(Daynight:attendance))
```

```
## # A tibble: 8 x 2
##   Daynight attendance
##   <chr>         <int>
## 1 N             48414
## 2 D             34743
## 3 D             44794
## 4 N             30430
## 5 D             42917
## 6 D             42419
## 7 D             33086
## 8 D             37929
```

There are eight games selected (see the eight rows in the result). Only two of them are night games, while the other six are day (weekend) games.

If you wanted to, you could automate the counting, like this:

```
jays %>% filter(attendance > 30000) %>% count(Daynight)
```

```
## # A tibble: 2 x 2
##   Daynight     n
##   <chr>    <int>
## 1 D            6
## 2 N            2
```

Six day games and two night games.

(d) Display the mean and standard deviation of attendances at all day and night games.

Solution

Two steps: the grouping according to what I want to group by, then summarizing according to what I want to summarize by. Since I am summarizing, only the summaries find their way into the final data frame, so I don't need to "select out" the other variables:

```
jays %>% group_by(Daynight) %>% summarize(mean.att = mean(attendance),
    sd.att = sd(attendance))
```

```
## # A tibble: 2 x 3
##   Daynight mean.att sd.att
##   <chr>       <dbl>  <dbl>
## 1 D          37885.  5775.
## 2 N          20087.  8084.
```

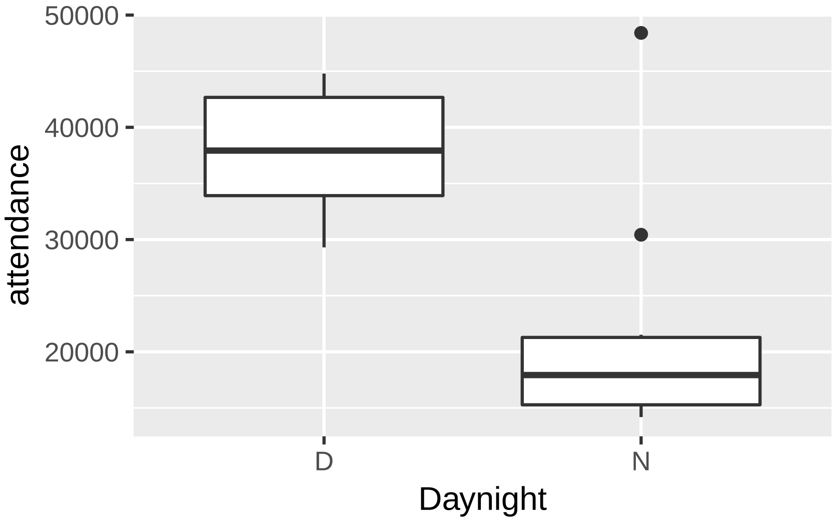
The mean attendances are about 38 thousand and about 20 thousand. Note that the night games have much the larger SD, possibly because of the large outlier night attendance (opening night). Which we can also investigate.

```
jays %>% group_by(Daynight) %>% summarize(median.att = median(attendance),
    iqr.att = IQR(attendance))
```

```
## # A tibble: 2 x 3
##   Daynight median.att iqr.att
##   <chr>         <dbl>   <dbl>
## 1 D            37929    8754.
## 2 N            17928.   6005.
```

This time, the night attendances have a *smaller* spread and a noticeably smaller median (compared to the mean), so it must have been the outlier that made the difference. There was another high value that R marked as an outlier:

```
ggplot(jays, aes(x = Daynight, y = attendance)) +
    geom_boxplot()
```



So when you take away those unusual values, the night game attendances are indeed less variable.

The right test, as you might have guessed, for comparing the medians of these non-normal data, is Mood's median test:

```
library(smmr)
median_test(jays, attendance, Daynight)
```

```
## $table
##      above
## group above below
##     D     7     0
##     N     5    12
##
## $test
##        what       value
## 1 statistic 9.882352941
## 2        df 1.000000000
## 3   P-value 0.001668714
```

There was one attendance exactly equal to the overall median (as you would expect: with an odd number of data values, the median is one of the data values). `smmr` removed it; if you did the test by hand, what happens to it depends on whether you counted aboves or belows, and this will have a small effect on the P-value, though not on the conclusion.

The overall median attendance was 21,000, and *none* of the day games had attendance less than that. With the small frequencies, the accuracy of the P-value is a bit questionable, but taking it at face value, there *is* a significant difference between median attendances at day and night games.

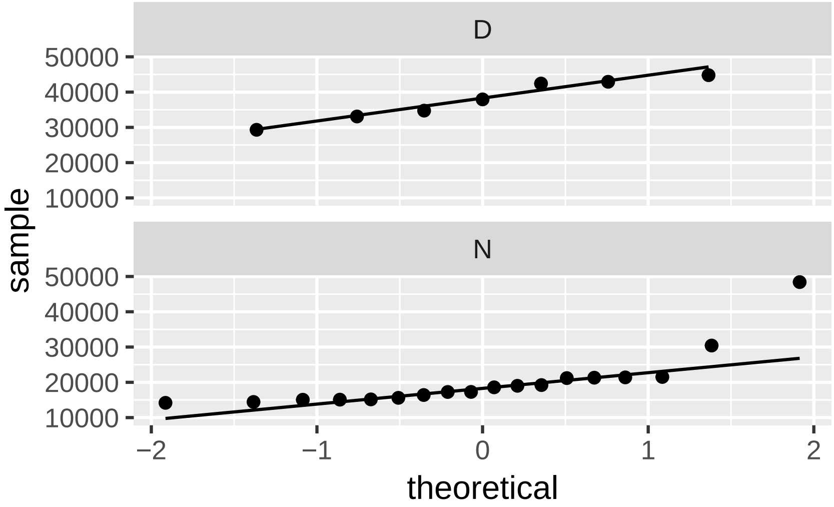
If you do this by hand, you'll get a warning about the chi-squared approximation being inaccurate. This is because of the small frequencies, and *not* because of the outliers. Those are not damaging the test at all.

(e) Make normal quantile plots of the day attendances and the night attendances, separately. Do you see any evidence of non-normality? (You would expect to on the night attendances because of the big opening-night value.)

Solution

The best way to do this is facetted normal quantile plots. Remember that the facetting part goes right at the end:

```
ggplot(jays, aes(sample = attendance)) + stat_qq() +
    stat_qq_line() + facet_wrap(~Daynight, ncol = 1)
```



The day attendances are pretty normal, though it is hard to be sure with only 7 of them.

The night attendances are not normal. The lone point top right is the outlier. On top of that, the lowest attendances are not quite low enough and the second-highest attendance is a bit too high, so there is a bit of evidence of right-skewness as well as just the one outlier.

If you leave out the `ncol=1`, you'll get the two normal quantile plots side by side (which means that each one is tall and skinny, and thus hard to read). The `ncol=1` displays all the facets in *one* column, and though it would be nice to have the graphs be about square, landscape mode is easier to read than portrait mode.

One of the reasons for skewness is often a limit on the values of the variable. The Rogers Centre has a capacity around 55,000. The day game attendances don't get especially close to that, which suggests that everyone who wants to go to the game can get a ticket. In that sort of situation, you'd expect attendances to vary around a "typical" value, with a random deviation that depends on things like the weather and the opposing team, which is the typical situation in which you get bell-shaped data. (If the Jays often sold out their stadium for day games, you'd see a lot of attendances close to the capacity, with a few lower: ie., a left skew.)

As for the night games, well, there seems to be a minimum attendance that the Blue Jays get, somewhere around 15,000: no matter who they're playing or what the weather's like, this many people will show up (season-ticket holders, for example). On special occasions, such as opening night, the attendance will be much bigger, which points to a *right* skew.

12.2 *Baseball and softball spaghetti*

On a previous assignment, we found that students could throw a baseball further than they could throw a softball. In this question, we will make a graph called a "spaghetti plot" to illustrate this graphically. (The issue previously was that the data were matched pairs: the same students threw both balls.)

This seems to work most naturally by building a pipe, a line or two at a time. See if you can do it that way. (If you can't, use lots of temporary data frames, one to hold the result of each part.)

(a) Read in the data again from link. The variables had no names, so supply some, as you did before.

Solution

Literal copy and paste:

```
myurl = "http://www.utsc.utoronto.ca/~butler/c32/throw.txt"
throws = read_delim(myurl, " ", col_names = c("student",
    "baseball", "softball"))
```

```
## Parsed with column specification:
```

```
## cols(
##   student = col_integer(),
##   baseball = col_integer(),
##   softball = col_integer()
## )
```

```
throws
```

```
## # A tibble: 24 x 3
##    student baseball softball
##      <int>    <int>    <int>
##  1       1       65       57
##  2       2       90       58
##  3       3       75       66
##  4       4       73       61
##  5       5       79       65
##  6       6       68       56
##  7       7       58       53
##  8       8       41       41
##  9       9       56       44
## 10      10       70       65
## # ... with 14 more rows
```

(b) Create a new column that is the students turned into a `factor`, adding it to your data frame.

Solution
Feed `student` into `factor`, creating a new column with `mutate`:

```
throws %>% mutate(fs = factor(student))
```

```
## # A tibble: 24 x 4
##    student baseball softball fs
##      <int>    <int>    <int> <fct>
##  1       1       65       57 1
##  2       2       90       58 2
##  3       3       75       66 3
##  4       4       73       61 4
##  5       5       79       65 5
##  6       6       68       56 6
##  7       7       58       53 7
##  8       8       41       41 8
##  9       9       56       44 9
## 10      10       70       65 10
## # ... with 14 more rows
```

This doesn't look any different from the original student numbers, but note the variable type at the top of the column.

(c) Gather together all the throwing distances into one column, making a second column that says which ball was thrown.

Solution
Literally `gather` (from `tidyr`):

```
throws %>% mutate(fs = factor(student)) %>% gather(ball,
    distance, baseball:softball)
```

```
## # A tibble: 48 x 4
##    student fs    ball     distance
##      <int> <fct> <chr>       <int>
##  1       1 1     baseball       65
##  2       2 2     baseball       90
##  3       3 3     baseball       75
##  4       4 4     baseball       73
##  5       5 5     baseball       79
##  6       6 6     baseball       68
##  7       7 7     baseball       58
##  8       8 8     baseball       41
##  9       9 9     baseball       56
## 10      10 10    baseball       70
## # ... with 38 more rows
```

Two columns to include, consecutive ones, or two to omit, the first and last. So I think it's easier to name the ones you want to include.

If you want to show off a little, you can use a select-helper, noting that the columns you want to gather up all end in "ball":

```
throws %>% mutate(fs = factor(student)) %>% gather(ball,
    distance, ends_with("ball"))
```

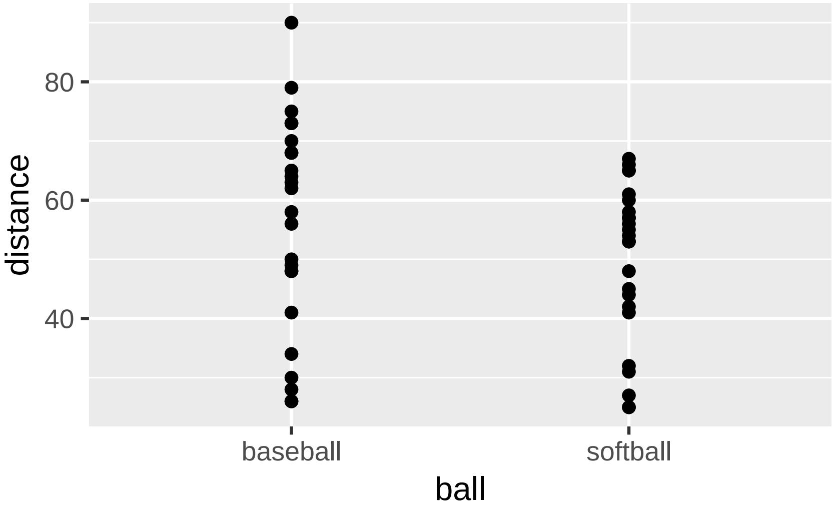
```
## # A tibble: 48 x 4
##    student fs    ball     distance
##      <int> <fct> <chr>       <int>
##  1       1 1     baseball       65
##  2       2 2     baseball       90
##  3       3 3     baseball       75
##  4       4 4     baseball       73
##  5       5 5     baseball       79
##  6       6 6     baseball       68
##  7       7 7     baseball       58
##  8       8 8     baseball       41
##  9       9 9     baseball       56
## 10      10 10    baseball       70
## # ... with 38 more rows
```

with the same result. Use whichever you like.

(d) Using your new data frame, make a "scatterplot" of throwing distance against type of ball.

Solution
The obvious thing:

```
throws %>% mutate(fs = factor(student)) %>% gather(ball,
    distance, baseball:softball) %>% ggplot(aes(x = ball,
    y = distance)) + geom_point()
```



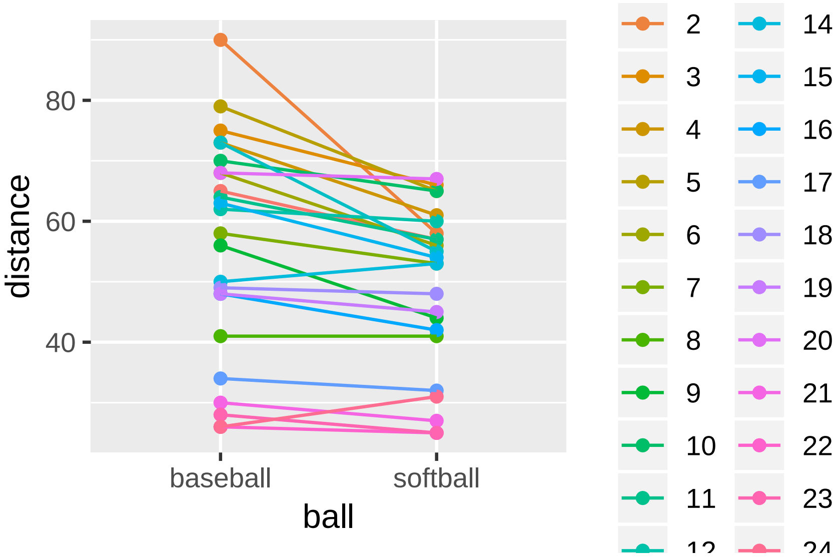
What this plot is missing is an indication of which student threw which ball. As it stands now, it could be an inferior version of a boxplot of distances thrown for each ball (which would imply that they are two independent sets of students, something that is not true).

(e) Add two things to your plot: something that will distinguish the students by colour (this works best if the thing distinguished by colour is a factor), and something that will join the two points for the same student by a line.

You can try it without. See below.

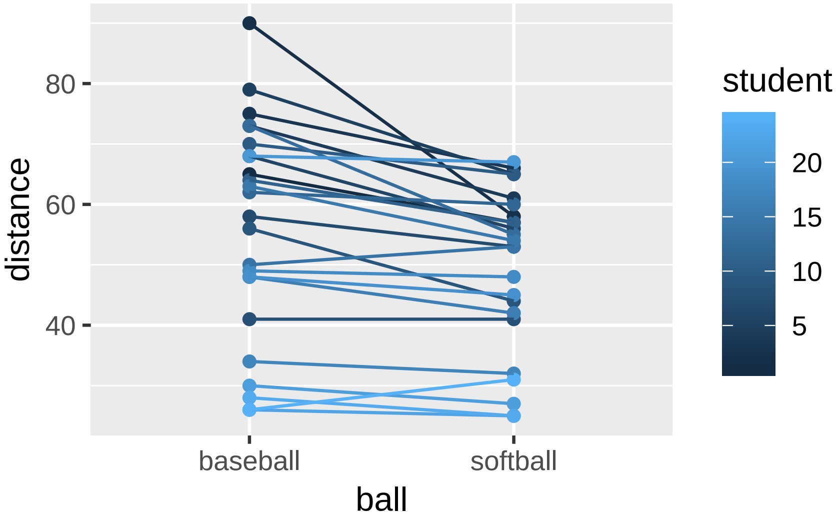
Solution
A colour and a group in the aes, and a geom_line:

```
throws %>% mutate(fs = factor(student)) %>% gather(ball,
    distance, baseball:softball) %>% ggplot(aes(x = ball,
    y = distance, group = fs, colour = fs)) +
    geom_point() + geom_line()
```



You can see what happens if you use the student as a number:

```
throws %>% mutate(fs = factor(student)) %>% gather(ball,
    distance, baseball:softball) %>% ggplot(aes(x = ball,
    y = distance, group = student, colour = student)) +
    geom_point() + geom_line()
```



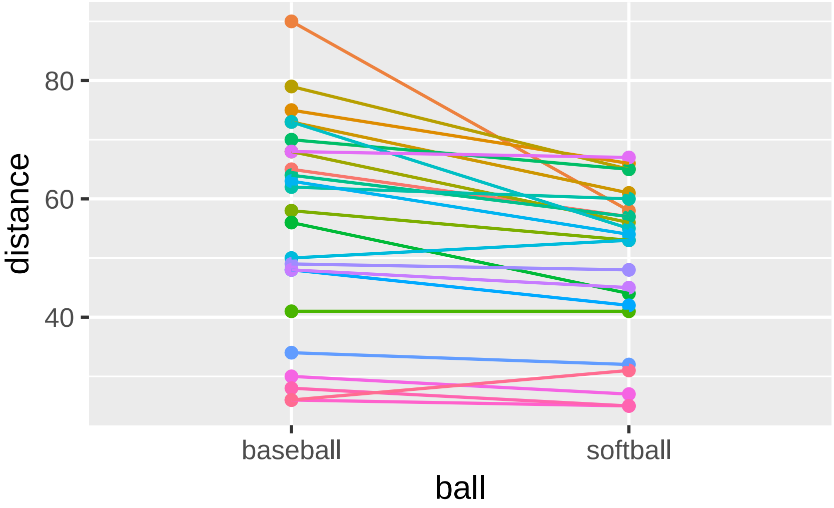
Now the student numbers are distinguished as a shade of blue (on an implied continuous scale: even a nonsensical fractional student number like 17.5 would be a shade of blue). This is not actually so bad here, because all we are trying to do is to distinguish the students sufficiently from each other so that we can see where the spaghetti strands go. But I like the multi-coloured one better.

(f) The legend is not very informative. Remove it from the plot, using `guides`.

Solution

You won't have seen this before. Here's what to do: Find what's at the top of the legend that you want to remove. Here that is fs. Find where fs appears in your aes. It actually appears in two places: in group and colour. I think the legend we want to get rid of is actually the colour one, so we do this:

```
throws %>% mutate(fs = factor(student)) %>% gather(ball,
    distance, baseball:softball) %>% ggplot(aes(x = ball,
    y = distance, group = fs, colour = fs)) +
    geom_point() + geom_line() + guides(colour = F)
```



That seems to have done it.

(g) What do you see on the final spaghetti plot? What does that tell you about the relative distances a student can throw a baseball vs. a softball? Explain briefly, blah blah blah.

Solution

Most of the spaghetti strands go downhill from baseball to softball, or at least very few of them go uphill. That tells us that most students can throw a baseball further than a softball. That was the same impression that the matched-pairs *t*-test gave us. But the spaghetti plot tells us something else. If you look carefully, you see that most of the big drops are for students who could throw a baseball a long way. These students also threw a softball further than the other students, but not by as much. Most of the spaghetti strands in the bottom half of the plot go more or less straight across. This indicates that students who cannot throw a baseball very far will throw a softball about the same distance as they threw the baseball. There is an argument you could make here that the difference between distances thrown is a *proportional* one, something like "a student typically throws a baseball 20% further than a softball". That could be assessed by comparing not the distances themselves, but the logs of the distances: in other words, making a log transformation of all the distances. (Distances have a lower limit of zero, so you might expect observed distances to be skewed to the right, which is another argument for making some kind of transformation.)

12.3 *Ethanol and sleep time in rats*

A biologist wished to study the effects of ethanol on sleep time in rats. A sample of 20 rats (all the same age) was selected, and each rat was given an injection having a particular concentration (0, 1, 2 or 4 grams per kilogram of body weight) of ethanol. These are labelled `e0, e1, e2, e4`. The "0" treatment was a control group. The rapid eye movement (REM) sleep time was then recorded for each rat. The data are in link.

(a) Read the data in from the file. Check that you have four rows of observations and five columns of sleep times.

Solution
Separated by single spaces:

```
sleep1 = read_delim("ratsleep.txt", " ")
```

```
## Parsed with column specification:
## cols(
##   treatment = col_character(),
##   obs1 = col_double(),
##   obs2 = col_double(),
##   obs3 = col_double(),
##   obs4 = col_double(),
##   obs5 = col_double()
## )
```

```
sleep1
```

```
## # A tibble: 4 x 6
##   treatment  obs1  obs2  obs3  obs4  obs5
##   <chr>     <dbl> <dbl> <dbl> <dbl> <dbl>
## 1 e0         88.6  73.2  91.4  68    75.2
## 2 e1         63    53.9  69.2  50.1  71.5
## 3 e2         44.9  59.5  40.2  56.3  38.7
## 4 e4         31    39.6  45.3  25.2  22.7
```

There are six columns, but one of them labels the groups, and there are correctly five columns of sleep times.

I used a "temporary" name for my data frame, because I'm going to be doing some processing on it in a minute, and I want to reserve the name `sleep` for my processed data frame.

(b) Unfortunately, the data are in the wrong format. All the sleep times for each treatment group are on one row, and we should have *one* column containing *all* the sleep times, and the corresponding row should show which treatment group that sleep time came from. If you prefer to skip this part: read in the data from link, and proceed to the boxplots in (c). The `tidyr` function `gather` turns wide format (which we have) into long format (which we want). `gather` needs four things fed into it: a data frame, what makes the columns different, what makes them the same, and finally which columns are to be `gather`ed together (combined into one column), the first one, a colon, and the last one. Save the result of `gather` into a data frame, and look at it. Do you have 20 rows of not-very-many variables?

Solution

What makes the columns `obs1` through `obs5` different is that they are different observation numbers ("replicates", in the jargon). I'll call that `rep`. What makes them the same is that they are all sleep times. Columns `obs1` through `obs5` are the ones we want to combine, thus. Here is where I use the name `sleep`: I save the result of the `gather` into a data frame `sleep`. Note that I also used the brackets-around-the-outside to display what I had, so that I didn't have to do a separate display. This is a handy way of saving *and* displaying in one shot:

```
(sleep <- sleep1 %>% gather(rep, sleeptime, obs1:obs5))
```

```
## # A tibble: 20 x 3
##    treatment rep   sleeptime
##    <chr>     <chr>     <dbl>
##  1 e0        obs1       88.6
##  2 e1        obs1       63
##  3 e2        obs1       44.9
##  4 e4        obs1       31
##  5 e0        obs2       73.2
##  6 e1        obs2       53.9
##  7 e2        obs2       59.5
##  8 e4        obs2       39.6
##  9 e0        obs3       91.4
## 10 e1        obs3       69.2
## 11 e2        obs3       40.2
## 12 e4        obs3       45.3
## 13 e0        obs4      68
## 14 e1        obs4      50.1
## 15 e2        obs4      56.3
## 16 e4        obs4      25.2
## 17 e0        obs5      75.2
## 18 e1        obs5      71.5
## 19 e2        obs5      38.7
## 20 e4        obs5      22.7
```

We have 20 rows of 3 columns. I got all the rows, but you will probably get an output with ten rows as usual, and will need to click Next to see the last ten rows. The initial display will say how many rows (20) and columns (3) you have.

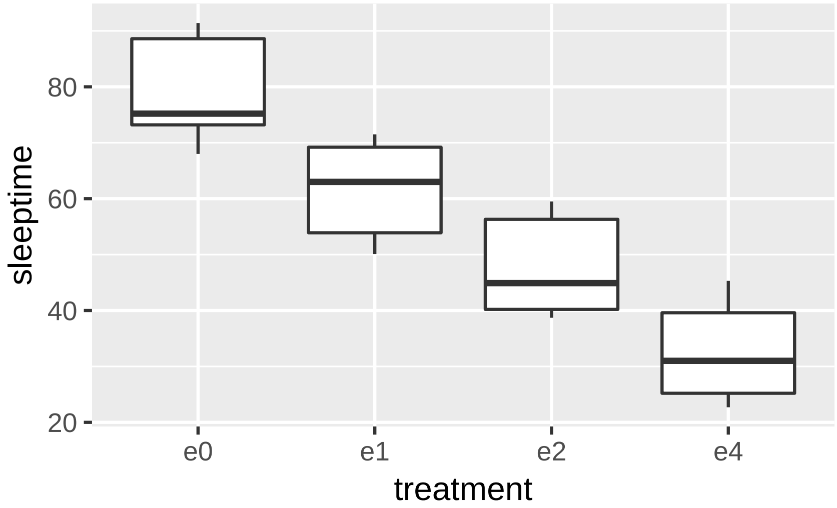
The column `rep` is not very interesting: it just says which observation each one was within its group. The interesting things are `treatment` and `sleeptime`, which are the two variables we'll need for our analysis of variance.

Sometimes the column playing the role of *rep* *is* interesting to us, but not here.

(c) Using your new data frame, make side-by-side boxplots of sleep time by treatment group.

Solution

```
ggplot(sleep, aes(x = treatment, y = sleeptime)) +
    geom_boxplot()
```



(d) In your boxplots, how does the median sleep time appear to depend on treatment group?

Solution

It appears to *decrease* as the dose of ethanol increases, and pretty substantially so (in that the differences ought to be significant, but that's coming up).

(e) There is an assumption about spread that the analysis of variance needs in order to be reliable. Do your boxplots indicate that this assumption is satisfied for these data, bearing in mind that you have only five observations per group?

Solution

The assumption is that the population SDs of each group are all equal. Now, the boxplots show IQRs, which are kind of a surrogate for SD, and because we only have five observations per group to base the IQRs on, the *sample* IQRs might vary a bit. So we should look at the heights of the boxes on the boxplot, and see whether they are grossly unequal. They appear to be to be of very similar heights, all things considered, so I am happy. If you want the SDs themselves:

```
sleep %>% group_by(treatment) %>% summarize(stddev = sd(sleeptime))
```

```
## # A tibble: 4 x 2
##   treatment stddev
##   <chr>      <dbl>
## 1 e0         10.2
## 2 e1          9.34
## 3 e2          9.46
## 4 e4          9.56
```

Those are *very* similar, given only 5 observations per group. No problems here.

(f) Run an analysis of variance to see whether sleep time differs significantly among treatment groups. What do you conclude?

Solution

I use aov here, because I might be following up with Tukey in a minute:

```
sleep.1 = aov(sleeptime ~ treatment, data = sleep)
summary(sleep.1)
```

```
##             Df Sum Sq Mean Sq F value
## treatment    3   5882    1961   21.09
## Residuals   16   1487      93
##               Pr(>F)
## treatment   8.32e-06 ***
## Residuals
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
```

This is a very small P-value, so my conclusion is that the mean sleep times are not all the same for the treatment groups. Further than that I am not entitled to say (yet).

The technique here is to save the output from `aov` in something, look at that (via `summary`), and then that same something gets fed into `TukeyHSD` later.

(g) Would it be a good idea to run Tukey's method here? Explain briefly why or why not, and if you think it would be a good idea, run it.

Solution

Tukey's method is useful when (i) we have run an analysis of variance and got a significant result and (ii) when we want to know which groups differ significantly from which. Both (i) and (ii) are true here. So:

```
TukeyHSD(sleep.1)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = sleeptime ~ treatment, data = sleep)
##
## $treatment
##         diff       lwr         upr     p adj
## e1-e0 -17.74 -35.18636  -0.2936428 0.0455781
## e2-e0 -31.36 -48.80636 -13.9136428 0.0005142
## e4-e0 -46.52 -63.96636 -29.0736428 0.0000056
## e2-e1 -13.62 -31.06636   3.8263572 0.1563545
## e4-e1 -28.78 -46.22636 -11.3336428 0.0011925
## e4-e2 -15.16 -32.60636   2.2863572 0.1005398
```

(h) What do you conclude from Tukey's method? (This is liable to be a bit complicated.) Is there a treatment that is clearly best, in terms of the sleep time being largest?

Solution

All the differences are significant except treatment `e2` vs. `e1` and `e4`. All the differences involving the control group `e0` are significant, and if you look back at the boxplots in (c), you'll see that the control group `e0` had the *highest* mean sleep time. So the control group is best (from this point of view), or another way of saying it is that *any* dose of ethanol is significantly reducing mean sleep time. The other comparisons are a bit confusing, because the 1-4 difference is significant, but neither of the differences involving 2 are. That is, 1 is better than 4, but 2 is not significantly worse than 1 nor better than 4. This seems like it should be a logical impossibility, but the story is that we don't have enough data to decide where 2 fits relative to 1 or 4. If we had 10 or 20 observations per group, we might be able to conclude that 2 is in between 1 and 4 as the boxplots suggest.

12.4 Growth of tomatoes

A biology graduate student exposed each of 32 tomato plants to one of four different colours of light (8 plants to each colour). The growth rate of each plant, in millimetres per week, was recorded. The data are in link.

(a) Read the data into R and confirm that you have 8 rows and 5 columns of data.

Solution
This kind of thing:

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/tomatoes.txt"
toms1 = read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   plant = col_integer(),
##   blue = col_double(),
##   red = col_double(),
##   yellow = col_double(),
##   green = col_double()
## )
```

```
toms1
```

```
## # A tibble: 8 x 5
##   plant  blue   red yellow green
##   <int> <dbl> <dbl>  <dbl> <dbl>
## 1     1  5.34  13.7   4.61  2.72
## 2     2  7.45  13.0   6.63  1.08
## 3     3  7.15  10.2   5.29  3.97
## 4     4  5.53  13.1   5.29  2.66
## 5     5  6.34  11.1   4.76  3.69
## 6     6  7.16  11.4   5.57  1.96
## 7     7  7.77  14.0   6.57  3.38
## 8     8  5.09  13.5   5.25  1.87
```

I do indeed have 8 rows and 5 columns.
With only 8 rows, listing the data like this is good.

(b) Re-arrange the data so that you have *one* column containing all the growth rates, and another column saying which colour light each plant was exposed to. (The aim here is to produce something suitable for feeding into aov later.)

Solution
This is a job for gather:

```
toms2 = toms1 %>% gather(colour, growthrate, blue:green)
toms2
```

```
## # A tibble: 32 x 3
##    plant colour growthrate
##    <int> <chr>       <dbl>
##  1     1 blue         5.34
##  2     2 blue         7.45
##  3     3 blue         7.15
##  4     4 blue         5.53
##  5     5 blue         6.34
##  6     6 blue         7.16
##  7     7 blue         7.77
##  8     8 blue         5.09
##  9     1 red         13.7
## 10     2 red         13.0
## # ... with 22 more rows
```

Reminder: data frame to gather, what makes the columns different (they're different colours), what makes them the same (they're all growth rates), which columns to gather together (all the colour ones).

Since the column plant was never mentioned, this gets repeated as necessary, so now it denotes "plant within colour group", which in this case is not very useful. (Where you have matched pairs, or repeated measures in general, you *do* want to keep track of which individual is which. But this is not repeated measures because plant number 1 in the blue group and plant number 1 in the red group are *different* plants.)

There were 8 rows originally and 4 different colours, so there should be, and are, $8 \times 4 = 32$ rows in the gathered-up data set.

(c) Save the data in the new format to a text file. This is most easily done using write_csv, which is the opposite of read_csv. It requires two things: a data frame, and the name of a file to save in, which should have a .csv extension.

Solution
The code is easy enough:

```
write_csv(toms2, "tomatoes2.csv")
```

If no error, it worked. That's all you need.

To verify (for my satisfaction) that it was saved correctly:

```
cat tomatoes2.csv
```

```
## plant,colour,growthrate
## 1,blue,5.34
## 2,blue,7.45
## 3,blue,7.15
## 4,blue,5.53
## 5,blue,6.34
## 6,blue,7.16
## 7,blue,7.77
## 8,blue,5.09
## 1,red,13.67
## 2,red,13.04
## 3,red,10.16
## 4,red,13.12
## 5,red,11.06
## 6,red,11.43
## 7,red,13.98
## 8,red,13.49
## 1,yellow,4.61
## 2,yellow,6.63
## 3,yellow,5.29
## 4,yellow,5.29
## 5,yellow,4.76
## 6,yellow,5.57
## 7,yellow,6.57
## 8,yellow,5.25
## 1,green,2.72
## 2,green,1.08
## 3,green,3.97
## 4,green,2.66
## 5,green,3.69
## 6,green,1.96
## 7,green,3.38
## 8,green,1.87
```

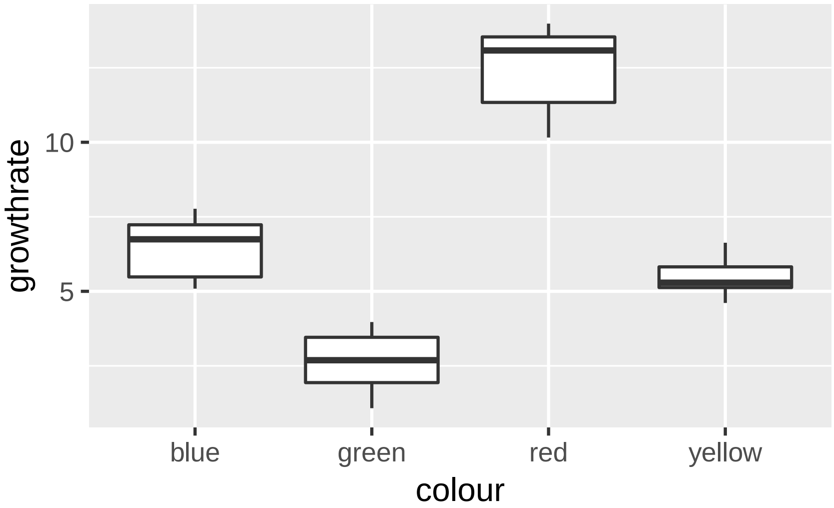
On my system, that will list the contents of the file. Or you can just open it in R Studio (if you saved it the way I did, it'll be in the same folder, and you can find it in the Files pane.)

(d) Make a suitable boxplot, and use it to assess the assumptions for ANOVA. What do you conclude? Explain briefly.

Solution

Nothing terribly surprising here. My data frame is called `toms2`, for some reason:

```
ggplot(toms2, aes(x = colour, y = growthrate)) +
    geom_boxplot()
```



There are no outliers, but there is a little skewness (compare the *whiskers*, not the placement of the median within the box, because what matters with skewness is the *tails*, not the middle of the distribution; it's problems in the tails that make the mean unsuitable as a measure of centre). The Red group looks the most skewed. Also, the Yellow group has smaller spread than the others (we assume that the population variances within each group are equal). The thing to bear in mind here, though, is that there are only eight observations per group, so the distributions could appear to have unequal variances or some non-normality by chance.

My take is that these data, all things considered, are *just about* OK for ANOVA. Another option would be to do Welch's ANOVA as well and compare with the regular ANOVA: if they give more or less the same P-value, that's a sign that I didn't need to worry.

Extra: some people like to run a formal test on the variances to test them for equality. My favourite (for reasons explained elsewhere) is the Levene test, if you insist on going this way. It lives in package `car`, and *does not* take a `data=`, so you need to do the `with` thing:

```
library(car)

## Loading required package: carData

##
## Attaching package: 'car'
## The following object is masked from 'package:dplyr':
##
##     recode

## The following object is masked from 'package:purrr':
##
##     some

with(toms2, leveneTest(growthrate, colour))

## Warning in leveneTest.default(growthrate,
## colour): colour coerced to factor.

## Levene's Test for Homogeneity of Variance (center = median)
##       Df F value Pr(>F)
## group  3  0.9075 0.4499
##       28
```

The warning is because `colour` was actually text, but the test did the right thing by turning it into a factor, so that's OK.

There is no way we can reject equal variances in the four groups. The *F*-statistic is less than 1, in fact, which says that if the four groups have the same population variances, the sample variances will be *more* different than the ones we observed on average, and so there is no way that these sample variances indicate different population variances. (This is because of 8 observations only per group; if there had been 80 observations per group, it would have been a different story.) Decide for yourself whether you're surprised by this.

With that in mind, I think the regular ANOVA will be perfectly good, and we would expect that and the Welch ANOVA to give very similar results.

I don't need `car` again, so let's get rid of it:

```
detach("package:car", unload = T)
```

(e) Run (regular) ANOVA on these data. What do you conclude? (Optional extra: if you think that some other variant of ANOVA would be better, run that as well and compare the results.)

Solution

`aov`, bearing in mind that Tukey is likely to follow:

```
toms.1 = aov(growthrate ~ colour, data = toms2)
summary(toms.1)

##             Df Sum Sq Mean Sq F value
## colour       3  410.5  136.82   118.2
## Residuals   28   32.4    1.16
##                Pr(>F)
## colour      5.28e-16 ***
## Residuals
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
```

This is a tiny P-value, so the mean growth rate for the different colours is definitely *not* the same for all colours. Or, if you like, one or more of the colours has a different mean growth rate than the others.

This, remember, is as far as we go right now.

Extra: if you thought that normality was OK but not equal spreads, then Welch ANOVA is the way to go:

```
toms.2 = oneway.test(growthrate ~ colour, data = toms2)
toms.2
```

```
##
##  One-way analysis of means (not
##  assuming equal variances)
##
## data:  growthrate and colour
## F = 81.079, num df = 3.000, denom df =
## 15.227, p-value = 1.377e-09
```

The P-value is not *quite* as small as for the regular ANOVA, but it is still very small, and the conclusion is the same.

If you had doubts about the normality (that were sufficiently great, even given the small sample sizes), then go with Mood's median test for multiple groups:

```
library(smmr)
median_test(toms2, growthrate, colour)
```

```
## $table
##         above
## group    above below
##   blue       5     3
##   green      0     8
##   red        8     0
##   yellow     3     5
##
## $test
##       what        value
## 1 statistic 1.700000e+01
## 2        df 3.000000e+00
## 3   P-value 7.067424e-04
```

The P-value is again extremely small (though not quite as small as for the other two tests, for the usual reason that Mood's median test doesn't use the data very efficiently: it doesn't use how *far* above or below the overall median the data values are.)

The story here, as ever, is consistency: whatever you thought was wrong, looking at the boxplots, needs to guide the test you do. This should probably be a flow chart, but this way works too:

- if you are not happy with normality, go with `median_test` from `smmr` (Mood's median test).
- if you are happy with normality and equal variances, go with `aov`.
- if you are happy with normality but not equal variances, go with `oneway.test` (Welch ANOVA).

So the first thing to think about is normality, and if you are OK with normality, then think about equal spreads. Bear in mind that you need to be willing to tolerate a certain amount of non-normality and inequality in the spreads, given that your data are only samples from their populations. (Don't expect perfection, in short.)

(f) If warranted, run a suitable follow-up. (If not warranted, explain briefly why not.)

Solution

Whichever flavour of ANOVA you ran (regular ANOVA, Welch ANOVA, Mood's median test), you got the same conclusion for these data: that the average growth rates were not all the same for the four colours. That, as you'll remember, is as far as you go. To find out which colours differ from which in terms of growth rate, you need to run some kind of multiple-comparisons follow-up, the right one for the analysis you did. Looking at the boxplots suggests that red is clearly best and green clearly worst, and it is possible that all the colours are significantly different from each other.) If you did regular ANOVA, Tukey is what you need:

```
TukeyHSD(toms.1)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = growthrate ~ colour, data = toms2)
```

```
##
## $colour
##                  diff       lwr        upr
## green-blue   -3.8125 -5.281129 -2.3438706
## red-blue      6.0150  4.546371  7.4836294
## yellow-blue  -0.9825 -2.451129  0.4861294
## red-green     9.8275  8.358871 11.2961294
## yellow-green  2.8300  1.361371  4.2986294
## yellow-red   -6.9975 -8.466129 -5.5288706
##                  p adj
## green-blue   0.0000006
## red-blue     0.0000000
## yellow-blue  0.2825002
## red-green    0.0000000
## yellow-green 0.0000766
## yellow-red   0.0000000
```

All of the differences are (strongly) significant, except for yellow and blue, the two with middling growth rates on the boxplot. Thus we would have no hesitation in saying that growth rate is biggest in red light and smallest in green light.

If you did Welch ANOVA, you need Games-Howell, which you have to get from one of the packages that offers it:

```
library(PMCMRplus)
gamesHowellTest(growthrate ~ factor(colour), data = toms2)
```

```
##
##  Pairwise comparisons using Games-Howell test

## data: growthrate by factor(colour)

##        blue    green   red
## green  1.6e-05 -       -
## red    1.5e-06 4.8e-09 -
## yellow 0.18707 0.00011 5.8e-07

##
## P value adjustment method: none

## alternative hypothesis: two.sided
```

The conclusions are the same as for the Tukey: all the means are significantly different except for yellow and blue. Finally, if you did Mood's median test, you need this one:

```
pairwise_median_test(toms2, growthrate, colour)
```

```
## # A tibble: 6 x 4
##   g1    g2       p_value adj_p_value
##   <chr> <chr>      <dbl>       <dbl>
## 1 blue  green  0.0000633    0.000380
## 2 blue  red    0.0000633    0.000380
## 3 blue  yellow 0.317        1.90
## 4 green red    0.0000633    0.000380
## 5 green yellow 0.0000633    0.000380
## 6 red   yellow 0.0000633    0.000380
```

Same conclusions again. This is what I would have guessed; the conclusions from Tukey were so clear-cut that it really didn't matter which way you went; you'd come to the same conclusion.

That said, what I am looking for from you is a sensible choice of analysis of variance (ANOVA, Welch's ANOVA or Mood's median test) for a good reason, followed by the *right* follow-up for the test you did. Even though the conclusions are all the same no matter what you do here, I want you to get used to following the right method, so that you will be able to do the right thing when it *does* matter.

12.5 *Pain relief in migraine headaches (again)*

The data in link are from a study of pain relief in migraine headaches. Specifically, 27 subjects were randomly assigned to receive *one* of three pain relieving drugs, labelled A, B and C. Each subject reported the number of hours of pain relief they obtained (that is, the number of hours between taking the drug and the migraine symptoms returning). A higher value is therefore better. Can we make some recommendation about which drug is best for the population of migraine sufferers?

(a) Read in and display the data. Take a look at the data file first, and see if you can say why `read_table` will work and `read_delim` will not.

Solution

The key is two things: the data values are *lined up in columns*, and *there is more than one space between values*. The second thing is why `read_delim` will not work. If you look carefully at the data file, you'll see that the column names are above and aligned with the columns, which is what `read_table` wants. If the column names had *not* been aligned with the columns, we would have needed `read_table2`.

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/migraine.txt"
migraine = read_table(my_url)
```

```
## Parsed with column specification:
## cols(
##   DrugA = col_integer(),
##   DrugB = col_integer(),
##   DrugC = col_integer()
## )
```

```
migraine
```

```
## # A tibble: 9 x 3
##   DrugA DrugB DrugC
##   <int> <int> <int>
## 1     4     6     6
## 2     5     8     7
## 3     4     4     6
## 4     3     5     6
## 5     2     4     7
## 6     4     6     5
## 7     3     5     6
## 8     4    11     5
## 9     4    10     5
```

Success.

(b) What is it about the experimental design that makes a one-way analysis of variance plausible for data like this?

Solution

Each experimental subject only tested *one* drug, so that we have 27 independent observations, nine from each drug. This is exactly the setup that a one-way ANOVA requires. Compare that to, for example, a situation where you had only 9 subjects, but they each tested *all* the drugs (so that each subject produced three measurements). That is like a three-measurement version of matched pairs, a so-called **repeated-measures design**, which requires its own kind of analysis.

To allow for the fact that measurements on the same subject are not independent but correlated.

(c) What is wrong with the current format of the data as far as doing a one-way ANOVA analysis is concerned? (This is related to the idea of whether or not the data are "tidy".)

Solution

For our analysis, we need one column of pain relief time and one column labelling the drug that the subject in question took. Or, if you prefer to think about what would make these data "tidy": there are 27 subjects, so there ought to be 27 rows, and all three columns are measurements of pain relief, so they ought to be in one column.

(d) "Tidy" the data to produce a data frame suitable for your analysis.

Solution

`gather` the columns that are all measurements of one thing. The syntax of `gather` is: what makes the columns different, what makes them the same, and which columns need to be gathered together. Use a pipe to name the dataframe to work with. I'm going to save my new data frame:

```
(migraine2 <- migraine %>% gather(drug, painrelief,
    DrugA:DrugC))
```

```
## # A tibble: 27 x 2
##    drug  painrelief
##    <chr>      <int>
##  1 DrugA          4
##  2 DrugA          5
##  3 DrugA          4
##  4 DrugA          3
##  5 DrugA          2
##  6 DrugA          4
##  7 DrugA          3
##  8 DrugA          4
##  9 DrugA          4
## 10 DrugB          6
## # ... with 17 more rows
```

The brackets around the whole thing print out the result as well as saving it. If you don't have those, you'll need to type `migraine2` again to display it.

We do indeed have a new data frame with 27 rows, one per observation, and 2 columns, one for each variable: the pain relief hours, plus a column identifying which drug that pain relief time came from. Exactly what `aov` needs.

You can probably devise a better name for your new data frame.

(e) Go ahead and run your one-way ANOVA (and Tukey if necessary). Assume for this that the pain relief hours in each group are sufficiently close to normally distributed with sufficiently equal spreads.

Solution

My last sentence absolves us from doing the boxplots that we would normally insist on doing.

```
painrelief.1 = aov(painrelief ~ drug, data = migraine2)
summary(painrelief.1)
```

```
##             Df Sum Sq Mean Sq F value
## drug         2  41.19   20.59   7.831
## Residuals   24  63.11    2.63
##              Pr(>F)
## drug        0.00241 **
## Residuals
## ---
## Signif. codes:
##   0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1  ’ ’ 1
```

There are (strongly) significant differences among the drugs, so it is definitely worth firing up Tukey to figure out where the differences are:

```
TukeyHSD(painrelief.1)
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = painrelief ~ drug, data = migraine2)
##
## $drug
##                    diff        lwr      upr
## DrugB-DrugA  2.8888889  0.9798731 4.797905
## DrugC-DrugA  2.2222222  0.3132065 4.131238
## DrugC-DrugB -0.6666667 -2.5756824 1.242349
##                 p adj
## DrugB-DrugA 0.0025509
## DrugC-DrugA 0.0203671
## DrugC-DrugB 0.6626647
```

Both the differences involving drug A are significant, and because a high value of `painrelief` is better, in both cases drug A is *worse* than the other drugs. Drugs B and C are not significantly different from each other.

Extra: we can also use the “pipe” to do this all in one go:

```
migraine %>% gather(drug, painrelief, DrugA:DrugC) %>%
    aov(painrelief ~ drug, data = .) %>% summary()
```

```
##             Df Sum Sq Mean Sq F value
## drug         2  41.19   20.59   7.831
## Residuals   24  63.11    2.63
##              Pr(>F)
## drug        0.00241 **
## Residuals
## ---
## Signif. codes:
##   0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1  ’ ’ 1
```

with the same results as before. Notice that I never actually created a second data frame by name; it was created by `gather` and then immediately used as input to `aov`. I also used the `data=.` trick to use "the data frame that came out of the previous step" as my input to `aov`.

And then thrown away.

Read the above like this: "take `migraine`, and then gather together the `DrugA` through `DrugC` columns into a column `painrelief`, labelling each by its drug, and then do an ANOVA of `painrelief` by `drug`, and then summarize the results."

What is even more alarming is that I can feed the output from `aov` straight into `TukeyHSD`:

```
migraine %>% gather(drug, painrelief, DrugA:DrugC) %>%
    aov(painrelief ~ drug, data = .) %>% TukeyHSD()
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = painrelief ~ drug, data = .)
##
## $drug
##                   diff        lwr      upr
## DrugB-DrugA  2.8888889  0.9798731 4.797905
## DrugC-DrugA  2.2222222  0.3132065 4.131238
## DrugC-DrugB -0.6666667 -2.5756824 1.242349
##                 p adj
## DrugB-DrugA 0.0025509
## DrugC-DrugA 0.0203671
## DrugC-DrugB 0.6626647
```

I wasn't sure whether this would work, since the output from `aov` is an R `list` rather than a data frame, but the output from `aov` is sent into `TukeyHSD` whatever kind of thing it is.

What I am missing here is to display the result of `aov` *and* use it as input to `TukeyHSD`. Of course, I had to discover that this could be solved, and indeed it can:

```
migraine %>% gather(drug, painrelief, DrugA:DrugC) %>%
    aov(painrelief ~ drug, data = .) %>% {
    print(summary(.))
    .
} %>% TukeyHSD()
```

```
##             Df Sum Sq Mean Sq F value
## drug         2  41.19   20.59   7.831
## Residuals   24  63.11    2.63
##              Pr(>F)
## drug        0.00241 **
## Residuals
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
```

```
##   Tukey multiple comparisons of means
##     95% family-wise confidence level
##
## Fit: aov(formula = painrelief ~ drug, data = .)
##
## $drug
##                   diff        lwr      upr
## DrugB-DrugA  2.8888889  0.9798731 4.797905
## DrugC-DrugA  2.2222222  0.3132065 4.131238
## DrugC-DrugB -0.6666667 -2.5756824 1.242349
##                  p adj
## DrugB-DrugA 0.0025509
## DrugC-DrugA 0.0203671
## DrugC-DrugB 0.6626647
```

The odd-looking second-last line of that uses that `.` trick for "whatever came out of the previous step". The thing inside the curly brackets is two commands one after the other; the first is to display the `summary` of that `aov` and the second part after the `;` is to just pass whatever came out of the previous line, the output from `aov`, on, unchanged, into `TukeyHSD`.

It needs *print* around it to display it, as you need *print* to display something within a loop or a function.

In the Unix world this is called `tee`, where you print something *and* pass it on to the next step. The name `tee` comes from a (real) pipe that plumbers would use to split water flow into two, which looks like a letter T.

(f) What recommendation would you make about the best drug or drugs? Explain briefly.

Solution

Drug A is significantly the worst, so we eliminate that. But there is no significant difference between drugs B and C, so we have no reproducible reason for preferring one rather than the other. Thus, we recommend "either B or C". If you weren't sure which way around the drugs actually came out, then you should work out the mean pain relief score by drug:

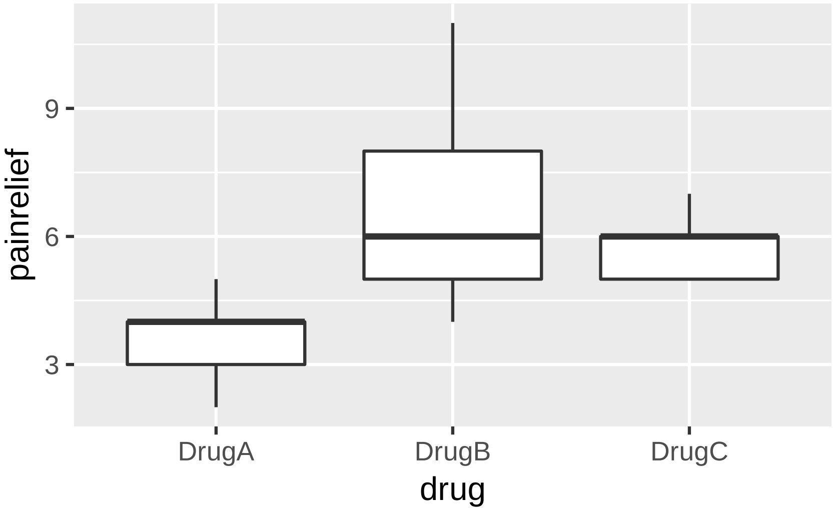
```
migraine2 %>% group_by(drug) %>% summarize(m = mean(painrelief))
```

```
## # A tibble: 3 x 2
##   drug      m
##   <chr> <dbl>
## 1 DrugA  3.67
## 2 DrugB  6.56
## 3 DrugC  5.89
```

These confirm that A is worst, and there is nothing much to choose between B and C. You should *not* recommend drug C over drug B on this evidence, just because its (sample) mean is higher than B's. The point about significant differences is that they are supposed to stand up to replication: in another experiment, or in real-life experiences with these drugs, the mean pain relief score for drug A is expected to be worst, but between drugs B and C, sometimes the mean of B will come out higher and sometimes C's mean will be higher, because there is no significant difference between them. Another way is to draw a boxplot of pain-relief scores:

This talks about *means* rather than individual observations; in individual cases, sometimes even drug *A* will come out best. But we're interested in population means, since we want to do the greatest good for the greatest number. *Greatest good for the greatest number* is from Jeremy Bentham, 1748–1832, British philosopher and advocate of utilitarianism.

```
ggplot(migraine2, aes(x = drug, y = painrelief)) +
    geom_boxplot()
```



The medians of drugs B and C are actually exactly the same. Because the pain relief values are all whole numbers (and there are only 9 in each group), you get that thing where enough of them are equal that the median and third quartiles are equal, actually for all three groups.

Despite the outlier, I'm willing to call these groups sufficiently symmetric for the ANOVA to be OK (but I didn't ask you to draw the boxplot, because I didn't want to confuse the issue with this. The point of this question was to get the data tidy enough to do an analysis.) Think about it for a moment: that outlier is a value of 8. This is really not that much bigger than the value of 7 that is the highest one on drug C. The 7 for drug C is not an outlier. The only reason the 8 came out as an outlier was because the IQR was only 1. If the IQR on drug B had happened to be a bit bigger, the 8 would not have been an outlier.

As I said, I didn't want you to have to get into this, but if you are worried, you know what the remedy is — Mood's median test. Don't forget to use the right data frame:

```
library(smmr)
median_test(migraine2, painrelief, drug)
```

```
## $table
##        above
## group   above below
##   DrugA     0     8
##   DrugB     5     2
##   DrugC     6     0
##
## $test
##        what        value
## 1 statistic 1.527273e+01
## 2        df 2.000000e+00
## 3   P-value 4.825801e-04
```

Because the pain relief scores are integers, there are probably a lot of them equal to the overall median. There were 27 observations altogether, but Mood's median test will discard any that are equal to this value. There must have been 9 observations in each group to start with, but if you look at each row of the table, there are only 8 observations listed for drug A, 7 for drug B and 6 for drug C, so there must have been 1, 2 and 3 (totalling 6) observations equal to the median that were discarded.

The P-value is a little bigger than came out of the *F*-test, but the conclusion is still that there are definitely differences among the drugs in terms of pain relief. The table at the top of the output again suggests that drug A is worse than the others, but to confirm that you'd have to do Mood's median test on all three *pairs* of drugs, and then use Bonferroni to allow for your having done three tests:

```
pairwise_median_test(migraine2, painrelief, drug)
```

```
## # A tibble: 3 x 4
##   g1    g2     p_value adj_p_value
##   <chr> <chr>    <dbl>       <dbl>
## 1 DrugA DrugB 0.00721     0.0216
## 2 DrugA DrugC 0.000183    0.000548
## 3 DrugB DrugC 0.921       2.76
```

Drug A gives worse pain relief (fewer hours) than both drugs B and C, which are not significantly different from each hour. This is exactly what you would have guessed from the boxplot.

I gotta do something about those adjusted P-values bigger than 1!

12.6 *Location, species and disease in plants*

The table below is a "contingency table", showing frequencies of diseased and undiseased plants of two different species in two different locations:

```
Species     Disease present         Disease absent
Location X Location Y  Location X Location Y
A             44         12           38        10
B             28         22           20        18
```

The data were saved as link. In that file, the columns are coded by two letters: a `p` or an `a` to denote presence or absence of disease, and an `x` or a `y` to denote location X or Y. The data are separated by multiple spaces and aligned with the variable names.

(a) Read in and display the data.

Solution

`read_table` again. You know this because, when you looked at the data file, which of course you did (didn't you?), you saw that the data values were aligned by columns with multiple spaces between them:

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/disease.txt"
tbl = read_table(my_url)
```

```
## Parsed with column specification:
## cols(
##   Species = col_character(),
##   px = col_integer(),
##   py = col_integer(),
##   ax = col_integer(),
##   ay = col_integer()
## )
```

```
tbl
```

```
## # A tibble: 2 x 5
##   Species    px    py    ax    ay
##   <chr>   <int> <int> <int> <int>
## 1 A          44    12    38    10
## 2 B          28    22    20    18
```

I was thinking ahead, since I'll be wanting to have one of my columns called `disease`, so I'm *not* calling the data frame `disease`.

You'll also have noticed that I simplified the data frame that I had you read in, because the original contingency table I showed you has *two* header rows, and we have to have *one* header row. So I mixed up the information in the two header rows into one.

(b)??part:nottidy?? Explain briefly how these data are not "tidy".

Solution

The simple answer is that there are 8 frequencies, that each ought to be in a row by themselves. Or, if you like, there are three variables, Species, Disease status and Location, and each of *those* should be in a *column* of its own. Either one of these ideas, or something like it, is good. I need you to demonstrate that you know something about "tidy data" in this context.

(c) Use a suitable `tidyr` tool to get all the things that are the same into a single column. (You'll need to make up a temporary name for the other new column that you create.) Show your result.

Solution

`gather` is the tool. All the columns apart from `Species` contain frequencies, so that's what's "the same". They are frequencies in disease-location combinations, so I'll call the column of "what's different" `disloc`. Feel free to call it `temp` for now if you prefer:

```
(tbl.2 <- tbl %>% gather(disloc, frequency, px:ay))
```

```
## # A tibble: 8 x 3
##   Species disloc frequency
##   <chr>   <chr>      <int>
## 1 A       px            44
## 2 B       px            28
## 3 A       py            12
## 4 B       py            22
## 5 A       ax            38
## 6 B       ax            20
## 7 A       ay            10
## 8 B       ay            18
```

This also works ("gather together everything but `Species`"):

```
(tbl.2 <- tbl %>% gather(disloc, frequency, -Species))
```

```
## # A tibble: 8 x 3
##   Species disloc frequency
##   <chr>   <chr>      <int>
## 1 A       px            44
## 2 B       px            28
## 3 A       py            12
## 4 B       py            22
## 5 A       ax            38
## 6 B       ax            20
## 7 A       ay            10
## 8 B       ay            18
```

(d) Explain briefly how the data frame you just created is still not "tidy" yet.

Solution

The column I called `disloc` actually contains *two* variables, disease and location, which need to be split up. A check on this is that we have two columns (not including the frequencies), but back in (??part:nottidy??) we found *three* variables, so there ought to be three non-frequency columns.

(e) Use one more `tidyr` tool to make these data tidy, and show your result.

Solution

This means splitting up `disloc` into two separate columns, splitting after the first character, thus:

```
(tbl.3 <- tbl.2 %>% separate(disloc, c("disease",
    "location"), 1))
```

```
## # A tibble: 8 x 4
##   Species disease location frequency
##   <chr>   <chr>   <chr>        <int>
## 1 A       p       x               44
## 2 B       p       x               28
## 3 A       p       y               12
## 4 B       p       y               22
## 5 A       a       x               38
## 6 B       a       x               20
## 7 A       a       y               10
## 8 B       a       y               18
```

This is now tidy: eight frequencies in rows, and three non-frequency columns. (Go back and look at your answer to part (??part:nottidy??) and note that the issues you found there have all been resolved now.)

(f) Let's see if we can re-construct the original contingency table (or something equivalent to it). Use the function `xtabs`. This requires first a model formula with the frequency variable on the left of the squiggle, and the other variables separated by plus signs on the right. Second it requires a data frame, with `data=`. Feed your data frame from the previous part into `xtabs`. Save the result in a variable and display the result.

Solution

```
tbl.4 = xtabs(frequency ~ Species + disease +
    location, data = tbl.3)
tbl.4
```

```
## , , location = x
##
##        disease
## Species  a  p
##       A 38 44
##       B 20 28
##
## , , location = y
##
##        disease
## Species  a  p
##       A 10 12
##       B 18 22
```

This shows a pair of contingency tables, one each for each of the two locations (in general, the variable you put last on the right side of the model formula). You can check that everything corresponds with the original data layout at the beginning of the question, possibly with some things rearranged (but with the same frequencies in the same places).

(g) Take the output from the last part and feed it into the function `ftable`. How has the output been changed? Which do you like better? Explain briefly.

Solution

This:

```
ftable(tbl.4)
```

```
##                 location  x  y
## Species disease
## A       a                38 10
##         p               44 12
## B       a               20 18
##         p               28 22
```

This is the same output, but shown more compactly. (Rather like a vertical version of the original data, in fact.) I like `ftable` better because it displays the data in the smallest amount of space, though I'm fine if you prefer the `xtabs` output because it spreads things out more. This is a matter of taste. Pick one and tell me why you prefer it, and I'm good.

That's the end of what you had to do, but I thought I would do some modelling and try to find out what's associated with disease. The appropriate modelling with frequencies is called "log-linear modelling", and it assumes that the log of the frequencies has a linear relationship with the effects of the other variables. This is not quite as simple as the log transformations we had before, because bigger frequencies are going to be more variable, so we fit a generalized linear model with a Poisson-distributed response and log link. (It's better if you know what that means, but you ought to be able to follow the logic if you don't.)

First, fit a model predicting frequency from everything, including all the interactions. (The reason for doing it this way will become clear later):

```
model.1 = glm(frequency ~ Species * location *
    disease, data = tbl.3, family = "poisson")
drop1(model.1, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## frequency ~ Species * location * disease
##                          Df Deviance    AIC
## <none>                      0.000000 55.291
## Species:location:disease  1 0.070257 53.362
##                               LRT Pr(>Chi)
## <none>
## Species:location:disease 0.070257    0.791
```

The residuals are all zero because this model fits perfectly. The problem is that it is very complicated, so it offers no insight. So what we do is to look at the highest-order interaction `Species:location:disease` and see whether it is significant. It is not, so we can remove it. This is reminiscent of variable selection in regression, where we pull the least significant thing out of the model in turn until we can go no further. But here, we have additional things to think about: we have to get rid of all the three-way interactions before we can tackle the two-way ones, and all the two-way ones before we can tackle the main effects. There is a so-called "nested" structure happening here that says you don't look at, say, `Species`, until you have removed *all* the higher-order interactions involving `Species`. Not clear yet? Don't fret. `drop1` allows you to assess what is currently up for grabs (here, only the three-way interaction, which is not significant, so out it comes).

Let's get rid of that three-way interaction. This is another use for `update` that we've seen in connection with multiple regression (to make small changes to a big model):

```
model.2 = update(model.1, . ~ . - Species:location:disease)
drop1(model.2, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## frequency ~ Species + location + disease + Species:location +
##     Species:disease + location:disease
##                  Df Deviance    AIC     LRT
## <none>                0.0703 53.362
## Species:location  1  13.0627 64.354 12.9924
## Species:disease   1   0.2696 51.561  0.1993
## location:disease  1   0.1043 51.396  0.0340
##                   Pr(>Chi)
## <none>
## Species:location 0.0003128 ***
## Species:disease  0.6552865
## location:disease 0.8536877
## ---
## Signif. codes:
##   0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1  ’ ’ 1
```

Notice how `update` saved us having to write the whole model out again.

Now the three two-way interactions are up for grabs: `Species:location`, `Species:disease` and `location:disease`. The last of these is the least significant, so out it comes. I did some copying and pasting, but I had to remember which model I was working with and what I was removing:

```
model.3 = update(model.2, . ~ . - location:disease)
drop1(model.3, test = "Chisq")
```

```
## Single term deletions
##
```

```
## Model:
## frequency ~ Species + location + disease + Species:location +
##     Species:disease
##                  Df Deviance    AIC     LRT
## <none>                0.1043 51.396
## Species:location  1  13.0678 62.359 12.9635
## Species:disease   1   0.2746 49.566  0.1703
##                   Pr(>Chi)
## <none>
## Species:location 0.0003176 ***
## Species:disease  0.6798021
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
```

`Species:disease` comes out, but it looks as if `Species:location` will have to stay:

```
model.4 = update(model.3, . ~ . - Species:disease)
drop1(model.4, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## frequency ~ Species + location + disease + Species:location
##                  Df Deviance    AIC     LRT
## <none>                0.2746 49.566
## disease           1   2.3617 49.653  2.0871
## Species:location  1  13.2381 60.530 12.9635
##                   Pr(>Chi)
## <none>
## disease          0.1485461
## Species:location 0.0003176 ***
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
```

`Species:location` indeed stays. That means that anything "contained in" it also has to stay, regardless of its main effect. So the only candidate for removal now is `disease`: not significant, out it comes:

```
model.5 = update(model.4, . ~ . - disease)
drop1(model.5, test = "Chisq")
```

```
## Single term deletions
##
```

```
## Model:
## frequency ~ Species + location + Species:location
##                   Df Deviance    AIC    LRT
## <none>                 2.3617 49.653
## Species:location  1  15.3252 60.617 12.963
##                    Pr(>Chi)
## <none>
## Species:location 0.0003176 ***
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
```

And now we have to stop.

What does this final model mean? Well, frequency depends significantly on the `Species:location` combination, but not on anything else. To see how, we make a contingency table of species by location (totalling up over disease status, since that is not significant):

```
xtabs(frequency ~ Species + location, data = tbl.3)
```

```
##        location
## Species  x  y
##       A 82 22
##       B 48 40
```

Most of the species A's are at location X, but the species B's are about evenly divided between the two locations. Or, if you prefer (equally good): location X has mostly species A, while location Y has mostly species B. You can condition on either variable and compare the conditional distribution of the other one.

Now, this is rather interesting, because this began as a study of disease, but disease has completely disappeared from our final model! That means that nothing in our final model has any relationship with disease. Indeed, if you check the original table, you'll find that disease is present slightly more than it's absent, for all combinations of species and location. That is, neither species nor location has any particular association with (effect on) disease, since disease prevalence doesn't change appreciably if you change location, species or the combination of them.

The way an association with disease would show up is if a `disease:`something interaction had been significant and had stayed in the model, that something would have been associated with disease. For example, if the `disease:Species` table had looked like this:

```
disease = c("a", "a", "p", "p")
Species = c("A", "B", "A", "B")
```

```
frequency = c(10, 50, 30, 30)
xx = data.frame(disease, Species, frequency)
xtabs(frequency ~ disease + Species)
```

```
##        Species
## disease  A  B
##       a 10 50
##       p 30 30
```

For species A, disease is present 75% of the time, but for species B it’s present less than 40% of the time. So in this one there ought to be a significant association between disease and species:

```
xx.1 = glm(frequency ~ disease * Species, data = xx,
    family = "poisson")
drop1(xx.1, test = "Chisq")
```

```
## Single term deletions
##
## Model:
## frequency ~ disease * Species
##                 Df Deviance    AIC    LRT
## <none>                0.000 28.400
## disease:Species  1   15.518 41.918 15.518
##                  Pr(>Chi)
## <none>
## disease:Species 8.171e-05 ***
## ---
## Signif. codes:
##   0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1  ’ ’ 1
```

And so there is. Nothing can come out of the model. (This is the same kind of test as a chi-squared test for association, if you know about that. The log-linear model is a multi-variable generalization of that.)

12.7 *Cars*

My cars data file can be found at link. The values in the data file are separated by commas; the car names are up to 29 characters long. Display your results for each part after (a). In R, displaying a `tibble` normally shows its first ten lines, which is all you need here; there’s no need to display all the lines.

(a) Read the data into R and list the values.

Solution

read_csv will do it:

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/cars.csv"
cars = read_csv(my_url)
```

```
## Parsed with column specification:
## cols(
##   car = col_character(),
##   MPG = col_double(),
##   weight = col_double(),
##   cylinders = col_integer(),
##   hp = col_integer(),
##   country = col_character()
## )
```

```
cars
```

```
## # A tibble: 38 x 6
##    car    MPG weight cylinders    hp country
##    <ch> <dbl>  <dbl>     <int> <int> <chr>
##  1 Bui~  28.4   2.67         4    90 U.S.
##  2 Dod~  30.9   2.23         4    75 U.S.
##  3 Mer~  20.8   3.07         6    85 U.S.
##  4 Fia~  37.3   2.13         4    69 Italy
##  5 Peu~  16.2   3.41         6   133 France
##  6 VW ~  31.9   1.92         4    71 Germany
##  7 Ply~  34.2   2.2          4    70 U.S.
##  8 Maz~  34.1   1.98         4    65 Japan
##  9 Bui~  16.9   4.36         8   155 U.S.
## 10 Aud~  20.3   2.83         5   103 Germany
## # ... with 28 more rows
```

(b) Display only the car names and the countries they come from.

Solution

```
cars %>% select(car, country)
```

```
## # A tibble: 38 x 2
##    car                country
##    <chr>              <chr>
##  1 Buick Skylark      U.S.
##  2 Dodge Omni         U.S.
##  3 Mercury Zephyr     U.S.
##  4 Fiat Strada        Italy
##  5 Peugeot 694 SL     France
##  6 VW Rabbit          Germany
##  7 Plymouth Horizon   U.S.
##  8 Mazda GLC          Japan
##  9 Buick Estate Wagon U.S.
## 10 Audi 5000          Germany
## # ... with 28 more rows
```

This *almost* works, but not quite:

```
cars %>% select(starts_with("c"))
```

```
## # A tibble: 38 x 3
##    car                cylinders country
##    <chr>                  <int> <chr>
##  1 Buick Skylark              4 U.S.
##  2 Dodge Omni                 4 U.S.
##  3 Mercury Zephyr             6 U.S.
##  4 Fiat Strada                4 Italy
##  5 Peugeot 694 SL             6 France
##  6 VW Rabbit                  4 Germany
##  7 Plymouth Horizon           4 U.S.
##  8 Mazda GLC                  4 Japan
##  9 Buick Estate Wagon         8 U.S.
## 10 Audi 5000                  5 Germany
## # ... with 28 more rows
```

It gets *all* the columns that start with c, which includes cylinders as well.

(c) Display everything *except* horsepower:

Solution
Naming what you *don't* want is sometimes easier:

```
cars %>% select(-hp)
```

```
## # A tibble: 38 x 5
##    car          MPG weight cylinders country
##    <chr>      <dbl>  <dbl>     <int> <chr>
##  1 Buick Sky~  28.4   2.67         4 U.S.
##  2 Dodge Omni  30.9   2.23         4 U.S.
##  3 Mercury Z~  20.8   3.07         6 U.S.
##  4 Fiat Stra~  37.3   2.13         4 Italy
##  5 Peugeot 6~  16.2   3.41         6 France
##  6 VW Rabbit   31.9   1.92         4 Germany
##  7 Plymouth ~  34.2   2.2          4 U.S.
##  8 Mazda GLC   34.1   1.98         4 Japan
##  9 Buick Est~  16.9   4.36         8 U.S.
## 10 Audi 5000   20.3   2.83         5 Germany
## # ... with 28 more rows
```

(d) Display only the cars that have 8-cylinder engines (but display all the variables for those cars).

Solution
This:

```
cars %>% filter(cylinders == 8)
```

```
## # A tibble: 8 x 6
##   car     MPG weight cylinders    hp country
##   <chr> <dbl>  <dbl>     <int> <int> <chr>
## 1 Buic~  16.9   4.36         8   155 U.S.
## 2 Chev~  19.2   3.60         8   125 U.S.
## 3 Chry~  18.5   3.94         8   150 U.S.
## 4 Ford~  17.6   3.72         8   129 U.S.
## 5 Dodg~  18.2   3.83         8   135 U.S.
## 6 Ford~  15.5   4.05         8   142 U.S.
## 7 Merc~  16.5   3.96         8   138 U.S.
## 8 Chev~  17     3.84         8   130 U.S.
```

8 of them, all from the US.

(e) Display the cylinders and horsepower for the cars that have horsepower 70 or less.

Solution
This one is selecting some observations and some variables:

```
cars %>% filter(hp <= 70) %>% select(cylinders:hp)
```

```
## # A tibble: 6 x 2
##   cylinders    hp
##       <int> <int>
## 1         4    69
## 2         4    70
## 3         4    65
## 4         4    65
## 5         4    68
## 6         4    68
```

Cylinders and horsepower are consecutive columns, so we can select them either using the colon `:` or by `c(cylinders,hp)`.

You can also do the `filter` and the `select` the other way around. This one works because the *rows* you want to choose are determined by a column you're going to keep. If you wanted to display the cylinders and horsepower of the cars with `mpg` over 30, you would have to choose the rows first, because after you've chosen the columns, there is no `mpg` any more.

(f) Find the mean and SD of gas mileage of the cars with 4 cylinders.

Solution

```
cars %>% filter(cylinders == 4) %>% summarize(m = mean(MPG),
    s = sd(MPG))
```

```
## # A tibble: 1 x 2
##       m     s
##   <dbl> <dbl>
## 1  30.0  4.18
```

Or you can get the mean and SD of gas mileage for all numbers of cylinders, and pick out the one you want:

```
cars %>% group_by(cylinders) %>% summarize(m = mean(MPG),
    s = sd(MPG))
```

```
## # A tibble: 4 x 3
##   cylinders     m     s
##       <int> <dbl> <dbl>
## 1         4  30.0  4.18
## 2         5  20.3 NA
## 3         6  21.1  4.08
## 4         8  17.4  1.19
```

Top row is the same as before. And since the output is a data frame, you can do any of these things with *that*, for example:

```
cars %>% group_by(cylinders) %>% summarize(m = mean(MPG),
    s = sd(MPG)) %>% filter(cylinders == 4)
```

```
## # A tibble: 1 x 3
##   cylinders     m     s
##       <int> <dbl> <dbl>
## 1         4  30.0  4.18
```

to pick out just the right row. This is a very easy kind of question to set on an exam. Just so you know.

12.8 Number 1 songs

The data file link contains a lot of information about songs popular in 2000. This dataset is untidy. Our ultimate aim is to answer "which song occupied the #1 position for the largest number of weeks?". To do that, we will build a pipe that starts from the data frame read in from the URL above, and finishes with an answer to the question. I will take you through this step by step. Each part will involve adding something to the pipe you built previously (possibly after removing a line or two that you used to display the previous result).

(a) Read the data and display what you have.

Solution

```
billboard = read_csv("http://stat405.had.co.nz/data/billboard.csv")
```

```
## Parsed with column specification:
## cols(
##   .default = col_integer(),
##   artist.inverted = col_character(),
##   track = col_character(),
##   time = col_time(format = ""),
##   genre = col_character(),
##   date.entered = col_date(format = ""),
##   date.peaked = col_date(format = ""),
##   x66th.week = col_character(),
##   x67th.week = col_character(),
##   x68th.week = col_character(),
##   x69th.week = col_character(),
##   x70th.week = col_character(),
##   x71st.week = col_character(),
##   x72nd.week = col_character(),
##   x73rd.week = col_character(),
##   x74th.week = col_character(),
##   x75th.week = col_character(),
##   x76th.week = col_character()
## )
```

```
## See spec(...) for full column specifications.
```

There are a *lot* of columns. What does this look like?

```
billboard
```

```
## # A tibble: 317 x 83
##     year artist.inverted track time  genre
##    <int> <chr>           <chr> <tim> <chr>
##  1  2000 Destiny's Child Inde~ 03:38 Rock
##  2  2000 Santana         Mari~ 04:18 Rock
##  3  2000 Savage Garden   I Kn~ 04:07 Rock
##  4  2000 Madonna         Music 03:45 Rock
##  5  2000 Aguilera, Chri~ Come~ 03:38 Rock
##  6  2000 Janet           Does~ 04:17 Rock
##  7  2000 Destiny’s Child Say ~ 04:31 Rock
##  8  2000 Iglesias, Enri~ Be W~ 03:36 Latin
##  9  2000 Sisqo           Inco~ 03:52 Rock
## 10  2000 Lonestar        Amaz~ 04:25 Coun~
## # ... with 307 more rows, and 78 more
## #   variables: date.entered <date>,
## #   date.peaked <date>, x1st.week <int>,
## #   x2nd.week <int>, x3rd.week <int>,
## #   x4th.week <int>, x5th.week <int>,
## #   x6th.week <int>, x7th.week <int>,
## #   x8th.week <int>, x9th.week <int>,
## #   x10th.week <int>, x11th.week <int>,
## #   x12th.week <int>, x13th.week <int>,
## #   x14th.week <int>, x15th.week <int>,
## #   x16th.week <int>, x17th.week <int>,
## #   x18th.week <int>, x19th.week <int>,
## #   x20th.week <int>, x21st.week <int>,
## #   x22nd.week <int>, x23rd.week <int>,
## #   x24th.week <int>, x25th.week <int>,
## #   x26th.week <int>, x27th.week <int>,
## #   x28th.week <int>, x29th.week <int>,
## #   x30th.week <int>, x31st.week <int>,
## #   x32nd.week <int>, x33rd.week <int>,
## #   x34th.week <int>, x35th.week <int>,
## #   x36th.week <int>, x37th.week <int>,
## #   x38th.week <int>, x39th.week <int>,
## #   x40th.week <int>, x41st.week <int>,
## #   x42nd.week <int>, x43rd.week <int>,
## #   x44th.week <int>, x45th.week <int>,
## #   x46th.week <int>, x47th.week <int>,
## #   x48th.week <int>, x49th.week <int>,
## #   x50th.week <int>, x51st.week <int>,
## #   x52nd.week <int>, x53rd.week <int>,
## #   x54th.week <int>, x55th.week <int>,
## #   x56th.week <int>, x57th.week <int>,
## #   x58th.week <int>, x59th.week <int>,
## #   x60th.week <int>, x61st.week <int>,
## #   x62nd.week <int>, x63rd.week <int>,
## #   x64th.week <int>, x65th.week <int>,
## #   x66th.week <chr>, x67th.week <chr>,
## #   x68th.week <chr>, x69th.week <chr>,
## #   x70th.week <chr>, x71st.week <chr>,
## #   x72nd.week <chr>, x73rd.week <chr>,
## #   x74th.week <chr>, x75th.week <chr>,
## #   x76th.week <chr>
```

On yours, you will definitely see a little arrow top right saying "there are more columns", and you will have to click on it several times to see them all.

(b) The columns `x1st.week` through `x76th.week` contain the rank of each song in the Billboard chart in that week, with week 1 being the first week that the song appeared in the chart. Convert all these columns into two: an indication of week, called `week`, and of rank, called `rank`. Most songs appeared in the Billboard chart for a lot less than 76 weeks, so there are missing values, which you want to remove. (I say "indication of week" since this will probably be text at the moment). Display your new data frame. Do you have fewer columns? Why do you have a lot more rows? Explain briefly.

Solution

This is `gather`ing up all those columns, with `na.rm=T` to get rid of the missings:

```
billboard %>% gather(week, rank, x1st.week:x76th.week,
    na.rm = T)
```

```
## # A tibble: 5,307 x 9
##     year artist.inverted track time  genre
##   * <int> <chr>           <chr> <tim> <chr>
##  1  2000 Destiny's Child Inde~ 03:38 Rock
##  2  2000 Santana         Mari~ 04:18 Rock
##  3  2000 Savage Garden   I Kn~ 04:07 Rock
##  4  2000 Madonna         Music 03:45 Rock
##  5  2000 Aguilera, Chri~ Come~ 03:38 Rock
##  6  2000 Janet           Does~ 04:17 Rock
##  7  2000 Destiny's Child Say ~ 04:31 Rock
##  8  2000 Iglesias, Enri~ Be W~ 03:36 Latin
##  9  2000 Sisqo           Inco~ 03:52 Rock
## 10  2000 Lonestar        Amaz~ 04:25 Coun~
## # ... with 5,297 more rows, and 4 more
## #   variables: date.entered <date>,
## #   date.peaked <date>, week <chr>,
## #   rank <chr>
```

Another way to do this is with a select-helper: all those column names end with `week`, so we can select them all thus:

```
billboard %>% gather(week, rank, ends_with("week"),
    na.rm = T)
```

```
## # A tibble: 5,307 x 9
##     year artist.inverted track time  genre
##   * <int> <chr>           <chr> <tim> <chr>
##   1  2000 Destiny's Child Inde~ 03:38 Rock
##   2  2000 Santana         Mari~ 04:18 Rock
##   3  2000 Savage Garden   I Kn~ 04:07 Rock
##   4  2000 Madonna         Music 03:45 Rock
##   5  2000 Aguilera, Chri~ Come~ 03:38 Rock
##   6  2000 Janet           Does~ 04:17 Rock
##   7  2000 Destiny's Child Say ~ 04:31 Rock
##   8  2000 Iglesias, Enri~ Be W~ 03:36 Latin
##   9  2000 Sisqo           Inco~ 03:52 Rock
## 10  2000 Lonestar        Amaz~ 04:25 Coun~
## # ... with 5,297 more rows, and 4 more
## #   variables: date.entered <date>,
## #   date.peaked <date>, week <chr>,
## #   rank <chr>
```

There are now only 9 columns, a lot fewer than we started with. This is (I didn't need you to say) because we have collected together all those week columns into one (a column called rank with an indication of which week it came from). The logic of the gather is that all those columns contain ranks (which is what make them the same), but they are ranks from different weeks (which is what makes them different).

What has actually happened is that we have turned "wide" format into "long" format. This is not very insightful, so I would like you to go a bit further in your explanation. The original data frame encodes the rank of each song in each week, and what the gather has done is to make that explicit: in the new data frame, each song's rank in each week appears in *one* row, so that there are as many rows as there are song-week combinations. The original data frame had 317 songs over 76 weeks, so this many:

```
317 * 76
```

```
## [1] 24092
```

song-week combinations.

Not every song appeared in the Billboard chart for 76 weeks, so our tidy data frame has a lot fewer rows than this.

You need to say that the original data frame had each song appearing once (on one line), but now each song appears on multiple rows, one for each week that the song was in the chart. Or something equivalent to that.

(c) Display just your two new columns (for the first few rows). Add something appropriate onto the end of your pipe to do this.

Solution
A select is the thing:

```
billboard %>% gather(week, rank, x1st.week:x76th.week,
    na.rm = T) %>% select(week, rank)
```

```
## # A tibble: 5,307 x 2
##    week      rank
##  * <chr>     <chr>
##  1 x1st.week 78
##  2 x1st.week 15
##  3 x1st.week 71
##  4 x1st.week 41
##  5 x1st.week 57
##  6 x1st.week 59
##  7 x1st.week 83
##  8 x1st.week 63
##  9 x1st.week 77
## 10 x1st.week 81
## # ... with 5,297 more rows
```

(d) Both your week and rank columns are (probably) text. Create new columns that contain just the numeric values, and display just your new columns, again adding onto the end of your pipe. (In the previous part, you probably had some code that picked out a few columns to display them. Get rid of that.)

Solution
parse_number is the easiest. Create new columns, with mutate, that are the parse_number-ed versions of the old ones.

```
billboard %>% gather(week, rank, x1st.week:x76th.week,
    na.rm = T) %>% mutate(week_number = parse_number(week),
    rank_number = parse_number(rank)) %>% select(ends_with("number"))
```

```
## # A tibble: 5,307 x 2
##    week_number rank_number
##          <dbl>       <dbl>
##  1           1          78
##  2           1          15
##  3           1          71
##  4           1          41
##  5           1          57
##  6           1          59
##  7           1          83
##  8           1          63
##  9           1          77
## 10           1          81
## # ... with 5,297 more rows
```

You see that these are indeed numbers. (I gave my new columns names that ended with `number`, which meant that I could select them with the select-helper `ends_with`. I'm not insisting that you do this, but it's a handy trick.)

Since `rank` already looks like a number, but happens to be text, you can also convert it with `as.numeric` (or `as.integer`, since it is actually text that looks like a whole number). For converting `rank`, these are also good, but for converting `week`, you need something that will pull out the number. (`str_extract` from `stringr` will also do it, but that's beyond our scope now. It's on page 212 of the R book if you wish to investigate it. But `parse_number` is a lot easier.)

(e) The meaning of your week-number column is that it refers to the number of weeks *after* the song first appeared in the Billboard chart. That is, if a song's first appearance (in `date.entered)` is July 24, then week 1 is July 24, week 2 is July 31, week 3 is August 7, and so on. Create a column `current` by adding the appropriate number of *days*, based on your week number, to `date.entered`. Display `date.entered`, your week number, and `current` to show that you have calculated the right thing. Note that you can add a number of days onto a date and you will get another date.

Solution

There is a (small) gotcha here: if you read carefully, you'll see that "week 1" is actually "week 0" in terms of the number of days to add on to `date.entered`. So you have to subtract one from the number of weeks before you multiply it by seven to get a number of days. After that thinking, this:

```
billboard %>% gather(week, rank, x1st.week:x76th.week,
    na.rm = T) %>% mutate(week_number = parse_number(week),
    rank_number = parse_number(rank)) %>% mutate(current = date.entered +
    (week_number - 1) * 7) %>% select(date.entered,
    week_number, current)
```

```
## # A tibble: 5,307 x 3
##    date.entered week_number current
##    <date>              <dbl> <date>
##  1 2000-09-23              1 2000-09-23
##  2 2000-02-12              1 2000-02-12
##  3 1999-10-23              1 1999-10-23
##  4 2000-08-12              1 2000-08-12
##  5 2000-08-05              1 2000-08-05
##  6 2000-06-17              1 2000-06-17
##  7 1999-12-25              1 1999-12-25
##  8 2000-04-01              1 2000-04-01
##  9 2000-06-24              1 2000-06-24
## 10 1999-06-05              1 1999-06-05
## # ... with 5,297 more rows
```

Don't forget to use your week-turned-into-number, or else it won't work! (This bit me too, so you don't need to feel bad.)

You can also combine the three column-definition statements into one mutate. It doesn't matter; as soon as you have defined a column, you can use it in defining another column, even within the same `mutate`.

Anyway, the rows displayed are all `week_number` 1, so the `current` date should be the same as `date.entered`, and is. (These are all the first week that a song is in the Billboard chart).

You might be thinking that this is not much of a check, and you would be right. A handy trick is to display a random sample of 10 (say) out of the 5,000-odd rows of the data frame. To do that, add the line `sample_n(10)` on the end, like this:

```
billboard %>% gather(week, rank, x1st.week:x76th.week,
    na.rm = T) %>% mutate(week_number = parse_number(week),
    rank_number = parse_number(rank)) %>% mutate(current = date.entered +
    (week_number - 1) * 7) %>% select(date.entered,
    week_number, current) %>% sample_n(10)
```

```
## # A tibble: 10 x 3
##    date.entered week_number current
##    <date>              <dbl> <date>
##  1 2000-03-18             27 2000-09-16
##  2 2000-08-12              3 2000-08-26
##  3 2000-09-23              4 2000-10-14
##  4 1999-12-04             11 2000-02-12
##  5 2000-01-22              8 2000-03-11
##  6 2000-05-27             16 2000-09-09
##  7 2000-04-29              5 2000-05-27
##  8 2000-06-10              4 2000-07-01
##  9 2000-04-15             12 2000-07-01
## 10 2000-08-26             18 2000-12-23
```

This gives a variety of rows to check. The first current should be $27 - 1 = 26$ weeks, or about 6 months, after the date the song entered the chart, and so it is; the second one should be $3 - 1 = 2$ weeks after entry, and it is. The third one should be 3 weeks after September 23; this is (as I figure it) September $23 + 21 = 44$, and September has 30 days, so this is really October 14. Check.

Your random selection of rows is likely to be different from mine, but the same kind of thinking will enable you to check whether it makes sense.

(f) Reaching the #1 rank on the Billboard chart is one of the highest accolades in the popular music world. List all the songs that reached rank 1. For these songs, list the artist (as given in the data set), the song title, and the date(s) for which the song was ranked number 1. Arrange the songs in date order of being ranked #1. Display all the songs (I found 55 of them).

Solution

To the previous pipe, add the last lines below. You can use either rank (text) or what I called rank_number (a number). It doesn't matter here, since we are only checking for equal-to, not something like "less than":

```
billboard %>% gather(week, rank, x1st.week:x76th.week,
    na.rm = T) %>% mutate(week_number = parse_number(week),
    rank_number = parse_number(rank)) %>% mutate(current = date.entered +
    (week_number - 1) * 7) %>% filter(rank ==
    1) %>% arrange(current) %>% select(artist.inverted,
    track, current)
```

```
## # A tibble: 55 x 3
##    artist.inverted   track        current
##    <chr>             <chr>        <date>
##  1 Aguilera, Christ~ What A Girl~ 2000-01-15
##  2 Aguilera, Christ~ What A Girl~ 2000-01-22
##  3 Savage Garden     I Knew I Lo~ 2000-01-29
##  4 Savage Garden     I Knew I Lo~ 2000-02-05
##  5 Savage Garden     I Knew I Lo~ 2000-02-12
##  6 Carey, Mariah     Thank God I~ 2000-02-19
##  7 Savage Garden     I Knew I Lo~ 2000-02-26
##  8 Lonestar          Amazed       2000-03-04
##  9 Lonestar          Amazed       2000-03-11
## 10 Destiny's Child   Say My Name  2000-03-18
## # ... with 45 more rows
```

You'll see the first ten rows, as here, but with clickable buttons to see the next 10 (and the previous 10 if you have moved beyond 1–10).

The "artist" column is called `artist.inverted` because, if the artist is a single person rather than a group, their last name is listed first. The song title appears in the column `track`.

The song by Destiny's Child spills into 2001 because it entered the chart in 2000, and the data set keeps a record of all such songs until they drop out of the chart. I'm not sure what happened to the song that was #1 on January 8, 2000; maybe it entered the chart in 1999 and so is not listed here.

Which was the title of a song by Prince.

(g) Use R to find out which song held the #1 rank for the largest number of weeks. For this, you can assume that the song titles are all unique (if it's the same song title, it's the same song), but the artists might not be (for example, Madonna might have had two different songs reach the #1 rank). The information you need is in the output you obtained for the previous part, so it's a matter of adding some code to the end of that. The last mark was for displaying *only* the song that was ranked #1 for the largest number of weeks, or for otherwise making it easy to see which song it was.

Solution

This is a question of using `count`, but on the `track` title:

```
billboard %>% gather(week, rank, x1st.week:x76th.week,
    na.rm = T) %>% mutate(week_number = parse_number(week),
    rank_number = parse_number(rank)) %>% mutate(current = date.entered +
    (week_number - 1) * 7) %>% filter(rank ==
    1) %>% arrange(current) %>% select(artist.inverted,
    track, current) %>% count(track)
```

```
## # A tibble: 17 x 2
##    track                                n
##    <chr>                            <int>
##  1 Amazed                               2
##  2 Bent                                 1
##  3 Be With You                          3
##  4 Come On Over Baby (All I Want Is Y~  4
##  5 Doesn't Really Matter                3
##  6 Everything You Want                  1
##  7 I Knew I Loved You                   4
##  8 Incomplete                           2
##  9 Independent Women Part I            11
## 10 It's Gonna Be Me                     2
## 11 Maria, Maria                        10
## 12 Music                                4
## 13 Say My Name                          3
## 14 Thank God I Found You                1
## 15 Try Again                                1
## 16 What A Girl Wants                        2
## 17 With Arms Wide Open                      1
```

Then you can scan down the n column, find that the biggest number is 11, and say: it's the song "Independent Women Part I" by Destiny's Child. This is 3 points (out of 4, when the question was to be handed in).

But, this is a data frame, so anything we can do to a data frame we can do to this, like listing out only the row(s) where n is equal to its maximum value:

```
billboard %>% gather(week, rank, x1st.week:x76th.week,
    na.rm = T) %>% mutate(week_number = parse_number(week),
    rank_number = parse_number(rank)) %>% mutate(current = date.entered +
    (week_number - 1) * 7) %>% filter(rank ==
    1) %>% arrange(current) %>% select(artist.inverted,
    track, current) %>% count(track) %>% filter(n ==
    max(n))
```

```
## # A tibble: 1 x 2
##   track                        n
##   <chr>                    <int>
## 1 Independent Women Part I    11
```

or arranging them in (most logically, descending) order by n to make it easier to pick out the top one:

```
billboard %>% gather(week, rank, x1st.week:x76th.week,
    na.rm = T) %>% mutate(week_number = parse_number(week),
    rank_number = parse_number(rank)) %>% mutate(current = date.entered +
    (week_number - 1) * 7) %>% filter(rank ==
    1) %>% arrange(current) %>% select(artist.inverted,
    track, current) %>% count(track) %>% arrange(desc(n))
```

```
## # A tibble: 17 x 2
##    track                                       n
##    <chr>                                   <int>
##  1 Independent Women Part I                   11
##  2 Maria, Maria                               10
##  3 Come On Over Baby (All I Want Is Y~         4
##  4 I Knew I Loved You                          4
##  5 Music                                       4
##  6 Be With You                                 3
##  7 Doesn't Really Matter                       3
##  8 Say My Name                                 3
##  9 Amazed                              2
## 10 Incomplete                          2
## 11 It’s Gonna Be Me                    2
## 12 What A Girl Wants                   2
## 13 Bent                                1
## 14 Everything You Want                 1
## 15 Thank God I Found You               1
## 16 Try Again                           1
## 17 With Arms Wide Open                 1
```

Either of those will net you the 4th point.

If you want to be a little bit more careful, you can make an artist-track combination as below. This would catch occasions where the same song by two different artists made it to #1, or two different songs that happened to have the same title did. It’s not very likely that the same artist would record two *different* songs with the same title, though it is possible that the same song by the same artist could appear in the Billboard chart on two different occasions.

As, for example, when Prince died.

I think I want to create an artist-song combo fairly early in my pipe, and then display *that* later, something like this. This means replacing `track` by my `combo` later in the pipe, wherever it appears:

```
billboard %>% gather(week, rank, x1st.week:x76th.week,
    na.rm = T) %>% mutate(week_number = parse_number(week),
    rank_number = parse_number(rank)) %>% mutate(combo = paste(track,
    artist.inverted, sep = " by ")) %>% mutate(current = date.entered +
    (week_number - 1) * 7) %>% filter(rank ==
    1) %>% arrange(current) %>% select(combo,
    current) %>% count(combo) %>% arrange(desc(n))
```

```
## # A tibble: 17 x 2
##    combo                                  n
##    <chr>                              <int>
##  1 Independent Women Part I by Destin~    11
##  2 Maria, Maria by Santana               10
##  3 Come On Over Baby (All I Want Is Y~     4
##  4 I Knew I Loved You by Savage Garden     4
##  5 Music by Madonna                        4
##  6 Be With You by Iglesias, Enrique        3
##  7 Doesn’t Really Matter by Janet          3
##  8 Say My Name by Destiny’s Child          3
##  9 Amazed by Lonestar                      2
## 10 Incomplete by Sisqo                     2
## 11 It’s Gonna Be Me by N’Sync              2
## 12 What A Girl Wants by Aguilera, Chr~     2
## 13 Bent by matchbox twenty                1
## 14 Everything You Want by Vertical Ho~     1
## 15 Thank God I Found You by Carey, Ma~     1
## 16 Try Again by Aaliyah                    1
## 17 With Arms Wide Open by Creed            1
```

I don't think it makes any difference here, but it might in other years, or if you look over several years where you might get cover versions of the same song performed by different artists.

Zero-point bonus: how many of these artists have you heard of? How many have your parents heard of? (I followed popular music quite closely much earlier than this, in the early 1980s in the UK. I remember both Madonna and U2 when they *first* became famous. U2's first single was called "Fire" and it just scraped into the UK top 40. Things changed after that.)

12.9 Bikes on College

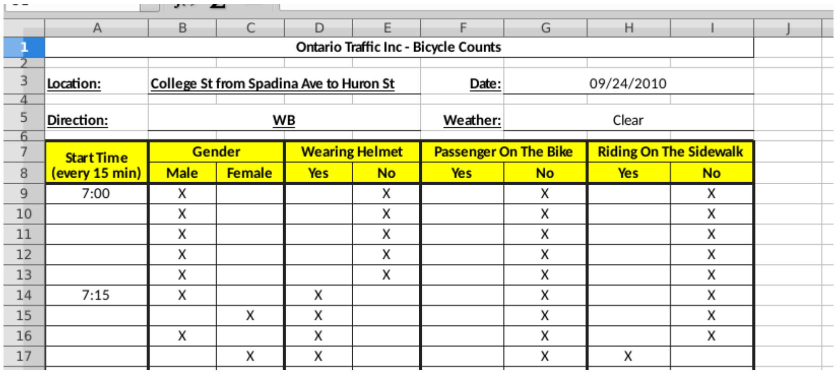
The City of Toronto collects all kinds of data on aspects of life in the city. See link. One collection of data is records of the number of cyclists on certain downtown streets. The data in link are a record of the cyclists on College Street on the block west from Huron to Spadina on September 24, 2010. In the spreadsheet, each row relates to one cyclist. The first column is the time the cyclist was observed (to the nearest 15 minutes). After that, there are four pairs of columns. The observer filled in (exactly) one X in each pair of columns, according to whether (i) the cyclist was male or female, (ii) was or was not wearing a helmet, (iii) was or was not carrying a passenger on the bike, (iv) was or was not riding on the sidewalk. We want to create a tidy data frame that has the time in each row, and has columns containing appropriate values, often `TRUE` or `FALSE`, for each of the four variables measured.

I will lead you through the process, which will involve developing a (long) pipe, one step at a time.

(a) Take a look at the spreadsheet (using Excel or similar: this may open when you click the link). Are there any obvious header rows? Is there any extra material before the data start? Explain briefly.

Solution

This is what I see (you should see something that looks like this):



	A	B	C	D	E	F	G	H	I	J
1	Ontario Traffic Inc - Bicycle Counts									
2										
3	Location:	College St from Spadina Ave to Huron St				Date:	09/24/2010			
4										
5	Direction:	WB				Weather:	Clear			
6										
7	Start Time (every 15 min)	Gender		Wearing Helmet		Passenger On The Bike		Riding On The Sidewalk		
8		Male	Female	Yes	No	Yes	No	Yes	No	
9	7:00	X			X		X		X	
10		X			X		X		X	
11		X			X		X		X	
12		X			X		X		X	
13		X			X		X		X	
14	7:15	X		X			X		X	
15			X	X			X		X	
16		X		X			X		X	
17			X	X			X	X		

There are really *two* rows of headers (the rows highlighted in yellow). The actual information that says what the column pair is about is in the first of those two rows, and the second row indicates which category of the information above this column refers to. This is not the usual way that the column headers encode what the columns are about: we are used to having *one* column `gender` that would take the values `female` or `male`, or a column `helmet` containing the values `yes` or `no`. (You might be sensing `gather` here, which may be one way of tackling this, but I lead you into another idea below.) There are also six lines above the highlighted ones that contain background information about this study. (This is where I got the information about the date of the study and which block of which street it is about.) I am looking for two things: the apparent header line is actually two lines (the ones in yellow), and there are extra lines above that which are not data.

(b)??part:firstpart?? Read the data into an R data frame. Read *without* headers, and instruct R how many lines to skip over using `skip=` and a suitable number. When this is working, display the first few lines of your data frame. Note that your columns have names `X1` through `X9`.

Solution

The actual data start on line 9, so we need to skip 8 lines. `col_names=F` is the way to say that we have no column names (not ones that we want to use, anyway). Just typing the name of the data frame will display "a few" (that is, 10) lines of it, so that you can check it for plausibleness:

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/bikes.csv"
bikes = read_csv(my_url, skip = 8, col_names = F)
```

```
## Parsed with column specification:
## cols(
##   X1 = col_time(format = ""),
##   X2 = col_character(),
##   X3 = col_character(),
##   X4 = col_character(),
##   X5 = col_character(),
##   X6 = col_character(),
##   X7 = col_character(),
##   X8 = col_character(),
##   X9 = col_character()
## )
```

```
bikes
```

```
## # A tibble: 1,958 x 9
##    X1     X2    X3    X4    X5    X6    X7
##    <time> <chr> <chr> <chr> <chr> <chr> <chr>
##  1 07:00  X     <NA>  <NA>  X     <NA>  X
##  2    NA  X     <NA>  <NA>  X     <NA>  X
##  3    NA  X     <NA>  <NA>  X     <NA>  X
##  4    NA  X     <NA>  <NA>  X     <NA>  X
##  5    NA  X     <NA>  <NA>  X     <NA>  X
##  6 07:15  X     <NA>  X     <NA>  <NA>  X
##  7    NA  <NA>  X     X     <NA>  <NA>  X
##  8    NA  X     <NA>  X     <NA>  <NA>  X
##  9    NA  <NA>  X     X     <NA>  <NA>  X
## 10    NA  X     <NA>  X     <NA>  <NA>  X
## # ... with 1,948 more rows, and 2 more
## #   variables: X8 <chr>, X9 <chr>
```

This seems to have worked: a column with times in it, and four pairs of columns, with exactly one of each pair having an X in it. The variable names X1 through X9 were generated by read_csv, as it does when you read in data with col_names=F. The times are correctly times, and the other columns are all text. The blank cells in the spreadsheet have appeared in our data frame as “missing” (NA). The notation <NA> means “missing text” (as opposed to a missing number, say).

The first line in our data frame contains the first 7:00 (am) cyclist, so it looks as if we skipped the right number of lines.

(c) What do you notice about the times in your first column? What do you think those “missing” times should be?

Solution

There are some times and some missing values. It seems a reasonable guess that the person recording the data only recorded a time when a new period of 15 minutes had begun, so that the missing times should be the same as the previous non-missing one: For example, the first five rows are cyclists observed at 7:00 am (or, at least, between 7:00 and 7:15). So they should be recorded as 7:00, and the ones in rows 7–10 should be recorded as 7:15, and so on.

(d) Find something from the `tidyverse` that will fill in those missing values with the right thing. Start a pipe from the data frame you read in, that updates the appropriate column with the filled-in times.

Oh, what a giveaway.

Solution

`fill` from `tidyr` fills in the missing times with the previous non-missing value. (This will mean finding the help for `fill` in R Studio or online.) I told you it was a giveaway. If you look in the help for `fill` via `?fill` (or if you Google `tidyr::fill`, which is the full name for "the `fill` that lives in `tidyr`"), you'll see that it requires up to two things (not including the data frame): a column to fill, and a direction to fill it (the default of "down" is exactly what we want). Thus:

```
bikes %>% fill(X1)
```

```
## # A tibble: 1,958 x 9
##    X1     X2    X3    X4    X5    X6    X7
##    <time> <chr> <chr> <chr> <chr> <chr> <chr>
##  1 07:00  X     <NA>  <NA>  X     <NA>  X
##  2 07:00  X     <NA>  <NA>  X     <NA>  X
##  3 07:00  X     <NA>  <NA>  X     <NA>  X
##  4 07:00  X     <NA>  <NA>  X     <NA>  X
##  5 07:00  X     <NA>  <NA>  X     <NA>  X
##  6 07:15  X     <NA>  X     <NA>  <NA>  X
##  7 07:15  <NA>  X     X     <NA>  <NA>  X
##  8 07:15  X     <NA>  X     <NA>  <NA>  X
##  9 07:15  <NA>  X     X     <NA>  <NA>  X
## 10 07:15  X     <NA>  X     <NA>  <NA>  X
## # ... with 1,948 more rows, and 2 more
## #   variables: X8 <chr>, X9 <chr>
```

Success!

We will probably want to rename `X1` to something like `time`, so let's do that now before we forget. There is a `rename` that does about what you'd expect:

```
bikes %>% fill(X1) %>% rename(Time = X1)
```

```
## # A tibble: 1,958 x 9
##    Time   X2    X3    X4    X5    X6    X7
##    <time> <chr> <chr> <chr> <chr> <chr> <chr>
##  1 07:00  X     <NA>  <NA>  X     <NA>  X
##   2 07:00  X     <NA>  <NA>  X     <NA>  X
##   3 07:00  X     <NA>  <NA>  X     <NA>  X
##   4 07:00  X     <NA>  <NA>  X     <NA>  X
##   5 07:00  X     <NA>  <NA>  X     <NA>  X
##   6 07:15  X     <NA>  X     <NA>  <NA>  X
##   7 07:15  <NA>  X     X     <NA>  <NA>  X
##   8 07:15  X     <NA>  X     <NA>  <NA>  X
##   9 07:15  <NA>  X     X     <NA>  <NA>  X
##  10 07:15  X     <NA>  X     <NA>  <NA>  X
## # ... with 1,948 more rows, and 2 more
## #   variables: X8 <chr>, X9 <chr>
```

The only thing I keep forgetting is that the syntax of rename is "new name equals old name". Sometimes I think it's the other way around, and then I wonder why it doesn't work.

I gave it a capital T so as not to confuse it with other things in R called time.

(e) R's ifelse function works like =IF in Excel. You use it to create values for a new variable, for example in a mutate. The first input to it is a logical condition (something that is either true or false); the second is the value your new variable should take if the condition is true, and the third is the value of your new variable if the condition is false. Create a new column gender in your data frame that is "male" or "female" depending on the value of your X2 column, using mutate. (You can assume that exactly one of the second and third columns has an X in it.) Add your code to the end of your pipe and display (the first 10 rows of) the result.

Solution

Under the assumption we are making, we only have to look at column X2 and we ignore X3 totally:

```
bikes %>% fill(X1) %>% rename(Time = X1) %>% mutate(gender = ifelse(X2 ==
    "X", "male", "female"))
```

```
## # A tibble: 1,958 x 10
##     Time   X2    X3    X4    X5    X6    X7
##     <time> <chr> <chr> <chr> <chr> <chr> <chr>
##   1 07:00  X     <NA>  <NA>  X     <NA>  X
##   2 07:00  X     <NA>  <NA>  X     <NA>  X
##   3 07:00  X     <NA>  <NA>  X     <NA>  X
##   4 07:00  X     <NA>  <NA>  X     <NA>  X
##   5 07:00  X     <NA>  <NA>  X     <NA>  X
##   6 07:15  X     <NA>  X     <NA>  <NA>  X
##   7 07:15  <NA>  X     X     <NA>  <NA>  X
##  8 07:15  X     <NA>  X     <NA>  <NA>  X
##  9 07:15  <NA>  X     X     <NA>  <NA>  X
## 10 07:15  X     <NA>  X     <NA>  <NA>  X
## # ... with 1,948 more rows, and 3 more
## #   variables: X8 <chr>, X9 <chr>,
## #   gender <chr>
```

Oh, that didn't work. The gender column is either male or missing; the two missing ones here should say female. What happened? Let's just look at our logical condition this time:

```
bikes %>% fill(X1) %>% rename(Time = X1) %>% mutate(isX = (X2 ==
    "X"))
```

```
## # A tibble: 1,958 x 10
##    Time   X2    X3    X4    X5    X6    X7
##    <time> <chr> <chr> <chr> <chr> <chr> <chr>
##  1 07:00  X     <NA>  <NA>  X     <NA>  X
##  2 07:00  X     <NA>  <NA>  X     <NA>  X
##  3 07:00  X     <NA>  <NA>  X     <NA>  X
##  4 07:00  X     <NA>  <NA>  X     <NA>  X
##  5 07:00  X     <NA>  <NA>  X     <NA>  X
##  6 07:15  X     <NA>  X     <NA>  <NA>  X
##  7 07:15  <NA>  X     X     <NA>  <NA>  X
##  8 07:15  X     <NA>  X     <NA>  <NA>  X
##  9 07:15  <NA>  X     X     <NA>  <NA>  X
## 10 07:15  X     <NA>  X     <NA>  <NA>  X
## # ... with 1,948 more rows, and 3 more
## #   variables: X8 <chr>, X9 <chr>, isX <lgl>
```

This is not true and false, it is true and missing. The idea is that if X2 is missing, we don't (in general) know what its value is: it might even be X! So if X2 is missing, any comparison of it with another value ought to be missing as well.

That's in general. Here, we know where those missing values came from: they were blank cells in the spreadsheet, so we actually have more information.

Perhaps a better way to go is to test whether X2 is missing (in which case, it's a female cyclist). R has a function is.na which is TRUE if the thing inside it is missing and FALSE if the thing inside it has some non-missing value. In our case, it goes like this:

```
bikes %>% fill(X1) %>% rename(Time = X1) %>% mutate(gender = ifelse(is.na(X2),
    "female", "male"))
```

```
## # A tibble: 1,958 x 10
##    Time   X2    X3    X4    X5    X6    X7
##    <time> <chr> <chr> <chr> <chr> <chr> <chr>
##  1 07:00  X     <NA>  <NA>  X     <NA>  X
##  2 07:00  X     <NA>  <NA>  X     <NA>  X
##  3 07:00  X     <NA>  <NA>  X     <NA>  X
##  4 07:00  X     <NA>  <NA>  X     <NA>  X
##  5 07:00  X     <NA>  <NA>  X     <NA>  X
##  6 07:15  X     <NA>  X     <NA>  <NA>  X
##  7 07:15  <NA>  X     X     <NA>  <NA>  X
##  8 07:15  X     <NA>  X     <NA>  <NA>  X
##  9 07:15  <NA>  X     X     <NA>  <NA>  X
## 10 07:15  X     <NA>  X     <NA>  <NA>  X
## # ... with 1,948 more rows, and 3 more
## #   variables: X8 <chr>, X9 <chr>,
## #   gender <chr>
```

Or you can test X3 for missingness: if missing, it's male, otherwise it's female. That also works.

This made an assumption that the person recording the X's actually *did* mark an X in exactly one of the columns. For example, the columns could *both* be missing, or *both* have an X in them. This gives us more things to check, at least three. ifelse is good for something with only two alternatives, but when you have more, case_when is much better. Here's how that goes. Our strategy is to check for three things: (i) X2 has an X and X3 is missing; (ii) X2 is missing and X3 has an X; (iii) anything else, which is an error:

In some languages it is called *switch*. Python appears not to have it. What you do there instead is to use a Python dictionary to pick out the value you want.

```
bikes %>% fill(X1) %>% rename(Time = X1) %>% mutate(gender = case_when(X2 ==
    "X" & is.na(X3) ~ "Male", is.na(X2) & X3 ==
    "X" ~ "Female", TRUE ~ "Error!"))
```

```
## # A tibble: 1,958 x 10
##    Time   X2    X3    X4    X5    X6    X7
##    <time> <chr> <chr> <chr> <chr> <chr> <chr>
##  1 07:00  X     <NA>  <NA>  X     <NA>  X
##  2 07:00  X     <NA>  <NA>  X     <NA>  X
##  3 07:00  X     <NA>  <NA>  X     <NA>  X
##  4 07:00  X     <NA>  <NA>  X     <NA>  X
##  5 07:00  X     <NA>  <NA>  X     <NA>  X
##  6 07:15  X     <NA>  X     <NA>  <NA>  X
##  7 07:15  <NA>  X     X     <NA>  <NA>  X
##  8 07:15  X     <NA>  X     <NA>  <NA>  X
##  9 07:15  <NA>  X     X     <NA>  <NA>  X
## 10 07:15  X     <NA>  X     <NA>  <NA>  X
## # ... with 1,948 more rows, and 3 more
## #   variables: X8 <chr>, X9 <chr>,
## #   gender <chr>
```

It seems nicest to format it like that, with the squiggles lining up, so you can see what possible values `gender` might take.

The structure of the `case_when` is that the thing you're checking for goes on the left of the squiggle, and the value you want your new variable to take goes on the right. What it does is to go down the list of conditions that you are checking for, and as soon as it finds one that is true, it grabs the value on the right of the squiggle and moves on to the next row. The usual way to write these is to have a catch-all condition at the end that is always true, serving to make sure that your new variable always gets *some* value. `TRUE` is, um, always true. If you want an English word for the last condition of your `case_when`, "otherwise" is a nice one.

I wanted to check that the observer did check exactly one of `V2` and `V3` as I asserted, which can be done by gluing this onto the end:

```
bikes %>% fill(X1) %>% rename(Time = X1) %>% mutate(gender = case_when(X2 ==
    "X" & is.na(X3) ~ "Male", is.na(X2) & X3 ==
    "X" ~ "Female", TRUE ~ "Error!")) %>% count(gender)
```

```
## # A tibble: 2 x 2
##   gender     n
##   <chr>  <int>
## 1 Female   861
## 2 Male    1097
```

There are only Males and Females, so the observer really did mark exactly one X. (As a bonus, you see that there were slightly more male cyclists than female ones.)

Extra: I was wondering how `gather` would play out here. The way to do it seems to be to rename the columns first:

```
bikes %>% fill(X1) %>% rename(Time = X1) %>% rename(male = X2,
    female = X3)
```

```
## # A tibble: 1,958 x 9
##     Time male  female X4    X5    X6    X7
##     <ti> <chr> <chr>  <chr> <chr> <chr> <chr>
##   1 07:~ X     <NA>   <NA>  X     <NA>  X
##   2 07:~ X     <NA>   <NA>  X     <NA>  X
##   3 07:~ X     <NA>   <NA>  X     <NA>  X
##   4 07:~ X     <NA>   <NA>  X     <NA>  X
##   5 07:~ X     <NA>   <NA>  X     <NA>  X
##   6 07:~ X     <NA>   X     <NA>  <NA>  X
##  7 07:~ <NA>  X      X     <NA>  <NA>  X
##  8 07:~ X     <NA>   X     <NA>  <NA>  X
##  9 07:~ <NA>  X      X     <NA>  <NA>  X
## 10 07:~ X     <NA>   X     <NA>  <NA>  X
## # ... with 1,948 more rows, and 2 more
## #   variables: X8 <chr>, X9 <chr>
```

and then gather them up:

```
bikes %>% fill(X1) %>% rename(Time = X1) %>% rename(male = X2,
    female = X3) %>% gather(gender, what, male:female)
```

```
## # A tibble: 3,916 x 9
##    Time   X4    X5    X6    X7    X8    X9
##    <time> <chr> <chr> <chr> <chr> <chr> <chr>
##  1 07:00  <NA>  X     <NA>  X     <NA>  X
##  2 07:00  <NA>  X     <NA>  X     <NA>  X
##  3 07:00  <NA>  X     <NA>  X     <NA>  X
##  4 07:00  <NA>  X     <NA>  X     <NA>  X
##  5 07:00  <NA>  X     <NA>  X     <NA>  X
##  6 07:15  X     <NA>  <NA>  X     <NA>  X
##  7 07:15  X     <NA>  <NA>  X     <NA>  X
##  8 07:15  X     <NA>  <NA>  X     <NA>  X
##  9 07:15  X     <NA>  <NA>  X     X     <NA>
## 10 07:15  X     <NA>  <NA>  X     <NA>  X
## # ... with 3,906 more rows, and 2 more
## #   variables: gender <chr>, what <chr>
```

I wasn't quite sure what to call "what makes them the same", at least not until I had seen how it came out. This is where the X or missing goes, so we want the lines where what is equal to X:

```
bikes %>% fill(X1) %>% rename(Time = X1) %>% rename(male = X2,
    female = X3) %>% gather(gender, what, male:female) %>%
    filter(what == "X")
```

```
## # A tibble: 1,958 x 9
##    Time   X4    X5    X6    X7    X8    X9
##    <time> <chr> <chr> <chr> <chr> <chr> <chr>
##  1 07:00  <NA>  X     <NA>  X     <NA>  X
##  2 07:00  <NA>  X     <NA>  X     <NA>  X
##  3 07:00  <NA>  X     <NA>  X     <NA>  X
##  4 07:00  <NA>  X     <NA>  X     <NA>  X
##  5 07:00  <NA>  X     <NA>  X     <NA>  X
##  6 07:15  X     <NA>  <NA>  X     <NA>  X
##  7 07:15  X     <NA>  <NA>  X     <NA>  X
##  8 07:15  X     <NA>  <NA>  X     <NA>  X
##  9 07:15  X     <NA>  <NA>  X     <NA>  X
## 10 07:15  X     <NA>  <NA>  X     <NA>  X
## # ... with 1,948 more rows, and 2 more
## #   variables: gender <chr>, what <chr>
```

Another way to do this is to remove the missings in the gather:

```
bikes %>% fill(X1) %>% rename(Time = X1) %>% rename(male = X2,
    female = X3) %>% gather(gender, what, male:female,
    na.rm = T)
```

```
## # A tibble: 1,958 x 9
##    Time   X4    X5    X6    X7    X8    X9
##  * <time> <chr> <chr> <chr> <chr> <chr> <chr>
##  1 07:00  <NA>  X     <NA>  X     <NA>  X
##  2 07:00  <NA>  X     <NA>  X     <NA>  X
##  3 07:00  <NA>  X     <NA>  X     <NA>  X
##  4 07:00  <NA>  X     <NA>  X     <NA>  X
##  5 07:00  <NA>  X     <NA>  X     <NA>  X
##  6 07:15  X     <NA>  <NA>  X     <NA>  X
##  7 07:15  X     <NA>  <NA>  X     <NA>  X
##  8 07:15  X     <NA>  <NA>  X     <NA>  X
##  9 07:15  X     <NA>  <NA>  X     <NA>  X
## 10 07:15  X     <NA>  <NA>  X     <NA>  X
## # ... with 1,948 more rows, and 2 more
## #   variables: gender <chr>, what <chr>
```

In case you are wondering where the females went, all the males are listed first this way, and then all the females. To verify this, we can count the males and females obtained this way, and we should get the same thing we got before:

```
bikes %>% fill(X1) %>% rename(Time = X1) %>% rename(male = X2,
    female = X3) %>% gather(gender, what, male:female,
    na.rm = T) %>% count(gender)
```

```
## # A tibble: 2 x 2
##   gender     n
##   <chr>  <int>
## 1 female   861
## 2 male    1097
```

And this is what we had before.

(f) Create variables helmet, passenger and sidewalk in your data frame that are TRUE if the "Yes" column contains X and FALSE otherwise. This will use mutate again, but you don't need ifelse:

just set the variable equal to the appropriate logical condition. As before, the best way to create these variables is to test the appropriate things for missingness. Note that you can create as many new variables as you like in one `mutate`. Show the first few lines of your new data frame. (Add your code onto the end of the pipe you made above.)

Solution

On the face of it, the way to do this is to go looking for `X`'s:

```
bikes %>% fill(X1) %>% rename(Time = X1) %>% mutate(gender = ifelse(is.na(X2),
    "female", "male")) %>% mutate(helmet = (X4 ==
    "X"), passenger = (X6 == "X"), sidewalk = (X8 ==
    "X"))
```

```
## # A tibble: 1,958 x 13
##    Time   X2    X3    X4    X5    X6    X7
##    <time> <chr> <chr> <chr> <chr> <chr> <chr>
##  1 07:00  X     <NA>  <NA>  X     <NA>  X
##  2 07:00  X     <NA>  <NA>  X     <NA>  X
##  3 07:00  X     <NA>  <NA>  X     <NA>  X
##  4 07:00  X     <NA>  <NA>  X     <NA>  X
##  5 07:00  X     <NA>  <NA>  X     <NA>  X
##  6 07:15  X     <NA>  X     <NA>  <NA>  X
##  7 07:15  <NA>  X     X     <NA>  <NA>  X
##  8 07:15  X     <NA>  X     <NA>  <NA>  X
##  9 07:15  <NA>  X     X     <NA>  <NA>  X
## 10 07:15  X     <NA>  X     <NA>  <NA>  X
## # ... with 1,948 more rows, and 6 more
## #   variables: X8 <chr>, X9 <chr>,
## #   gender <chr>, helmet <lgl>,
## #   passenger <lgl>, sidewalk <lgl>
```

But, we run into the same problem that we did with `gender`: the new variables are either `TRUE` or missing, never `FALSE`.

The solution is the same: look for the things that are *missing* if the cyclist is wearing a helmet, carrying a passenger or riding on the sidewalk. These are `X5, X7, X9` respectively:

```
bikes %>% fill(X1) %>% rename(Time = X1) %>% mutate(gender = ifelse(is.na(X2),
    "female", "male")) %>% mutate(helmet = is.na(X5),
    passenger = is.na(X7), sidewalk = is.na(X9))
```

```
## # A tibble: 1,958 x 13
##    Time   X2    X3    X4    X5    X6    X7
##    <time> <chr> <chr> <chr> <chr> <chr> <chr>
##   1 07:00  X     <NA>  <NA>  X     <NA>  X
##   2 07:00  X     <NA>  <NA>  X     <NA>  X
##   3 07:00  X     <NA>  <NA>  X     <NA>  X
##   4 07:00  X     <NA>  <NA>  X     <NA>  X
##   5 07:00  X     <NA>  <NA>  X     <NA>  X
##   6 07:15  X     <NA>  X     <NA>  <NA>  X
##   7 07:15  <NA>  X     X     <NA>  <NA>  X
##   8 07:15  X     <NA>  X     <NA>  <NA>  X
##   9 07:15  <NA>  X     X     <NA>  <NA>  X
##  10 07:15  X     <NA>  X     <NA>  <NA>  X
## # ... with 1,948 more rows, and 6 more
## #   variables: X8 <chr>, X9 <chr>,
## #   gender <chr>, helmet <lgl>,
## #   passenger <lgl>, sidewalk <lgl>
```

Again, you can do the mutate all on one line if you want to, or all four variable assignments in one mutate, but I used newlines and indentation to make the structure clear.

It is less elegant, though equally good for the purposes of the assignment, to use ifelse for these as well, which would go like this, for example:

```
bikes %>% fill(X1) %>% rename(Time = X1) %>% mutate(gender = ifelse(X2 ==
    "X", "male", "female")) %>% mutate(helmet = ifelse(is.na(X5),
    T, F))
```

```
## # A tibble: 1,958 x 11
##     Time   X2    X3    X4    X5    X6    X7
##     <time> <chr> <chr> <chr> <chr> <chr> <chr>
##   1 07:00  X     <NA>  <NA>  X     <NA>  X
##   2 07:00  X     <NA>  <NA>  X     <NA>  X
##   3 07:00  X     <NA>  <NA>  X     <NA>  X
##   4 07:00  X     <NA>  <NA>  X     <NA>  X
##   5 07:00  X     <NA>  <NA>  X     <NA>  X
##   6 07:15  X     <NA>  X     <NA>  <NA>  X
##   7 07:15  <NA>  X     X     <NA>  <NA>  X
##   8 07:15  X     <NA>  X     <NA>  <NA>  X
##   9 07:15  <NA>  X     X     <NA>  <NA>  X
##  10 07:15  X     <NA>  X     <NA>  <NA>  X
## # ... with 1,948 more rows, and 4 more
## #   variables: X8 <chr>, X9 <chr>,
## #   gender <chr>, helmet <lgl>
```

and the same for passenger and sidewalk. The warning is, whenever you see a T and an F in an ifelse, that you could probably get rid of the ifelse and use the logical condition directly. For

If I was helping you, and you were struggling with *ifelse* but finally mastered it, it seemed easier to suggest that you used it again for the others.

texttt{gender}, though, you need the `ifelse` (or a `case_when`) because the values you want it to take are `male` and `female`, something other than `TRUE` and `FALSE`.

I like to put brackets around logical conditions when I am assigning them to a variable. If I don't, I get something like

```
helmet = V4 == "X"
```

which actually works, but is very hard to read. Well, I *think* it works. Let's check:

```
exes = c("X", "", "X", "", "X")
y = exes == "X"
y
```

```
## [1]  TRUE FALSE  TRUE FALSE  TRUE
```

Yes it does. But I would never recommend writing it this way, because unless you are paying attention, you won't notice which `=` is saving in a variable, and which one is "logically equal".

It works because of a thing called "operator precedence": the logical-equals is evaluated first, and the result of that is saved in the variable. But unless you or your readers remember that, it's better to write

```
y = (exes == "X")
```

to draw attention to the order of calculation. This is the same reason that

```
4 + 5 * 6
```

```
## [1] 34
```

evaluates this way rather than doing the addition first and getting 54. BODMAS and all that.

The `gather` approach works for these too. Rename the columns as `yes` and `no`, and then give the "what makes them the same" column a name like `helmet`. Give the "what makes them different" column a name like `what2`, to make it easier to remove later. And then do the same with the others, one `gather` at a time.

(g)??part:lastpart?? Finally (for the data manipulation), get rid of all the original columns, keeping only the new ones that you created. Save the results in a data frame and display its first few rows.

Solution

This is a breath of fresh air after all the thinking needed above: this is just `select`, added to the end:

```
mybikes = bikes %>% fill(X1) %>% rename(Time = X1) %>%
    mutate(gender = ifelse(is.na(X2), "female",
        "male")) %>% mutate(helmet = is.na(X5),
    passenger = is.na(X7), sidewalk = is.na(X9)) %>%
    select(-(X2:X9))
mybikes
```

```
## # A tibble: 1,958 x 5
##    Time   gender helmet passenger sidewalk
##    <time> <chr>  <lgl>  <lgl>     <lgl>
##  1 07:00  male   FALSE  FALSE     FALSE
##  2 07:00  male   FALSE  FALSE     FALSE
##  3 07:00  male   FALSE  FALSE     FALSE
##  4 07:00  male   FALSE  FALSE     FALSE
##  5 07:00  male   FALSE  FALSE     FALSE
##  6 07:15  male   TRUE   FALSE     FALSE
##  7 07:15  female TRUE   FALSE     FALSE
##  8 07:15  male   TRUE   FALSE     FALSE
##  9 07:15  female TRUE   FALSE     TRUE
## 10 07:15  male   TRUE   FALSE     FALSE
## # ... with 1,948 more rows
```

You might not have renamed your `X1`, in which case, you still have it, but need to keep it (because it holds the times).

Another way to do this is to use a "select-helper", thus:

```
bikes %>% fill(X1) %>% rename(Time = X1) %>% mutate(gender = ifelse(is.na(X2),
    "female", "male")) %>% mutate(helmet = is.na(X5),
    passenger = is.na(X7), sidewalk = is.na(X9)) %>%
    select(-num_range("X", 2:9))
```

```
## # A tibble: 1,958 x 5
##    Time   gender helmet passenger sidewalk
##    <time> <chr>  <lgl>  <lgl>     <lgl>
##  1 07:00  male   FALSE  FALSE     FALSE
##  2 07:00  male   FALSE  FALSE     FALSE
##  3 07:00  male   FALSE  FALSE     FALSE
##  4 07:00  male   FALSE  FALSE     FALSE
##  5 07:00  male   FALSE  FALSE     FALSE
##  6 07:15  male   TRUE   FALSE     FALSE
##  7 07:15  female TRUE   FALSE     FALSE
##  8 07:15  male   TRUE   FALSE     FALSE
##  9 07:15  female TRUE   FALSE     TRUE
## 10 07:15  male   TRUE   FALSE     FALSE
## # ... with 1,948 more rows
```

This means "get rid of all the columns whose names are *X* followed by a number 2 through 9".

The pipe looks long and forbidding, but you built it (and tested it) a little at a time. Which is how you do it.

(h) The next few parts are a quick-fire analysis of the data set. They can all be solved using `count`. How many male and how many female cyclists were observed in total?

Solution

I already got this one when I was checking for observer-notation errors earlier:

```
mybikes %>% count(gender)
```

```
## # A tibble: 2 x 2
##   gender     n
##   <chr>  <int>
## 1 female   861
## 2 male    1097
```

861 females and 1097 males.

(i) How many male and female cyclists were not wearing helmets?

Solution

You can count two variables at once, in which case you get counts of all combinations of them:

```
mybikes %>% count(gender, helmet)
```

```
## # A tibble: 4 x 3
##   gender helmet     n
##   <chr>  <lgl>  <int>
## 1 female FALSE    403
## 2 female TRUE     458
## 3 male   FALSE    604
## 4 male   TRUE     493
```

403 females and 604 males were not wearing helmets, picking out what we need.

The real question of interest here is "what *proportion* of male and female cyclists were not wearing helmets?" This has a rather elegant solution that I will have to explain. First, let's go back to the `group_by` and `summarize` version of the `count` here:

But I didn't want to complicate this question any farther.

```
mybikes %>% group_by(gender, helmet) %>% summarize(the_ount = n())
```

```
## # A tibble: 4 x 3
## # Groups:   gender [?]
##   gender helmet the_ount
##   <chr>  <lgl>     <int>
## 1 female FALSE       403
## 2 female TRUE        458
## 3 male   FALSE       604
## 4 male   TRUE        493
```

That's the same table we got just now. Now, let's calculate a proportion and see what happens:

```
mybikes %>% group_by(gender, helmet) %>% summarize(the_count = n()) %>%
    mutate(prop = the_count/sum(the_count))
```

```
## # A tibble: 4 x 4
## # Groups:   gender [2]
##   gender helmet the_count  prop
##   <chr>  <lgl>      <int> <dbl>
## 1 female FALSE        403 0.468
## 2 female TRUE         458 0.532
## 3 male   FALSE        604 0.551
## 4 male   TRUE         493 0.449
```

We seem to have the proportions of males and females who were and were not wearing a helmet, and you can check that this is indeed the case, for example:

```
403/(403 + 458)
```

```
## [1] 0.4680604
```

47% of females were not wearing helmets, while 55% of males were helmetless. (You can tell from the original frequencies that a small majority of females wore helmets and a small majority of males did not.)

Now, we have to ask ourselves: how on earth did that work?

When you calculate a summary (like our `sum(count)` above), it figures that you can't want the sum by gender-helmet combination, since you already have those in `count`. You must want the sum *over* something. What? What happens is that it goes back to the `group_by` and "peels off" the last thing there, which in this case is `helmet`, leaving only `gender`. It then sums the counts for each gender, giving us what we wanted.

It just blows my mind that someone (ie., Hadley Wickham) could (i) think that this would be a nice syntax to have (instead of just being an error), (ii) find a way to implement it and (iii) find a nice logical explanation ("peeling off") to explain how it worked.

What happens if we switch the order of the things in the group_by?

```
mybikes %>% group_by(helmet, gender) %>% summarize(the_count = n()) %>%
    mutate(prop = the_count/sum(the_count))
```

```
## # A tibble: 4 x 4
## # Groups:   helmet [2]
##   helmet gender the_count  prop
##   <lgl>  <chr>      <int> <dbl>
## 1 FALSE  female       403 0.400
## 2 FALSE  male         604 0.600
## 3 TRUE   female       458 0.482
## 4 TRUE   male         493 0.518
```

Now we get the proportion of helmeted riders of each gender, which is not the same as what we had before. Before, we had "out of males" and "out of females"; now we have "out of helmeted riders" and "out of helmetless riders". (The riders with helmets are almost 50–50 males and females, but the riders without helmets are about 60% male.)

This is row and column proportions in a contingency table, B22 style.

Now, I have to see whether the count variant of this works:

```
mybikes %>% count(gender, helmet) %>% mutate(prop = n/sum(n))
```

```
## # A tibble: 4 x 4
##   gender helmet     n  prop
##   <chr>  <lgl>  <int> <dbl>
## 1 female FALSE    403 0.206
## 2 female TRUE     458 0.234
## 3 male   FALSE    604 0.308
## 4 male   TRUE     493 0.252
```

It doesn't. Well, it kind of does, but it divided by the sum of all of them rather than "peeling off", so these are overall proportions rather than row or column proportions.

So I think you have to do this the group_by and summarize way.

(j) How many cyclists were riding on the sidewalk *and* carrying a passenger?

Solution

Not too many, I'd hope. Again:

```
mybikes %>% count(passenger, sidewalk)
```

```
## # A tibble: 3 x 3
##   passenger sidewalk     n
##   <lgl>     <lgl>    <int>
## 1 FALSE     FALSE     1880
## 2 FALSE     TRUE        73
## 3 TRUE      FALSE        5
```

We're looking for the "true", "true" entry of that table, which seems to have vanished. That means the count is *zero*: none at all. (There were only 5 passenger-carrying riders, and they were all on the road.)

(k) What was the busiest 15-minute period of the day, and how many cyclists were there then?

Solution

The obvious way is to list every 15-minute period and eyeball the largest frequency. There are quite a few 15-minute periods, so be prepared to hit Next a few times (or use `View`):

```
mybikes %>% count(Time) %>% print(n = Inf)
```

```
## # A tibble: 48 x 2
##    Time       n
##    <time> <int>
##  1 07:00      5
##  2 07:15      8
##  3 07:30      9
##  4 07:45      5
##  5 08:00     18
##  6 08:15     14
##  7 08:30     12
##  8 08:45     22
##  9 09:00     17
## 10 09:15     15
## 11 09:30     16
## 12 09:45     12
## 13 10:00      8
## 14 10:15     21
## 15 10:30     22
## 16 10:45     19
## 17 11:00     30
## 18 11:15     14
## 19 11:30     27
## 20 11:45     28
## 21 12:00     22
## 22 12:15     35
## 23 12:30     40
## 24 12:45     33
## 25 13:00     44
## 26 13:15     46
## 27 13:30     29
## 28 13:45     41
## 29 14:00     36
## 30 14:15     45
## 31 14:30     33
## 32 14:45     50
## 33 15:00     49
## 34 15:15     51
## 35 15:30     61
## 36 15:45     79
## 37 16:00    101
## 38 16:15     56
## 39 16:30     51
## 40 16:45     75
## 41 17:00    104
## 42 17:15    128
## 43 17:30     80
## 44 17:45     73
## 45 18:00     75
## 46 18:15     78
## 47 18:30     63
## 48 18:45     58
```

17:15, or 5:15 pm, with 128 cyclists.

But, computers are meant to save us that kind of effort. How? Note that the output from `count` is itself a data frame, so anything you can do to a data frame, you can do to *it*: for example, display only the rows where the frequency equals the maximum frequency:

```
mybikes %>% count(Time) %>% filter(n == max(n))
```

```
## # A tibble: 1 x 2
##   Time       n
##   <time> <int>
## 1 17:15    128
```

That will actually display *all* the times where the cyclist count equals the maximum, of which there might be more than one.

13
Regression

```
library(tidyverse)

## -- Attaching packages ---- tidyverse 1.2.1 --

## v ggplot2 3.0.0     v purrr   0.2.5
## v tibble  1.4.2     v dplyr   0.7.6
## v tidyr   0.8.1     v stringr 1.3.1
## v readr   1.1.1     v forcats 0.3.0

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

13.1 *Rainfall in California*

The data in link are rainfall and other measurements for 30 weather stations in California. Our aim is to understand how well the annual rainfall at these stations (measured in inches) can be predicted from the other measurements, which are the altitude (in feet above sea level), the latitude (degrees north of the equator) and the distance from the coast (in miles).

(a) Read the data into R. You'll have to be careful here, since the values are space-delimited, but sometimes by more than one space, to make the columns line up. `read_table2`, with filename or url, will read it in. One of the variables is called `rainfall`, so as long as you *do not* call the data frame that, you should be safe.

Solution
I used `rains` as the name of my data frame:

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/calirain.txt"
rains = read_table2(my_url)
```

```
## Parsed with column specification:
## cols(
##   station = col_character(),
##   rainfall = col_double(),
##   altitude = col_integer(),
##   latitude = col_double(),
##   fromcoast = col_integer()
## )
```

I have the right number of rows and columns.

There is also `read_table`, but that requires *all* the columns, including the header row, to be lined up. You can try that here and see how it fails.

I don't need you to investigate the data yet (that happens in the next part), but this is interesting (to me):

```
rains
```

```
## # A tibble: 30 x 5
##    station rainfall altitude latitude
##    <chr>      <dbl>    <int>    <dbl>
##  1 Eureka      39.6       43     40.8
##  2 RedBlu~     23.3      341     40.2
##  3 Thermal     18.2     4152     33.8
##  4 FortBr~     37.5       74     39.4
##  5 SodaSp~     49.3     6752     39.3
##  6 SanFra~     21.8       52     37.8
##  7 Sacram~     18.1       25     38.5
##  8 SanJose     14.2       95     37.4
##  9 GiantF~     42.6     6360     36.6
## 10 Salinas     13.8       74     36.7
## # ... with 20 more rows, and 1 more
## #   variable: fromcoast <int>
```

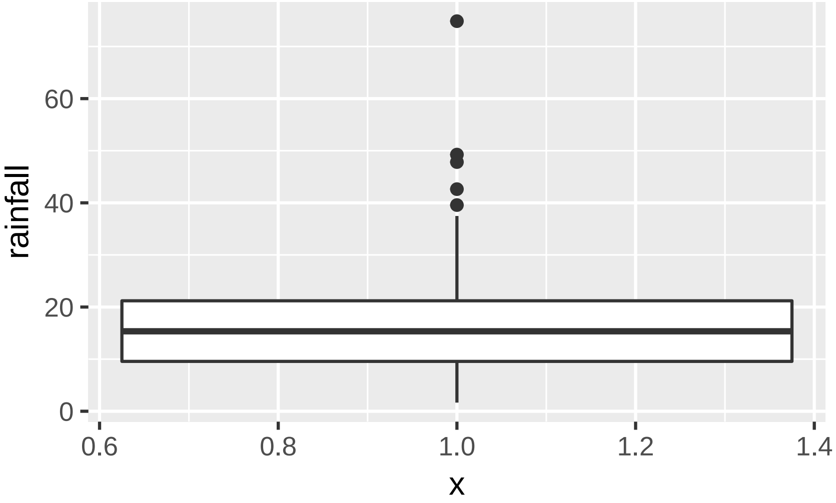
Some of the station names are two words, but they have been smooshed into one word, so that `read_table2` will recognize them as a single thing. Someone had already done that for us, so I didn't even have to do it myself.

If the station names had been two genuine words, a `.csv` would probably have been the best choice (the actual data values being separated by commas then, and not spaces).

(b) Make a boxplot of the rainfall figures, and explain why the values are reasonable. (A rainfall cannot be negative, and it is unusual for a annual rainfall to exceed 60 inches.) A `ggplot` boxplot needs *something* on the *x*-axis: the number 1 will do.

Solution

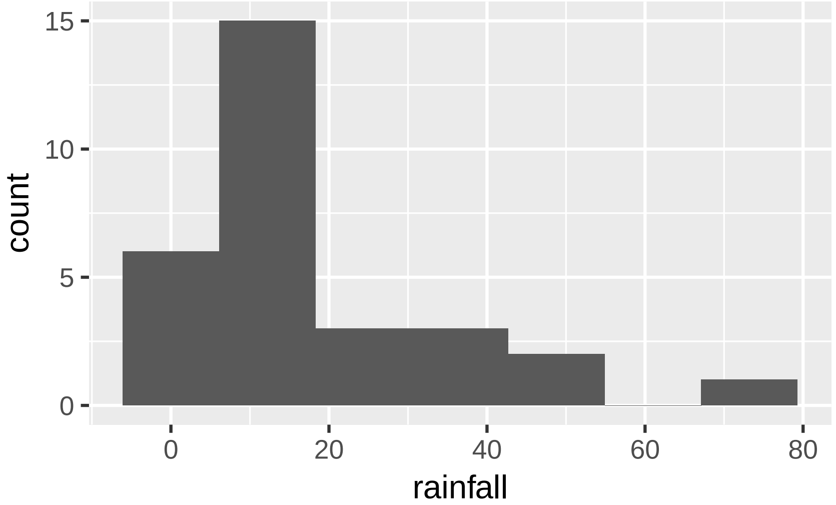
```
ggplot(rains, aes(y = rainfall, x = 1)) + geom_boxplot()
```



There is only one rainfall over 60 inches, and the smallest one is close to zero but positive, so that is good.

Another possible plot here is a histogram, since there is only one quantitative variable:

```
ggplot(rains, aes(x = rainfall)) + geom_histogram(bins = 7)
```



This clearly shows the rainfall value above 60 inches, but some other things are less clear: are those two rainfall values around 50 inches above or below 50, and are those six rainfall values near zero actually above zero? Extra: What stations have those extreme values? Should you wish to find out:

```
rains %>% filter(rainfall > 60)
```

```
## # A tibble: 1 x 5
##   station rainfall altitude latitude
##   <chr>      <dbl>    <int>    <dbl>
## 1 Cresce~     74.9       35     41.7
## # ... with 1 more variable: fromcoast <int>
```

This is a place right on the Pacific coast, almost up into Oregon (it's almost the northernmost of all the stations). So it makes sense that it would have a high rainfall, if anywhere does. (If you know anything about rainy places, you'll probably think of Vancouver and Seattle, in the Pacific Northwest.) Here it is: link. Which station has less than 2 inches of annual rainfall?

```
rains %>% filter(rainfall < 2)
```

```
## # A tibble: 1 x 5
##   station rainfall altitude latitude
##   <chr>      <dbl>    <int>    <dbl>
## 1 DeathV~     1.66     -178     36.5
## # ... with 1 more variable: fromcoast <int>
```

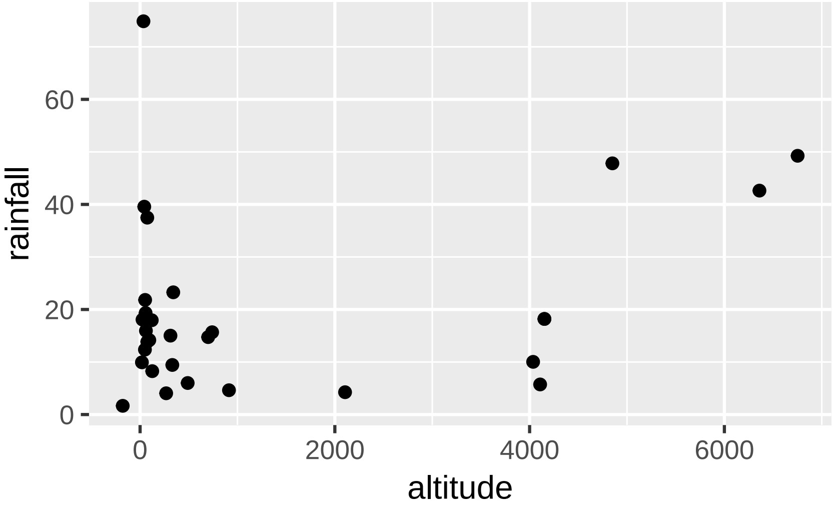
The name of the station is a clue: this one is in the desert. So you'd expect very little rain. Its altitude is *negative*, so it's actually *below* sea level. This is correct. Here is where it is: link.

(c) Plot `rainfall` against each of the other quantitative variables (that is, not `station`).

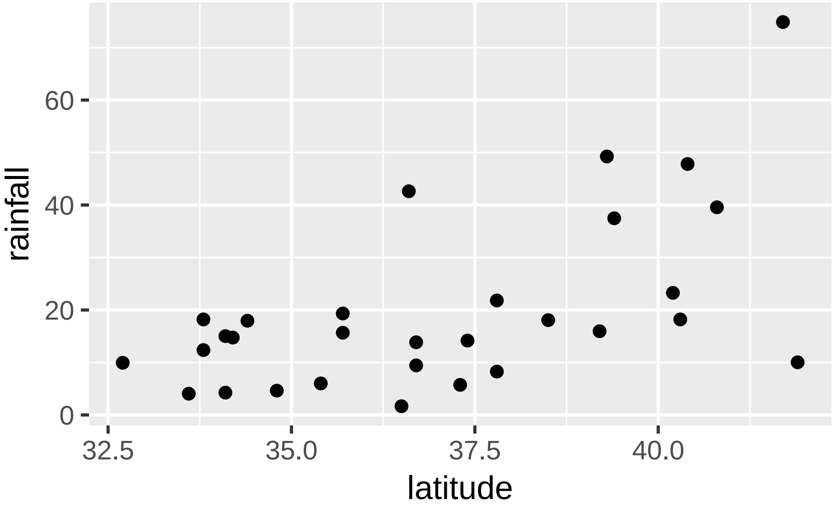
Solution

That is, `altitude`, `latitude` and `fromcoast`. The obvious way to do this (perfectly acceptable) is one plot at a time:

```
ggplot(rains, aes(y = rainfall, x = altitude)) +
    geom_point()
```

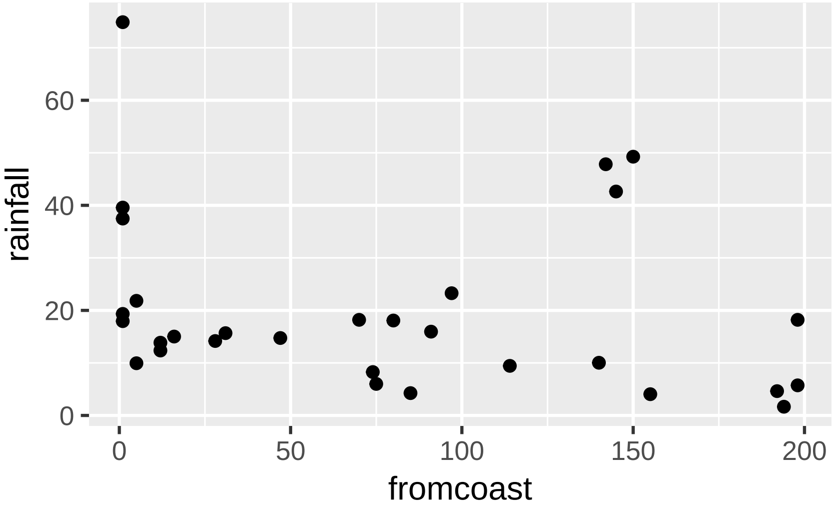


```
ggplot(rains, aes(y = rainfall, x = latitude)) +
    geom_point()
```



and finally

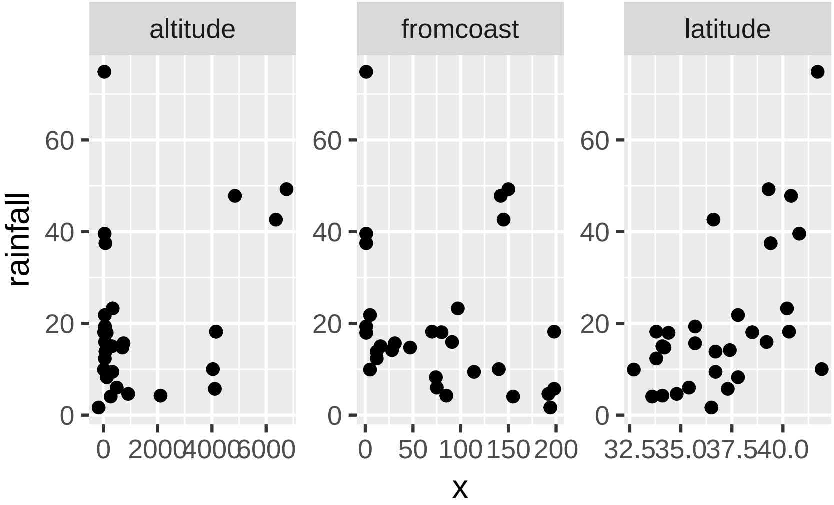
```
ggplot(rains, aes(y = rainfall, x = fromcoast)) +
    geom_point()
```



You can add a smooth trend to these if you want. Up to you. Just the points is fine with me.

Here is a funky way to get all three plots in one shot:

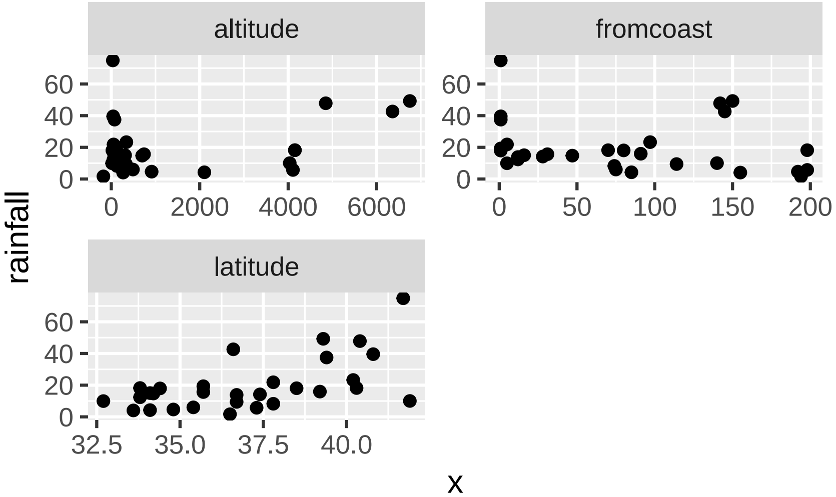
```
rains %>% gather(xname, x, altitude:fromcoast) %>%
    ggplot(aes(x = x, y = rainfall)) + geom_point() +
    facet_wrap(~xname, scales = "free")
```



This always seems extraordinarily strange if you haven't run into it before. The strategy is to put *all* the *x*-variables you want to plot into *one* column and then plot your *y* against the *x*-column. A nice side-effect of the way `gather` works is that what makes the *x*-columns different is that they are *x*-variables with different *names*, which is exactly what you want later for the facets. Thus: make a column of all the *x*'s glued together, labelled by which *x* they are, then plot *y* against *x* but make a different sub-plot or "facet" for each different *x*-name. The last thing is that each *x* is measured on a different scale, and unless we take steps, all the sub-plots will have the *same* scale on each axis, which we don't want.

I'm not sure I like how it came out, with three very tall plots. `facet_wrap` can also take an `nrow` or an `ncol`, which tells it how many rows or columns to use for the display. Here, for example, two columns because I thought three was too many:

```
rains %>% gather(xname, x, altitude:fromcoast) %>%
    ggplot(aes(x = x, y = rainfall)) + geom_point() +
    facet_wrap(~xname, scales = "free", ncol = 2)
```



Now, the three plots have come out about square, which I like a lot better.

(d) Look at the relationship of each other variable with `rainfall`. Justify the assertion that `latitude` seems most strongly related with `rainfall`. Is that relationship positive or negative? linear? Explain briefly.

Solution
Let's look at the three variables in turn:

- `altitude`: not much of anything. The stations near sea level have rainfall all over the place, though the three highest-altitude stations have the three highest rainfalls apart from Crescent City.
- `latitude`: there is a definite upward trend here, in that stations further north (higher latitude) are likely to have a higher rainfall. I'd call this trend linear (or, not obviously curved), though the two most northerly stations have one higher and one much lower rainfall than you'd expect.
- `fromcoast`: this is a weak downward trend, though the trend is spoiled by those three stations about 150 miles from the coast that have more than 40 inches of rainfall.

Out of those, only `latitude` seems to have any meaningful relationship with `rainfall`.

(e) Fit a regression with `rainfall` as the response variable, and `latitude` as your explanatory variable. What are the intercept, slope and R-squared values? Is there a *significant* relationship between `rainfall` and your explanatory variable? What does that mean?

Solution

Save your `lm` into a variable, since it will get used again later:

```
rainfall.1 = lm(rainfall ~ latitude, data = rains)
summary(rainfall.1)
```

```
##
## Call:
## lm(formula = rainfall ~ latitude, data = rains)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -27.297  -7.956  -2.103   6.082  38.262
##
## Coefficients:
##              Estimate Std. Error t value
## (Intercept) -113.3028    35.7210  -3.172
## latitude       3.5950     0.9623   3.736
##             Pr(>|t|)
## (Intercept)  0.00366 **
## latitude     0.00085 ***
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 13.82 on 28 degrees of freedom
## Multiple R-squared:  0.3326, Adjusted R-squared:  0.3088
## F-statistic: 13.96 on 1 and 28 DF,  p-value: 0.0008495
```

My intercept is -113.3, slope is 3.6 and R-squared is 0.33 or 33%. (I want you to pull these numbers out of the output and round them off to something sensible.) The slope is significantly nonzero, its P-value being 0.00085: rainfall really does depend on latitude, although not strongly so.

Extra: Of course, I can easily do the others as well, though you don't have to:

```
rainfall.2 = lm(rainfall ~ fromcoast, data = rains)
summary(rainfall.2)
```

```
##
## Call:
## lm(formula = rainfall ~ fromcoast, data = rains)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -15.240  -9.431  -6.603   2.871  51.147
##
## Coefficients:
##             Estimate Std. Error t value
## (Intercept) 23.77306    4.61296   5.154
## fromcoast   -0.05039    0.04431  -1.137
##             Pr(>|t|)
## (Intercept) 1.82e-05 ***
## fromcoast      0.265
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 16.54 on 28 degrees of freedom
## Multiple R-squared:  0.04414,    Adjusted R-squared:   0.01
## F-statistic: 1.293 on 1 and 28 DF,  p-value: 0.2651
```

Here, the intercept is 23.8, the slope is -0.05 and R-squared is a dismal 0.04 (4%). This is a way of seeing that this relationship is really weak, and it doesn't even have a curve to the trend or anything that would compensate for this. I looked at the scatterplot again and saw that if it were not for the point bottom right which is furthest from the coast and has almost no rainfall, there would be almost no trend at all. The slope here is not significantly different from zero, with a P-value of 0.265.

Finally:

```
rainfall.3 = lm(rainfall ~ altitude, data = rains)
summary(rainfall.3)
```

```
##
## Call:
## lm(formula = rainfall ~ altitude, data = rains)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -20.620  -8.479  -2.729   4.555  58.271
##
## Coefficients:
##              Estimate Std. Error t value
## (Intercept) 16.514799   3.539141   4.666
## altitude     0.002394   0.001428   1.676
##             Pr(>|t|)
## (Intercept)  6.9e-05 ***
## altitude       0.105
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 16.13 on 28 degrees of freedom
## Multiple R-squared:  0.09121,    Adjusted R-squared:  0.05875
## F-statistic:  2.81 on 1 and 28 DF,  p-value: 0.1048
```

The intercept is 16.5, the slope is 0.002 and the R-squared is 0.09 or 9%, also terrible. The P-value is 0.105, which is not small enough to be significant.

So it looks as if it's only `latitude` that has any impact at all. This is the only explanatory variable with a significantly nonzero slope. On its own, at least.

(f) Fit a multiple regression predicting `rainfall` from all three of the other (quantitative) variables. Display the results. Comment is coming up later.

Solution

This, then:

```
rainfall.4 = lm(rainfall ~ latitude + altitude +
    fromcoast, data = rains)
summary(rainfall.4)
```

```
##
## Call:
## lm(formula = rainfall ~ latitude + altitude + fromcoast, data = rains)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -28.722  -5.603  -0.531   3.510  33.317
##
## Coefficients:
##               Estimate Std. Error t value
## (Intercept) -1.024e+02  2.921e+01  -3.505
## latitude     3.451e+00  7.949e-01   4.342
## altitude     4.091e-03  1.218e-03   3.358
## fromcoast   -1.429e-01  3.634e-02  -3.931
##             Pr(>|t|)
## (Intercept) 0.001676 **
## latitude    0.000191 ***
## altitude    0.002431 **
## fromcoast   0.000559 ***
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 11.1 on 26 degrees of freedom
## Multiple R-squared:  0.6003, Adjusted R-squared:  0.5542
## F-statistic: 13.02 on 3 and 26 DF,  p-value: 2.205e-05
```

(g) What is the R-squared for the regression of the last part? How does that compare with the R-squared of your regression in part (e)?

Solution

The R-squared is 0.60 (60%), which is quite a bit bigger than the R-squared of 0.33 (33%) we got back in (e).

(h) What do you conclude about the importance of the variables that you did *not* include in your model in (e)? Explain briefly.

Solution

Both variables `altitude` and `fromcoast` are significant in this regression, so they have *something to add* over and above `latitude` when it comes to predicting rainfall, even though (and this seems odd) they have no apparent relationship with `rainfall` on their own. Another way to say this is that the three variables work together as a team to predict rainfall, and together they do much better than any one of them can do by themselves.

This also goes to show that the scatterplots we began with don't get to the heart of multi-variable relationships, because they are only looking at the variables two at a time.

(i) Make a suitable hypothesis test that the variables `altitude` and `fromcoast` significantly improve the prediction of `rainfall` over the use of `latitude` alone. What do you conclude?

Solution

This calls for `anova`. Feed this two fitted models, smaller (fewer explanatory variables) first. The null hypothesis is that the two models are equally good (so we should go with the smaller); the alternative is that the larger model is better, so that the extra complication is worth it:

```
anova(rainfall.1, rainfall.4)
```

```
## Analysis of Variance Table
##
## Model 1: rainfall ~ latitude
## Model 2: rainfall ~ latitude + altitude + fromcoast
##   Res.Df    RSS Df Sum of Sq      F   Pr(>F)
## 1     28 5346.8
## 2     26 3202.3  2    2144.5 8.7057 0.001276
##
## 1
## 2 **
## ---
## Signif. codes:
##   0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1  ’ ’ 1
```

The P-value is small, so we reject the null in favour of the alternative: the regression with all three explanatory variables fits better than the one with just `latitude`, so the bigger model is the one we should go with.

If you have studied these things: this one is a "multiple-partial *F*-test", for testing the combined significance of more than one x but less than all the x's.

If you had just one x, you'd use a t-test for its slope, and if you were testing all the x's, you'd use the global F-test that appears in the regression output.

13.2 *Carbon monoxide in cigarettes*

The (US) Federal Trade Commission assesses cigarettes according to their tar, nicotine and carbon monoxide contents. In a particular year, 25 brands were assessed. For each brand, the tar, nicotine and carbon monoxide (all in milligrams) were measured, along with the weight in grams. Our aim is to predict carbon monoxide from any or all of the other variables. The data are in link. These are aligned by column (except for the variable names), with more than one space between each column of data.

(a) Read the data into R, and check that you have 25 observations and 4 variables.

Solution

This specification calls for `read_table2`:

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/ftccigar.txt"
cigs = read_table2(my_url)
```

```
## Parsed with column specification:
## cols(
##   tar = col_double(),
##   nicotine = col_double(),
##   weight = col_double(),
##   co = col_double()
## )
```

```
cigs
```

```
## # A tibble: 25 x 4
##      tar nicotine weight    co
##    <dbl>    <dbl>  <dbl> <dbl>
##  1  14.1     0.86  0.985  13.6
##  2  16       1.06  1.09   16.6
##  3  29.8     2.03  1.16   23.5
##  4   8       0.67  0.928  10.2
##  5   4.1     0.4   0.946   5.4
##  6  15       1.04  0.888  15
##  7   8.8     0.76  1.03    9
##  8  12.4     0.95  0.922  12.3
##  9  16.6     1.12  0.937  16.3
## 10  14.9     1.02  0.886  15.4
## # ... with 15 more rows
```

Yes, I have 25 observations on 4 variables indeed.

`read_delim` won't work (try it and see what happens), because that would require the values to be separated by *exactly one* space.

(b)??part:regone?? Run a regression to predict carbon monoxide from the other variables, and obtain a summary of the output.

Solution

The word "summary" is meant to be a big clue that `summary` is what you need:

```
cigs.1 = lm(co ~ tar + nicotine + weight, data = cigs)
summary(cigs.1)
```

```
##
## Call:
## lm(formula = co ~ tar + nicotine + weight, data = cigs)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.89261 -0.78269  0.00428  0.92891  2.45082
##
## Coefficients:
##             Estimate Std. Error t value
## (Intercept)   3.2022     3.4618   0.925
## tar           0.9626     0.2422   3.974
## nicotine     -2.6317     3.9006  -0.675
## weight       -0.1305     3.8853  -0.034
##             Pr(>|t|)
## (Intercept) 0.365464
## tar         0.000692 ***
## nicotine    0.507234
## weight      0.973527
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 1.446 on 21 degrees of freedom
## Multiple R-squared:  0.9186, Adjusted R-squared:  0.907
## F-statistic: 78.98 on 3 and 21 DF,  p-value: 1.329e-11
```

(c)??part:regtwo?? Which one of your explanatory variables would you remove from this regression? Explain (very) briefly. Go ahead and fit the regression without it, and describe how the change in R-squared from the regression in (??part:regone??) was entirely predictable.

Solution

First, the x-variable to remove. The obvious candidate is `weight`, since it has easily the highest, and clearly non-significant, P-value. So, out it comes:

```
cigs.2 = lm(co ~ tar + nicotine, data = cigs)
summary(cigs.2)
```

```
##
## Call:
## lm(formula = co ~ tar + nicotine, data = cigs)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.89941 -0.78470 -0.00144  0.91585  2.43064
##
## Coefficients:
##             Estimate Std. Error t value
## (Intercept)   3.0896     0.8438   3.662
## tar           0.9625     0.2367   4.067
## nicotine     -2.6463     3.7872  -0.699
##             Pr(>|t|)
## (Intercept) 0.001371 **
## tar         0.000512 ***
## nicotine    0.492035
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 1.413 on 22 degrees of freedom
## Multiple R-squared:  0.9186, Adjusted R-squared:  0.9112
## F-statistic: 124.1 on 2 and 22 DF,  p-value: 1.042e-12
```

R-squared has dropped from 0.9186 to . . . 0.9186! That is, taking out `weight` has not just had a minimal effect on R-squared; it's not changed R-squared at all. This is because `weight` was so far from being significant: it literally had *nothing* to add.

Another way of achieving the same thing is via the function `update`, which takes a fitted model object and describes the *change* that you want to make:

```
cigs.2a = update(cigs.1, . ~ . - weight)
summary(cigs.2a)
```

```
##
## Call:
## lm(formula = co ~ tar + nicotine, data = cigs)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -2.89941 -0.78470 -0.00144  0.91585  2.43064
##
## Coefficients:
##             Estimate Std. Error t value
## (Intercept)   3.0896     0.8438   3.662
## tar           0.9625     0.2367   4.067
## nicotine     -2.6463     3.7872  -0.699
##             Pr(>|t|)
## (Intercept) 0.001371 **
## tar         0.000512 ***
## nicotine    0.492035
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 1.413 on 22 degrees of freedom
## Multiple R-squared:  0.9186, Adjusted R-squared:  0.9112
## F-statistic: 124.1 on 2 and 22 DF,  p-value: 1.042e-12
```

This can be shorter than describing the whole model again, as you do with the `cigs.2` version of `lm`. The syntax is that you first specify a "base" fitted model object that you're going to update. Because the model `cigs.1` contains all the information about the kind of model it is, and which data frame the data come from, R already knows that this is a linear multiple regression and which x's it contains. The second thing to describe is the change from the "base". In this case, we want to use the same response variable and all the same explanatory variables that we had before, except for weight. This is specified by a special kind of model formula where . means "whatever was there before": in English, "same response and same explanatories except take out weight".

(d)??part:regthree?? Fit a regression predicting carbon monoxide from nicotine *only*, and display the summary.

Solution

As you would guess:

```
cigs.3 = lm(co ~ nicotine, data = cigs)
summary(cigs.3)
```

```
##
## Call:
## lm(formula = co ~ nicotine, data = cigs)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.3273 -1.2228  0.2304  1.2700  3.9357
##
## Coefficients:
##             Estimate Std. Error t value
## (Intercept)   1.6647     0.9936   1.675
## nicotine     12.3954     1.0542  11.759
##             Pr(>|t|)
## (Intercept)    0.107
## nicotine    3.31e-11 ***
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 1.828 on 23 degrees of freedom
## Multiple R-squared:  0.8574, Adjusted R-squared:  0.8512
## F-statistic: 138.3 on 1 and 23 DF,  p-value: 3.312e-11
```

(e) nicotine was far from being significant in the model of (??part:regtwo??), and yet in the model of (??part:regthree??), it was *strongly* significant, and the R-squared value of (??part:regthree??) was almost as high as that of (??part:regtwo??). What does this say about the importance of nicotine as an explanatory variable? Explain, as briefly as you can manage.

Solution

What this says is that you *cannot* say anything about the "importance" of nicotine without also describing the context that you're talking about. *By itself*, `nicotine` is important, but *when you have 'tar' in the model*, `nicotine` is not important: precisely, it now has nothing to add over and above the predictive value that `tar` has. You might guess that this is because `tar` and `nicotine` are "saying the same thing" in some fashion. We'll explore that in a moment.

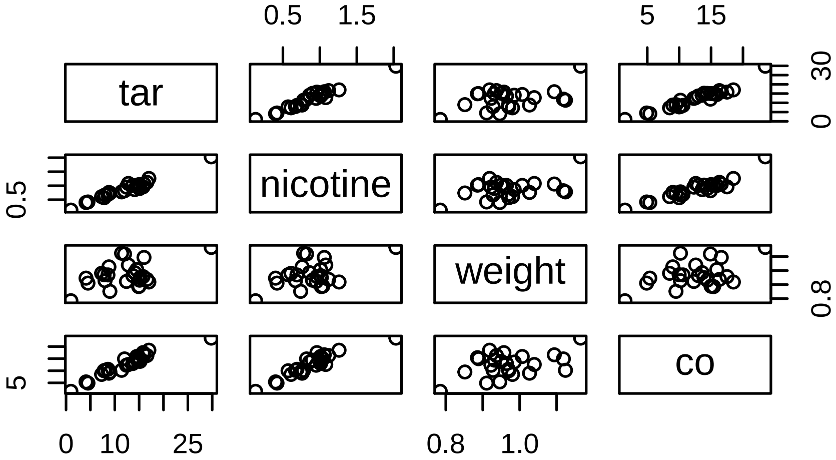
(f) Make a "pairs plot": that is, scatter plots between all pairs of variables. This can be done by feeding the whole data frame into `plot`. Do you see any strong relationships that do *not* include `co`? Does that shed any light on the last part? Explain briefly (or "at length" if that's how it comes out).

This is a base graphics graph rather than a ggplot one, but it will do for our purposes.

Solution

Plot the entire data frame:

```
plot(cigs)
```



We're supposed to ignore `co`, but I comment that strong relationships between `co` and *both* of `tar` and `nicotine` show up here, along with `weight` being at most weakly related to anything else.

That leaves the relationship of `tar` and `nicotine` with each other. That also looks like a strong linear trend. When you have correlations between explanatory variables, it is called "multicollinearity".

I mentioned a while back (in class) that having correlated x's was trouble. Here is where we find out why. The problem is that when `co` is large, `nicotine` is large, and a large value of `tar` will come along with it. So we don't know whether a large value of `co` is caused by a large value of `tar` or a large value of `nicotine`: there is no way to separate out their effects because in effect they are "glued together".

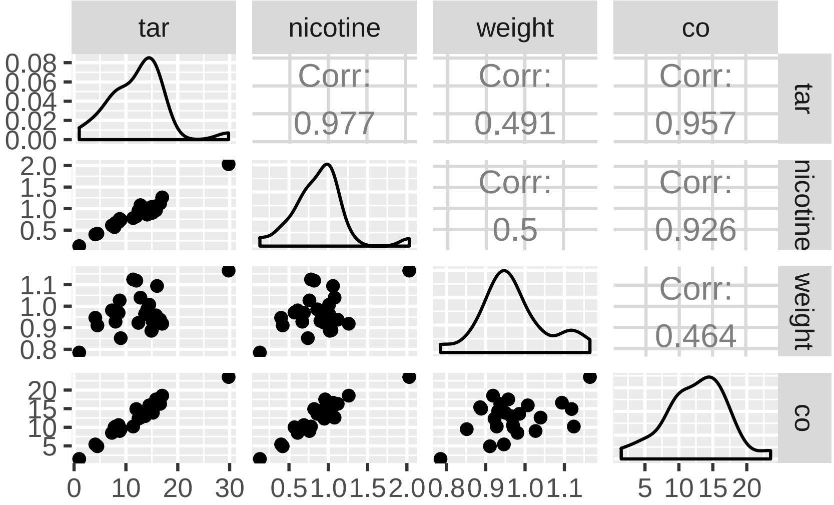
You might know of this effect (in an experimental design context) as "confounding": the effect of `tar` on `co` is confounded with the effect of `nicotine` on `co`, and you can't tell which one deserves the credit for predicting `co`.

If you were able to design an experiment here, you could (in principle) manufacture a bunch of cigarettes with high tar; some of them would have high nicotine and some would have low. Likewise for low tar. Then the correlation between `nicotine` and `tar` would go away, their effects on `co` would no longer be confounded, and you could see unambiguously which one of the variables deserves credit for predicting `co`. Or maybe it depends on both, genuinely, but at least then you'd know.

We, however, have an observational study, so we have to make do with the data we have. Confounding is one of the risks we take when we work with observational data.

This was a "base graphics" plot. There is a way of doing a `ggplot`-style "pairs plot", as this is called, thus:

```
library(GGally)

##
## Attaching package: 'GGally'

## The following object is masked from 'package:dplyr':
##
##     nasa

cigs %>% ggpairs()
```

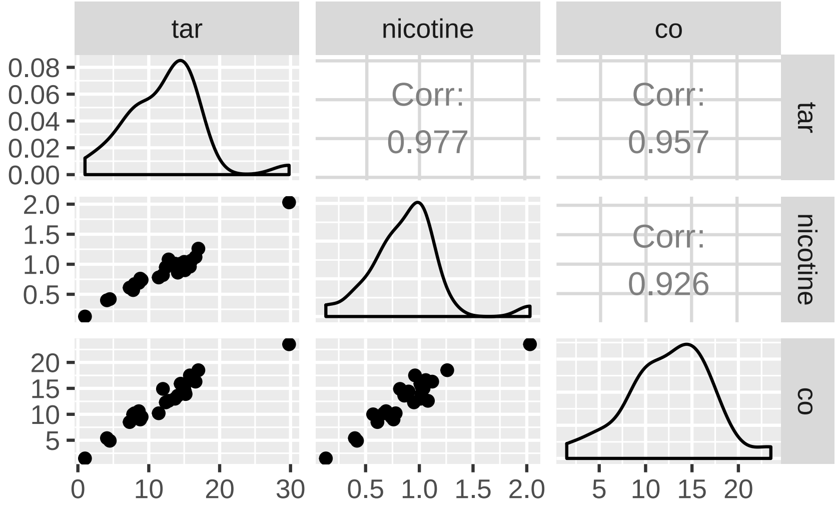


As ever, `install.packages` first, in the likely event that you don't have this package installed yet. Once you do, though, I think this is a nicer way to get a pairs plot.

This plot is a bit more sophisticated: instead of just having the scatterplots of the pairs of variables in the row and column, it uses the diagonal to show a "kernel density" (a smoothed-out histogram), and upper-right it shows the correlation between each pair of variables. The three correlations between `co`, `tar` and `nicotine` are clearly the highest.

If you want only some of the columns to appear in your pairs plot, `select` them first, and then pass that data frame into `ggpairs`. Here, we found that `weight` was not correlated with anything much, so we can take it out and then make a pairs plot of the other variables:

```
cigs %>% select(-weight) %>% ggpairs()
```



The three correlations that remain are all very high, which is entirely consistent with the strong linear relationships that you see bottom left.

13.3 *Maximal oxygen uptake in young boys*

A physiologist wanted to understand the relationship between physical characteristics of pre-adolescent boys and their maximal oxygen uptake (millilitres of oxygen per kilogram of body weight). The data are in link for a random sample of 10 pre-adolescent boys. The variables are (with units):

- `uptake`: Oxygen uptake (millitres of oxygen per kilogram of body weight)
- `age`: boy's age (years)
- `height`: boy's height (cm)
- `weight`: boy's weight (kg)
- `chest`: chest depth (cm).

(a) Read the data into R and confirm that you do indeed have 10 observations.

Solution

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/youngboys.txt"
boys = read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   uptake = col_double(),
##   age = col_double(),
##   height = col_double(),
##   weight = col_double(),
##   chest = col_double()
## )
```

```
boys
```

```
## # A tibble: 10 x 5
##    uptake   age height weight chest
##     <dbl> <dbl>  <dbl>  <dbl> <dbl>
##  1   1.54   8.4   132    29.1  14.4
##  2   1.74   8.7   136.   29.7  14.5
##  3   1.32   8.9   128.   28.4  14
##  4   1.5    9.9   131.   28.8  14.2
##  5   1.46   9     130    25.9  13.6
##  6   1.35   7.7   128.   27.6  13.9
##  7   1.53   7.3   130.   29    14
##  8   1.71   9.9   138.   33.6  14.6
##  9   1.27   9.3   127.   27.7  13.9
## 10   1.5    8.1   132.   30.8  14.5
```

10 boys (rows) indeed.

(b) Fit a regression predicting oxygen uptake from all the other variables, and display the results.

Solution

Fitting four explanatory variables with only ten observations is likely to be pretty shaky, but we press ahead regardless:

```
boys.1 = lm(uptake ~ age + height + weight + chest,
    data = boys)
summary(boys.1)
```

```
##
```

```
## Call:
## lm(formula = uptake ~ age + height + weight + chest, data = boys)
##
## Residuals:
##         1         2         3         4
## -0.020697  0.019741 -0.003649  0.038470
##         5         6         7         8
## -0.023639 -0.026026  0.050459 -0.014380
##         9        10
##  0.004294 -0.024573
##
## Coefficients:
##              Estimate Std. Error t value
## (Intercept) -4.774739   0.862818  -5.534
## age         -0.035214   0.015386  -2.289
## height       0.051637   0.006215   8.308
## weight      -0.023417   0.013428  -1.744
## chest        0.034489   0.085239   0.405
##             Pr(>|t|)
## (Intercept) 0.002643 **
## age         0.070769 .
## height      0.000413 ***
## weight      0.141640
## chest       0.702490
## ---
## Signif. codes:
##   0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1  ’ ’ 1
##
## Residual standard error: 0.03721 on 5 degrees of freedom
## Multiple R-squared:  0.9675, Adjusted R-squared:  0.9415
## F-statistic:  37.2 on 4 and 5 DF,  p-value: 0.0006513
```

(c) (A one-mark question.) Would you say, on the evidence so far, that the regression fits well or badly? Explain (very) briefly.

Solution

R-squared of 0.97 (97%) is very high, so I’d say this regression fits very well. That’s all. I said “on the evidence so far” to dissuade you from overthinking this, or thinking that you needed to produce some more evidence. That, plus the fact that this was only one mark.

(d) It seems reasonable that an older boy should have a greater oxygen uptake, all else being equal. Is this supported by your output? Explain briefly.

Solution

If an older boy has greater oxygen uptake (the "all else equal" was a hint), the slope of age should be positive. It is not: it is -0.035, so it is suggesting (all else equal) that a greater age goes with a *smaller* oxygen uptake. The reason why this happens (which you didn't need, but you can include it if you like) is that age has a non-small P-value of 0.07, so that the age slope is not significantly different from zero. With all the other variables, age has nothing to *add* over and above them, and we could therefore remove it.

(e) It seems reasonable that a boy with larger weight should have larger lungs and thus a *statistically significantly* larger oxygen uptake. Is that what happens here? Explain briefly.

Solution

Look at the P-value for weight. This is 0.14, not small, and so a boy with larger weight does not have a significantly larger oxygen uptake, all else equal. (The slope for weight is not significantly different from zero either.) I emphasized "statistically significant" to remind you that this means to do a test and get a P-value.

(f) Fit a model that contains only the significant explanatory variables from your first regression. How do the R-squared values from the two regressions compare? (The last sentence asks for more or less the same thing as the next part. Answer it either here or there. Either place is good.)

Solution

Only height is significant, so that's the only explanatory variable we need to keep. I would just do the regression straight rather than using update here:

```
boys.2 = lm(uptake ~ height, data = boys)
summary(boys.2)
```

```
##
## Call:
## lm(formula = uptake ~ height, data = boys)
##
## Residuals:
##       Min        1Q    Median        3Q
## -0.069879 -0.033144  0.001407  0.009581
##       Max
##  0.084012
##
## Coefficients:
##              Estimate Std. Error t value
## (Intercept) -3.843326   0.609198  -6.309
## height       0.040718   0.004648   8.761
##             Pr(>|t|)
## (Intercept) 0.000231 ***
## height      2.26e-05 ***
## ---
## Signif. codes:
##   0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1  ’ ’ 1
##
## Residual standard error: 0.05013 on 8 degrees of freedom
## Multiple R-squared:  0.9056, Adjusted R-squared:  0.8938
## F-statistic: 76.75 on 1 and 8 DF,  p-value: 2.258e-05
```

If you want, you can use `update` here, which looks like this:

```
boys.2a = update(boys.1, . ~ . - age - weight -
    chest)
summary(boys.2a)
```

```
##
## Call:
## lm(formula = uptake ~ height, data = boys)
##
## Residuals:
##       Min        1Q    Median        3Q
## -0.069879 -0.033144  0.001407  0.009581
##       Max
##  0.084012
##
## Coefficients:
##              Estimate Std. Error t value
## (Intercept) -3.843326   0.609198  -6.309
## height       0.040718   0.004648   8.761
##             Pr(>|t|)
## (Intercept) 0.000231 ***
## height      2.26e-05 ***
## ---
## Signif. codes:
##   0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1  ’ ’ 1
##
## Residual standard error: 0.05013 on 8 degrees of freedom
## Multiple R-squared:  0.9056, Adjusted R-squared:  0.8938
## F-statistic: 76.75 on 1 and 8 DF,  p-value: 2.258e-05
```

This doesn’t go quite so smoothly here because there are three variables being removed, and it’s a bit of work to type them all.

(g) How has R-squared changed between your two regressions? Describe what you see in a few words.

Solution

R-squared has dropped by a bit, from 97% to 91%. (Make your own call: pull out the two R-squared numbers, and say a word or two about how they compare. I don't much mind what you say: "R-squared has decreased (noticeably)", "R-squared has hardly changed". But say something.)

(h) Carry out a test comparing the fit of your two regression models. What do you conclude, and therefore what recommendation would you make about the regression that would be preferred?

Solution

The word "test" again implies something that produces a P-value with a null hypothesis that you might reject. In this case, the test that compares two models differing by more than one x uses `anova`, testing the null hypothesis that the two regressions are equally good, against the alternative that the bigger (first) one is better. Feed `anova` two fitted model objects, smaller first:

```
anova(boys.2, boys.1)
```

```
## Analysis of Variance Table
##
## Model 1: uptake ~ height
## Model 2: uptake ~ age + height + weight + chest
##   Res.Df       RSS Df Sum of Sq      F
## 1      8 0.0201016
## 2      5 0.0069226  3  0.013179 3.1729
##   Pr(>F)
## 1
## 2  0.123
```

This P-value of 0.123 is not small, so we do not reject the null hypothesis. There is not a significant difference in fit between the two models. Therefore, we should go with the smaller model `boys.2` because it is simpler.

That drop in R-squared from 97% to 91% was, it turns out, *not* significant: the three extra variables could have produced a change in R-squared like that, *even if they were worthless*.

Recall that adding x's to a regression will always make R-squared go up, even if they are just random noise.

If you have learned about "adjusted R-squared", you might recall that this is supposed to go down *only* if the variables you took out should not have been taken out. But adjusted R-squared goes down here as well, from 94% to 89% (not quite as much, therefore). What happens is that adjusted R-squared is rather more relaxed about keeping variables than the anova F-test is; if we had used an α of something like 0.10, the decision between the two models would have been a lot closer, and this is reflected in the adjusted R-squared values.

(i) Obtain a table of correlations between all the variables in the data frame. Do this by feeding the whole data frame into cor. We found that a regression predicting oxygen uptake from just height was acceptably good. What does your table of correlations say about why that is? (Hint: look for all the correlations that are *large*.)

Solution
Correlations first:

```
cor(boys)
```

```
##           uptake       age    height
## uptake 1.0000000 0.1361907 0.9516347
## age    0.1361907 1.0000000 0.3274830
## height 0.9516347 0.3274830 1.0000000
## weight 0.6576883 0.2307403 0.7898252
## chest  0.7182659 0.1657523 0.7909452
##           weight     chest
## uptake 0.6576883 0.7182659
## age    0.2307403 0.1657523
## height 0.7898252 0.7909452
## weight 1.0000000 0.8809605
## chest  0.8809605 1.0000000
```

The correlations with age are all on the low side, but all the other correlations are high, not just between uptake and the other variables, but between the explanatory variables as well.

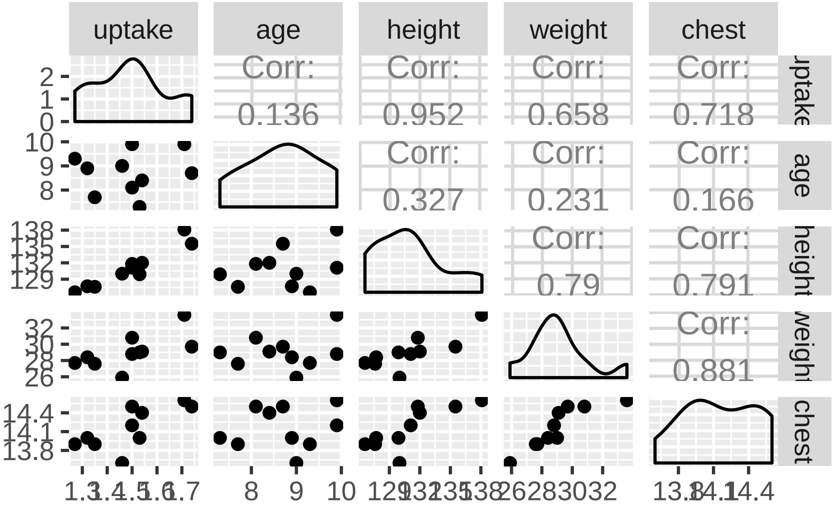
Why is this helpful in understanding what's going on? Well, imagine a boy with large height (a tall one). The regression boys.2 says that this alone is enough to predict that such a boy's oxygen uptake is likely to be large, since the slope is positive. But the correlations tell you more: a boy with large height is also (somewhat) likely to be older (have large age), heavier (large weight) and to have larger chest cavity. So oxygen uptake does depend on those other variables as well, but once you know height you can make a good guess at their values; you don't need to know them.

Further remarks: age has a low correlation with uptake, so its non-significance earlier appears to be "real": it really does have nothing extra to say, because the other variables have a stronger link with `uptake` than `age`. Height, however, seems to be the best way of relating oxygen uptake to any of the other variables. I think the suppositions from earlier about relating oxygen uptake to "bigness" in some sense are actually sound, but age and weight and `chest` capture "bigness" worse than height does. Later, when you learn about Principal Components, you will see that the first principal component, the one that best captures how the variables vary together, is often "bigness" in some sense.

This is not, I don't think, a real word, but I mean size emphasizing how big a boy is generally, rather than how small.

Another way to think about these things is via pairwise scatterplots. The nicest way to produce these is via `ggpairs` from package `GGally`:

```
boys %>% ggpairs()
```



A final remark: with five variables, we really ought to have more than ten observations (something like 50 would be better). But with more observations and the same correlation structure, the same issues would come up again, so the question would not be materially changed.

13.4 *Mating songs in crickets*

Male tree crickets produce "mating songs" by rubbing their wings together to produce a chirping sound. It is hypothesized that female tree crickets identify males of the correct species by how fast (in chirps per second) the male's mating song is. This is called the "pulse rate". Some data for two species of crickets are in link. The columns, which are unlabelled, are temperature and pulse rate (respectively) for *Oecanthus exclamationis* (first two columns) and *Oecanthus niveus* (third and fourth columns). The columns are separated by tabs. There are some missing values in the first two columns because fewer *exclamationis* crickets than *niveus* crickets were measured. The research question is whether males of the different species have different average pulse rates. It is also of interest to see whether temperature has an effect, and if so, what.

(a) Read in the data, allowing for the fact that you have no column names. You'll see that the columns have names X1 through X4. This is OK.

Solution

Tab-separated, so read_tsv; no column names, so col_names=F:

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/crickets.txt"
crickets = read_tsv(my_url, col_names = F)
```

```
## Parsed with column specification:
## cols(
##   X1 = col_double(),
##   X2 = col_double(),
##   X3 = col_double(),
##   X4 = col_double()
## )
```

```
crickets
```

```
## # A tibble: 17 x 4
##       X1    X2    X3    X4
##    <dbl> <dbl> <dbl> <dbl>
##  1  20.8  67.9  17.2  44.3
##  2  20.8  65.1  18.3  47.2
##  3  24    77.3  18.3  47.6
##  4  24    78.7  18.3  49.6
##  5  24    79.4  18.9  50.3
##  6  24    80.4  18.9  51.8
##  7  26.2  85.8  20.4  60
##  8  26.2  86.6  21    58.5
##  9  26.2  87.5  21    58.9
## 10  26.2  89.1  22.1  60.7
## 11  28.4  98.6  23.5  69.8
## 12  29   101.   24.2  70.9
## 13  30.4  99.3  25.9  76.2
## 14  30.4 102.   26.5  76.1
## 15  NA    NA    26.5  77
## 16  NA    NA    26.5  77.7
## 17  NA    NA    28.6  84.7
```

As promised.

If you didn't catch the tab-separated part, this probably happened to you:

```
d = read_delim(my_url, " ", col_names = F)
```

```
## Parsed with column specification:
## cols(
##   X1 = col_character()
## )
```

```
## Warning in rbind(names(probs), probs_f):
## number of columns of result is not a multiple
## of vector length (arg 1)
```

```
## Warning: 3 parsing failures.
## row # A tibble: 3 x 5 col     row col   expected  actual file          expected   <int> <chr> <chr>
```

This doesn't look good:

```
problems(d)
```

```
## # A tibble: 3 x 5
##     row col   expected  actual file
##   <int> <chr> <chr>     <chr>  <chr>
## 1    15 <NA>  1 columns 2 col~ 'http://www.~
## 2    16 <NA>  1 columns 2 col~ 'http://www.~
## 3    17 <NA>  1 columns 2 col~ 'http://www.~
```

The "expected columns" being 1 should bother you, since we know there are supposed to be 4 columns. At this point, we take a look at what got read in:

```
d
```

```
## # A tibble: 17 x 1
##    X1
##    <chr>
##  1 "20.8\t67.9\t17.2\t44.3"
##  2 "20.8\t65.1\t18.3\t47.2"
##  3 "24.0\t77.3\t18.3\t47.6"
##  4 "24.0\t78.7\t18.3\t49.6"
##  5 "24.0\t79.4\t18.9\t50.3"
##  6 "24.0\t80.4\t18.9\t51.8"
##  7 "26.2\t85.8\t20.4\t60.0"
##  8 "26.2\t86.6\t21.0\t58.5"
##  9 "26.2\t87.5\t21.0\t58.9"
## 10 "26.2\t89.1\t22.1\t60.7"
## 11 "28.4\t98.6\t23.5\t69.8"
## 12 "29.0\t100.8\t24.2\t70.9"
## 13 "30.4\t99.3\t25.9\t76.2"
## 14 "30.4\t101.7\t26.5\t76.1"
## 15 "NA\tNA"
## 16 "NA\tNA"
## 17 "NA\tNA"
```

and there you see the t or "tab" characters separating the values, instead of spaces. (This is what I tried first, and once I looked at this, I realized that read_tsv was what I needed.)

(b) These data are rather far from being tidy. There need to be three variables, temperature, pulse rate and species, and there are $14 + 17 = 31$ observations altogether. This one is tricky in that there are temperature and pulse rate for each of two levels of a factor, so I'll suggest combining the temperature and chirp rate together into one thing for each species, then gathering them, then splitting them again. Create new columns, named for each species, that contain the temperature and pulse rate for that species in that order, united together. For the rest of this question, start from the data frame you read in, and build a pipe, one or two steps at a time, to save creating a lot of temporary data frames.

Solution

Breathe, and then begin. unite creates new columns by joining together old ones:

As *str-c* or *paste* do, actually, but the advantage of *unite* is that it gets rid of the other columns, which you probably no longer need.

```
crickets %>% unite(exclamationis, X1:X2) %>% unite(niveus,
    X3:X4)
```

```
## # A tibble: 17 x 2
##    exclamationis niveus
##    <chr>         <chr>
##  1 20.8_67.9     17.2_44.3
##  2 20.8_65.1     18.3_47.2
##  3 24_77.3       18.3_47.6
##  4 24_78.7       18.3_49.6
##  5 24_79.4       18.9_50.3
##  6 24_80.4       18.9_51.8
##  7 26.2_85.8     20.4_60
##  8 26.2_86.6     21_58.5
##  9 26.2_87.5     21_58.9
## 10 26.2_89.1     22.1_60.7
## 11 28.4_98.6     23.5_69.8
## 12 29_100.8      24.2_70.9
## 13 30.4_99.3     25.9_76.2
## 14 30.4_101.7    26.5_76.1
## 15 NA_NA         26.5_77
## 16 NA_NA         26.5_77.7
## 17 NA_NA         28.6_84.7
```

Note that the original columns X1:X4 are *gone*, which is fine, because the information we needed from them is contained in the two new columns. unite by default uses an underscore to separate the joined-together values, which is generally safe since you won't often find those in data.

Digression: unite-ing with a space could cause problems if the data values have spaces in them already. Consider this list of names:

```
names = c("Cameron McDonald", "Durwin Yang", "Ole Gunnar Solskjaer",
    "Mahmudullah")
```

Two very former students of mine, a Norwegian soccer player, and a Bangladeshi cricketer. Only one of these has played for Manchester United:

```
manu = c(F, F, T, F)
```

and let's make a data frame:

```
d = tibble(name = names, manu = manu)
d
```

```
## # A tibble: 4 x 2
##   name                 manu
##   <chr>                <lgl>
## 1 Cameron McDonald     FALSE
## 2 Durwin Yang          FALSE
## 3 Ole Gunnar Solskjaer TRUE
## 4 Mahmudullah          FALSE
```

Now, what happens if we unite those columns, separating them by a space?

```
d %>% unite(joined, name:manu, sep = " ")
```

```
## # A tibble: 4 x 1
##   joined
##   <chr>
## 1 Cameron McDonald FALSE
## 2 Durwin Yang FALSE
## 3 Ole Gunnar Solskjaer TRUE
## 4 Mahmudullah FALSE
```

If we then try to separate them again, what happens?

```
d %>% unite(joined, name:manu, sep = " ") %>%
    separate(joined, c("one", "two"), " ")
```

```
## Warning: Expected 2 pieces. Additional pieces
## discarded in 3 rows [1, 2, 3].
```

```
## # A tibble: 4 x 2
##   one         two
##   <chr>       <chr>
## 1 Cameron     McDonald
## 2 Durwin      Yang
## 3 Ole         Gunnar
## 4 Mahmudullah FALSE
```

Things have gotten lost: most of the original values of `manu` and some of the names. If we use a different separator character, either choosing one deliberately or going with the default underscore, everything works swimmingly:

```
d %>% unite(joined, name:manu, sep = ":") %>%
    separate(joined, c("one", "two"), ":")
```

```
## # A tibble: 4 x 2
##   one                  two
##   <chr>                <chr>
## 1 Cameron McDonald     FALSE
## 2 Durwin Yang          FALSE
## 3 Ole Gunnar Solskjaer TRUE
## 4 Mahmudullah          FALSE
```

and we are back to where we started.

If you run just the `unite` line (move the pipe symbol to the next line so that the `unite` line is complete as it stands), you'll see what happened.

(c) The two columns `exclamationis` and `niveus` that you just created are both temperature-pulse rate combos, but for different species. `gather` them together into one column, labelled by species. (This is a straight `tidyr` `gather`, even though they contain something odd-looking.)

Solution

Thus, this, naming the new column `temp_pulse` since it contains both of those things. Add to the end of the pipe you started building in the previous part:

```
crickets %>% unite(exclamationis, X1:X2) %>% unite(niveus,
    X3:X4) %>% gather(species, temp_pulse, exclamationis:niveus)
```

```
## # A tibble: 34 x 2
##    species       temp_pulse
##    <chr>         <chr>
##  1 exclamationis 20.8_67.9
##  2 exclamationis 20.8_65.1
##  3 exclamationis 24_77.3
##  4 exclamationis 24_78.7
##  5 exclamationis 24_79.4
##  6 exclamationis 24_80.4
##  7 exclamationis 26.2_85.8
##  8 exclamationis 26.2_86.6
##  9 exclamationis 26.2_87.5
## 10 exclamationis 26.2_89.1
## # ... with 24 more rows
```

Yep. If you scroll down with Next, you'll see the other species of crickets, and you'll see some missing values at the bottom, labelled, at the moment, NA_NA.

This is going to get rather long, but don't fret: we debugged the two unite lines before, so if you get any errors, they must have come from the gather. So that would be the place to check.

(d) Now split up the temperature-pulse combos at the underscore, into two separate columns. This is separate. When specifying what to separate by, you can use a number ("split after this many characters") or a piece of text, in quotes ("when you see this text, split at it").

Solution

The text to split by is an underscore (in quotes), since unite by default puts an underscore in between the values it pastes together. Glue the separate onto the end. We are creating two new variables temperature and pulse_rate:

```
crickets %>% unite(exclamationis, X1:X2) %>% unite(niveus,
    X3:X4) %>% gather(species, temp_pulse, exclamationis:niveus) %>%
    separate(temp_pulse, c("temperature", "pulse_rate"),
        "_")
```

```
## # A tibble: 34 x 3
##    species       temperature pulse_rate
##    <chr>         <chr>       <chr>
##  1 exclamationis 20.8        67.9
##  2 exclamationis 20.8       65.1
##  3 exclamationis 24         77.3
##  4 exclamationis 24         78.7
##  5 exclamationis 24         79.4
##  6 exclamationis 24         80.4
##  7 exclamationis 26.2       85.8
##  8 exclamationis 26.2       86.6
##  9 exclamationis 26.2       87.5
## 10 exclamationis 26.2       89.1
## # ... with 24 more rows
```

You'll note that unite and separate are opposites ("inverses") of each other, but we haven't just done something and then undone it, because we have a gather in between; in fact, arranging it this way has done precisely the tidying we wanted.

(e) Almost there. Temperature and pulse rate are still text (because unite turned them into text), but they should be numbers. Create new variables that are numerical versions of temperature and pulse rate (using as.numeric). Check that you have no extraneous variables (and, if necessary, get rid of the ones you don't want). (Species is also text and really ought to be a factor, but having it as text doesn't seem to cause any problems.) You can, if you like, use parse_number instead of as.numeric. They should both work. The distinction I prefer to make is that parse_number is good for text with a number in it (that we want to pull the number out of), while as.numeric is for turning something that looks like a number but isn't one into a genuine number.

You could just as well make the point that the text 20.8 contains the number 20.8 and nothing else, so that parsing it as text in search of a number will pull out 20.8 as a number. If that logic works for you, go with it.

Solution

mutate-ing into a column that already exists overwrites the variable that's already there (which saves us some effort here).

```
crickets.1 = crickets %>% unite(exclamationis,
    X1:X2) %>% unite(niveus, X3:X4) %>% gather(species,
    temp_pulse, exclamationis:niveus) %>% separate(temp_pulse,
    c("temperature", "pulse_rate"), "_") %>% mutate(temperature = as.numeric(temperature)) %>%
    mutate(pulse_rate = as.numeric(pulse_rate))
```

```
## Warning in evalq(as.numeric(temperature),
## <environment>): NAs introduced by coercion
```

```
## Warning in evalq(as.numeric(pulse_rate),
## <environment>): NAs introduced by coercion
```

```
crickets.1
```

```
## # A tibble: 34 x 3
##    species       temperature pulse_rate
##    <chr>               <dbl>      <dbl>
##  1 exclamationis        20.8       67.9
##  2 exclamationis        20.8       65.1
##  3 exclamationis        24         77.3
##  4 exclamationis        24         78.7
##  5 exclamationis        24         79.4
##  6 exclamationis        24         80.4
##  7 exclamationis        26.2       85.8
##  8 exclamationis        26.2       86.6
##  9 exclamationis        26.2       87.5
## 10 exclamationis        26.2       89.1
## # ... with 24 more rows
```

I saved the data frame this time, since this is the one we will use for our analysis.

The warning message tells us that we got genuine missing-value NAs back, which is probably what we want. Specifically, they got turned from missing *text* to missing *numbers*! The R word "coercion" means values being changed from one type of thing to another type of thing. (We'll ignore the missings and see if they cause us any trouble. The same warning messages will show up on graphs later.) So I have 34 rows (including three rows of missings) instead of the 31 rows I would have liked. Otherwise, success.

You might think that missing is just missing, but R distinguishes between types of missing.

There is (inevitably) another way to do this. We are doing the as.numeric twice, exactly the same on two different columns, and when you are doing the same thing on a number of columns, here a mutate with the same function, you have the option of using mutate_if or mutate_at. These are like summarize_if and summarize_at that we used way back to compute numerical summaries of a bunch of columns: the if variant works on columns that share a property, like being numeric, and the at variant works on columns whose names have something in common or that we can list, which is what we want here:

```
crickets %>% unite(exclamationis, X1:X2) %>% unite(niveus,
    X3:X4) %>% gather(species, temp_pulse, exclamationis:niveus) %>%
    separate(temp_pulse, c("temperature", "pulse_rate"),
        "_") %>% mutate_at(vars(temperature:pulse_rate),
    funs(as.numeric))
```

```
## Warning in evalq(as.numeric(temperature),
## <environment>): NAs introduced by coercion

## Warning in evalq(as.numeric(pulse_rate),
## <environment>): NAs introduced by coercion
```

```
## # A tibble: 34 x 3
##    species       temperature pulse_rate
##    <chr>               <dbl>      <dbl>
##  1 exclamationis        20.8       67.9
##  2 exclamationis        20.8       65.1
##  3 exclamationis        24         77.3
##  4 exclamationis        24         78.7
##  5 exclamationis        24         79.4
##  6 exclamationis        24         80.4
##  7 exclamationis        26.2       85.8
##  8 exclamationis        26.2       86.6
##  9 exclamationis        26.2       87.5
## 10 exclamationis        26.2       89.1
## # ... with 24 more rows
```

Can't I just say that these are columns 2 and 3?

```
crickets %>% unite(exclamationis, X1:X2) %>% unite(niveus,
    X3:X4) %>% gather(species, temp_pulse, exclamationis:niveus) %>%
    separate(temp_pulse, c("temperature", "pulse_rate"),
        "_") %>% mutate_at(vars(2:3), funs(as.numeric))
```

```
## Warning in evalq(as.numeric(temperature),
## <environment>): NAs introduced by coercion
```

```
## Warning in evalq(as.numeric(pulse_rate),
## <environment>): NAs introduced by coercion
```

```
## # A tibble: 34 x 3
##    species       temperature pulse_rate
##    <chr>               <dbl>      <dbl>
##  1 exclamationis        20.8       67.9
##  2 exclamationis        20.8       65.1
##  3 exclamationis        24         77.3
##  4 exclamationis        24         78.7
##  5 exclamationis        24         79.4
##  6 exclamationis        24         80.4
##  7 exclamationis        26.2       85.8
##  8 exclamationis        26.2       86.6
##  9 exclamationis        26.2       87.5
## 10 exclamationis        26.2       89.1
## # ... with 24 more rows
```

Yes. Equally good. What goes into the `vars` is the same as can go into a `select`: column numbers, names, or any of those "select helpers" like `starts_with`.

You might think of `mutate_if` here, but if you scroll back, you'll find that all the columns are text, before you convert temperature and pulse rate to numbers, and so there's no way to pick out just the two columns you want that way.

Check that the temperature and pulse rate columns are now labelled `dbl`, which means they actually *are* decimal numbers (and don't just look like decimal numbers).

Either way, using `unite` and then `separate` means that all the columns we created we want to keep (or, all the ones we would have wanted to get rid of have already been gotten rid of).

Now we can actually do some statistics.

(f) Do a two-sample *t*-test to see whether the mean pulse rates differ between species. What do you conclude?

Solution

Drag your mind way back to this:

```
t.test(pulse_rate ~ species, data = crickets.1)
```

```
##
##  Welch Two Sample t-test
##
## data:  pulse_rate by species
## t = 5.2236, df = 28.719, p-value =
## 1.401e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  14.08583 32.22677
## sample estimates:
## mean in group exclamationis
##                    85.58571
##       mean in group niveus
##                    62.42941
```

There is strong evidence of a difference in means (a P-value around 0.00001), and the confidence interval says that the mean chirp rate is higher for *exclamationis*. That is, not just for the crickets that were observed here, but for *all* crickets of these two species.

(g) The analysis in the last part did not use temperature, however. Is it possible that temperature also has an effect? To assess this, draw a scatterplot of pulse rate against temperature, with the points distinguished, somehow, by the species they are from.

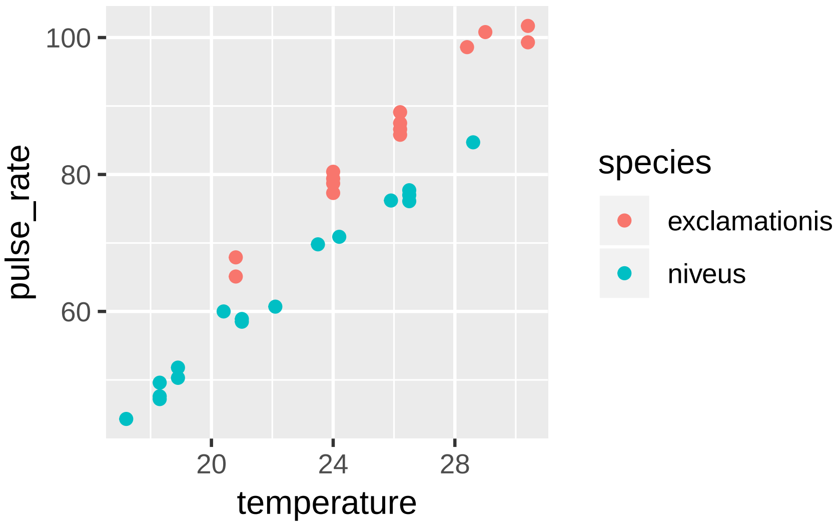
This was the actual reason I gave you this question: I wanted you to do this. It sort of morphed into all the other stuff as well.

Solution

One of the wonderful things about `ggplot` is that doing the obvious thing works:

```
ggplot(crickets.1, aes(x = temperature, y = pulse_rate,
    colour = species)) + geom_point()
```

```
## Warning: Removed 3 rows containing missing values
## (geom_point).
```



(h) What does the plot tell you that the *t*-test doesn't? How would you describe differences in pulse rates between species now?

Solution

The plot tells you that (for both species) as temperature goes up, pulse rate goes up as well. *Allowing for that*, the difference in pulse rates between the two species is even clearer than it was before. To see an example, pick a temperature, and note that the mean pulse rate at that temperature seems to be at least 10 higher for *exclamationis*, with a high degree of consistency. The *t*-test mixed up all the pulse rates at all the different temperatures. Even though the conclusion was clear enough, it could be clearer if we incorporated temperature into the analysis. There was also a potential source of unfairness in that the *exclamationis* crickets tended to be observed at higher temperatures than *niveus* crickets; since pulse rates increase with temperature, the apparent difference in pulse rates between the species might have been explainable by one species being observed mainly in higher temperatures. This was *utterly invisible* to us when we did the *t*-test, but it shows the importance of accounting for all the relevant variables when you do your analysis. If the species had been observed at opposite temperatures, we might have concluded that *niveus* have the higher pulse rates on average. I come back to this later when I discuss the confidence interval for species difference that comes out of the regression model with temperature.

And it shows the value of looking at relevant plots.

Mistakenly.

(i) Fit a regression predicting pulse rate from species and temperature. Compare the P-value for species in this regression to the one from the *t*-test. What does that tell you?

Solution

This is actually a so-called "analysis of covariance model", which properly belongs in D29, but it's really just a regression:

```
pulse.1 = lm(pulse_rate ~ species + temperature,
    data = crickets.1)
summary(pulse.1)
```

```
##
## Call:
## lm(formula = pulse_rate ~ species + temperature, data = crickets.1)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.0128 -1.1296 -0.3912  0.9650  3.7800
##
## Coefficients:
##                 Estimate Std. Error t value
## (Intercept)     -7.21091    2.55094  -2.827
## speciesniveus -10.06529    0.73526 -13.689
## temperature      3.60275    0.09729  37.032
##                Pr(>|t|)
## (Intercept)     0.00858 **
## speciesniveus 6.27e-14 ***
## temperature    < 2e-16 ***
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 1.786 on 28 degrees of freedom
##   (3 observations deleted due to missingness)
## Multiple R-squared:  0.9896, Adjusted R-squared:  0.9888
## F-statistic:  1331 on 2 and 28 DF,  p-value: < 2.2e-16
```

The P-value for species is now 6.27×10^{-14} or 0.00000000000006, which is even less than the P-value of 0.00001 that came out of the *t*-test. That is to say, when you know temperature, you can be even more sure of your conclusion that there is a difference between the species.

The R-squared for this regression is almost 99%, which says that if you know both temperature and species, you can predict the pulse rate almost exactly.

In the regression output, the slope for species is about −10. It is labelled `speciesniveus`. Since species is categorical, `lm` uses the first category, *exclamationis*, as the baseline and expresses each other species relative to that. Since the slope is about −10, it says that at any given temperature, the mean pulse rate for *niveus* is about 10 less than for *exclamationis*. This is pretty much what the scatterplot told us.

We can go a little further here:

```
confint(pulse.1)
```

```
##                    2.5 %    97.5 %
## (Intercept)   -12.436265 -1.985547
## speciesniveus -11.571408 -8.559175
## temperature     3.403467  3.802038
```

The second line says that the pulse rate for *niveus* is between about 8.5 and 11.5 less than for *exclamationis*, at any given temperature (comparing the two species at the same temperature as each other, but that temperature could be anything). This is a lot shorter than the CI that came out of the *t*-test, that went from 14 to 32. This is because we are now accounting for temperature, which also makes a difference. (In the *t*-test, the temperatures were all mixed up). What we also see is that the *t*-interval is shifted up compared to the one from the regression. This is because the *t*-interval conflates two things: the textsl{exclamationis} crickets do have a higher pulse rate, but they were also observed at higher temperatures, which makes it look as if their pulse rates are more higher than they really are, when you account for temperature.

Mixes up.

This is actually grammatically correct.

This particular model constrains the slope with temperature to be the same for both species (just the intercepts differ). If you want to allow the slopes to differ between species, you add an interaction between temperature and species:

```
pulse.2 = lm(pulse_rate ~ species * temperature,
    data = crickets.1)
summary(pulse.2)
```

```
##
## Call:
## lm(formula = pulse_rate ~ species * temperature, data = crickets.1)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.7031 -1.3417 -0.1235  0.8100  3.6330
##
```

```
## Coefficients:
##                            Estimate
## (Intercept)                -11.0408
## speciesniveus               -4.3484
## temperature                  3.7514
## speciesniveus:temperature   -0.2340
##                            Std. Error t value
## (Intercept)                    4.1515  -2.659
## speciesniveus                  4.9617  -0.876
## temperature                    0.1601  23.429
## speciesniveus:temperature      0.2009  -1.165
##                            Pr(>|t|)
## (Intercept)                   0.013 *
## speciesniveus                 0.389
## temperature                  <2e-16 ***
## speciesniveus:temperature     0.254
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 1.775 on 27 degrees of freedom
##   (3 observations deleted due to missingness)
## Multiple R-squared:  0.9901, Adjusted R-squared:  0.989
## F-statistic: 898.9 on 3 and 27 DF,  p-value: < 2.2e-16
```

To see whether adding the interaction term added anything to the prediction, \marginnote{Though it's hard to imagine being able to improve on an R-squared of 99%.} compare the model with and without using texttt{anova}:

```
anova(pulse.1, pulse.2)
```

```
## Analysis of Variance Table
##
## Model 1: pulse_rate ~ species + temperature
## Model 2: pulse_rate ~ species * temperature
##   Res.Df    RSS Df Sum of Sq     F Pr(>F)
## 1     28 89.350
## 2     27 85.074  1    4.2758 1.357 0.2542
```

There's no significant improvement by adding the interaction, so there's no evidence that having different slopes for each species is necessary. Note that `anova` gave the same P-value as did the *t*-test for the slope coefficient for the interaction in `summary`, 0.254 in both cases. This is because there were only two species and therefore only one slope coefficient was required to distinguish them. If there had been three species, we would have had to look at the anova output to hunt for a difference among species, since there would have been two slope coefficients, each with its own P-value.

This wouldn't have told us about the overall effect of species.

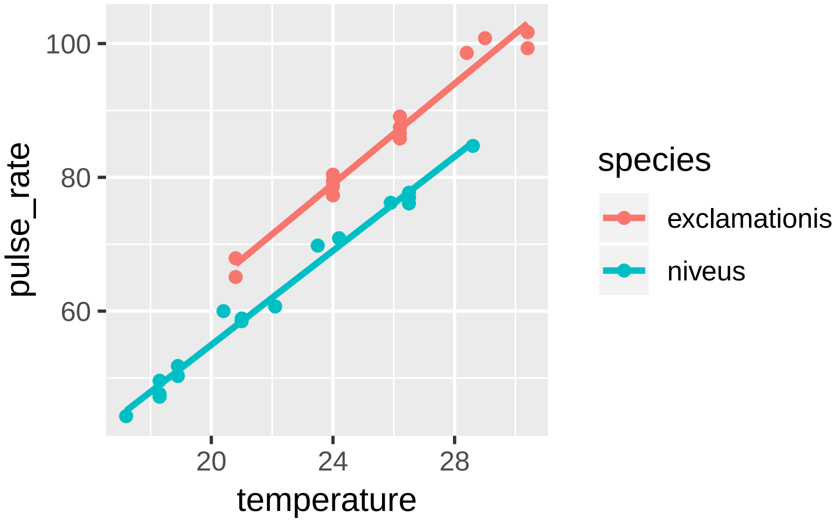
The upshot is that we do not need different slopes; the model pulse.1 with the same slope for each species describes what is going on.

ggplot makes it almost laughably easy to add regression lines for each species to our plot, thus:

```
ggplot(crickets.1, aes(x = temperature, y = pulse_rate,
    colour = species)) + geom_point() + geom_smooth(method = "lm",
    se = F)
```

```
## Warning: Removed 3 rows containing non-finite
## values (stat_smooth).
```

```
## Warning: Removed 3 rows containing missing values
## (geom_point).
```



The lines are almost exactly parallel, so having the same slope for each species makes perfect sense.

13.5 Facebook friends and grey matter

Is there a relationship between the number of Facebook friends a person has, and the density of grey matter in the areas of the brain associated with social perception and associative memory? To find out, a 2012 study measured both of these variables for a sample of 40 students at City University in London (England). The data are at link. The grey matter density is on a *z*-score standardized scale. The values are separated by *tabs*.

The aim of this question is to produce an R Markdown report that contains your answers to the questions below.

You should aim to make your report flow smoothly, so that it would be pleasant for a grader to read, and can stand on its own as an analysis (rather than just being the answer to a question that I set you). Some suggestions: give your report a title and arrange it into sections with an Introduction; add a small amount of additional text here and there explaining what you are doing and why. I don't expect you to spend a large amount of time on this, but I *do* hope you will make some effort. (My report came out to 4 Word pages.)

(a) Read in the data and make a scatterplot for predicting the number of Facebook friends from the grey matter density. On your scatterplot, add a smooth trend.

Solution

Begin your document with a code chunk containing `library(tidyverse)`. The data values are separated by tabs, which you will need to take into account:

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/facebook.txt"
fb = read_tsv(my_url)
```

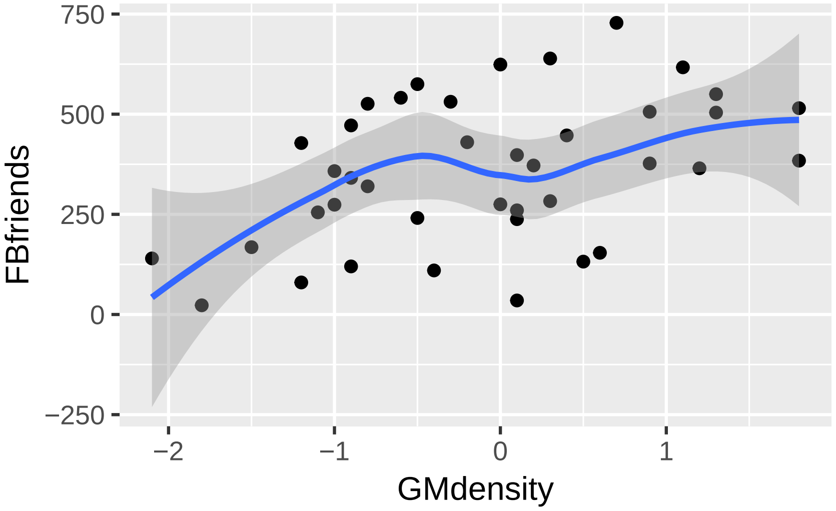
```
## Parsed with column specification:
## cols(
##   GMdensity = col_double(),
##   FBfriends = col_integer()
## )
```

```
fb
```

```
## # A tibble: 40 x 2
##    GMdensity FBfriends
##        <dbl>     <int>
##  1      -1.8        23
##  2       0.1        35
##  3      -1.2        80
##  4      -0.4       110
##  5      -0.9       120
##  6      -2.1       140
##  7      -1.5       168
##  8       0.5       132
##  9       0.6       154
## 10      -0.5       241
## # ... with 30 more rows
```

```
ggplot(fb, aes(x = GMdensity, y = FBfriends)) +
    geom_point() + geom_smooth()
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



(b)??part:scatterconc?? Describe what you see on your scatterplot: is there a trend, and if so, what kind of trend is it? (Don't get too taken in by the exact shape of your smooth trend.) Think "form, direction, strength".

Solution

I'd say there seems to be a weak, upward, apparently linear trend. The points are not especially close to the trend, so I don't think there's any justification for calling this other than "weak". (If you think the trend is, let's say, "moderate", you ought to say what makes you think that: for example, that the people with a lot of Facebook friends also tend to have a higher grey matter density. I can live with a reasonably-justified "moderate".) The reason I said not to get taken in by the shape of the smooth trend is that this has a "wiggle" in it: it goes down again briefly in the middle. But this is likely a quirk of the data, and the trend, if there is any, seems to be an upward one.

(c) Fit a regression predicting the number of Facebook friends from the grey matter density, and display the output.

Solution

That looks like this. You can call the "fitted model object" whatever you like, but you'll need to get the capitalization of the variable names correct:

```
fb.1 = lm(FBfriends ~ GMdensity, data = fb)
summary(fb.1)
```

```
##
## Call:
## lm(formula = FBfriends ~ GMdensity, data = fb)
```

```
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -339.89 -110.01   -5.12   99.80  303.64
##
## Coefficients:
##             Estimate Std. Error t value
## (Intercept)   366.64      26.35  13.916
## GMdensity      82.45      27.58   2.989
##             Pr(>|t|)
## (Intercept)  < 2e-16 ***
## GMdensity    0.00488 **
## ---
## Signif. codes:
##   0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1  ’ ’ 1
##
## Residual standard error: 165.7 on 38 degrees of freedom
## Multiple R-squared:  0.1904, Adjusted R-squared:  0.1691
## F-statistic: 8.936 on 1 and 38 DF,  p-value: 0.004882
```

I observe, though I didn’t ask you to, that the R-squared is pretty awful, going with a correlation of

```
sqrt(0.1904)
```

```
## [1] 0.4363485
```

which *would* look like as weak of a trend as we saw.

Correlations have to go up beyond 0.50 before they start looking at all interesting.

(d)??part:regtest?? Is the slope of your regression line significantly different from zero? What does that mean, in the context of the data?

Solution

The P-value of the slope is 0.005, which is less than 0.05. Therefore the slope *is* significantly different from zero. That means that the number of Facebook friends really does depend on the grey matter density, for the whole population of interest and not just the 40 students observed here (that were a sample from that population). I don’t mind so much what you think the population is, but it needs to be clear that the relationship applies to a population. Another way to approach this is to say that you would expect this relationship to show up again in another similar experiment. That also works, because it gets at the idea of reproducibility.

(e) Are you surprised by the results of parts (??part:scatterconc??) and (??part:regtest??)? Explain briefly.

Solution

I *am* surprised, because I thought the trend on the scatterplot was so weak that there would not be a significant slope. I guess there was enough of an upward trend to be significant, and with $n = 40$ observations we were able to get a significant slope out of that scatterplot. With this many observations, even a weak correlation can be significantly nonzero. You can be surprised or not, but you need to have some kind of consideration of the strength of the trend on the scatterplot as against the significance of the slope. For example, if you decided that the trend was "moderate" in strength, you would be justified in being less surprised than I was. Here, there is the usual issue that we have proved that the slope is not zero (that the relationship is not flat), but we may not have a very clear idea of what the slope actually *is*. There are a couple of ways to get a confidence interval. The obvious one is to use R as a calculator and go up and down twice its standard error (to get a rough idea):

```
82.45 + 2 * 27.58 * c(-1, 1)
```

```
## [1]  27.29 137.61
```

The `c()` thing is to get both confidence limits at once. The smoother way is this:

```
confint(fb.1)
```

```
##                 2.5 %   97.5 %
## (Intercept) 313.30872 419.9810
## GMdensity    26.61391 138.2836
```

Feed `confint` a "fitted model object" and it'll give you confidence intervals (by default 95%) for all the parameters in it.

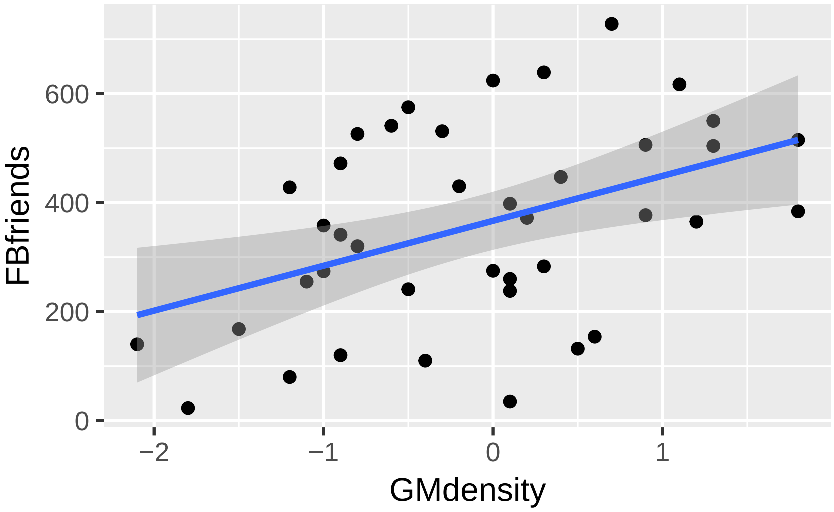
The confidence interval for the slope goes from about 27 to about 138. That is to say, a one-unit increase in grey matter density goes with an increase in Facebook friends of this much. This is not especially insightful: it's bigger than zero (the test was significant), but other than that, it could be almost anything. *This* is where the weakness of the trend comes back to bite us. With this much scatter in our data, we need a *much* larger sample size to estimate accurately how big an effect grey matter density has.

(f) Obtain a scatterplot with the regression line on it.

Solution

Just a modification of (a):

```
ggplot(fb, aes(x = GMdensity, y = FBfriends)) +
    geom_point() + geom_smooth(method = "lm")
```

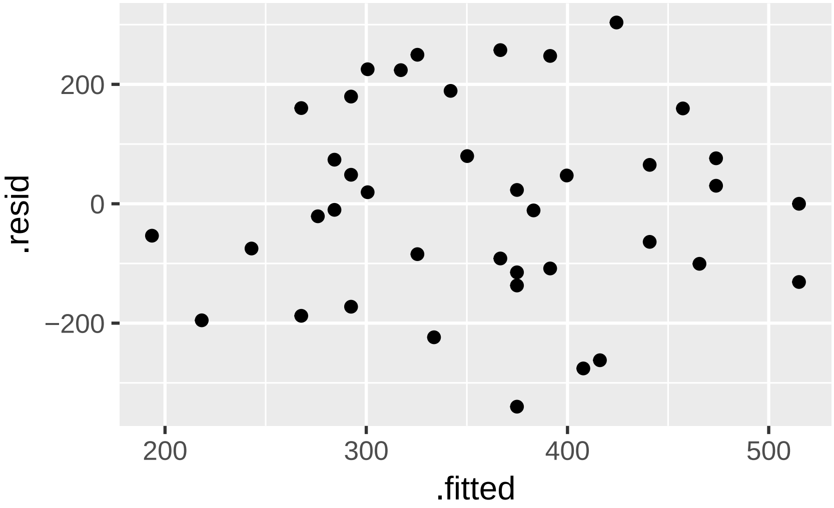


(g) Obtain a plot of the residuals from the regression against the fitted values, and comment briefly on it.

Solution

This is, to my mind, the easiest way:

```
ggplot(fb.1, aes(x = .fitted, y = .resid)) + geom_point()
```

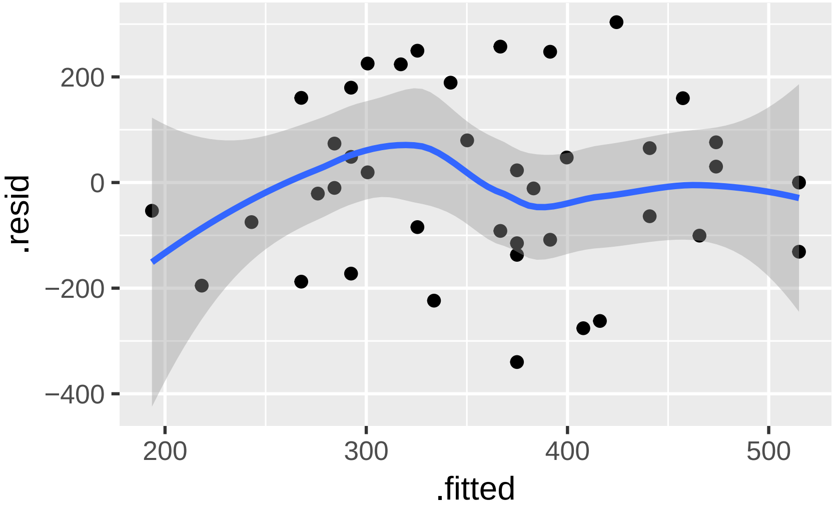


There is some "magic" here, since the fitted model object is not actually a data frame, but it works this way. That looks to me like a completely random scatter of points. Thus, I am completely happy with the straight-line regression that we fitted, and I see no need to improve it.

(You should make two points here: one, describe what you see, and two, what it implies about whether or not your regression is satisfactory.)

Compare that residual plot with this one:

```
ggplot(fb.1, aes(x = .fitted, y = .resid)) + geom_point() +
    geom_smooth()

## ‘geom_smooth()‘ using method = ’loess’ and formula ’y ~ x’
```



Now, why did I try adding a smooth trend, and why is it not necessarily a good idea? The idea of a residual plot is that there should be no trend, and so the smooth trend curve ought to go straight across. The problem is that it will tend to wiggle, just by chance, as here: it looks as if it goes up and down before flattening out. But if you look at the points, *they* are all over the place, not close to the smooth trend at all. So the smooth trend is rather deceiving. Or, to put it another way, to indicate a real problem, the smooth trend would have to be a *lot* farther from flat than this one is. I'd call this one basically flat.

13.6 Endogenous nitrogen excretion in carp

A paper in Fisheries Science reported on variables that affect "endogenous nitrogen excretion" or ENE in carp raised in Japan. A number of carp were divided into groups based on body weight, and each group was placed in a different tank. The mean body weight of the carp placed in each tank was recorded. The carp were then fed a protein-free diet three times daily for a period of 20 days. At the end of the experiment, the amount of ENE in each tank was measured, in milligrams of total fish body weight per day. (Thus it should not matter that some of the tanks had more fish than others, because the scaling is done properly.)

For this question, write a report in R Markdown that answers the questions below and contains some narrative that describes your analysis. Create an HTML document from your R Markdown.

(a) Read the data in from link. There are 10 tanks.

Solution

Just this. Listing the data is up to you, but doing so and commenting that the values appear to be correct will improve your report.

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/carp.txt"
carp = read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   tank = col_integer(),
##   bodyweight = col_double(),
##   ENE = col_double()
## )
```

```
carp
```

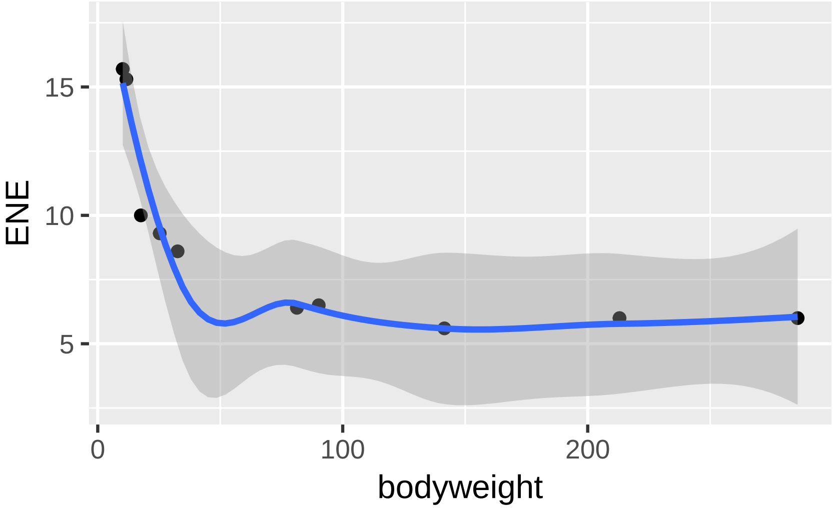
```
## # A tibble: 10 x 3
##     tank bodyweight   ENE
##    <int>      <dbl> <dbl>
##  1     1       11.7  15.3
##  2     2       25.3   9.3
##  3     3       90.2   6.5
##  4     4      213     6
##  5     5       10.2  15.7
##  6     6       17.6  10
##  7     7       32.6   8.6
##  8     8       81.3   6.4
##  9     9      142.    5.6
## 10    10      286.    6
```

(b)??scatter-one?? Create a scatterplot of ENE (response) against bodyweight (explanatory). Add a smooth trend to your plot.

Solution

```
ggplot(carp, aes(x = bodyweight, y = ENE)) + geom_point() +
    geom_smooth()
```

```
## ‘geom_smooth()‘ using method = ’loess’ and formula ’y ~ x’
```



This part is just about getting the plot. Comments are coming in a minute. Note that `ENE` is capital letters, so that `ene` will not work.

(c) Is there an upward or downward trend (or neither)? Is the relationship a line or a curve? Explain briefly.

Solution

The trend is downward: as bodyweight increases, ENE decreases. However, the decrease is rapid at first and then levels off, so the relationship is nonlinear. I want some kind of support for an assertion of non-linearity: anything that says that the slope or rate of decrease is not constant is good.

(d)??linear?? Fit a straight line to the data, and obtain the R-squared for the regression.

Solution

`lm`. The first stage is to fit the straight line, saving the result in a variable, and the second stage is to look at the "fitted model object", here via `summary`:

```
carp.1 = lm(ENE ~ bodyweight, data = carp)
summary(carp.1)
```

```
##
## Call:
## lm(formula = ENE ~ bodyweight, data = carp)
##
## Residuals:
##    Min     1Q Median     3Q    Max
## -2.800 -1.957 -1.173  1.847  4.572
##
## Coefficients:
##             Estimate Std. Error t value
## (Intercept) 11.40393    1.31464   8.675
## bodyweight  -0.02710    0.01027  -2.640
##             Pr(>|t|)
## (Intercept) 2.43e-05 ***
## bodyweight    0.0297 *
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 2.928 on 8 degrees of freedom
## Multiple R-squared:  0.4656, Adjusted R-squared:  0.3988
## F-statistic: 6.971 on 1 and 8 DF,  p-value: 0.0297
```

Finally, you need to give me a (suitably rounded) value for R-squared: 46.6% or 47% or the equivalents as a decimal. I just need the value at this point. This kind of R-squared is actually pretty good for natural data, but the issue is whether we can improve it by fitting a non-linear model.

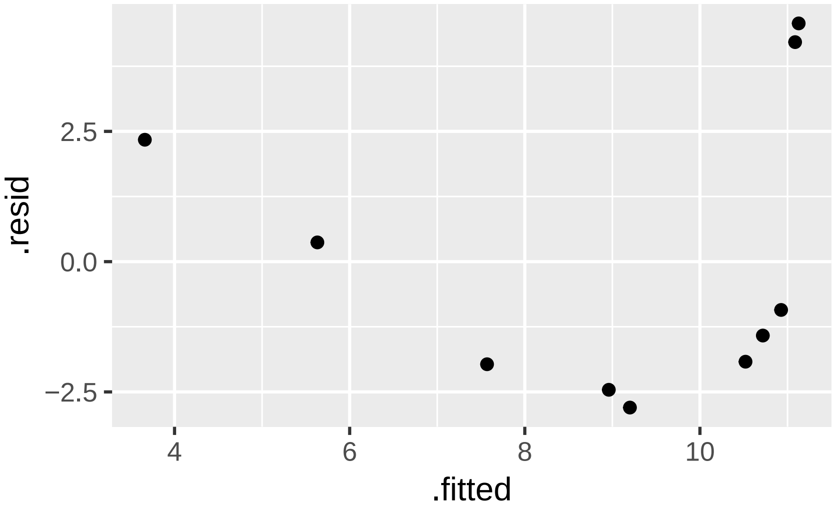
The suspicion being that we can, since the scatterplot suggested serious non-linearity.

(e) Obtain a residual plot (residuals against fitted values) for this regression. Do you see any problems? If so, what does that tell you about the relationship in the data?

Solution

This is the easiest way: feed the output of the regression straight into ggplot:

```
ggplot(carp.1, aes(x = .fitted, y = .resid)) +
    geom_point()
```



(f) Fit a parabola to the data (that is, including an x-squared term). Compare the R-squared values for the models in this part and part (??linear??). Does that suggest that the parabola model is an improvement here over the linear model?

Solution

Add bodyweight-squared to the regression. Don’t forget the `I()`:

```
carp.2 = lm(ENE ~ bodyweight + I(bodyweight^2),
    data = carp)
summary(carp.2)
```

```
##
## Call:
## lm(formula = ENE ~ bodyweight + I(bodyweight^2), data = carp)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -2.0834 -1.7388 -0.5464  1.3841  2.9976
##
## Coefficients:
##                   Estimate Std. Error
## (Intercept)     13.7127373  1.3062494
## bodyweight      -0.1018390  0.0288109
## I(bodyweight^2)  0.0002735  0.0001016
##                 t value Pr(>|t|)
## (Intercept)      10.498 1.55e-05 ***
## bodyweight       -3.535  0.00954 **
## I(bodyweight^2)   2.692  0.03101 *
## ---
## Signif. codes:
##   0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1  ’ ’ 1
##
## Residual standard error: 2.194 on 7 degrees of freedom
## Multiple R-squared:  0.7374, Adjusted R-squared:  0.6624
## F-statistic: 9.829 on 2 and 7 DF,  p-value: 0.009277
```

R-squared has gone up from 47% to 74%, a substantial improvement. This suggests to me that the parabola model is a substantial improvement.

Again, not a surprise, given our initial scatterplot.

I try to avoid using the word “significant” in this context, since we haven’t actually done a test of significance.

The reason for the `I()` is that the up-arrow has a special meaning in `lm`, relating to interactions between factors (as in ANOVA), that we don’t want here. Putting `I()` around it means “use as is”, that is, raise bodyweight to power 2, rather than using the special meaning of the up-arrow in `lm`.

Because it's the up-arrow that is the problem, this applies whenever you're raising an explanatory variable to a power (or taking a reciprocal or a square root, say).

(g) Is the test for the slope coefficient for the squared term significant? What does this mean?

Solution

Look along the `bodyweight`-squared line to get a P-value of 0.031. This is less than the default 0.05, so it *is* significant. This means, in short, that the quadratic model is a significant *improvement* over the linear one. Said longer: the null hypothesis being tested is that the slope coefficient of the squared term is zero (that is, that the squared term has nothing to add over the linear model). This is rejected, so the squared term has *something* to add in terms of quality of prediction.

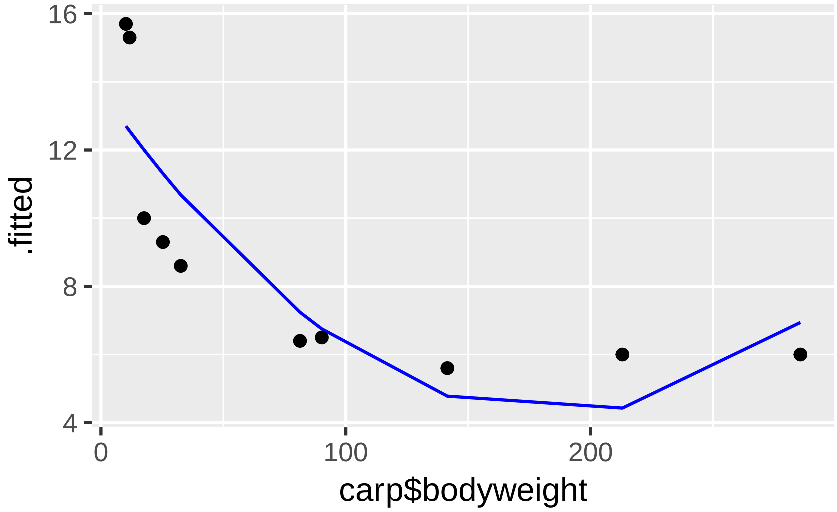
Now we can use that word *significant*.

(h) Make the scatterplot of part (??scatter-one??), but add the fitted curve. Describe any way in which the curve fails to fit well.

Solution

This is a bit slippery, because the points to plot and the fitted curve are from different data frames. What you do in this case is to put a `data=` in one of the `geoms`, which says "don't use the data frame that was in the `ggplot`, but use this one instead". I would think about starting with the regression object `carp.2` as my base data frame, since we want (or I want) to do two things with that: plot the fitted values and join them with lines. Then I want to add the original data, just the points:

```
ggplot(carp.2, aes(x = carp$bodyweight, y = .fitted),
    colour = "blue") + geom_line(colour = "blue") +
    geom_point(data = carp, aes(x = bodyweight,
        y = ENE))
```



This works, but is not very aesthetic, because the bodyweight that is plotted against the fitted values is in the wrong data frame, and so we have to use the dollar-sign thing to get it from the right one.

A better way around this is "augment" the data with output from the regression object. This is done using `augment` from package `broom`:

```
library(broom)
carp.2a = augment(carp.2, carp)
carp.2a
```

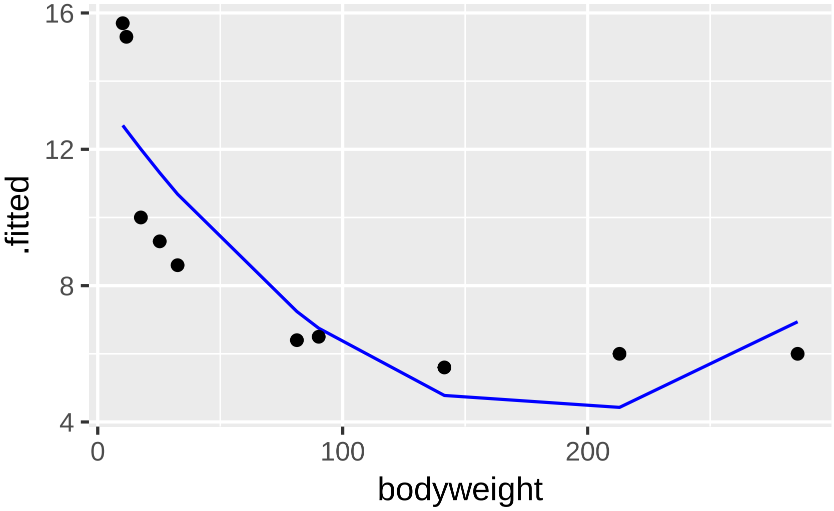
```
## # A tibble: 10 x 10
##     tank bodyweight   ENE .fitted .se.fit
##   * <int>      <dbl> <dbl>   <dbl>   <dbl>
##   1     1       11.7  15.3   12.6    1.07
##   2     2       25.3   9.3   11.3    0.886
##   3     3       90.2   6.5    6.75   1.07
##   4     4      213     6      4.43   1.25
##   5     5       10.2  15.7   12.7    1.10
##   6     6       17.6  10     12.0    0.980
##   7     7       32.6   8.6   10.7    0.828
##   8     8       81.3   6.4    7.24   1.01
##   9     9      142.    5.6    4.78   1.31
## 10    10      286.    6      6.94   2.05
## # ... with 5 more variables: .resid <dbl>,
## #   .hat <dbl>, .sigma <dbl>, .cooksd <dbl>,
## #   .std.resid <dbl>
```

so now you see what `carp.2a` has in it, and then:

```
g = ggplot(carp.2a, aes(x = bodyweight, y = .fitted)) +
    geom_line(colour = "blue") + geom_point(aes(y = ENE))
```

This is easier coding: there are only two non-standard things. The first is that the fitted-value lines should be a distinct colour like blue so that you can tell them from the data points. The second thing is that for the second `geom_point`, the one that plots the data, the x coordinate `bodyweight` is correct so that we don't have to change that; we only have to change the y-coordinate, which is `ENE`. The plot is this:

```
g
```



Concerning interpretation, you have a number of possibilities here. The simplest is that the points in the middle are above the curve, and the points at the ends are below. (That is, negative residuals at the ends, and positive ones in the middle, which gives you a hint for the next part.) Another is that the parabola curve fails to capture the *shape* of the relationship; for example, I see nothing much in the data suggesting that the relationship should go back up, and even given that, the fitted curve doesn't go especially near any of the points.

I was thinking that the data should be fit better by something like the left half of an upward-opening parabola, but I guess the curvature on the left half of the plot suggests that it needs most of the left half of the parabola just to cover the left half of the plot.

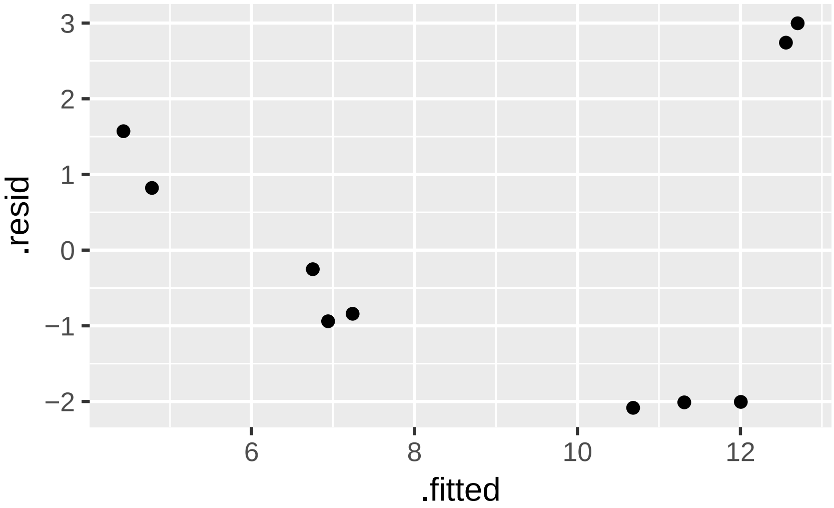
The moral of the story, as we see in the next part, is that the parabola is the wrong curve for the job.

(i) Obtain a residual plot for the parabola model. Do you see any problems with it? (If you do, I'm not asking you to do anything about them in this question, but I will.)

Solution

The same idea as before for the other residual plot. Use the fitted model object `carp.2` as your data frame for the `ggplot`:

```
ggplot(carp.2, aes(x = .fitted, y = .resid)) +
    geom_point()
```



I think this is *still* a curve (or, it goes down and then sharply up at the end). Either way, there is still a pattern.

That was all I needed, but as to what this means: our parabola was a curve all right, but it appears not to be the right *kind* of curve. I think the original data looks more like a hyperbola (a curve like $y = 1/x$) than a parabola, in that it seems to decrease fast and then gradually to a limit, and *that* suggests, as in the class example, that we should try an asymptote model. Note how I specify it, with the `I()` thing again, since `/` has a special meaning to `lm` in the same way that ˆ does:

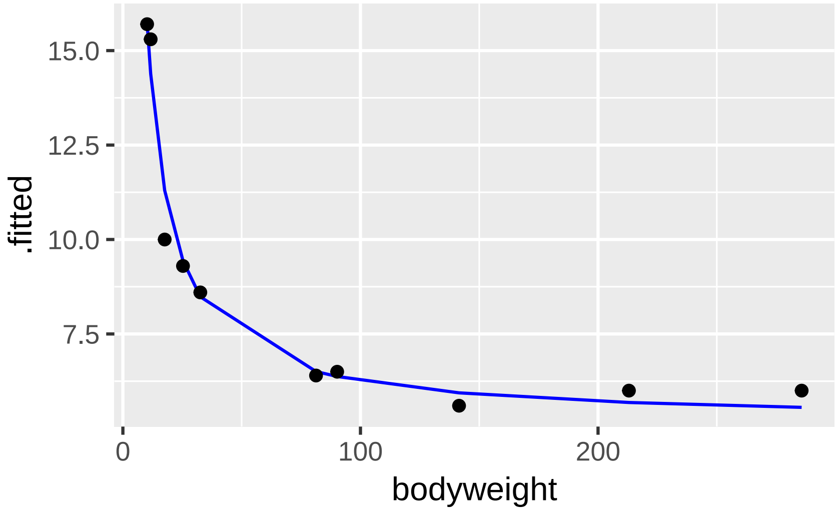
```
carp.3 = lm(ENE ~ I(1/bodyweight), data = carp)
summary(carp.3)
```

```
##
## Call:
## lm(formula = ENE ~ I(1/bodyweight), data = carp)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -1.29801 -0.12830  0.04029  0.26702  0.91707
##
## Coefficients:
##                 Estimate Std. Error t value
## (Intercept)       5.1804     0.2823   18.35
## I(1/bodyweight) 107.6690     5.8860   18.29
##                 Pr(>|t|)
## (Intercept)     8.01e-08 ***
## I(1/bodyweight) 8.21e-08 ***
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 0.6121 on 8 degrees of freedom
## Multiple R-squared:  0.9766, Adjusted R-squared:  0.9737
## F-statistic: 334.6 on 1 and 8 DF,  p-value: 8.205e-08
```

That fits *extraordinarily* well, with an R-squared up near 98%. The intercept is the asymptote, which suggests a (lower) limit of about 5.2 for ENE (in the limit for large bodyweight). We would have to ask the fisheries scientist whether this kind of thing is a reasonable biological mechanism. It says that a carp always has some ENE, no matter how big it gets, but a smaller carp will have a lot more.

Does the fitted value plot look reasonable now? This is augment again since the fitted values and observed data come from different data frames:

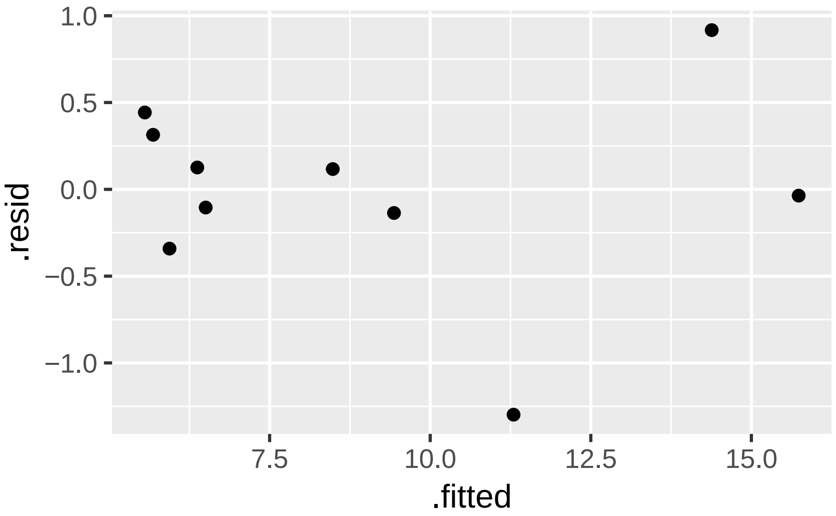
```
library(broom)
augment(carp.3, carp) %>% ggplot(aes(x = bodyweight,
    y = .fitted)) + geom_line(colour = "blue") +
    geom_point(aes(y = ENE))
```



I'd say that does a really nice job of fitting the data. But it would be nice to have a few more tanks with large-bodyweight fish, to convince us that we have the shape of the trend right.

And, as ever, the residual plot. That's a lot easier than the plot we just did:

```
ggplot(carp.3, aes(x = .fitted, y = .resid)) +
    geom_point()
```



All in all, that looks pretty good (and certainly a vast improvement over the ones you got before).

When you write up your report, you can make it flow better by writing it in a way that suggests that each thing was the obvious thing to do next: that is, that *you* would have thought to do it next, rather than me telling you what to do.

My report (as an R Markdown file) is at link. Download it, knit it, play with it.

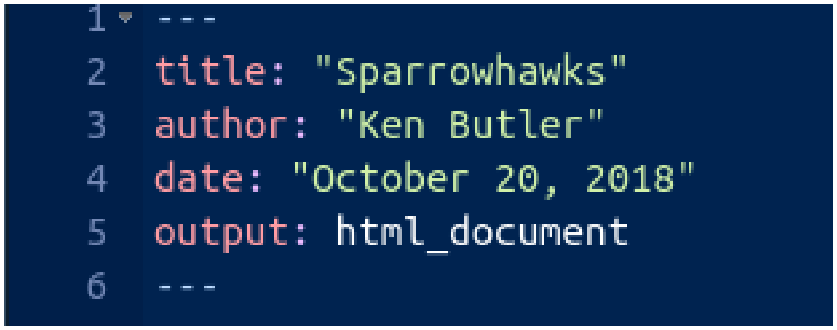
13.7 *Sparrowhawks*

??q:hawks?? One of nature's patterns is the relationship between the percentage of adult birds in a colony that return from the previous year, and the number of new adults that join the colony. Data for 13 colonies of sparrowhawks can be found at link. The columns are the percentage of adults returning from the previous year, and the number of new adults that join the colony.

(a) Create a new R Markdown report, give it a suitable title, and ask for HTML output. Answer the questions that follow in your report. At any stage, you can Knit HTML to see how the report looks so far.

Solution

In R Studio, select File, New File, R Markdown. Fill in the Title, Author and leave the Default Output Format at HTML. You'll see a template report with the document info at the top. This is my document info:



```
---
title: "Sparrowhawks"
author: "Ken Butler"
date: "October 20, 2018"
output: html_document
---
```

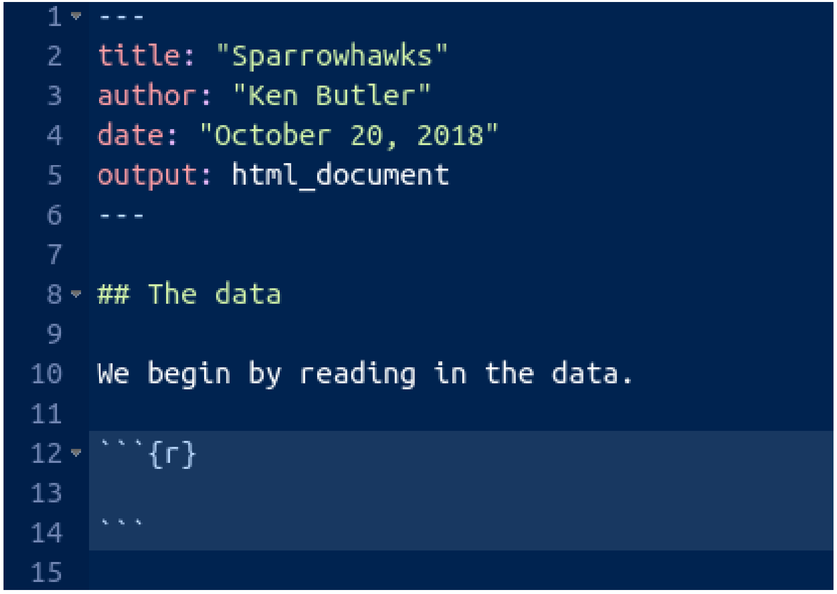
This is known in the jargon as a "YAML block". Below that is the template R Markdown document, which you can delete now or later.

YAML stands for *Yet Another Markup Language*, but we're not using it in this course, other than as the top bit of an R Markdown document.

(b) Read in the data and display the first few values. Add some text saying how many rows of data there are.

Solution

Read the data into a data frame. In your report, add some text like "we read in the data", perhaps after a section heading like "The data". Then add a *code chunk* by selecting Chunks and Insert Chunk, or by pressing control-alt-I. So far you have something like this.



~~~
---
title: "Sparrowhawks"
author: "Ken Butler"
date: "October 20, 2018"
output: html_document
---

## The data

We begin by reading in the data.

```{r}

```

~~~

Inside the code chunk, that is, in the bit between the backtick characters, put R code, just as you would type it at the Console or put in an R notebook. In this case, that would be the following code, minus the message that comes out of read_delim:

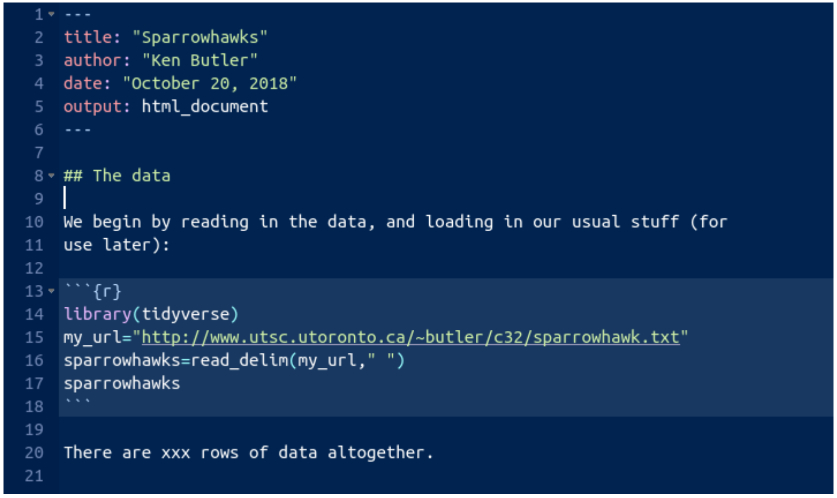
```
library(tidyverse)
my_url = "http://www.utsc.utoronto.ca/~butler/c32/sparrowhawk.txt"
sparrowhawks = read_delim(my_url, " ")
```

```
## Parsed with column specification:
```

```
## cols(
##   returning = col_integer(),
##   newadults = col_integer()
## )
```

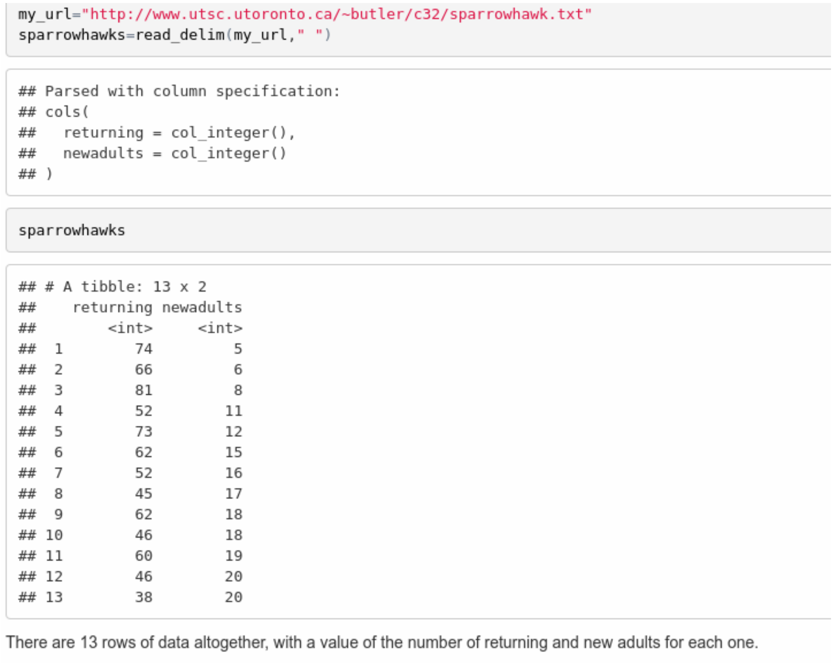
```
sparrowhawks
```

For you, it looks like this:



~~~
---
title: "Sparrowhawks"
author: "Ken Butler"
date: "October 20, 2018"
output: html_document
---

## The data

We begin by reading in the data, and loading in our usual stuff (for
use later):

```{r}
library(tidyverse)
my_url="http://www.utsc.utoronto.ca/~butler/c32/sparrowhawk.txt"
sparrowhawks=read_delim(my_url," ")
sparrowhawks
```

There are xxx rows of data altogether.

~~~

We don't know how many rows of data there are yet, so I've left a "placeholder" for it, when we figure it out. The file is annoyingly called `sparrowhawk.txt`, singular. Sorry about that. If you knit this (click on "Knit HTML" next to the ball of wool, or press control-shift-K), it should run, and you'll see a viewer pop up with the HTML output. Now you can see how many rows there are, and you can go back and edit the R Markdown and put in 13 in place of xxx, and knit again. You might be worried about how hard R is working with all this knitting. Don't worry about that. R can take it. Mine looked like this:



```
my_url="http://www.utsc.utoronto.ca/~butler/c32/sparrowhawk.txt"
sparrowhawks=read_delim(my_url," ")
```

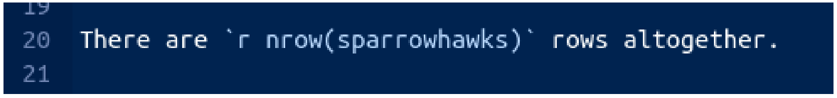
```
## Parsed with column specification:
## cols(
##   returning = col_integer(),
##   newadults = col_integer()
## )
```

```
sparrowhawks
```

```
## # A tibble: 13 x 2
##    returning newadults
##        <int>     <int>
##  1        74         5
##  2        66         6
##  3        81         8
##  4        52        11
##  5        73        12
##  6        62        15
##  7        52        16
##  8        45        17
##  9        62        18
## 10        46        18
## 11        60        19
## 12        46        20
## 13        38        20
```

There are 13 rows of data altogether, with a value of the number of returning and new adults for each one.

There is a better way of adding values that come from the output, which I mention here in case you are interested (if you are not, feel free to skip this). What you do is to make what is called an "inline code chunk". Where you want a number to appear in the text, you have some R Markdown that looks like this:



```
There are `r nrow(sparrowhawks)` rows altogether.
```

The piece inside the backticks is the letter `r`, a space, and then one line of R code. The one line of code will be run, and all of the stuff within the backticks will be replaced in the output by the result of running the R code, in this case the number 13. Typically, you are extracting a number from the data, like the number of rows or a mean of something. If it's a decimal number, it will come out with a lot of decimal places unless you explicitly `round` it. OK, let me try it: the data frame has 13 rows altogether. I didn't type that number; it was calculated from the data frame. Woo hoo!

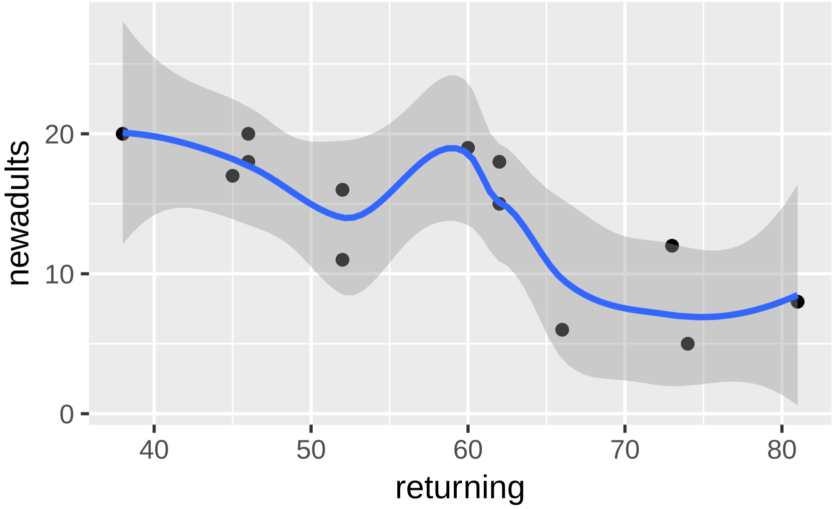
(c) Create a new section entitled "Exploratory analysis", and create a scatterplot for predicting number of new adults from the percentage of returning adults. Describe what you see, adding some suitable text to your report.

Solution

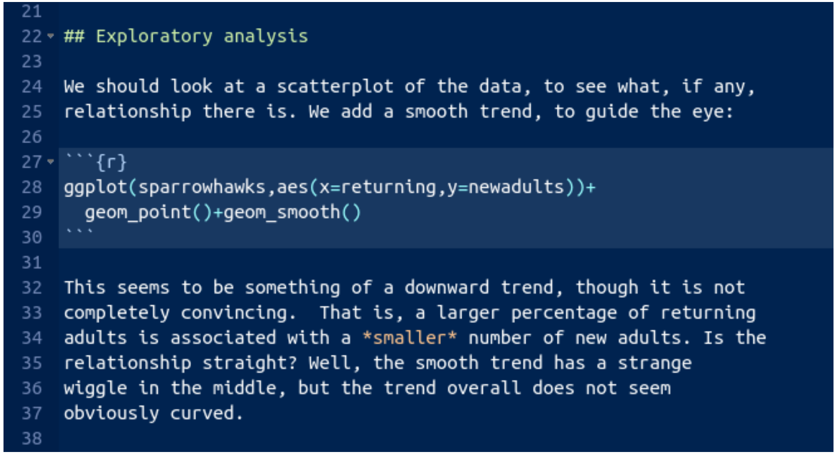
The R code you add should look like this, with the results shown (when you knit the report again):

```
library(tidyverse)
```

```
ggplot(sparrowhawks, aes(x = returning, y = newadults)) +
    geom_point() + geom_smooth()

## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



The piece of report that I added looks like this:



~~~
## Exploratory analysis

We should look at a scatterplot of the data, to see what, if any,
relationship there is. We add a smooth trend, to guide the eye:

```{r}
ggplot(sparrowhawks,aes(x=returning,y=newadults))+
  geom_point()+geom_smooth()
```

This seems to be something of a downward trend, though it is not
completely convincing.  That is, a larger percentage of returning
adults is associated with a *smaller* number of new adults. Is the
relationship straight? Well, the smooth trend has a strange
wiggle in the middle, but the trend overall does not seem
obviously curved.

~~~

Note (i) that you have to do nothing special to get the plot to appear, and (ii) that I put "smaller" in italics, and you see how.

(d) Obtain the correlation between the two variables. Is this consistent with the scatterplot? Explain briefly. (The R function you need is `cor`. You can feed it a data frame.)

Solution

The appropriate R code is this, in another code chunk:

```
with(sparrowhawks, cor(newadults, returning))

## [1] -0.7484673
```

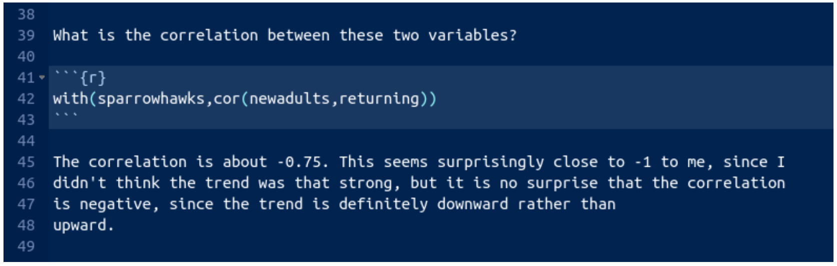
Or you can ask for the correlations of the whole data frame:

```
cor(sparrowhawks)
```

```
##             returning  newadults
## returning  1.0000000 -0.7484673
## newadults -0.7484673  1.0000000
```

This latter is a “correlation matrix” with a correlation between each column and each other column. Obviously the correlation between a column and itself is 1, and that is *not* the one we want.

I added this to the report (still in the Exploratory Analysis section, since it seems to belong there):



~~~
What is the correlation between these two variables?

```{r}
with(sparrowhawks,cor(newadults,returning))
```

The correlation is about -0.75. This seems surprisingly close to -1 to me, since I
didn't think the trend was that strong, but it is no surprise that the correlation
is negative, since the trend is definitely downward rather than
upward.
~~~

(e) Obtain the regression line for predicting the number of new adults from the percentage of returning adults.

Solution

This R code, in another code chunk:

```
newadults.1 = lm(newadults ~ returning, data = sparrowhawks)
summary(newadults.1)
```

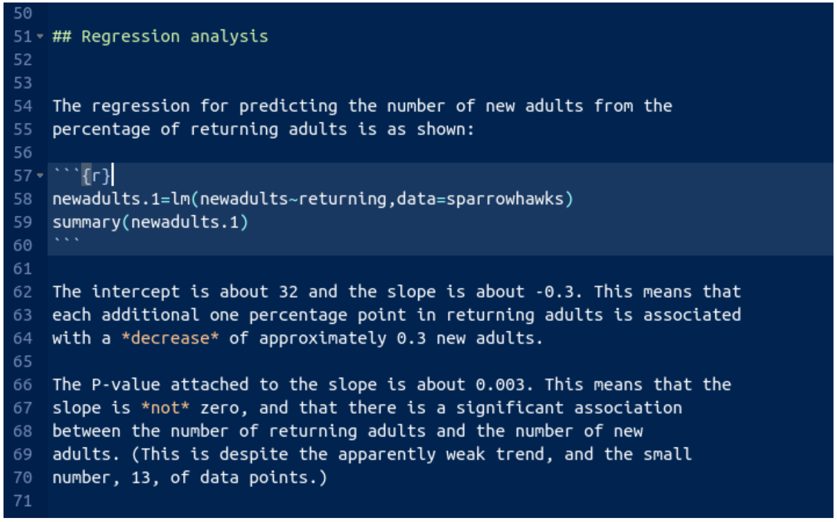
```
##
## Call:
## lm(formula = newadults ~ returning, data = sparrowhawks)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -5.8687 -1.2532  0.0508  2.0508  5.3071
##
## Coefficients:
##             Estimate Std. Error t value
## (Intercept) 31.93426    4.83762   6.601
## returning   -0.30402    0.08122  -3.743
##             Pr(>|t|)
## (Intercept) 3.86e-05 ***
## returning    0.00325 **
## ---
## Signif. codes:
##   0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1  ’ ’ 1
```

```
##
## Residual standard error: 3.667 on 11 degrees of freedom
## Multiple R-squared:  0.5602, Adjusted R-squared:  0.5202
## F-statistic: 14.01 on 1 and 11 DF,  p-value: 0.003248
```

(f) What are the intercept and slope of your regression line? Is the slope significant? What does that mean, in the context of the data?

Solution

See the output in the previous part. That's what we need to talk about. I added this to the report. I thought we deserved a new section here:



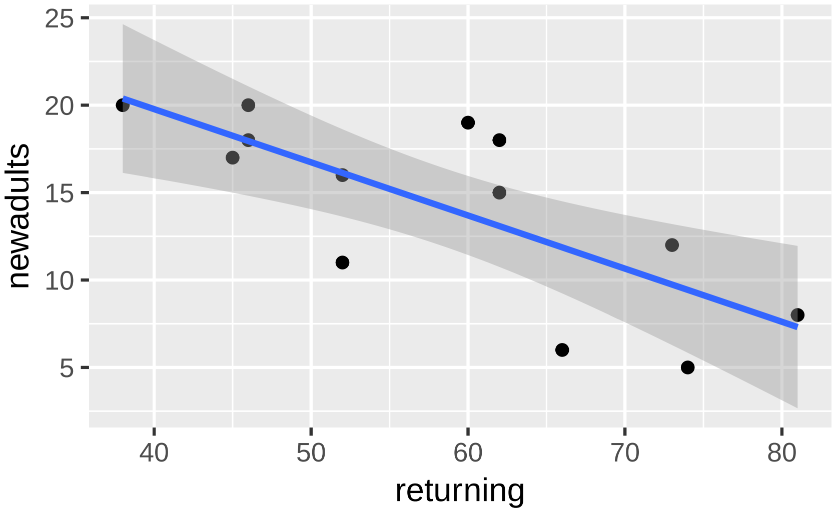
~~~

Regression analysis

The regression for predicting the number of new adults from the
percentage of returning adults is as shown:

```{r}
newadults.1=lm(newadults~returning,data=sparrowhawks)
summary(newadults.1)
```

The intercept is about 32 and the slope is about -0.3. This means that
each additional one percentage point in returning adults is associated
with a *decrease* of approximately 0.3 new adults.

The P-value attached to the slope is about 0.003. This means that the
slope is *not* zero, and that there is a significant association
between the number of returning adults and the number of new
adults. (This is despite the apparently weak trend, and the small
number, 13, of data points.)

~~~

(g) Create a scatterplot of the data with the regression line on it.

Solution

This code. Using `geom_smooth` with `method="lm"` will add the regression line to the plot:

```r
ggplot(sparrowhawks, aes(x = returning, y = newadults)) +
    geom_point() + geom_smooth(method = "lm")
```

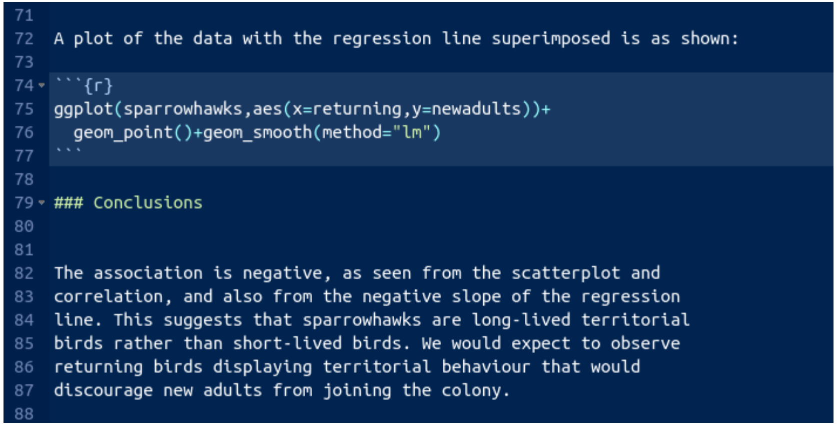


I added a bit of text to the report, which I will show in a moment.

(h) For short-lived birds, the association between these two variables is positive: changes in weather and food supply cause the populations of new and returning birds to increase together. For long-lived territorial birds, however, the association is negative because returning birds claim their territories in the colony and do not leave room for new recruits. Which type of species is the sparrowhawk? Add a short Conclusions section to your report with discussion of this issue.

Solution

My addition to the report looks like this:



~~~
A plot of the data with the regression line superimposed is as shown:

```{r}
ggplot(sparrowhawks,aes(x=returning,y=newadults))+
  geom_point()+geom_smooth(method="lm")
```

### Conclusions


The association is negative, as seen from the scatterplot and
correlation, and also from the negative slope of the regression
line. This suggests that sparrowhawks are long-lived territorial
birds rather than short-lived birds. We would expect to observe
returning birds displaying territorial behaviour that would
discourage new adults from joining the colony.
~~~

I think that rounds off the report nicely.

13.8 Salaries of social workers

Another salary-prediction question: does the number of years of work experience that a social worker has help to predict their salary? Data for 50 social workers are in link.

(a) Read the data into R. Check that you have 50 observations on two variables. Also do something to check that the years of experience and annual salary figures look reasonable overall.

Solution

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/socwork.txt"
soc = read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   experience = col_integer(),
##   salary = col_integer()
## )
```

```
soc
```

```
## # A tibble: 50 x 2
##    experience salary
##         <int>  <int>
##  1          7  26075
##  2         28  79370
##  3         23  65726
##  4         18  41983
##  5         19  62308
##  6         15  41154
##  7         24  53610
##  8         13  33697
##  9          2  22444
## 10          8  32562
## # ... with 40 more rows
```

That checks that we have the right *number* of observations; to check that we have sensible *values*, something like `summary` is called for:

```
summary(soc)
```

```
##    experience        salary
##  Min.   : 1.00   Min.   :16105
##  1st Qu.:13.50   1st Qu.:36990
##  Median :20.00   Median :50948
##  Mean   :18.12   Mean   :50171
##  3rd Qu.:24.75   3rd Qu.:65204
##  Max.   :28.00   Max.   :99139
```

A person working in any field cannot have a negative number of years of experience, and cannot have more than about 40 years of experience (or else they would have retired). Our experience numbers fit that. Salaries had better be five or six figures, and salaries for social workers are not generally all that high, so these figures look reasonable.

A rather more `tidyverse` way is this:

```
soc %>% summarize_all(c("min", "max"))
```

```
## # A tibble: 1 x 4
##   experience_min salary_min experience_max
##            <dbl>      <dbl>          <dbl>
## 1              1      16105             28
## # ... with 1 more variable: salary_max <dbl>
```

This gets the minimum and maximum of all the variables. I would have liked them arranged in a nice rectangle (`min` and `max` as rows, the variables as columns), but that's not how this comes out.

Here is another:

```
soc %>% map_df(~quantile(.))
```

```
## # A tibble: 5 x 2
##   experience salary
##        <dbl>  <dbl>
## 1        1   16105
## 2       13.5 36990.
## 3       20   50948.
## 4       24.8 65204.
## 5       28   99139
```

These are the five-number summaries of each variable. Normally, they come with percentiles attached:

```
quantile(soc$experience)
```

```
##    0%   25%   50%   75%  100%
##  1.00 13.50 20.00 24.75 28.00
```

but the percentiles get lost in the transition to a `tibble`, and I haven't found out how to get them back.

This almost works:

```
soc %>% map_df(~enframe(quantile(.)))
```

```
## # A tibble: 10 x 2
##    name    value
##    <chr>   <dbl>
##  1 0%        1
##  2 25%      13.5
##  3 50%      20
##  4 75%      24.8
##  5 100%     28
##  6 0%    16105
##  7 25%   36990.
##  8 50%   50948.
##  9 75%   65204.
## 10 100%  99139
```

but, though we now have the percentiles, we've lost the names of the variables, so it isn't much better.

In this context, `map` says "do whatever is in the brackets for each column of the data frame". (That's the implied "for each".) The output from `quantile` is a vector that we would like to have display as a data frame, so `map_df` instead of any other form of `map`.

As you know, the `map` family is actually very flexible: they run a function "for each" anything and glue the results together, like this:

```
soc %>% map_dbl(median)
```

```
## experience     salary
##       20.0    50947.5
```

which gets the median for each variable. That's the same thing as this:

```
soc %>% summarize_all("median")
```

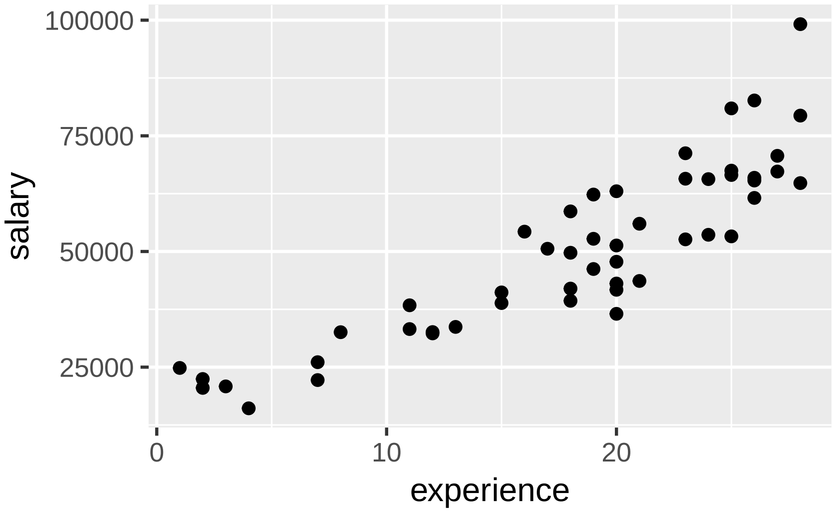
```
## # A tibble: 1 x 2
##   experience salary
##        <dbl>  <dbl>
## 1         20 50948.
```

(b) Make a scatterplot showing how salary depends on experience. Does the nature of the trend make sense?

Solution

The usual:

```
ggplot(soc, aes(x = experience, y = salary)) +
    geom_point()
```



As experience goes up, salary also goes up, as you would expect. Also, the trend seems more or less straight.

(c) Fit a regression predicting salary from experience, and display the results. Is the slope positive or negative? Does that make sense?

Solution

```
soc.1 = lm(salary ~ experience, data = soc)
summary(soc.1)
```

```
##
## Call:
## lm(formula = salary ~ experience, data = soc)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -17666.3  -5498.2   -726.7   4667.7  27811.6
##
## Coefficients:
##             Estimate Std. Error t value
## (Intercept)  11368.7     3160.3   3.597
## experience    2141.4      160.8  13.314
##             Pr(>|t|)
## (Intercept) 0.000758 ***
## experience   < 2e-16 ***
## ---
## Signif. codes:
##   0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1  ’ ’ 1
##
## Residual standard error: 8642 on 48 degrees of freedom
## Multiple R-squared:  0.7869, Adjusted R-squared:  0.7825
## F-statistic: 177.3 on 1 and 48 DF,  p-value: < 2.2e-16
```

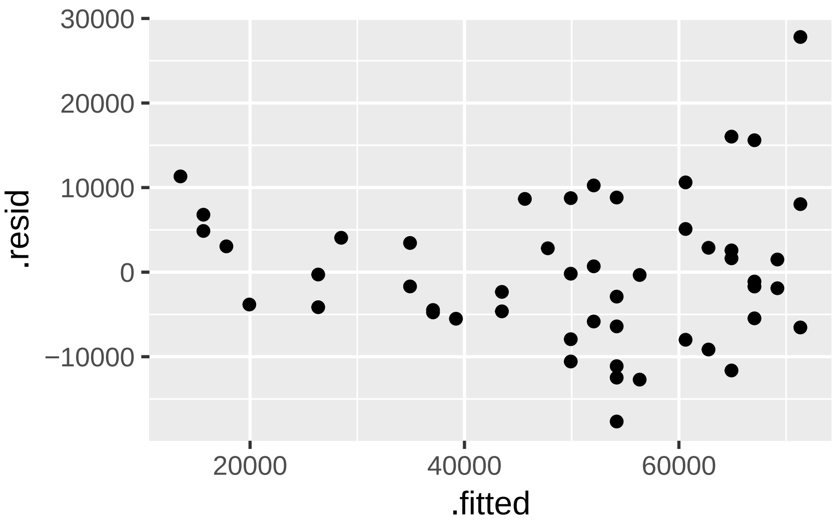
The slope is (significantly) positive, which squares with our guess (more experience goes with greater salary), and also the upward trend on the scatterplot. The value of the slope is about 2,000; this means that one more year of experience goes with about a $2,000 increase in salary.

(d) Obtain and plot the residuals against the fitted values. What problem do you see?

Solution

The easiest way to do this with `ggplot` is to plot the *regression object* (even though it is not actually a data frame), and plot the `.fitted` and `.resid` columns in it, not forgetting the initial dots:

```
ggplot(soc.1, aes(x = .fitted, y = .resid)) +
    geom_point()
```

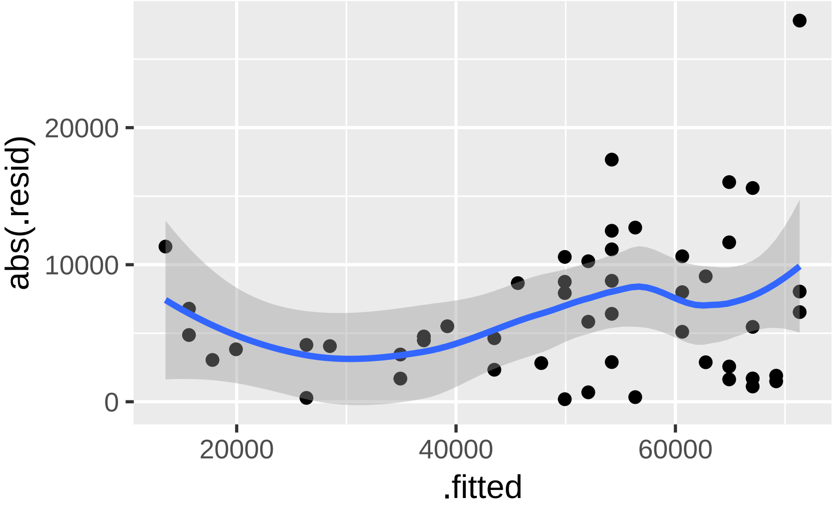


I see a "fanning-out": the residuals are getting bigger *in size* (further away from zero) as the fitted values get bigger. That is, when the (estimated) salary gets larger, it also gets more variable.

Fanning-out is sometimes hard to see. What you can do if you suspect that it might have happened is to plot the *absolute value* of the residuals against the fitted values. The absolute value is the residual without its plus or minus sign, so if the residuals are getting bigger in size, their absolute values are getting bigger. That would look like this:

```
ggplot(soc.1, aes(x = .fitted, y = abs(.resid))) +
    geom_point() + geom_smooth()
```

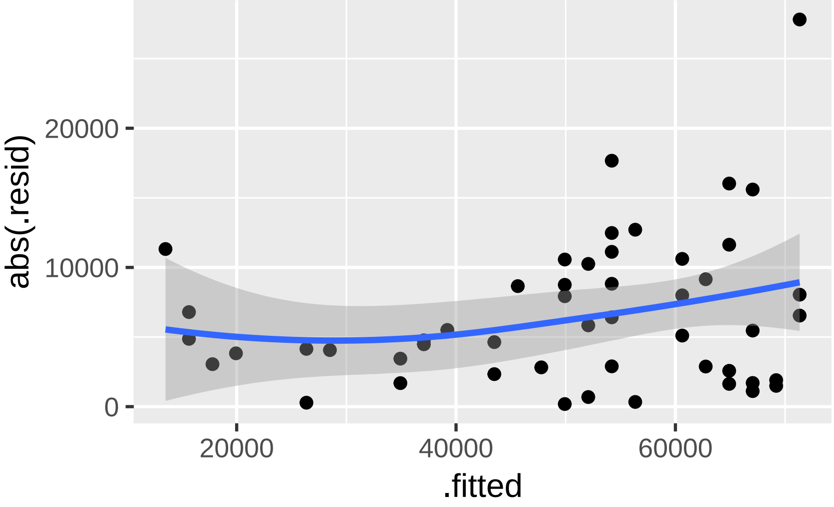
```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



I added a smooth trend to this to help us judge whether the absolute-value-residuals are getting bigger as the fitted values get bigger. It looks to me as if the overall trend is an increasing one, apart from those few small fitted values that have larger-sized residuals. Don't get thrown off by the kinks in the smooth trend. Here is a smoother version:

```
ggplot(soc.1, aes(x = .fitted, y = abs(.resid))) +
    geom_point() + geom_smooth(span = 2)
```

```
## `geom_smooth()` using method = 'loess' and formula 'y ~ x'
```



The larger fitted values, according to this, have residuals larger in size.

The thing that controls the smoothness of the smooth trend is the value of span in geom_smooth. The default is 0.75. The larger the value you use, the smoother the trend; the smaller, the more wiggly. I'm inclined to think that the default value is a bit too small. Possibly this value is too big, but it shows you the idea.

(e) The problem you unearthed in the previous part is often helped by a transformation. Run Box-Cox on your data to find a suitable transformation. What transformation is suggested?

Solution

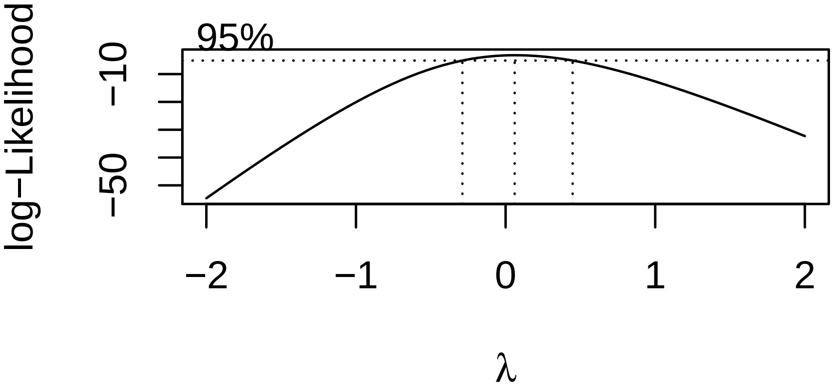
You'll need to call in (and install if necessary) the package `MASS` that contains `boxcox`:

```
library(MASS)
```

```
##
## Attaching package: 'MASS'

## The following object is masked from 'package:dplyr':
##
##     select
```

I explain that "masked" thing below.

```
boxcox(salary ~ experience, data = soc)
```



That one looks like $\lambda = 0$ or log. You could probably also justify fourth root (power 0.25), but log is a very common transformation, which people won't need much persuasion to accept.

There's one annoyance with `MASS`: it has a `select` (which I have never used), and if you load `tidyverse` first and `MASS` second, as I have done here, when you mean to run the column-selection `select`, it will actually run the `select` that comes from `MASS`, and give you an error that you will have a terrible time debugging. That's what that "masked" message was when you loaded `MASS`.

So I'm going to be tidy and get rid of `MASS`, now that I'm finished with it. Let's first see which packages are loaded, rather a lot in my case:

The packages before *tidyverse* other than *MASS* are all loaded by the *tidyverse*, which is why there are so many.

```
search()
```

```
##  [1] ".GlobalEnv"        "package:MASS"
##  [3] "package:broom"     "package:GGally"
##  [5] "package:bindrcpp"  "package:forcats"
##  [7] "package:stringr"   "package:dplyr"
##  [9] "package:purrr"     "package:readr"
## [11] "package:tidyr"     "package:tibble"
## [13] "package:ggplot2"   "package:tidyverse"
## [15] "package:stats"     "package:graphics"
## [17] "package:grDevices" "package:utils"
## [19] "package:datasets"  "package:methods"
## [21] "Autoloads"         "package:base"
```

then get rid of `MASS`:

```
detach("package:MASS", unload = T)
```

Now check that it has gone:

```
search()
```

```
##  [1] ".GlobalEnv"        "package:broom"
##  [3] "package:GGally"    "package:bindrcpp"
##  [5] "package:forcats"   "package:stringr"
##  [7] "package:dplyr"     "package:purrr"
##  [9] "package:readr"     "package:tidyr"
## [11] "package:tibble"    "package:ggplot2"
## [13] "package:tidyverse" "package:stats"
## [15] "package:graphics"  "package:grDevices"
## [17] "package:utils"     "package:datasets"
## [19] "package:methods"   "Autoloads"
## [21] "package:base"
```

It has. Now any calls to `select` will use the right one. We hope.

The output of `search` is called the **search list**, and it tells you where R will go looking for things. The first one `.GlobalEnv` is where all your variables, data frames etc. get stored, and that is what gets searched first. Then R will go looking in each thing in turn until it finds what it is looking for. When you load a package with `library()`, it gets added to the list *in second place*, behind `.GlobalEnv`. So, when we had `MASS` loaded (the first `search()`), if we called `select`, then it would find the one in `MASS` first.

If you want to insist on something like "the `select` that lives in `dplyr`", you can do that by saying `dplyr::select`. But this is kind of cumbersome if you don't need to do it, which is why I got rid of `MASS` here.

All the ones that are part of this project, anyway.

That means that if you write a function with the same name as one that is built into R or a package, yours is the one that will get called. This is probably a bad idea, since you won't be able to get at R's function by that name.

(f) Calculate a new variable as suggested by your transformation. Use your transformed response in a regression, showing the summary.

Solution

The best way is to add the new variable to the data frame using mutate, and save that new data frame. That goes like this:

```
soc.2 = soc %>% mutate(log_salary = log(salary))
```

and then

```
soc.3 = lm(log_salary ~ experience, data = soc.2)
summary(soc.3)
```

```
##
## Call:
## lm(formula = log_salary ~ experience, data = soc.2)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.35435 -0.09046 -0.01725  0.09739  0.26355
##
## Coefficients:
##             Estimate Std. Error t value
## (Intercept) 9.841315   0.056356  174.63
## experience  0.049979   0.002868   17.43
##             Pr(>|t|)
## (Intercept)   <2e-16 ***
## experience    <2e-16 ***
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 0.1541 on 48 degrees of freedom
## Multiple R-squared:  0.8635, Adjusted R-squared:  0.8607
## F-statistic: 303.7 on 1 and 48 DF,  p-value: < 2.2e-16
```

I think it's best to save the data frame with log_salary in it, since we'll be doing a couple of things with it, and it's best to be able to start from soc.2. But you can also do this:

```
soc %>% mutate(log_salary = log(salary)) %>% lm(log_salary ~
    experience, data = .) %>% summary()
```

```
##
## Call:
```

```
## lm(formula = log_salary ~ experience, data = .)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.35435 -0.09046 -0.01725  0.09739  0.26355
##
## Coefficients:
##             Estimate Std. Error t value
## (Intercept) 9.841315   0.056356  174.63
## experience  0.049979   0.002868   17.43
##             Pr(>|t|)
## (Intercept)   <2e-16 ***
## experience    <2e-16 ***
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 0.1541 on 48 degrees of freedom
## Multiple R-squared:  0.8635, Adjusted R-squared:  0.8607
## F-statistic: 303.7 on 1 and 48 DF,  p-value: < 2.2e-16
```

The second line is where the fun starts: `lm` wants the data frame as a `data=` at the end. So, to specify a data frame in something like `lm`, we have to use the special symbol `.`, which is another way to say "the data frame that came out of the previous step".

Got that? All right. The last line is a piece of cake in comparison. Normally `summary` would require a data frame or a fitted model object, but the second line produces one (a fitted model object) as output, which goes into `summary` as the first (and only) thing, so all is good and we get the regression output.

What we lose by doing this is that if we need something later from this fitted model object, we are out of luck since we didn't save it. That's why I created `soc.2` and `soc.3` above.

You can also put functions of things directly into `lm`:

```
soc.1a = lm(log(salary) ~ experience, data = soc)
summary(soc.1a)
```

```
##
## Call:
## lm(formula = log(salary) ~ experience, data = soc)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.35435 -0.09046 -0.01725  0.09739  0.26355
```

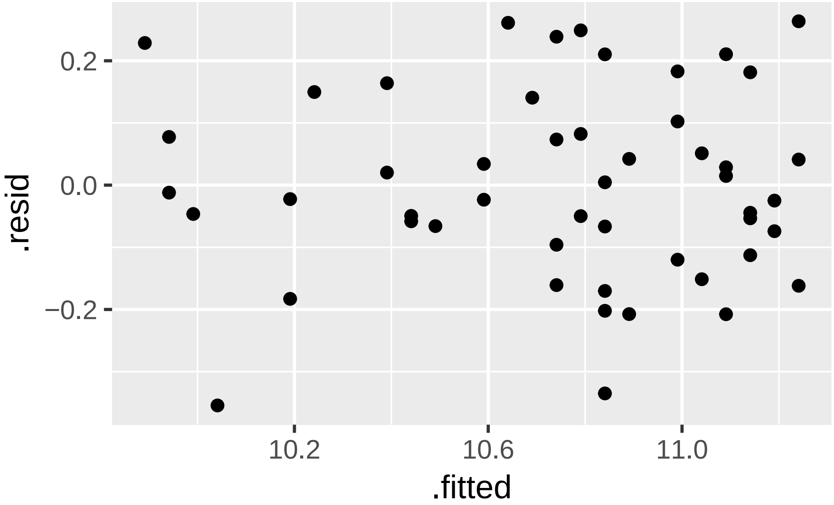
```
##
## Coefficients:
##             Estimate Std. Error t value
## (Intercept) 9.841315   0.056356  174.63
## experience  0.049979   0.002868   17.43
##             Pr(>|t|)
## (Intercept)   <2e-16 ***
## experience    <2e-16 ***
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 0.1541 on 48 degrees of freedom
## Multiple R-squared:  0.8635, Adjusted R-squared:  0.8607
## F-statistic: 303.7 on 1 and 48 DF,  p-value: < 2.2e-16
```

(g) Obtain and plot the residuals against the fitted values for this regression. Do you seem to have solved the problem with the previous residual plot?

Solution

As we did before, treating the regression object as if it were a data frame:

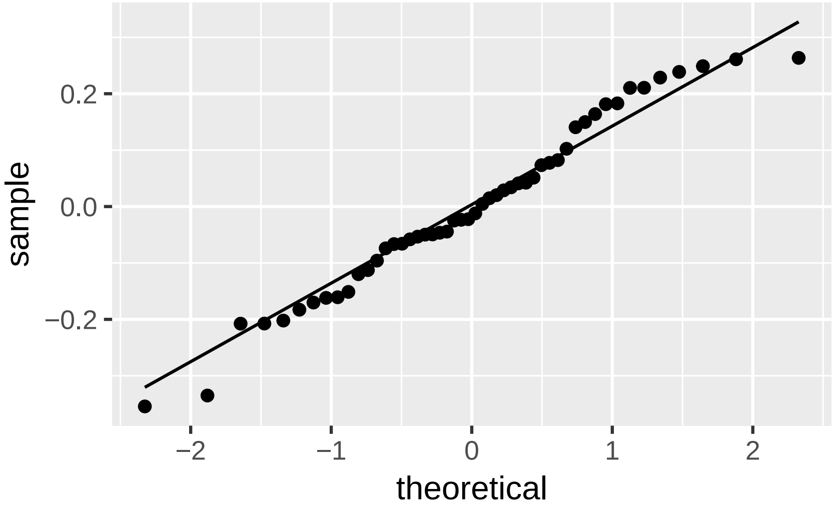
```
ggplot(soc.3, aes(x = .fitted, y = .resid)) +
    geom_point()
```



That, to my mind, is a horizontal band of points, so I would say yes, I have solved the fanning out.

One concern I have about the residuals is that there seem to be a couple of very negative values: that is, are the residuals normally distributed as they should be? Well, that's easy enough to check:

```
ggplot(soc.3, aes(sample = .resid)) + stat_qq() +
    stat_qq_line()
```



The issues here are that those bottom two values are a bit too low, and the top few values are a bit bunched up (that curve at the top). It is really not bad, though, so I am making the call that I don't think I needed to worry. Note that the transformation we found here is the same as the log-salary used by the management consultants in the backward-elimination question, and with the same effect: an extra year of experience goes with a *percent* increase in salary.

What increase? Well, the slope is about 0.05, so adding a year of experience is predicted to increase log-salary by 0.05, or to multiply actual salary by

```
exp(0.05)
```

```
## [1] 1.051271
```

or to increase salary by about 5%.

Mathematically, e^x is approximately $1 + x$ for small x, which winds up meaning that the slope in a model like this, if it is small, indicates about the percent increase in the response associated with a 1-unit change in the explanatory variable. Note that this only works with e^x and natural logs, not base 10 logs or anything like that.

13.9 *Predicting volume of wood in pine trees*

In forestry, the financial value of a tree is the volume of wood that it contains. This is difficult to estimate while the tree is still standing, but the diameter is easy to measure with a tape measure (to measure the circumference) and a calculation involving π, assuming that the cross-section of the tree is at least approximately circular. The standard measurement is "diameter at breast height" (that is, at the height of a human breast or chest), defined as being 4.5 feet above the ground.

Several pine trees had their diameter measured shortly before being cut down, and for each tree, the volume of wood was recorded.

The data are in link. The diameter is in inches and the volume is in cubic inches. Is it possible to predict the volume of wood from the diameter?

(a) Read the data into R and display the values (there are not very many).

Solution

Observe that the data values are separated by spaces, and therefore that read_delim will do it:

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/pinetrees.txt"
trees = read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   diameter = col_integer(),
##   volume = col_integer()
## )
```

```
trees
```

```
## # A tibble: 10 x 2
##    diameter volume
##       <int>  <int>
##  1       32    185
##  2       29    109
##  3       24     95
##  4       45    300
##  5       20     30
##  6       30    125
##  7       26     55
##  8       40    246
##  9       24     60
## 10       18     15
```

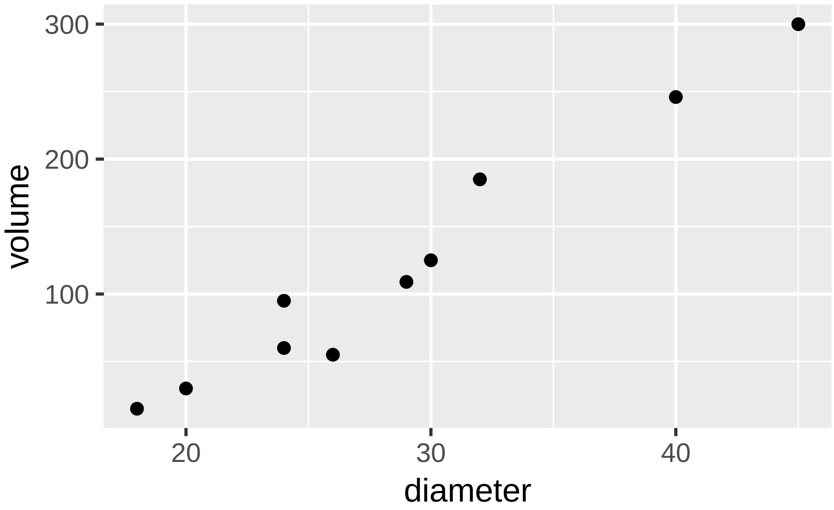
That looks like the data file.

(b) Make a suitable plot.

Solution

No clues this time. You need to recognize that you have two quantitative variables, so that a scatterplot is called for. Also, the volume is the response, so that should go on the y-axis:

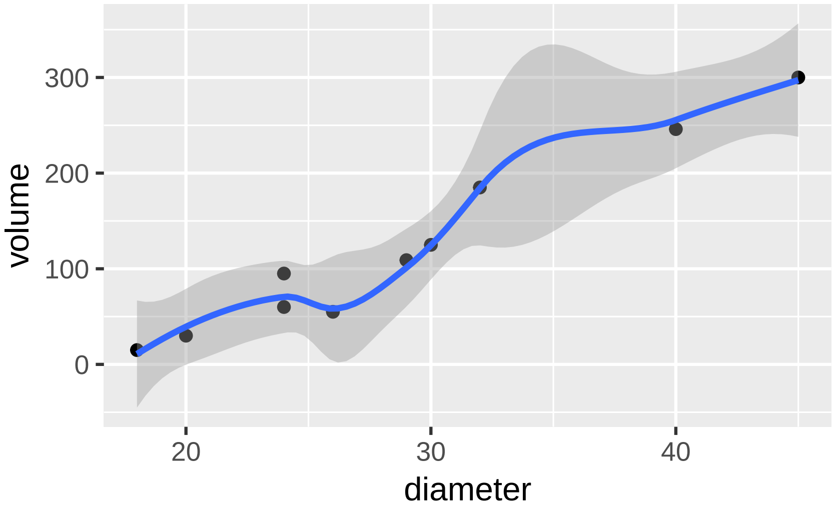
```
ggplot(trees, aes(x = diameter, y = volume)) +
    geom_point()
```



You can put a smooth trend on it if you like, which would look like this:

```
ggplot(trees, aes(x = diameter, y = volume)) +
    geom_point() + geom_smooth()
```

```
## ‘geom_smooth()‘ using method = ’loess’ and formula ’y ~ x’
```



I’ll take either of those for this part, though I think the smooth trend actually obscures the issue here (because there is not so much data).

(c) Describe what you learn from your plot about the relationship between diameter and volume, if anything.

Solution

The word “relationship” offers a clue that a scatterplot would have been a good idea, if you hadn’t realized by now. I am guided by “form, direction, strength” in looking at a scatterplot:

- Form: it is an apparently linear relationship.
- Direction: it is an upward trend: that is, a tree with a larger diameter also has a larger volume of wood. (This is not very surprising.)
- Strength: I'd call this a strong (or moderate-to-strong) relationship. (We'll see in a minute what the R-squared is.)

You don't need to be as formal as this, but you *do* need to get at the idea that it is an upward trend, apparently linear, and at least fairly strong.

When this was graded, it was 3 marks, to clue you in that there are three things to say.

(d) Fit a (linear) regression, predicting volume from diameter, and obtain the summary. How would you describe the R-squared?

Solution

My naming convention is (usually) to call the fitted model object by the name of the response variable and a number. (I have always used dots, but in the spirit of the tidyverse I suppose I should use underscores.)

```
volume.1 = lm(volume ~ diameter, data = trees)
summary(volume.1)

##
## Call:
## lm(formula = volume ~ diameter, data = trees)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -36.497  -9.982   1.751   8.959  28.139
##
## Coefficients:
##             Estimate Std. Error t value
## (Intercept) -191.749     23.954  -8.005
## diameter      10.894      0.801  13.600
##             Pr(>|t|)
## (Intercept) 4.35e-05 ***
## diameter    8.22e-07 ***
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 20.38 on 8 degrees of freedom
## Multiple R-squared:  0.9585, Adjusted R-squared:  0.9534
## F-statistic:   185 on 1 and 8 DF,  p-value: 8.217e-07
```

R-squared is nearly 96%, so the relationship is definitely a strong one.

I also wanted to mention the broom package, which was installed with the tidyverse but which you need to load separately. It provides two handy ways to summarize a fitted model (regression, analysis of variance or whatever):

```
library(broom)
glance(volume.1)

## # A tibble: 1 x 11
##   r.squared adj.r.squared sigma statistic
## *     <dbl>         <dbl> <dbl>     <dbl>
## 1     0.959         0.953  20.4      185.
## # ... with 7 more variables: p.value <dbl>,
## #   df <int>, logLik <dbl>, AIC <dbl>,
## #   BIC <dbl>, deviance <dbl>,
## #   df.residual <int>
```

This gives a one-line summary of a model, including things like R-squared. This is handy if you're fitting more than one model, because you can collect the one-line summaries together into a data frame and eyeball them.

The other summary is this one:

```
tidy(volume.1)

## # A tibble: 2 x 5
##   term  estimate std.error statistic p.value
##   <chr>    <dbl>     <dbl>     <dbl>   <dbl>
## 1 (Int~   -192.     24.0       -8.01 4.35e-5
## 2 diam~     10.9     0.801     13.6  8.22e-7
```

This gives a table of intercepts, slopes and their P-values, but the value to this one is that it is a *data frame*, so if you want to pull anything out of it, you know how to do that:

The *summary* output is more designed for looking at than for extracting things from.

```
tidy(volume.1) %>% filter(term == "diameter")

## # A tibble: 1 x 5
##   term  estimate std.error statistic p.value
##   <chr>    <dbl>     <dbl>     <dbl>   <dbl>
## 1 diam~     10.9     0.801      13.6 8.22e-7
```

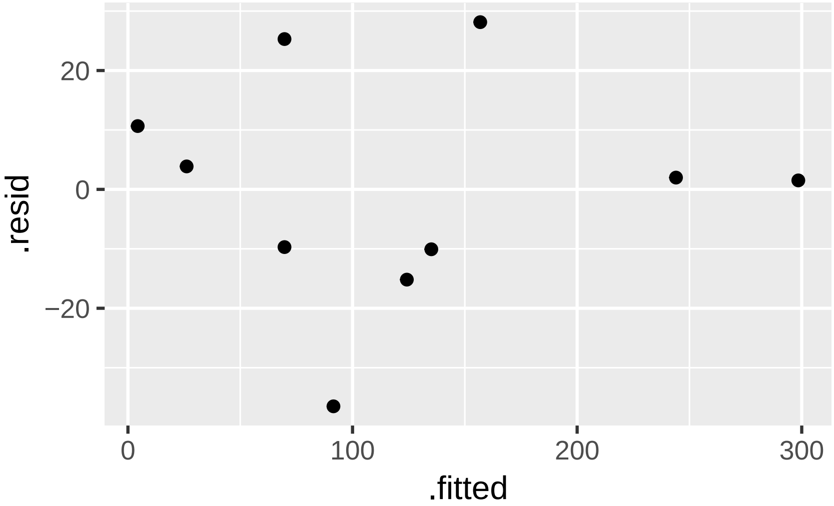
This gets the estimated slope and its P-value, without worrying about the corresponding things for the intercept, which are usually of less interest anyway.

(e) Draw a graph that will help you decide whether you trust the linearity of this regression. What do you conclude? Explain briefly.

Solution

The thing I'm fishing for is a residual plot (of the residuals against the fitted values), and on it you are looking for a random mess of nothingness:

```
ggplot(volume.1, aes(x = .fitted, y = .resid)) +
    geom_point()
```



Make a call. You could say that there's no discernible pattern, especially with such a small data set, and therefore that the regression is fine. Or you could say that there is fanning-in: the two points on the right have residuals close to 0 while the points on the left have residuals larger in size. Say something.

I don't think you can justify a curve or a trend, because the residuals on the left are both positive and negative.

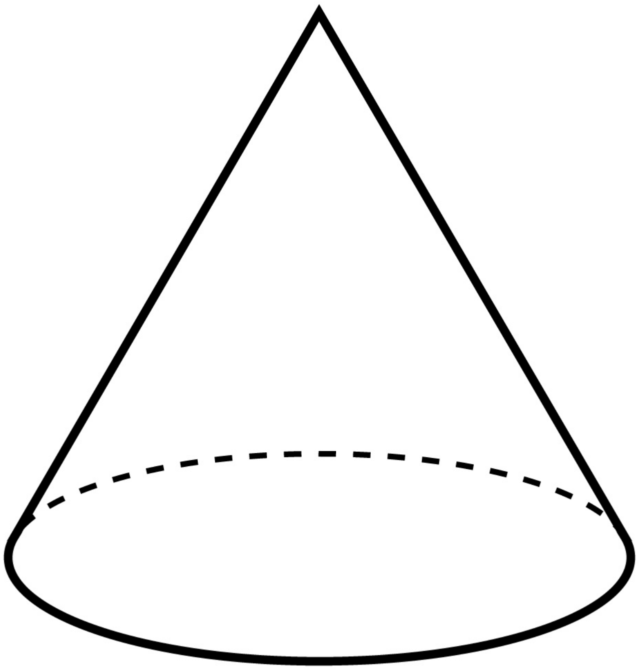
My feeling is that the residuals on the right are close to 0 because these points have noticeably larger diameter than the others, and they are *influential* points in the regression that will pull the line closer to themselves. This is why their residuals are close to zero. But I am happy with either of the points made in the paragraph under the plot.

(f) What would you guess would be the volume of a tree of diameter zero? Is that what the regression predicts? Explain briefly.

Solution

Logically, a tree that has diameter zero is a non-existent tree, so its volume should be zero as well. In the regression, the quantity that says what volume is when diameter is zero is the *intercept*. Here the intercept is -192, which is definitely not zero. In fact, if you look at the P-value, the intercept is significantly *less* than zero. Thus, the model makes no logical sense for trees of small diameter. The smallest tree in the data set has diameter 18, which is not really small, I suppose, but it is a little disconcerting to have a model that makes no logical sense.

(g) A simple way of modelling a tree's shape is to pretend it is a cone, like this, but probably taller and skinnier:



with its base on the ground. What is the relationship between the *diameter* (at the base) and volume of a cone? (If you don't remember, look it up. You'll probably get a formula in terms of the radius, which you'll have to convert. Cite the website you used.)

Solution

According to link, the volume of a cone is $V = \pi r^2 h/3$, where V is the volume, r is the radius (at the bottom of the cone) and h is the height. The diameter is twice the radius, so replace r by $d/2$, d being the diameter. A little algebra gives

$$V = \pi d^2 h/12.$$

(h) Fit a regression model that predicts volume from diameter according to the formula you obtained in the previous part. You can assume that the trees in this data set are of similar heights, so that the height can be treated as a constant.

Display the results.

Solution

According to my formula, the volume depends on the diameter squared, which I include in the model thus:

```
volume.2 = lm(volume ~ I(diameter^2), data = trees)
summary(volume.2)
```

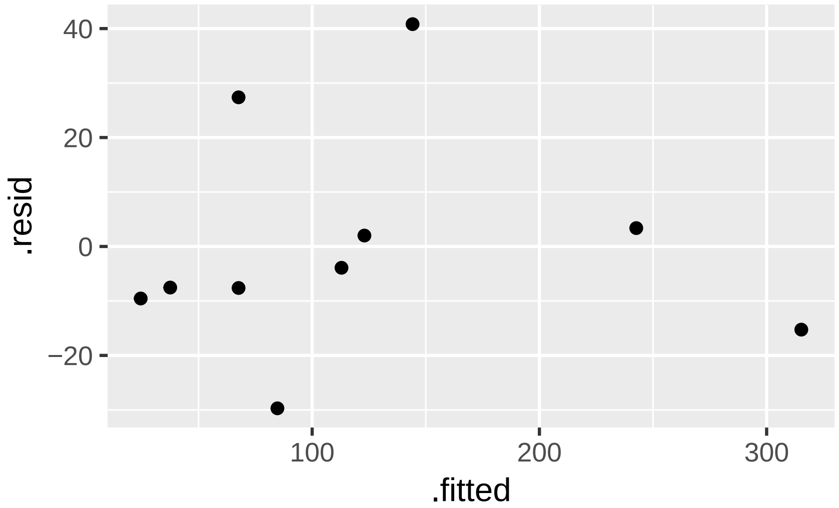
```
##
## Call:
## lm(formula = volume ~ I(diameter^2), data = trees)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -29.708  -9.065  -5.722   3.032  40.816
##
## Coefficients:
##                Estimate Std. Error t value
## (Intercept)   -30.82634   13.82243   -2.23
## I(diameter^2)   0.17091    0.01342   12.74
##               Pr(>|t|)
## (Intercept)     0.0563 .
## I(diameter^2) 1.36e-06 ***
## ---
## Signif. codes:
##   0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1  ’ ’ 1
##
## Residual standard error: 21.7 on 8 degrees of freedom
## Multiple R-squared:  0.953,  Adjusted R-squared:  0.9471
## F-statistic: 162.2 on 1 and 8 DF,  p-value: 1.359e-06
```

This adds an intercept as well, which is fine (there are technical difficulties around removing the intercept).

That's as far as I wanted you to go, but (of course) I have a few comments.

The intercept here is still negative, but not significantly different from zero, which is a step forward. The R-squared for this regression is very similar to that from our linear model (the one for which the intercept made no sense). So, from that point of view, either model predicts the data well. I should look at the residuals from this one:

```
ggplot(volume.2, aes(x = .fitted, y = .resid)) +
    geom_point()
```



I really don't think there are any problems there.

Now, I said to assume that the trees are all of similar height. This seems entirely questionable, since the trees vary quite a bit in diameter, and you would guess that trees with bigger diameter would also be taller. It seems more plausible that the same kind of trees (pine trees in this case) would have the same "shape", so that if you knew the diameter you could *predict* the height, with larger-diameter trees being taller. Except that we don't have the heights here, so we can't build a model for that.

So I went looking in the literature. I found this paper: link. This gives several models for relationships between volume, diameter and height. In the formulas below, there is an implied "plus error" on the right, and the α_i are parameters to be estimated.

For predicting height from diameter (equation 1 in paper):

$$h = \exp(\alpha_1 + \alpha_2 d^{\alpha_3})$$

For predicting volume from height and diameter (equation 6):

$$V = \alpha_1 d^{\alpha_2} h^{\alpha_3}$$

This is a take-off on our assumption that the trees were cone-shaped, with cone-shaped trees having $\alpha_1 = \pi/12$, $\alpha_2 = 2$ and $\alpha_3 = 1$. The paper uses different units, so α_1 is not comparable, but α_2 and α_3 are (as estimated from the data in the paper, which were for longleaf pine) quite close to 2 and 1.

Last, the actual relationship that helps us: predicting volume from just diameter (equation 5):

$$V = \alpha_1 d^{\alpha_2}$$

This is a power law type of relationship. For example, if you were willing to pretend that a tree was a cone with height proportional to diameter (one way of getting at the idea of a bigger tree typically being taller, instead of assuming constant height as we did), that would imply $\alpha_2 = 3$ here.

This is non-linear as it stands, but we can bash it into shape by taking logs:

$$\ln V = \ln \alpha_1 + \alpha_2 \ln d$$

so that log-volume has a linear relationship with log-diameter and we can go ahead and estimate it:

```
volume.3 = lm(log(volume) ~ log(diameter), data = trees)
summary(volume.3)
```

```
##
## Call:
## lm(formula = log(volume) ~ log(diameter), data = trees)
##
## Residuals:
##      Min       1Q   Median       3Q      Max
## -0.40989 -0.22341  0.01504  0.10459  0.53596
##
## Coefficients:
##               Estimate Std. Error t value
## (Intercept)    -5.9243     1.1759  -5.038
## log(diameter)   3.1284     0.3527   8.870
##               Pr(>|t|)
## (Intercept)      0.001 **
## log(diameter) 2.06e-05 ***
## ---
## Signif. codes:
##   0 ’***’ 0.001 ’**’ 0.01 ’*’ 0.05 ’.’ 0.1  ’ ’ 1
##
## Residual standard error: 0.3027 on 8 degrees of freedom
## Multiple R-squared:  0.9077, Adjusted R-squared:  0.8962
## F-statistic: 78.68 on 1 and 8 DF,  p-value: 2.061e-05
```

The parameter that I called α_2 above is the slope of this model, 3.13. This is a bit different from the figure in the paper, which was 2.19. I think these are comparable even though the other parameter is not (again, measurements in different units, plus, this time we need to take the log of it). I think the “slopes” are comparable because we haven’t estimated our slope all that accurately:

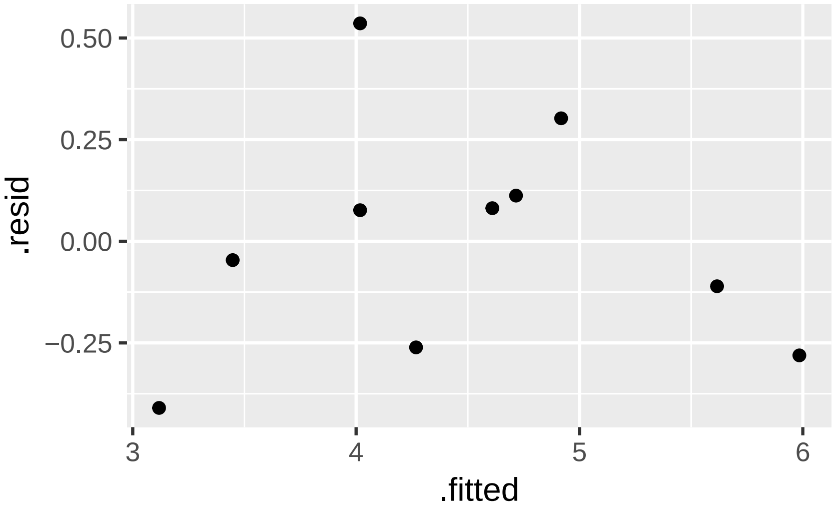
```
confint(volume.3)
```

```
##                     2.5 %    97.5 %
## (Intercept)   -8.635791 -3.212752
## log(diameter)  2.315115  3.941665
```

From 2.3 to 3.9. It is definitely not zero, but we are rather less sure about what it is, and 2.19 is not completely implausible.

The R-squared here, though it is less than the other ones we got, is still high. The residuals are these:

```
ggplot(volume.3, aes(x = .fitted, y = .resid)) +
    geom_point()
```



which again seem to show no problems. The residuals are smaller in size now because of the log transformation: the actual and predicted log-volumes are smaller numbers than the actual and predicted volumes, so the residuals are now closer to zero.

Does this model behave itself at zero? Well, roughly at least: if the diameter is very small, its log is very negative, and the predicted log-volume is also very negative (the slope is positive). So the predicted actual volume will be close to zero. If you want to make that mathematically rigorous, you can take limits, but that's the intuition. We can also do some predictions: set up a data frame that has a column called `diameter` with some diameters to predict for:

```
d = tibble(diameter = c(1, 2, seq(5, 50, 5)))
d
```

```
## # A tibble: 12 x 1
##    diameter
##       <dbl>
##  1        1
##  2        2
##   3         5
##   4        10
##   5        15
##   6        20
##   7        25
##   8        30
##   9        35
## 10        40
## 11        45
## 12        50
```

and then feed that into `predict`:

```
p = predict(volume.3, d)
d %>% mutate(pred = p)
```

```
## # A tibble: 12 x 2
##    diameter   pred
##       <dbl>  <dbl>
##   1         1 -5.92
##   2         2 -3.76
##   3         5 -0.889
##   4        10  1.28
##   5        15  2.55
##   6        20  3.45
##   7        25  4.15
##   8        30  4.72
##   9        35  5.20
## 10        40  5.62
## 11        45  5.98
## 12        50  6.31
```

These are predicted log-volumes, so we'd better anti-log them. `log` in R is natural logs, so this is inverted using `exp`:

```
d %>% mutate(pred = exp(p))
```

```
## # A tibble: 12 x 2
##    diameter      pred
##       <dbl>     <dbl>
##   1         1   0.00267
##   2         2   0.0234
##   3         5   0.411
##   4        10   3.59
##   5        15  12.8
##   6        20  31.4
##  7       25  63.2
##  8       30 112.
##  9       35 181.
## 10       40 275.
## 11       45 397.
## 12       50 552.
```

For a diameter near zero, the predicted volume appears to be near zero as well.

I mentioned broom earlier. We can make a data frame out of the one-line summaries of our three models:

```
bind_rows(glance(volume.1), glance(volume.2),
    glance(volume.3))
```

```
## # A tibble: 3 x 11
##   r.squared adj.r.squared  sigma statistic
##       <dbl>         <dbl>  <dbl>     <dbl>
## 1     0.959         0.953 20.4       185.
## 2     0.953         0.947 21.7       162.
## 3     0.908         0.896  0.303      78.7
## # ... with 7 more variables: p.value <dbl>,
## #   df <int>, logLik <dbl>, AIC <dbl>,
## #   BIC <dbl>, deviance <dbl>,
## #   df.residual <int>
```

(I mistakenly put glimpse instead of glance there the first time. The former is for a quick look at a *data frame*, while the latter is for a quick look at a *model*.)

The three R-squareds are all high, with the one from the third model being a bit lower as we saw before.

My code is rather repetitious. There has to be a way to streamline it. I was determined to find out how. My solution involves putting the three models in a list, and then using map to get the glance output for each one, and bind_rows to glue the results together into one data frame. I was inspired to try this by remembering that map_df will work for a function like glance that outputs a data frame:

```
model_list = list(volume.1, volume.2, volume.3)
map_df(model_list, ~glance(.))
```

```
## # A tibble: 3 x 11
##   r.squared adj.r.squared  sigma statistic
##       <dbl>         <dbl>  <dbl>     <dbl>
## 1     0.959         0.953 20.4       185.
## 2     0.953         0.947 21.7       162.
## 3     0.908         0.896  0.303      78.7
## # ... with 7 more variables: p.value <dbl>,
## #   df <int>, logLik <dbl>, AIC <dbl>,
## #   BIC <dbl>, deviance <dbl>,
## #   df.residual <int>
```

It works. You see the three R-squared values in the first column. The third model is otherwise a lot different from the others because it has a different response variable.

Other thoughts:

How might you measure or estimate the height of a tree (other than by climbing it and dropping a tape measure down)? One way, that works if the tree is fairly isolated, is to walk away from its base. Periodically, you point at the top of the tree, and when the angle between your arm and the ground reaches 45 degrees, you stop walking. (If it's greater than 45 degrees, you walk further away, and if it's less, you walk back towards the tree.) The distance between you and the base of the tree is then equal to the height of the tree, and if you have a long enough tape measure you can measure it.

The above works because the tangent of 45 degrees is 1. If you have a device that will measure the actual angle, you can be any distance away from the tree, point the device at the top, record the angle, and do some trigonometry to estimate the height of the tree (to which you add the height of your eyes).

These days, there are apps that will let you do this with your phone. I found one called Clinometer. See also [link](https://gabrielhemery.com/how-to-calculate-tree-height-using-a-smartphone/).

13.10 Crickets revisited

This is a reorganization of the crickets problem that you may have seen before (minus the data tidying).

Male tree crickets produce "mating songs" by rubbing their wings together to produce a chirping sound. It is hypothesized that female tree crickets identify males of the correct species by how fast (in chirps per second) the male's mating song is. This is called the "pulse rate". Some data for two species of crickets are in link as a CSV file. The columns are species (text), temperature, and pulse rate (numbers). This is the tidied version of the data set that the previous version of this question had you create. The research question is whether males of the different species have different average pulse rates. It is also of interest to see whether temperature has an effect, and if so, what.

(a) Read the data into R and display what you have.

Solution

Nothing terribly surprising here:

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/crickets2.csv"
crickets = read_csv(my_url)
```

```
## Parsed with column specification:
## cols(
##   species = col_character(),
##   temperature = col_double(),
##   pulse_rate = col_double()
## )
```

```
crickets
```

```
## # A tibble: 31 x 3
##    species       temperature pulse_rate
##    <chr>               <dbl>      <dbl>
##  1 exclamationis        20.8       67.9
##  2 exclamationis        20.8       65.1
##  3 exclamationis        24         77.3
##  4 exclamationis        24         78.7
##  5 exclamationis        24         79.4
##  6 exclamationis        24         80.4
##  7 exclamationis        26.2       85.8
##  8 exclamationis        26.2       86.6
##  9 exclamationis        26.2       87.5
## 10 exclamationis        26.2       89.1
## # ... with 21 more rows
```

31 crickets, which is what I remember. What species are there?

```
crickets %>% count(species)
```

```
## # A tibble: 2 x 2
##   species           n
##   <chr>         <int>
## 1 exclamationis    14
## 2 niveus           17
```

That looks good. We proceed.

(b) Do a two-sample *t*-test to see whether the mean pulse rates differ between species. What do you conclude?

Solution
Drag your mind way back to this:

```
t.test(pulse_rate ~ species, data = crickets)
```

```
##
##  Welch Two Sample t-test
##
## data:  pulse_rate by species
## t = 5.2236, df = 28.719, p-value =
## 1.401e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  14.08583 32.22677
## sample estimates:
## mean in group exclamationis
##                    85.58571
##        mean in group niveus
##                    62.42941
```

There is strong evidence of a difference in means (a P-value around 0.00001), and the confidence interval says that the mean chirp rate is higher for *exclamationis*. That is, not just for the crickets that were observed here, but for *all* crickets of these two species.

(c) Can you do that two-sample *t*-test as a regression?

Solution

Hang onto the "pulse rate depends on species" idea and try that in `lm`:

```
pulse.0 = lm(pulse_rate ~ species, data = crickets)
summary(pulse.0)
```

```
##
## Call:
## lm(formula = pulse_rate ~ species, data = crickets)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -20.486  -9.458  -1.729  13.342  22.271
##
## Coefficients:
##                Estimate Std. Error t value
## (Intercept)      85.586      3.316  25.807
## speciesniveus   -23.156      4.478  -5.171
##                Pr(>|t|)
## (Intercept)     < 2e-16 ***
## speciesniveus 1.58e-05 ***
## ---
## Signif. codes:
```

```
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 12.41 on 29 degrees of freedom
## Multiple R-squared:  0.4797, Adjusted R-squared:  0.4617
## F-statistic: 26.74 on 1 and 29 DF,  p-value: 1.579e-05
```

I had to use "model 0" for this since I already have a `pulse.1` below and I didn't want to go down and renumber everything.

Look along the `speciesniveus` line. Ignoring the fact that it is negative, the *t*-statistic is almost the same as before (5.17 vs. 5.22) and so is the P-value (1.4×10^{-5} vs. 1.6×10^{-5}).

Why aren't they exactly the same? Regression is assuming equal variances everywhere (that is, within the two `species`), and before, we did the Welch-Satterthwaite test that does not assume equal variances. What if we do the pooled *t*-test instead?

```
t.test(pulse_rate ~ species, data = crickets,
    var.equal = T)
```

```
##
##  Two Sample t-test
##
## data:  pulse_rate by species
## t = 5.1706, df = 29, p-value =
## 1.579e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  13.99690 32.31571
## sample estimates:
## mean in group exclamationis
##                    85.58571
##        mean in group niveus
##                    62.42941
```

Now the regression and the *t*-test *do* give exactly the same answers. We'll think about that equal-spreads assumption again later.

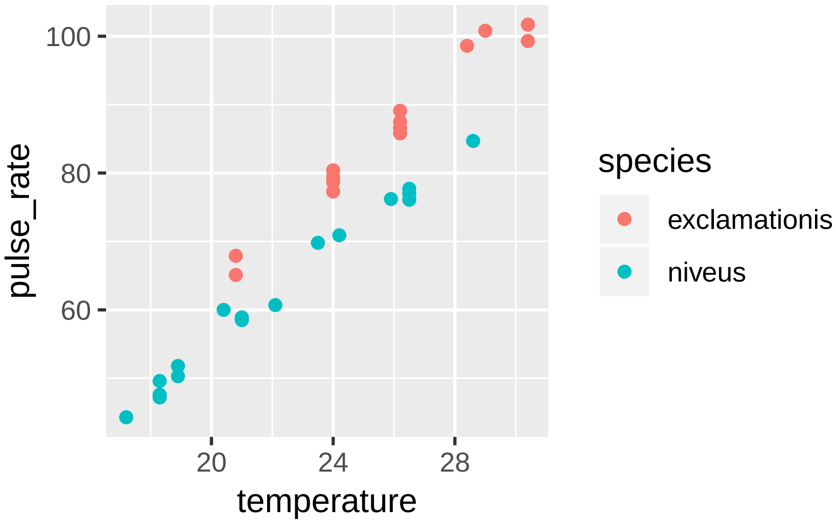
(d) The analysis in the last part did not use temperature, however. Is it possible that temperature also has an effect? To assess this, draw a scatterplot of pulse rate against temperature, with the points distinguished, somehow, by the species they are from.

This was the actual reason I thought of this question originally: I wanted you to do this.

Solution

One of the wonderful things about `ggplot` is that doing the obvious thing works:

```
ggplot(crickets, aes(x = temperature, y = pulse_rate,
    colour = species)) + geom_point()
```



(e) What does the plot tell you that the *t*-test doesn't? How would you describe differences in pulse rates between species now?

Solution

The plot tells you that (for both species) as temperature goes up, pulse rate goes up as well. *Allowing for that*, the difference in pulse rates between the two species is even clearer than it was before. To see an example, pick a temperature, and note that the mean pulse rate at that temperature seems to be at least 10 higher for *exclamationis*, with a high degree of consistency. The *t*-test mixed up all the pulse rates at all the different temperatures. Even though the conclusion was clear enough, it could be clearer if we incorporated temperature into the analysis. There was also a potential source of unfairness in that the *exclamationis* crickets tended to be observed at higher temperatures than *niveus* crickets; since pulse rates increase with temperature, the apparent difference in pulse rates between the species might have been explainable by one species being observed mainly in higher temperatures. This was *utterly invisible* to us when we did the *t*-test, but it shows the importance of accounting for all the relevant variables when you do your analysis. If the species had been observed at opposite temperatures, we might have concluded that textsl{niveus} have the higher pulse rates on average. I come back to this later when I discuss the confidence interval for species difference that comes out of the regression model with temperature.

And it shows the value of looking at relevant plots.

Mistakenly.

(f) Fit a regression predicting pulse rate from species and temperature. Compare the P-value for species in this regression to the one from the *t*-test. What does that tell you?

Solution

This is actually a so-called “analysis of covariance model”, which properly belongs in D29, but it’s really just a regression:

```
pulse.1 = lm(pulse_rate ~ species + temperature,
    data = crickets)
summary(pulse.1)
```

```
##
## Call:
## lm(formula = pulse_rate ~ species + temperature, data = crickets)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.0128 -1.1296 -0.3912  0.9650  3.7800
##
## Coefficients:
##                 Estimate Std. Error t value
## (Intercept)    -7.21091    2.55094  -2.827
## speciesniveus -10.06529    0.73526 -13.689
## temperature     3.60275    0.09729  37.032
##               Pr(>|t|)
## (Intercept)    0.00858 **
## speciesniveus 6.27e-14 ***
## temperature    < 2e-16 ***
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 1.786 on 28 degrees of freedom
## Multiple R-squared:  0.9896, Adjusted R-squared:  0.9888
## F-statistic:  1331 on 2 and 28 DF,  p-value: < 2.2e-16
```

The P-value for species is now 6.27×10^{-14} or 0.0000000000006, which is even less than the P-value of 0.00001 that came out of the *t*-test. That is to say, when you know temperature, you can be even more sure of your conclusion that there is a difference between the species.

The R-squared for this regression is almost 99%, which says that if you know both temperature and species, you can predict the pulse rate almost exactly.

In the regression output, the slope for species is about -10. It is labelled `speciesniveus`. Since species is categorical, `lm` uses the first category, *exclamationis*, as the baseline and expresses each other species relative to that. Since the slope is about -10, it says that at any given temperature, the mean pulse rate for *niveus* is about 10 less than for *exclamationis*. This is pretty much what the scatterplot told us.

We can go a little further here:

```
confint(pulse.1)
```

```
##                    2.5 %    97.5 %
## (Intercept)   -12.436265 -1.985547
## speciesniveus -11.571408 -8.559175
## temperature     3.403467  3.802038
```

The second line says that the pulse rate for *niveus* is between about 8.5 and 11.5 less than for *exclamationis*, at any given temperature (comparing the two species at the same temperature as each other, but that temperature could be anything). This is a lot shorter than the CI that came out of the *t*-test, that went from 14 to 32. This is because we are now accounting for temperature, which also makes a difference. (In the *t*-test, the temperatures were all mixed up). What we also see is that the *t*-interval is shifted up compared to the one from the regression. This is because the *t*-interval conflates two things: the textsl{exclamationis} crickets do have a higher pulse rate, but they were also observed at higher temperatures, which makes it look as if their pulse rates are more higher than they really are, when you account for temperature.

Mixes up.

This is actually grammatically correct.

This particular model constrains the slope with temperature to be the same for both species (just the intercepts differ). If you want to allow the slopes to differ between species, you add an interaction between temperature and species:

```
pulse.2 = lm(pulse_rate ~ species * temperature,
    data = crickets)
summary(pulse.2)
```

```
##
## Call:
## lm(formula = pulse_rate ~ species * temperature, data = crickets)
##
## Residuals:
##     Min      1Q  Median      3Q     Max
## -3.7031 -1.3417 -0.1235  0.8100  3.6330
##
## Coefficients:
##                           Estimate
## (Intercept)               -11.0408
## speciesniveus              -4.3484
## temperature                 3.7514
## speciesniveus:temperature  -0.2340
##                            Std. Error t value
## (Intercept)                    4.1515  -2.659
## speciesniveus                  4.9617  -0.876
## temperature                    0.1601  23.429
## speciesniveus:temperature      0.2009  -1.165
##                            Pr(>|t|)
## (Intercept)                   0.013 *
## speciesniveus                 0.389
## temperature                  <2e-16 ***
## speciesniveus:temperature     0.254
## ---
## Signif. codes:
##   0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1  ' ' 1
##
## Residual standard error: 1.775 on 27 degrees of freedom
## Multiple R-squared:  0.9901, Adjusted R-squared:  0.989
## F-statistic: 898.9 on 3 and 27 DF,  p-value: < 2.2e-16
```

To see whether adding the interaction term added anything to the prediction, \marginnote{Though it's hard to imagine being able to improve on an R-squared of 99%.} compare the model with and without using anova:

```
anova(pulse.1, pulse.2)
```

```
## Analysis of Variance Table
##
## Model 1: pulse_rate ~ species + temperature
## Model 2: pulse_rate ~ species * temperature
##   Res.Df    RSS Df Sum of Sq     F Pr(>F)
## 1     28 89.350
## 2     27 85.074  1    4.2758 1.357 0.2542
```

There's no significant improvement by adding the interaction, so there's no evidence that having different slopes for each species is necessary. This is the same interpretation as any anova for comparing two regressions: the two models are not significantly different in fit, so go with the simpler one, that is, the one without the interaction.

Note that anova gave the same P-value as did the *t*-test for the slope coefficient for the interaction in summary, 0.254 in both cases. This is because there were only two species and therefore only one slope coefficient was required to distinguish them. If there had been three species, we would have had to look at the anova output to hunt for a difference among species, since there would have been two slope coefficients, each with its own P-value.

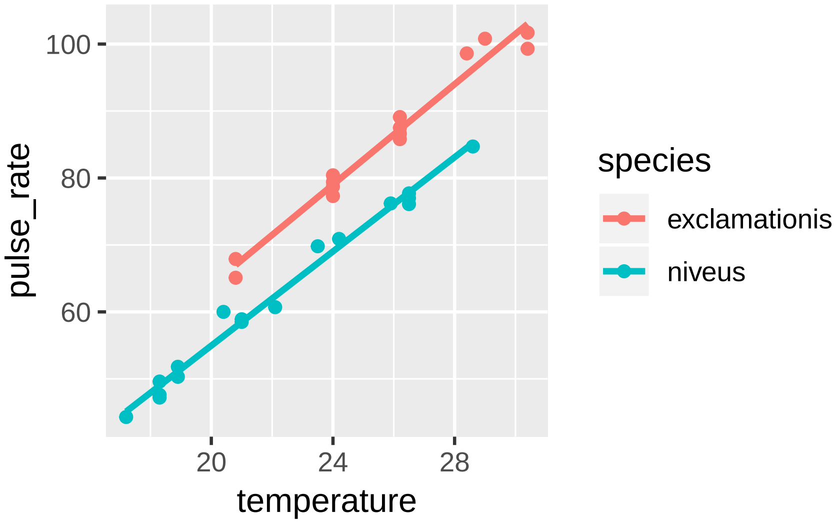
This wouldn't have told us about the overall effect of species.

If you haven't seen interactions before, don't worry about this. The idea behind it is that we are testing whether we needed lines with different slopes and we concluded that we don't. Don't worry so much about the mechanism behind `pulse.2`; just worry about how it somehow provides a way of modelling two different slopes, one for each species, which we can then test to see whether it helps.

The upshot is that we do not need different slopes; the model `pulse.1` with the same slope for each species describes what is going on.

`ggplot` makes it almost laughably easy to add regression lines for each species to our plot, thus:

```
ggplot(crickets, aes(x = temperature, y = pulse_rate,
    colour = species)) + geom_point() + geom_smooth(method = "lm",
    se = F)
```



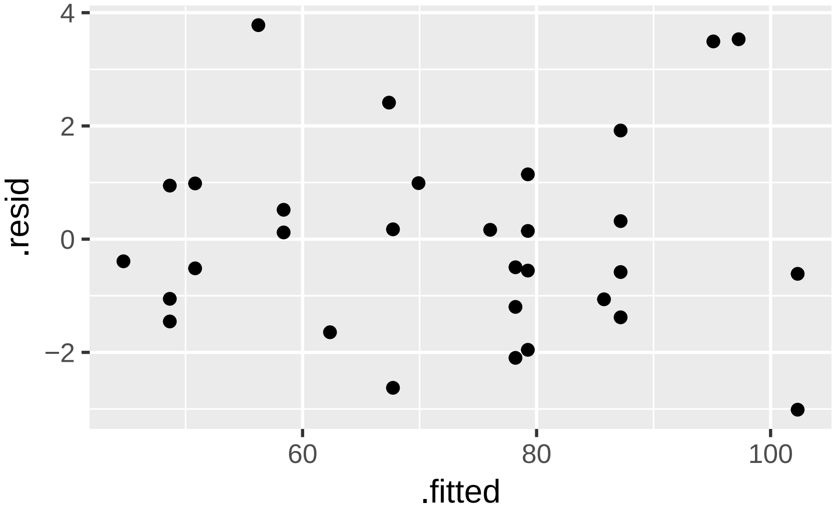
The lines are almost exactly parallel, so having the same slope for each species makes perfect sense.

(g) Make suitable residual plots for the regression `pulse.1`.

Solution

First, the plot of residuals against fitted values (after all, it *is* a regression):

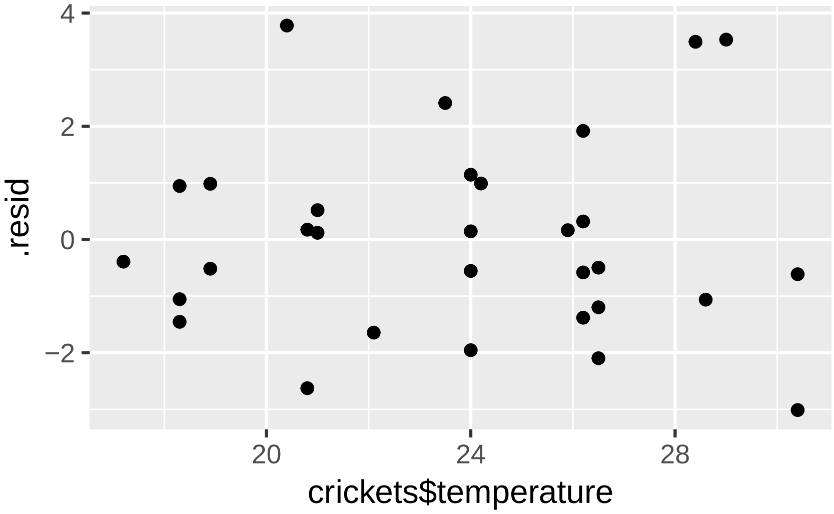
```
ggplot(pulse.1, aes(x = .fitted, y = .resid)) +
    geom_point()
```



This looks nice and random.

Now, we plot the residuals against the explanatory variables. There are two, temperature and species, but the latter is categorical. We'll have some extra issues around species, but before we get to that, we have to remember that the data and the output from the regression are in different places when we plot them. There are different ways to get around that. Perhaps the simplest is to use `pulse.1` as our "default" data frame and then get `temperature` from the right place:

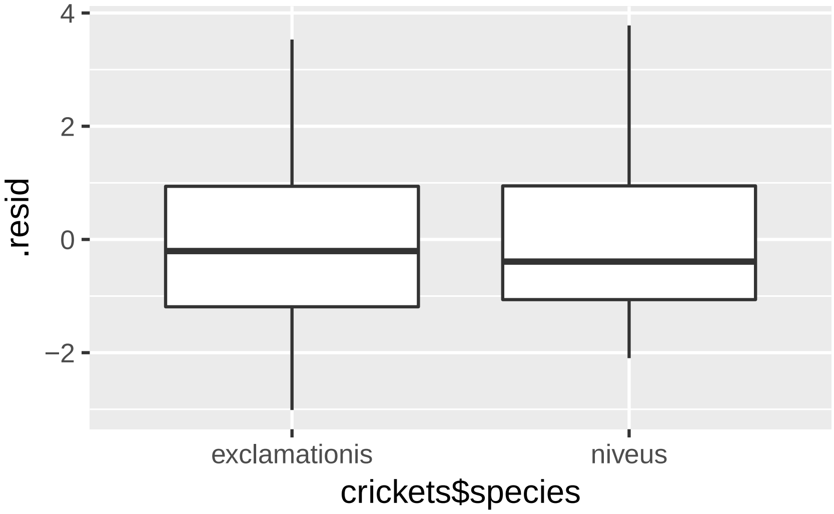
```
ggplot(pulse.1, aes(x = crickets$temperature,
    y = .resid)) + geom_point()
```



I don't see anything untoward there.

Species. We want to compare the residuals for the two species, which is categorical. Since the residuals are quantitative, this suggests a boxplot. Remembering to get species from the right place again, that goes like this:

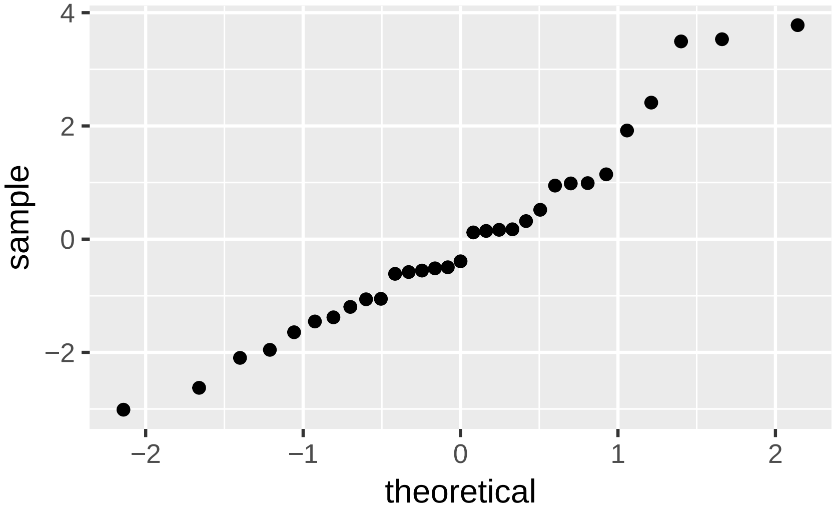
```
ggplot(pulse.1, aes(x = crickets$species, y = .resid)) +
    geom_boxplot()
```



For the residuals, the median should be zero within each group, and the two groups should be approximately normal with mean 0 and about the same spread. Same spread looks OK, since the boxes are almost exactly the same height, but the normality is not quite there, since both distributions are a little bit skewed to the right. That would also explain why the median residual in each group is a little bit less than zero, because the mathematics requires the overall *mean* residual to be zero, and the right-skewness would make the mean higher than the median.

Is that non-normality really problematic? Well, I could look at the normal quantile plot of all the residuals together. This is the one without the line:

```
ggplot(pulse.1, aes(sample = .resid)) + stat_qq()
```



There's a little weirdness at the top, and a tiny indication of a curve (that would suggest a little right-skewedness), but not really much to worry about. If that third-highest residual were a bit lower (say, 3 rather than 3.5) and maybe if the lowest residual was a bit lower, I don't think we'd have anything to complain about at all.

So, I'm not worried.

13.11 *Roller coasters*

A poll on the Discovery Channel asked people to nominate the best roller-coasters in the United States. We will examine the 10 roller-coasters that received the most votes. Two features of a roller-coaster that are of interest are the distance it drops from start to finish, measured here in feet and the duration of the ride, measured in seconds. Is it true that roller-coasters with a bigger drop also tend to have a longer ride? The data are at link.

Roller-coasters work by gravity, so there must be some drop.

These are not to be confused with what your mom insists that you place between your coffee mug and the table.

(a) Read the data into R and verify that you have a sensible number of rows and columns.

Solution

A .csv, so the usual for that:

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/coasters.csv"
coasters = read_csv(my_url)
```

```
## Parsed with column specification:
## cols(
##   coaster_name = col_character(),
##   state = col_character(),
##   drop = col_integer(),
##   duration = col_integer()
## )
```

```
coasters
```

```
## # A tibble: 10 x 4
##    coaster_name    state       drop duration
##    <chr>           <chr>      <int>    <int>
##  1 Incredible Hulk Florida      105      135
##  2 Millennium For~ Ohio         300      105
##  3 Goliath         California   255      180
##  4 Nitro           New Jersey   215      240
##  5 Magnum XL-2000  Ohio         195      120
##  6 The Beast       Ohio         141       65
##  7 Son of Beast    Ohio         214      140
##  8 Thunderbolt     Pennsylva~    95       90
##  9 Ghost Rider     California   108      160
## 10 Raven           Indiana       86       90
```

The number of marks for this kind of thing has been decreasing through the course, since by now you ought to have figured out how to do it without looking it up.

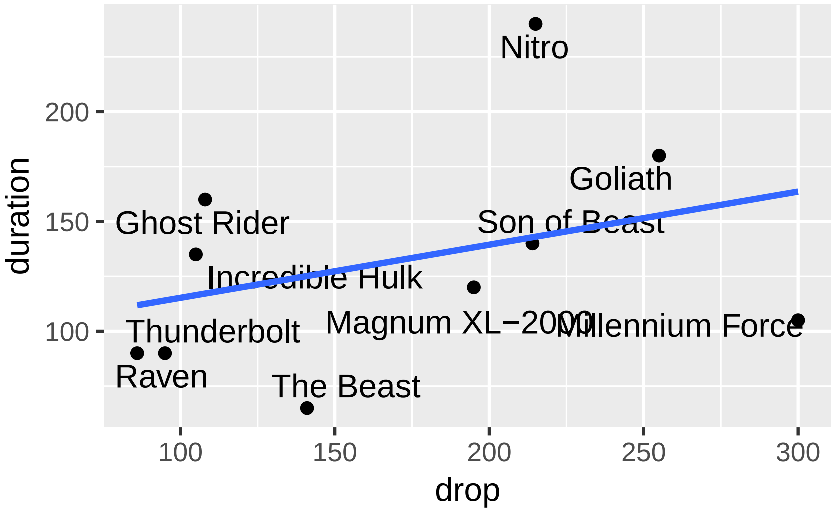
There are 10 rows for the promised 10 roller-coasters, and there are several columns: the drop for each roller-coaster and the duration of its ride, as promised, as well as the name of each roller-coaster and the state that it is in. (A lot of them seem to be in Ohio, for some reason that I don't know.) So this all looks good.

(b) Make a scatterplot of duration (response) against drop (explanatory), labelling each roller-coaster with its name in such a way that the labels do not overlap. Add a regression line to your plot.

Solution

The last part, about the labels not overlapping, is an invitation to use `ggrepel`, which is the way I'd recommend doing this. (If not, you have to do potentially lots of work organizing where the labels sit relative to the points, which is time you probably don't want to spend.) Thus:

```
library(ggrepel)
ggplot(coasters, aes(x = drop, y = duration, label = coaster_name)) +
    geom_point() + geom_text_repel() + geom_smooth(method = "lm",
    se = F)
```



The `se=F` at the end is optional; if you omit it, you get that "envelope" around the line, which is fine here.

Note that with the labelling done this way, you can easily identify which roller-coaster is which.

(c) Would you say that roller-coasters with a larger drop tend to have a longer ride? Explain briefly.

Solution

I think there are two good answers here: "yes" and "kind of". Supporting "yes" is the fact that the regression line does go uphill, so that overall, or on average, roller-coasters with a larger drop do tend to have a longer duration of ride as well. Supporting "kind of" is the fact that, though the regression line goes uphill, there are a lot of roller-coasters that are some way off the trend, far from the regression line. I am happy to go with either of those. I could also go with "not really" and the same discussion that I attached to "kind of".

(d) Find a roller-coaster that is unusual compared to the others. What about its combination of `drop` and `duration` is unusual?

Solution

This is an invitation to find a point that is a long way off the line. I think the obvious choice is my first one below, but I would take either of the others as well:

- "Nitro" is a long way above the line. That means it has a long duration, relative to its drop. There are two other roller-coasters that have a larger drop but not as long a duration. In other words, this roller-coaster drops slowly, presumably by doing a lot of twisting, loop-the-loop and so on.

- "The Beast" is a long way below the line, so it has a short duration relative to its drop. It is actually the shortest ride of all, but is only a bit below average in terms of drop. This suggests that The Beast is one of those rides that drops a long way quickly.
- "Millennium Force" has the biggest drop of all, but a shorter-than-average duration. This looks like another ride with a big drop in it.

A roller-coaster that is "unusual" will have a residual that is large in size (either positive, like Nitro, or negative, like the other two). I didn't ask you to find the residuals, but if you want to, augment from broom is the smoothest way to go:

```
library(broom)
duration.1 = lm(duration ~ drop, data = coasters)
augment(duration.1, coasters) %>% select(coaster_name,
    duration, drop, .resid) %>% arrange(desc(abs(.resid)))
```

```
## # A tibble: 10 x 4
##    coaster_name     duration  drop .resid
##    <chr>               <int> <int>  <dbl>
##  1 Nitro                 240   215  97.0
##  2 The Beast              65   141 -60.1
##  3 Millennium Force      105   300 -58.6
##  4 Ghost Rider           160   108  42.8
##  5 Goliath               180   255  27.3
##  6 Thunderbolt            90    95 -24.0
##  7 Raven                  90    86 -21.8
##  8 Incredible Hulk       135   105  18.6
##  9 Magnum XL-2000        120   195 -18.2
## 10 Son of Beast          140   214  -2.81
```

augment produces a data frame (of the original data frame with some new columns that come from the regression), so I can feed it into a pipe to do things with it, like only displaying the columns I want, and arranging them in order by absolute value of residual, so that the roller-coasters further from the line come out first. This identifies the three that we found above. The fourth one, "Ghost Rider", is like Nitro in that it takes a (relatively) long time to fall not very far. You can also put augment in the *middle* of a pipe, but then you seem to lose things that were not in the regression:

```
coasters %>% lm(duration ~ drop, data = .) %>%
    augment() %>% arrange(desc(abs(.resid)))
```

```
## # A tibble: 10 x 9
##    duration  drop .fitted .se.fit .resid
##       <int> <int>   <dbl>   <dbl>  <dbl>
##  1      240   215    143.    18.9  97.0
##  2       65   141    125.    17.5 -60.1
##  3      105   300    164.    33.4 -58.6
##  4      160   108    117.    21.6  42.8
##  5      180   255    153.    24.9  27.3
##  6       90    95    114.    23.7 -24.0
##  7       90    86    112.    25.2 -21.8
##  8      135   105    116.    22.1  18.6
##  9      120   195    138.    17.0 -18.2
## 10      140   214    143.    18.8  -2.81
## # ... with 4 more variables: .hat <dbl>,
## #   .sigma <dbl>, .cooksd <dbl>,
## #   .std.resid <dbl>
```

I wanted to hang on to the roller-coaster names, so I went the other way. The advantage of this way is less typing. You have to specify the `data=.` thing in the regression because the data frame is *not* the first input to `lm` (the model is), but you have a much simpler `augment` because its first input is the model that came out of the previous step. If the second input to `augment` is missing, as it is here, it "attempts to reconstruct the data from the model" which I think means that things like the coaster names that were not part of the regression won't be part of `augment`'s output either. That's my understanding. My first way explicitly supplies the original data frame to `augment` so there is no question about what it is using.

A quote from the package vignette.

14
Dates and times

The usual to begin with:

```
library(tidyverse)
```

```
## -- Attaching packages ---- tidyverse 1.2.1 --
```

```
## v ggplot2 3.0.0     v purrr   0.2.5
## v tibble  1.4.2     v dplyr   0.7.6
## v tidyr   0.8.1     v stringr 1.3.1
## v readr   1.1.1     v forcats 0.3.0
```

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

14.1 *Dealing with dates in the Worcester Heart Attack study*

The Worcester Heart Attack Study is an ongoing study of heart attacks in the Worcester, MA area. The main purpose of the study is to investigate changes over time in incidence and death rates, and also the use of different treatment approaches. We will be mainly using this data set to investigate data handling and dealing with dates. The data can be found at link.

(a) Read the data into R. The reading-in part is straightforward, but check what type of thing each column is. Is that what it should be?

Solution
This is `read_delim`:

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/whas500.txt"
whas = read_delim(my_url, " ")
```

```
## Parsed with column specification:
```

```
## cols(
##   .default = col_integer(),
##   bmi = col_double(),
##   admitdate = col_character(),
##   disdate = col_character(),
##   fdate = col_character()
## )

## See spec(...) for full column specifications.
```

```
whas
```

```
## # A tibble: 500 x 22
##       id   age gender    hr sysbp diasbp
##    <int> <int>  <int> <int> <int>  <int>
##  1     1    83      0    89   152     78
##  2     2    49      0    84   120     60
##  3     3    70      1    83   147     88
##  4     4    70      0    65   123     76
##  5     5    70      0    63   135     85
##  6     6    70      0    76    83     54
##  7     7    57      0    73   191    116
##  8     8    55      0    91   147     95
##  9     9    88      1    63   209    100
## 10    10    54      0   104   166    106
## # ... with 490 more rows, and 16 more
## #   variables: bmi <dbl>, cvd <int>,
## #   afb <int>, sho <int>, chf <int>,
## #   av3 <int>, miord <int>, mitype <int>,
## #   year <int>, admitdate <chr>,
## #   disdate <chr>, fdate <chr>, los <int>,
## #   dstat <int>, lenfol <int>, fstat <int>
```

To see what type everything is, note that when you display a `tibble`, the type of all the columns on the screen is displayed at the top. Click the little right-arrow to see more columns and to check their type.

All the numbers are properly integer (`int`) or decimal (`dbl`) numbers, but the date columns are `chr` or text. This means that they haven't been read as `Date`s (because they were not in year-month-day order). This is (as we will see) unlike SAS, which determined that they were dates, and even used the first 20 rows of the file to determine what format of dates they were.

(b) The date columns should be R dates. They are not year-month-day, so converting them via `as.Date` (which is what `read_delim` tries to do) will not work. Load the `lubridate` package, and create new columns in your data frame that are properly dates. Save your data frame, and list it to demonstrate that it worked.

Solution
Load `lubridate` first:

```
library(lubridate)

##
## Attaching package: 'lubridate'

## The following object is masked from 'package:base':
##
##     date
```

These dates are day-month-year, so we need `dmy` from `lubridate`:

```
whas2 = whas %>% mutate(admit = dmy(admitdate),
    dis = dmy(disdate), f = dmy(fdate))
glimpse(whas2)

## Observations: 500
## Variables: 25
## $ id        <int> 1, 2, 3, 4, 5, 6, 7, 8...
## $ age       <int> 83, 49, 70, 70, 70, 70...
## $ gender    <int> 0, 0, 1, 0, 0, 0, 0, 0...
## $ hr        <int> 89, 84, 83, 65, 63, 76...
## $ sysbp     <int> 152, 120, 147, 123, 13...
## $ diasbp    <int> 78, 60, 88, 76, 85, 54...
## $ bmi       <dbl> 25.54051, 24.02398, 22...
## $ cvd       <int> 1, 1, 0, 1, 1, 1, 1, 1...
## $ afb       <int> 1, 0, 0, 0, 0, 0, 0, 0...
## $ sho       <int> 0, 0, 0, 0, 0, 0, 0, 0...
## $ chf       <int> 0, 0, 0, 1, 0, 0, 0, 0...
## $ av3       <int> 0, 0, 0, 0, 0, 1, 0, 0...
## $ miord     <int> 1, 0, 0, 0, 0, 0, 0, 0...
## $ mitype    <int> 0, 1, 1, 1, 1, 0, 1, 1...
## $ year      <int> 1, 1, 1, 1, 1, 1, 1, 1...
## $ admitdate <chr> "13-01-1997", "19-01-1...
## $ disdate   <chr> "18-01-1997", "24-01-1...
## $ fdate     <chr> "31-12-2002", "31-12-2...
## $ los       <int> 5, 5, 5, 10, 6, 1, 5, ...
## $ dstat     <int> 0, 0, 0, 0, 0, 1, 0, 0...
## $ lenfol    <int> 2178, 2172, 2190, 297,...
## $ fstat     <int> 0, 0, 0, 1, 0, 1, 0, 1...
## $ admit      <date> 1997-01-13, 1997-01-1...
## $ dis        <date> 1997-01-18, 1997-01-2...
## $ f          <date> 2002-12-31, 2002-12-3...
```

There are a lot of columns, so I used `glimpse`. The three new variables we created are at the end of the list. They are correctly `Dates`, and they have the right values, the ones we can see at least.

The indentation is up to you. I think it's nice to make the creations of the three new variables line up. You can also make the opening and closing brackets on the long `mutate` aligned, or you can do as I have done here and put two closing brackets on the end. The rationale for this is that each of the variable definition lines in the `mutate` ends either with a comma or an extra closing bracket, the latter being on the last line. Your choice here is a matter of taste or (in your working life) the coding norms of the team you're working with.

You may have been offended by the repetition above. It so happens that these columns' names all end in `date` and they are the only ones that do, so we can use a "select helper" to select only them, and then submit all of them to a `mutate` via `mutate_at`, which goes like this:

```
whas %>% mutate_at(vars(ends_with("date")), funs(d = dmy)) %>%
    glimpse()
```

```
## Observations: 500
## Variables: 25
## $ id          <int> 1, 2, 3, 4, 5, 6, 7,...
## $ age         <int> 83, 49, 70, 70, 70, ...
## $ gender      <int> 0, 0, 1, 0, 0, 0, 0,...
## $ hr          <int> 89, 84, 83, 65, 63, ...
## $ sysbp       <int> 152, 120, 147, 123, ...
## $ diasbp      <int> 78, 60, 88, 76, 85, ...
## $ bmi         <dbl> 25.54051, 24.02398, ...
## $ cvd         <int> 1, 1, 0, 1, 1, 1, 1,...
## $ afb         <int> 1, 0, 0, 0, 0, 0, 0,...
## $ sho         <int> 0, 0, 0, 0, 0, 0, 0,...
## $ chf         <int> 0, 0, 0, 1, 0, 0, 0,...
## $ av3         <int> 0, 0, 0, 0, 0, 1, 0,...
## $ miord       <int> 1, 0, 0, 0, 0, 0, 0,...
## $ mitype      <int> 0, 1, 1, 1, 1, 0, 1,...
## $ year        <int> 1, 1, 1, 1, 1, 1, 1,...
## $ admitdate   <chr> "13-01-1997", "19-01...
## $ disdate     <chr> "18-01-1997", "24-01...
## $ fdate       <chr> "31-12-2002", "31-12...
## $ los         <int> 5, 5, 5, 10, 6, 1, 5...
## $ dstat       <int> 0, 0, 0, 0, 0, 1, 0,...
## $ lenfol      <int> 2178, 2172, 2190, 29...
## $ fstat       <int> 0, 0, 0, 1, 0, 1, 0,...
## $ admitdate_d <date> 1997-01-13, 1997-01...
## $ disdate_d   <date> 1997-01-18, 1997-01...
## $ fdate_d     <date> 2002-12-31, 2002-12...
```

One line, as you see, not three. The syntax of this is that we first say which columns we want to mutate. We can use any of the select-helpers for this, including listing the column numbers or names; in this case our date variables all ended with `date`. Then we have to give a function, or more than one function, to mutate them with; in this case we wanted to run all the dates-as-text through `dmy`. Because I said `d=dmy`, it takes the original date variable names, glues an underscore on the end and then the `d` that I said, so we create new variables by those names (at the end of the `glimpse` output). If I had just said `funs(dmy)`, we would have *overwritten* the original values, and `admitdate`, `disdate` and `fdate` would now be `dates`. Losing the original variables would have been OK here, but I wanted to show you how to create new variables.

(c) Create three new variables `diff1, diff2, diff3` that are the numbers of days between each of your dates, and save the data frame in which they have been created. Verify that at least some of them are the same as `los` and `lenfol`.

Solution

I don't know what R's internal storage is for dates (it might be seconds or milliseconds or anything, not necessarily days), so subtracting them requires care; you have to divide by the length of a day (in whatever units), thus:

```
whas3 = whas2 %>% mutate(diff1 = (dis - admit)/ddays(1),
    diff2 = (f - admit)/ddays(1), diff3 = (f -
        dis)/ddays(1))
glimpse(whas3)
```

```
## Observations: 500
## Variables: 28
## $ id        <int> 1, 2, 3, 4, 5, 6, 7, 8...
## $ age       <int> 83, 49, 70, 70, 70, 70...
## $ gender    <int> 0, 0, 1, 0, 0, 0, 0, 0...
## $ hr        <int> 89, 84, 83, 65, 63, 76...
## $ sysbp     <int> 152, 120, 147, 123, 13...
## $ diasbp    <int> 78, 60, 88, 76, 85, 54...
## $ bmi       <dbl> 25.54051, 24.02398, 22...
## $ cvd       <int> 1, 1, 0, 1, 1, 1, 1, 1...
## $ afb       <int> 1, 0, 0, 0, 0, 0, 0, 0...
## $ sho       <int> 0, 0, 0, 0, 0, 0, 0, 0...
## $ chf       <int> 0, 0, 0, 1, 0, 0, 0, 0...
## $ av3       <int> 0, 0, 0, 0, 0, 1, 0, 0...
## $ miord     <int> 1, 0, 0, 0, 0, 0, 0, 0...
## $ mitype    <int> 0, 1, 1, 1, 1, 0, 1, 1...
## $ year      <int> 1, 1, 1, 1, 1, 1, 1, 1...
## $ admitdate <chr> "13-01-1997", "19-01-1...
## $ disdate   <chr> "18-01-1997", "24-01-1...
## $ fdate     <chr> "31-12-2002", "31-12-2...
## $ los       <int> 5, 5, 5, 10, 6, 1, 5, ...
## $ dstat     <int> 0, 0, 0, 0, 0, 1, 0, 0...
## $ lenfol    <int> 2178, 2172, 2190, 297,...
## $ fstat     <int> 0, 0, 0, 1, 0, 1, 0, 1...
## $ admit     <date> 1997-01-13, 1997-01-1...
## $ dis       <date> 1997-01-18, 1997-01-2...
## $ f         <date> 2002-12-31, 2002-12-3...
## $ diff1     <dbl> 5, 5, 5, 10, 6, 1, 5, ...
## $ diff2     <dbl> 2178, 2172, 2190, 297,...
## $ diff3     <dbl> 2173, 2167, 2185, 287,...
```

The extra `d` on the front of `ddays` indicates that these are what is known to `lubridate` as "durations": a period of time 1 day long that could be any day (as opposed to "June 1, 1970" which is 1 day long, but tied to a particular day).

`los` should be the number of days in hospital, what I calculated as `diff1`, and `lenfol` should be the time from being admitted to last followup, which is my `diff2`. My output from `glimpse` confirms that.

Of course, checking that the first few values match is a nice confirmation, but is not actually a *proof*. For that, we should compare all 500 values, and it would be best to do it in such a way that R is comparing all 500 values for us, since it would be a lot more reliable than the human eye. R has a function `all.equal` which does exactly that. By way of warmup:

```
x = 1:4
y = 1:4
z = c(1, 2, 3, 5)
all.equal(x, y)

## [1] TRUE

all.equal(x, z)

## [1] "Mean relative difference: 0.25"
```

I thought the second one was just going to say FALSE, but it gave us a message instead, saying how close x and z were on average, so that we could decide whether they were close enough to call equal, or, as in this case, not.

Anyway:

```
with(whas3, all.equal(lenfol, diff2))

## [1] TRUE

with(whas3, all.equal(los, diff1))

## [1] TRUE
```

so they really are all equal, all 500 of them.

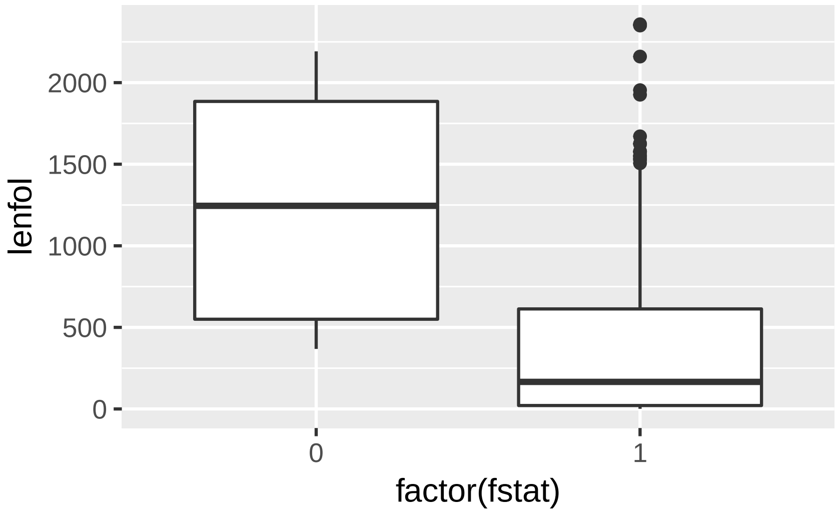
The computer scientists among you will note that I shouldn't have done this, because *diff1* through *diff3* are double-precision decimal numbers, so I should have tested their equality with *lenfol* and *los* by working out the absolute differences and testing whether they were all *small*. On consulting the help for *all.equal*, though, I find that it *does* work properly, because it actually tests whether the things being compared differ by less than a quantity *tolerance* which defaults to 0.000000015, and if they do it calls them equal. This is all tied in with the difference between integers and decimal numbers as they are represented on a computer: exactly and approximately, respectively. A double-precision number has about 16 significant digits of accuracy; equal things won't have all 16 digits equal, most likely, but they would be expected to have at least 8 of those digits the same. CSCA08 stuff, I imagine. This is where you can casually toss around terms like *machine epsilon*. Oh! I just realized something. You know how very very small P-values are shown in R as *<2.2e-16*? *That's* the machine epsilon. Anything smaller than that is indistinguishable from zero, and you can't have a P-value be *exactly* zero. The default *tolerance* I mentioned above is the square root of this, which is normally used for such things.

(d) Construct side-by-side boxplots of the length of followup by each followup status. You'll need to make sure that the followup status, as it gets fed into ggplot, is a factor, or, at least, not the number that it is now.

Solution

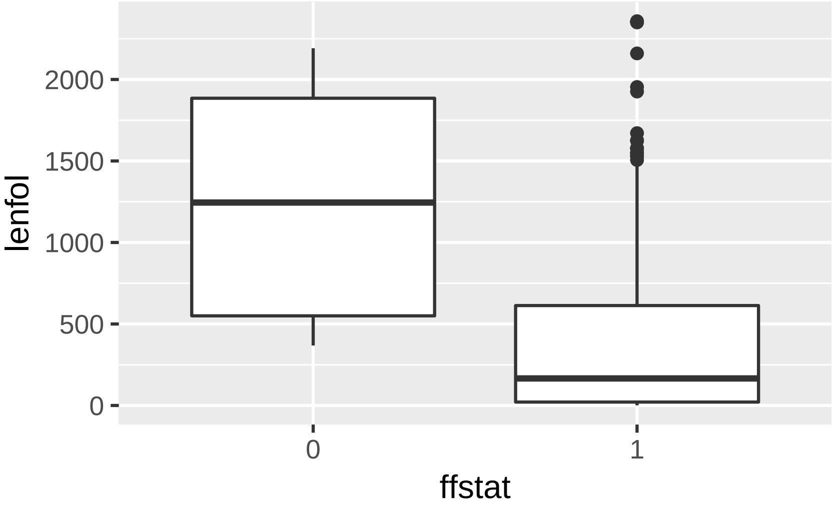
The easiest way to make a factor is to wrap fstat, which is a numeric 0 or 1, in factor():

```
ggplot(whas3, aes(x = factor(fstat), y = lenfol)) +
    geom_boxplot()
```



Or create a factor version of fstat first:

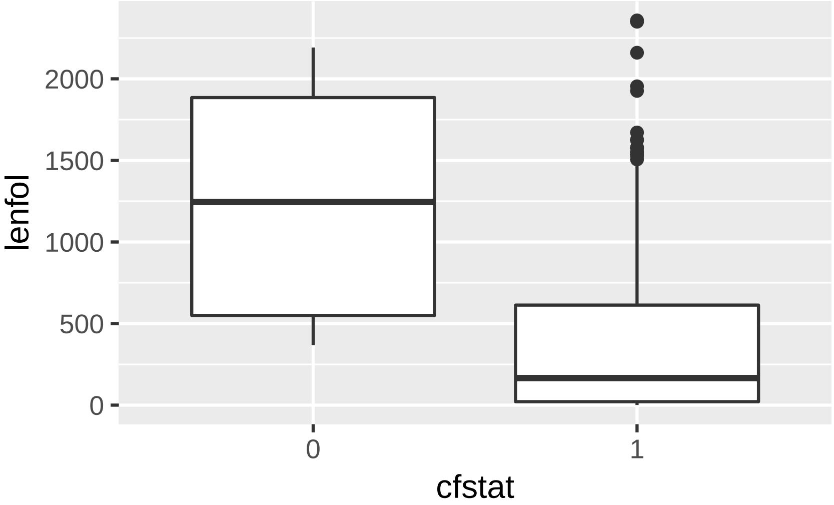
```
whas3 %>% mutate(ffstat = factor(fstat)) %>% ggplot(aes(x = ffstat,
    y = lenfol)) + geom_boxplot()
```



I think the second way looks better, because you get a cleaner *x*-axis on your plot. But if you're doing this for exploration, rather than as something that's going to appear in a report for your boss, the first way is fine.

`ggplot` also treats text stuff as categorical where needed, so this also works:

```
whas3 %>% mutate(cfstat = as.character(fstat)) %>%
    ggplot(aes(x = cfstat, y = lenfol)) + geom_boxplot()
```



14.2 *Growth of Mizuna lettuce seeds*

In 2010, a group of students planted some Mizuna lettuce seeds, and recorded how they grew. The data were saved in an Excel spreadsheet, which is at link. The columns are: the date, the height (in cm) of (I presume) the tallest plant, the amount of water added since the previous date (ml), the temperature in the container where the seedlings were growing, and any additional notes that the students made (edited for length by me). The top line of the data file is variable names.

(a) Read the spreadsheet data.

Solution

This is read_excel from package readxl. I'm not sure what will happen to the dates yet. Note that this needs a "local" copy of the spreadsheet (that is, you have to download it and save it on your computer, then upload it to rstudio.cloud), possibly using file.choose to help R find it. I put my copy in the same project folder as I was working in, so I just need the file name:

```
library(readxl)
mizuna = read_excel("mizuna.xlsx")
mizuna
```

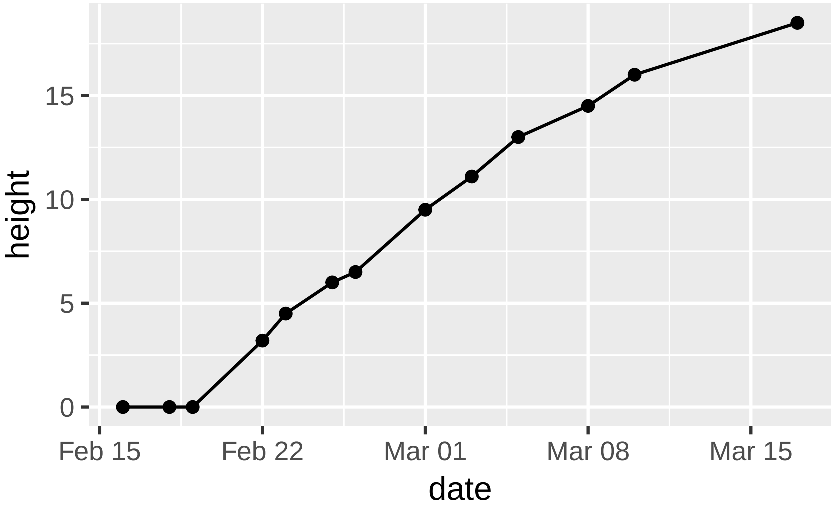
```
## # A tibble: 13 x 5
##    date                height water
##    <dttm>               <dbl> <dbl>
##  1 2010-02-16 00:00:00    0     400
##  2 2010-02-18 00:00:00    0       0
##  3 2010-02-19 00:00:00    0     200
##  4 2010-02-22 00:00:00    3.2   100
##  5 2010-02-23 00:00:00    4.5   100
##  6 2010-02-25 00:00:00    6     100
##  7 2010-02-26 00:00:00    6.5   200
##  8 2010-03-01 00:00:00    9.5   200
##  9 2010-03-03 00:00:00   11.1   200
## 10 2010-03-05 00:00:00   13     250
## 11 2010-03-08 00:00:00   14.5   500
## 12 2010-03-10 00:00:00   16     200
## 13 2010-03-17 00:00:00   18.5   800
## # ... with 2 more variables:
## #   temperature <dbl>, notes <chr>
```

The dates *did* get read properly. dttm is "date-time", so I guess it's allowing for the possibility that my dates had times attached as well. Unlike with SAS (as we see later), the years came out right.

(b) Make a plot of height against your dates, with the points joined by lines.

Solution

```
ggplot(mizuna, aes(x = date, y = height)) + geom_point() +
    geom_line()
```

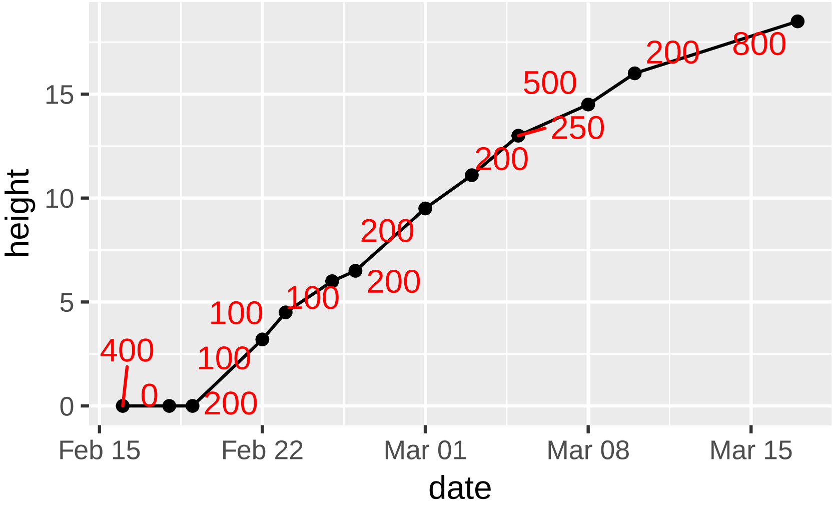


(c) Label each point on the plot with the amount of water added up to that point.

Solution

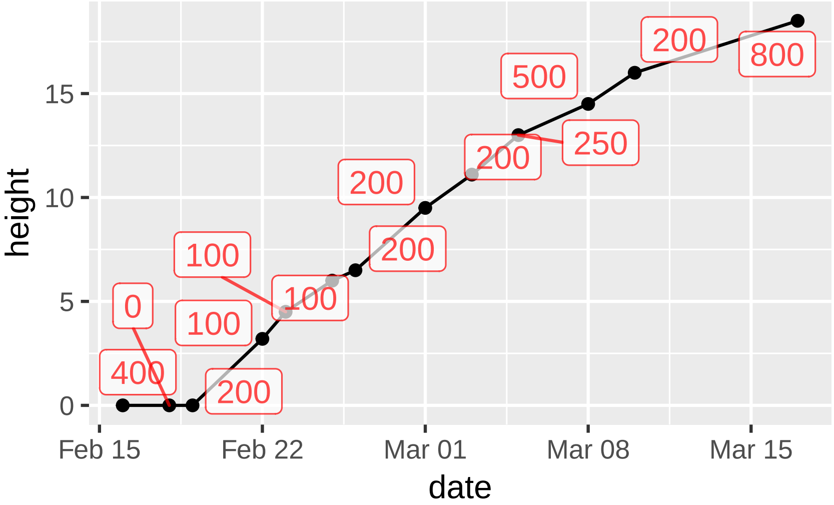
This is `water` again. The way to do this is to load `ggrepel`, then add `geom_text_repel` to the plot, by adding `label=water` to the *original* `aes`:

```
library(ggrepel)
ggplot(mizuna, aes(x = date, y = height, label = water)) +
    geom_point() + geom_line() + geom_text_repel(colour = "red")
```



I made the text red, so that you can see it more easily. It "repels" away from the points, but not from the lines joining them. Which makes me wonder whether this would work better (I explain `alpha` afterwards):

```r
library(ggrepel)
ggplot(mizuna, aes(x = date, y = height, label = water)) +
    geom_point() + geom_line() + geom_label_repel(colour = "red",
    alpha = 0.7)
```



The difference between `text` and `label` is that `text` just uses the text of the variable to mark the point, while `label` puts that text in a box.

I think it works better. You can see where the line goes (under the boxes with the labels in them), but you can see the labels clearly.

What that `alpha` does is to make the thing it's attached to (the labels) partly *transparent*. If you leave it out (try it), the black line disappears completely under the label boxes and you can't see where it goes at all. The value you give for `alpha` says how transparent the thing is, from 1 (not transparent at all) down to 0 (invisible). I first tried 0.3, and you could hardly see the boxes; then I tried 0.7 so that the boxes were a bit more prominent but the lines underneath were still slightly visible, and I decided that this is what I liked. I think making the labels a different colour was a good idea, since that helps to distinguish the number on the label from the line underneath.

You can apply `alpha` to pretty much any `ggplot` thing that might be on top of something else, to make it possible to see what's underneath it. The commonest use for it is if you have a scatterplot with a lot of points; normally, you only see some of the points, because the plot is then a sea of black. But if you make the points partly transparent, you can see more of what's nearby that would otherwise have been hidden.

At some point, I also have to show you folks `jitter`, which plots in slightly different places points that would otherwise overprint each other exactly, and you wouldn't know how many of them there were, like the outliers on the boxplots of German children near the new airport.

14.3 Types of childbirth

Childbirths can be of two types: a "vaginal" birth in which the child is born through the mother's vagina in the normal fashion, and a "cesarean section" where a surgeon cuts through the wall of the mother's abdomen, and the baby is delivered through the incision. Cesarean births are used when there are difficulties in pregnancy or during childbirth that would make a vaginal birth too risky. A hospital kept track of the number of vaginal and Cesarean births for the twelve months of 2012. Of interest is whether the Cesarean rate (the ratio of Cesarean births to all births) was increasing, decreasing or remaining stable over that time. The data may be found at link. The columns are the names of the months (in 2012), the number of cesarean births and the number of vaginal births. (The data are not real, but are typical of the kind of thing you would observe.)

(a) Read the data into R and display your data frame.

Solution
This is a space-delimited text file, which means:

```
my_url = "http://www.utsc.utoronto.ca/~butler/c32/birthtypes.txt"
births = read_delim(my_url, " ")
```

```
## Parsed with column specification:
## cols(
##   month = col_character(),
##   cesarean = col_integer(),
##   vaginal = col_integer()
## )
```

```
births
```

```
## # A tibble: 12 x 3
##    month cesarean vaginal
##    <chr>    <int>   <int>
##  1 Jan         11      68
##  2 Feb          9      63
##  3 Mar         10      72
##  4 Apr         18     105
##  5 May         10      90
##  6 Jun         10      92
##  7 Jul         11      78
##  8 Aug          9      83
##  9 Sep          9      90
## 10 Oct         15     101
## 11 Nov         12     130
## 12 Dec          8     101
```

Some text and two numbers for each month. Check.

(b) Create a column of actual dates and also a column of cesarean rates, as defined above. Store your new data frame in a variable and display it. For the dates, assume that each date is of the 1st of the month that it belongs to.

Solution

The easiest way is to use `str_c` or `paste` to create a text date with year, month and day in some order, and then to use the appropriate function from `lubridate` to turn that into an actual `date`. If you use `str_c`, you (probably) need the `sep` thing to make sure the values get a space between them; `paste` does this automatically. (The next question is whether `ymd` or whatever can cope without spaces, but I'm not exploring that.) The cesarean rate is `cesarean` divided by `cesarean` plus `vaginal`:

```
library(lubridate)
b2 = births %>% mutate(datestr = str_c("2012",
    month, "1", sep = " ")) %>% mutate(thedate = ymd(datestr)) %>%
    mutate(cesarean_rate = cesarean/(cesarean +
        vaginal))
b2
```

```
## # A tibble: 12 x 6
##    month cesarean vaginal datestr thedate
##    <chr>    <int>   <int> <chr>   <date>
##  1 Jan         11      68 2012 J~ 2012-01-01
##  2 Feb          9      63 2012 F~ 2012-02-01
##  3 Mar         10      72 2012 M~ 2012-03-01
##  4 Apr         18     105 2012 A~ 2012-04-01
##  5 May         10      90 2012 M~ 2012-05-01
##  6 Jun         10      92 2012 J~ 2012-06-01
##  7 Jul         11      78 2012 J~ 2012-07-01
##  8 Aug          9      83 2012 A~ 2012-08-01
##  9 Sep          9      90 2012 S~ 2012-09-01
## 10 Oct         15     101 2012 O~ 2012-10-01
## 11 Nov         12     130 2012 N~ 2012-11-01
## 12 Dec          8     101 2012 D~ 2012-12-01
## # ... with 1 more variable:
## #   cesarean_rate <dbl>
```

If you don't like that, create columns that contain 2012 and 1 all the way down. If you set a column name equal to a single value, that single value gets repeated the right number of times:

This is an example of R's so-called *recycling rules*.

```
births %>% mutate(year = 2012, day = 1)
```

```
## # A tibble: 12 x 5
##    month cesarean vaginal  year   day
##    <chr>    <int>   <int> <dbl> <dbl>
##  1 Jan         11      68  2012     1
##  2 Feb          9      63  2012     1
##  3 Mar         10      72  2012     1
##  4 Apr         18     105  2012     1
##  5 May         10      90  2012     1
##  6 Jun         10      92  2012     1
##  7 Jul         11      78  2012     1
##  8 Aug          9      83  2012     1
##  9 Sep          9      90  2012     1
## 10 Oct         15     101  2012     1
## 11 Nov         12     130  2012     1
## 12 Dec          8     101  2012     1
```

and then use `unite` as in class. The distinction is that `unite` *only* works on columns. It also "swallows up" the columns that it is made out of; in this case, the original year, month and day disappear:

```
b3 = births %>% mutate(year = 2012, day = 1) %>%
    unite(datestr, year, month, day) %>% mutate(thedate = ymd(datestr)) %>%
    mutate(cesarean_rate = cesarean/(cesarean +
        vaginal))
b3
```

```
## # A tibble: 12 x 5
##    datestr cesarean vaginal thedate
##    <chr>      <int>   <int> <date>
##  1 2012_J~       11      68 2012-01-01
##  2 2012_F~        9      63 2012-02-01
##  3 2012_M~       10      72 2012-03-01
##  4 2012_A~       18     105 2012-04-01
##  5 2012_M~       10      90 2012-05-01
##  6 2012_J~       10      92 2012-06-01
##  7 2012_J~       11      78 2012-07-01
##  8 2012_A~        9      83 2012-08-01
##  9 2012_S~        9      90 2012-09-01
## 10 2012_O~       15     101 2012-10-01
## 11 2012_N~       12     130 2012-11-01
## 12 2012_D~        8     101 2012-12-01
## # ... with 1 more variable:
## #   cesarean_rate <dbl>
```

I don't mind which order you glue your year, month and day together, as long as you construct the dates with the consistent `lubridate` function.

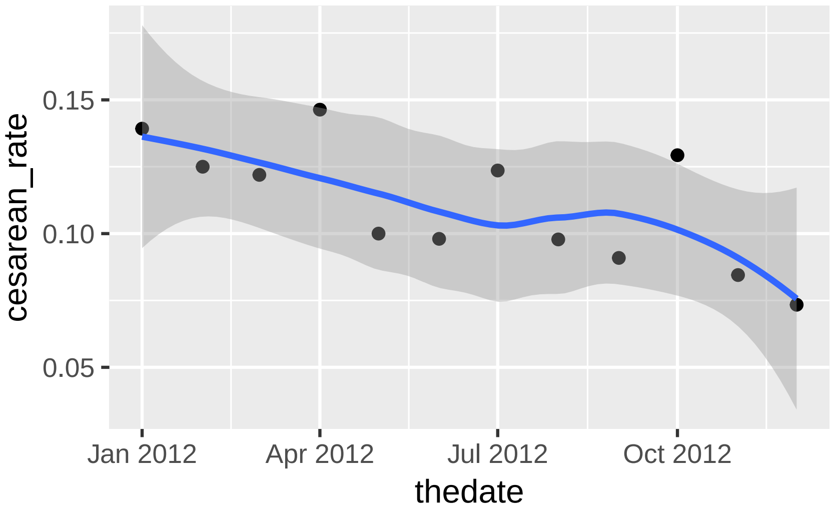
(c) Plot the cesarean rate against time, with a smooth trend. Do you see an upward trend, a downward trend, no trend, or something else?

Solution

This is a scatterplot with time on the x axis:

```
ggplot(b2, aes(x = thedate, y = cesarean_rate)) +
    geom_point() + geom_smooth()
```

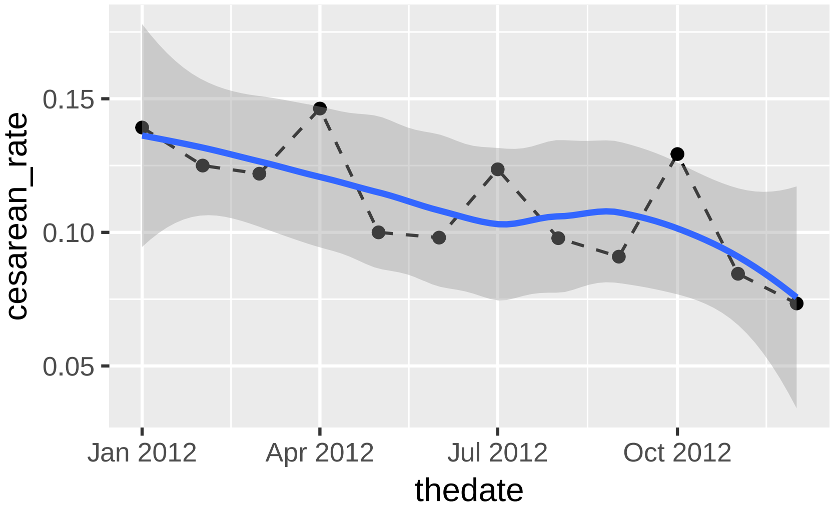
```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



I like this better than joining the points by lines, since we already have a trend on the plot, but you can do that in some contrasting way:

```
ggplot(b2, aes(x = thedate, y = cesarean_rate)) +
    geom_point() + geom_line(linetype = "dashed") +
    geom_smooth()
```

```
## 'geom_smooth()' using method = 'loess' and formula 'y ~ x'
```



I see a downward trend. ("A downward trend with a wiggle" if you like.) I didn't ask for any explanation. There is a certain unevenness in the trend of the actual data, but the overall picture appears to be downhill.

(d) Try to summarize the trend you just found with a correlation. What goes wrong? How can you fix it?

Solution
Something like this is the obvious guess:

```
with(b2, cor(thedate, cesarean_rate))
```

```
## Error in cor(thedate, cesarean_rate): 'x' must be numeric
```

This fails because `thedate` is not of itself a number. But lurking in the background is how the date is actually *represented*: as a number of days since Jan 1, 1970. Thus, passing it through `as.numeric` might turn it into that:

```
b5 <- b2 %>% mutate(numeric_date = as.numeric(thedate))
b5
```

```
## # A tibble: 12 x 7
##    month cesarean vaginal datestr thedate
##    <chr>    <int>   <int> <chr>   <date>
##  1 Jan         11      68 2012 J~ 2012-01-01
##  2 Feb          9      63 2012 F~ 2012-02-01
##  3 Mar         10      72 2012 M~ 2012-03-01
##  4 Apr         18     105 2012 A~ 2012-04-01
##  5 May         10      90 2012 M~ 2012-05-01
##  6 Jun         10      92 2012 J~ 2012-06-01
##  7 Jul         11      78 2012 J~ 2012-07-01
##  8 Aug          9      83 2012 A~ 2012-08-01
##  9 Sep          9      90 2012 S~ 2012-09-01
## 10 Oct         15     101 2012 O~ 2012-10-01
## 11 Nov         12     130 2012 N~ 2012-11-01
## 12 Dec          8     101 2012 D~ 2012-12-01
## # ... with 2 more variables:
## #   cesarean_rate <dbl>, numeric_date <dbl>
```

A little mental calculation suggests that these dates in 2012 are a bit over 40 years, that is $40 \times 365 \simeq 14000$ days, since the "zero" date of Jan 1, 1970, and so it turns out. This suggests that we can calculate a correlation with the numeric dates:

```
with(b5, cor(numeric_date, cesarean_rate))
```

```
## [1] -0.7091219
```

and we can make a test of the null hypothesis that the correlation is zero (against a two-sided alternative) thus:

```
with(b5, cor.test(numeric_date, cesarean_rate))
```

```
##
##  Pearson's product-moment correlation
##
## data:  numeric_date and cesarean_rate
## t = -3.1804, df = 10, p-value =
## 0.009813
## alternative hypothesis: true correlation is not equal to 0
## 95 percent confidence interval:
##  -0.9119078 -0.2280145
## sample estimates:
##       cor
## -0.7091219
```

That downward trend is more than just chance, with a P-value just under 0.01. Having said that, though, if you look at the confidence interval for the correlation, it includes almost all the negative values it could be, so that with only 12 observations we really know very little about the correlation other than that it appears to be negative.

Extra: In practice, you would typically have a much longer time series of measurements than this, such as monthly measurements for several years. In looking at only one year, like we did here, we could get trapped by seasonal effects: for example, cesarean rates might always go down through the year and then jump up again in January. Looking at several years would enable us to disentangle seasonal effects that happen every year from long-term trends. (As an example of this, think of Toronto snowfall: there is almost always snow in the winter and there is never snow in the summer, a seasonal effect, but in assessing climate change, you want to think about long-term trends in snowfall, after allowing for which month you're looking at.)

14.4 Wolves and caribou

In Denali National Park, Alaska, the size of the wolf population depends on the size of the caribou population (since wolves hunt and kill caribou). This is a large national park, so caribou are found in very large herds, so big, in fact, that the well-being of the entire herd is not threatened by wolf attacks. Can the size of the caribou population be used to predict the size of the wolf population? The data can be found at link. The columns are: the date of the survey, the name of the park employee in charge of the survey, the caribou population (in hundreds) and the wolf population (actual count).

In fact, it is believed that wolves help keep caribou herds strong by preventing over-population: that is, the weakest caribou are the ones taken by wolves.

The survey is always taken in the fall, but the date varies.

Counting animals in a region, especially rare, hard-to-find animals, is a whole science in itself. These numbers are probably estimates (with some uncertainty).

(a) Take a look at the data file. How would you describe its format? Read it into R, and check that you got something sensible.

Solution

This looks at first sight as if it's separated by spaces, but most of the data values are separated by *more than one* space. If you look further, you'll see that the values are *lined up in columns*, with the variable names aligned at the top. This is exactly the kind of thing that `read_table` will read. We start with the usual `library(tidyverse)`:

```
library(tidyverse)
my_url = "http://www.utsc.utoronto.ca/~butler/c32/caribou.txt"
denali = read_table(my_url)
```

```
## Parsed with column specification:
## cols(
##   date = col_character(),
##   name = col_character(),
##   caribou = col_integer(),
##   wolf = col_integer()
## )
```

```
denali
```

```
## # A tibble: 7 x 4
##   date       name          caribou  wolf
##   <chr>      <chr>           <int> <int>
## 1 09/01/1995 David S.           30    66
## 2 09/24/1996 Youngjin K.        34    79
## 3 10/03/1997 Srinivasan M.      27    70
## 4 09/15/1998 Lee Anne J.        25    60
## 5 09/08/1999 Stephanie T.       17    48
## 6 09/03/2000 Angus Mc D.        23    55
## 7 10/06/2001 David S.           20    60
```

That worked: four columns with the right names, and the counts of caribou and wolf are numbers. There are only seven years of surveys; in real-life data you would have more. But the point here is working with dates.

The only (small) weirdness is that the dates are text rather than having been converted into dates. This is because they are not year-month-day, which is the only format that gets automatically converted into dates when read in. (You could use `mdy` from `lubridate` to make them dates.)

Extra: you might have wondered how the names survived, even though they have spaces in them, sometimes more than one. Here's how the file looks:

```
date       name             caribou wolf
09/01/1995 David S.         30       66
09/24/1996 Youngjin K.      34       79
10/03/1997 Srinivasan M.    27       70
09/15/1998 Lee Anne J.      25       60
09/08/1999 Stephanie T.     17       48
09/03/2000 Angus Mc D.      23       55
10/06/2001 David S.         20       60
```

What `read_table` looks for is columns that contain spaces *all the way down*, and separates the values there. For example, between the year of`date` and the first name in `name` there is a space all the way down. After the names and before the caribou counts there are several spaces, and there is one space between the words `caribou` and `wolf` in the header line that goes all the way down. Thus four columns, `date`, `name`, `caribou` and `wolf`. This means that the spaces within the names don't cause any problems at all, since the spaces aren't in the same place in *every* line.

The only way this would fail is if *every* first name had the same number of letters in it; then the space between first name and initial of last name *would* be in the same place in every line.

(b) Create a new data frame where the column labelled `date` is now a genuine R `Date`, using something from `lubridate`.

Solution

What you do is to look at the format of the dates as they are now. They appear to be month-day-year, American style.

Not a surprise since Denali National Park is in Alaska.

Thus the function needed is mdy. It doesn't matter whether the months are names or numbers:

```
denali <- denali %>% mutate(date = mdy(date))
denali
```

```
## # A tibble: 7 x 4
##   date       name           caribou  wolf
##   <date>     <chr>            <int> <int>
## 1 1995-09-01 David S.            30    66
## 2 1996-09-24 Youngjin K.         34    79
## 3 1997-10-03 Srinivasan M.       27    70
## 4 1998-09-15 Lee Anne J.         25    60
## 5 1999-09-08 Stephanie T.        17    48
## 6 2000-09-03 Angus Mc D.         23    55
## 7 2001-10-06 David S.            20    60
```

I lived on the edge and overwrote both my column and the whole data frame.

It's actually not *really* living on the edge, because if it doesn't work, you go back and read the data in from the file again.

The dates are displayed in ISO format, year-month-day. You see at the top of the column that they now really *are* dates, not just pieces of text that look like dates.

(c) Create new columns containing the days of the week and the month names for the dates.

Solution

This involves digging in the lubridate help to find out how to extract things from a date. It turns out that wday extracts the day of the week from a date, by default as a number, and month gets the month, also by default as a number:

```
denali %>% mutate(mon = month(date), wd = wday(date))
```

```
## # A tibble: 7 x 6
##   date       name  caribou  wolf   mon    wd
##   <date>     <chr>   <int> <int> <dbl> <dbl>
## 1 1995-09-01 Davi~      30    66     9     6
## 2 1996-09-24 Youn~      34    79     9     3
## 3 1997-10-03 Srin~      27    70    10     6
## 4 1998-09-15 Lee ~      25    60     9     3
## 5 1999-09-08 Step~      17    48     9     4
## 6 2000-09-03 Angu~      23    55     9     1
## 7 2001-10-06 Davi~      20    60    10     7
```

This is not what we wanted, though; we wanted the names of the months and of the days. To fix that, add label=T to both functions:

```
denali %>% mutate(mon = month(date, label = T),
    wd = wday(date, label = T))
```

```
## # A tibble: 7 x 6
##   date       name  caribou  wolf mon   wd
##   <date>     <chr>   <int> <int> <ord> <ord>
## 1 1995-09-01 Davi~      30    66 Sep   Fri
## 2 1996-09-24 Youn~      34    79 Sep   Tue
## 3 1997-10-03 Srin~      27    70 Oct   Fri
## 4 1998-09-15 Lee ~      25    60 Sep   Tue
## 5 1999-09-08 Step~      17    48 Sep   Wed
## 6 2000-09-03 Angu~      23    55 Sep   Sun
## 7 2001-10-06 Davi~      20    60 Oct   Sat
```

and that cracks it.

No need to save this data frame anywhere, since we're not using any of this later.

Extra: the ord means "ordered factor", which makes sense since these are categorical variables with a natural order. This means that you could do something like counting the number of surveys in each month like this:

```
denali %>% mutate(mon = month(date, label = T),
    wd = wday(date, label = T)) %>% count(mon)
```

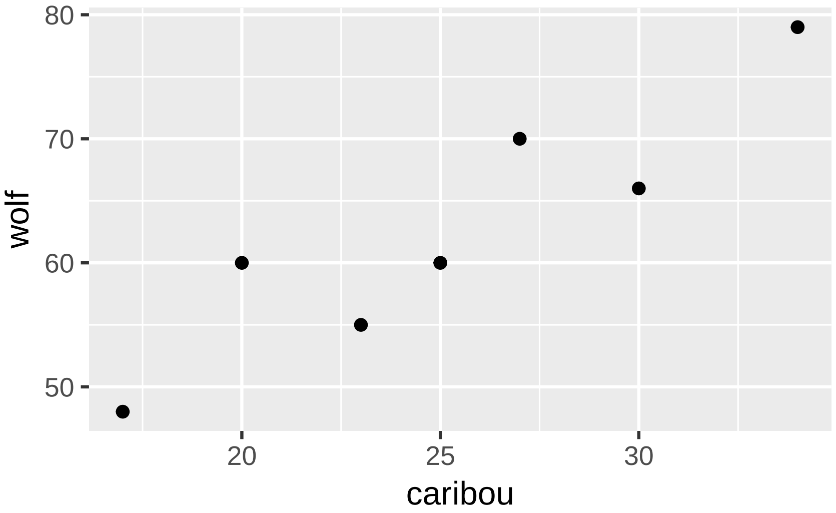
```
## # A tibble: 2 x 2
##   mon       n
##   <ord> <int>
## 1 Sep       5
## 2 Oct       2
```

(d)??part:scatter?? Enough playing around with dates. Make a scatterplot of caribou population (explanatory) against wolf population (response). Do you see any relationship?

Solution

Nothing terribly surprising here:

```
ggplot(denali, aes(x = caribou, y = wolf)) + geom_point()
```

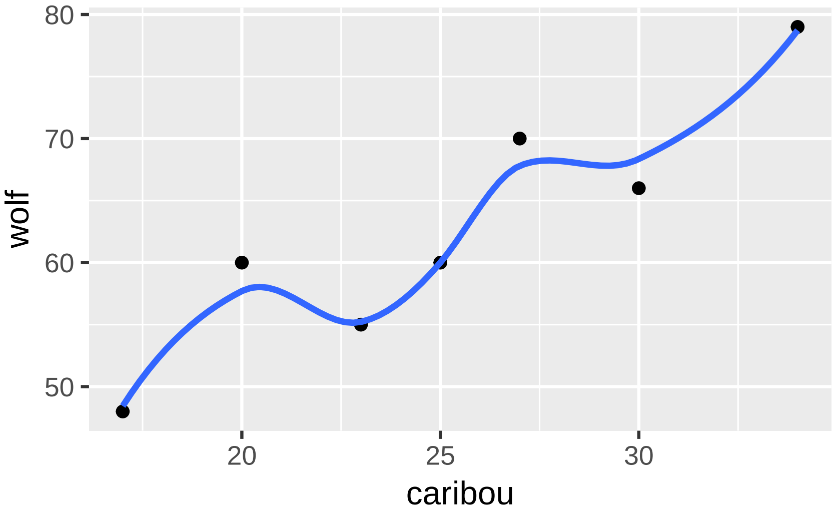


If you like, add a smooth trend to it:

This wiggles more than I would like, with such a small number of observations. Try putting someting like *span=2* in the smooth to make it less wiggly.

```
ggplot(denali, aes(x = caribou, y = wolf)) + geom_point() +
    geom_smooth(se = F)
```

```
## ‘geom_smooth()‘ using method = ’loess’ and formula ’y ~ x’
```



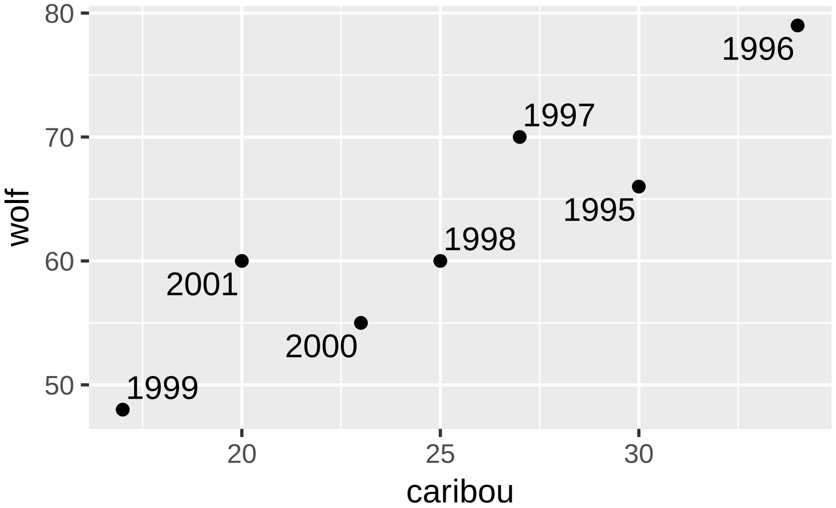
This is an upward trend: when one population is large, the other one is large too. This is typical for predator-prey relationships: when there is more to eat (more caribou) the wolf population goes up, and when less, it goes down.

(e) On your plot from the previous part, label each point with the year it belongs to. You can do this in two steps: first make a new column containing just the years, and then use it as labels for the points on the plot.

Solution

I'm going to use geom_text_repel for the labels from package ggrepel. The year values are gotten using the lubridate function year:

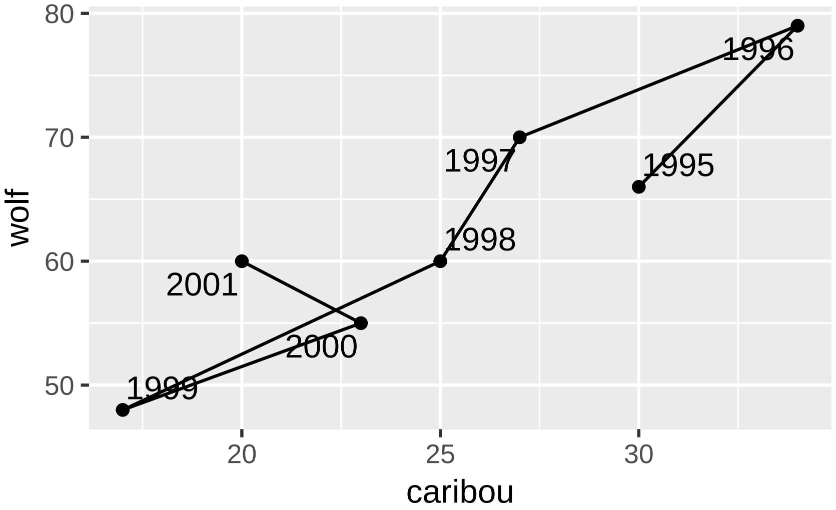
```
denali %>% mutate(year = year(date)) %>% ggplot(aes(x = caribou,
    y = wolf, label = year)) + geom_point() +
    geom_text_repel()
```



I thought about joining up the points in year order. This is actually *not* geom_line as you would have guessed, since what that does is to join points in the order of the variable on the *x*-axis. To join points in the order that they are in the data (what we want here, because the points are in time order in the data), use instead geom_path:

I have to say that I didn't know that until just now.

```
denali %>% mutate(year = year(date)) %>% ggplot(aes(x = caribou,
    y = wolf, label = year)) + geom_point() +
    geom_text_repel() + geom_path()
```



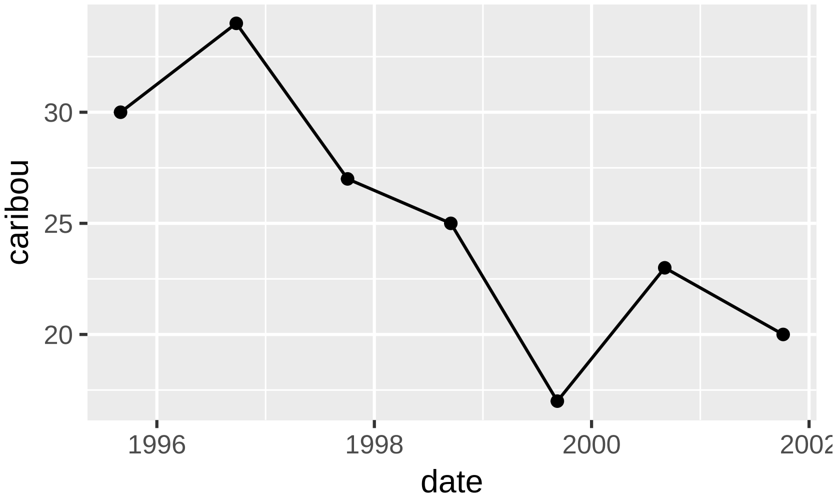
In 1996, both populations were large, and both showed a steady decline until 1999. In 2000 and 2001, both populations seemed to be on the way up again, and you can imagine that in a couple of years, things would go back to about where they were in 1995.

(f) Make a plot of caribou population against time (this is done the obvious way). What seems to be happening to the caribou population over time?

Solution

Make a scatterplot, with the survey date as explanatory variable, and caribou population as response (since time always goes on the *x*-axis):

```
ggplot(denali, aes(x = date, y = caribou)) + geom_point() +
    geom_line()
```



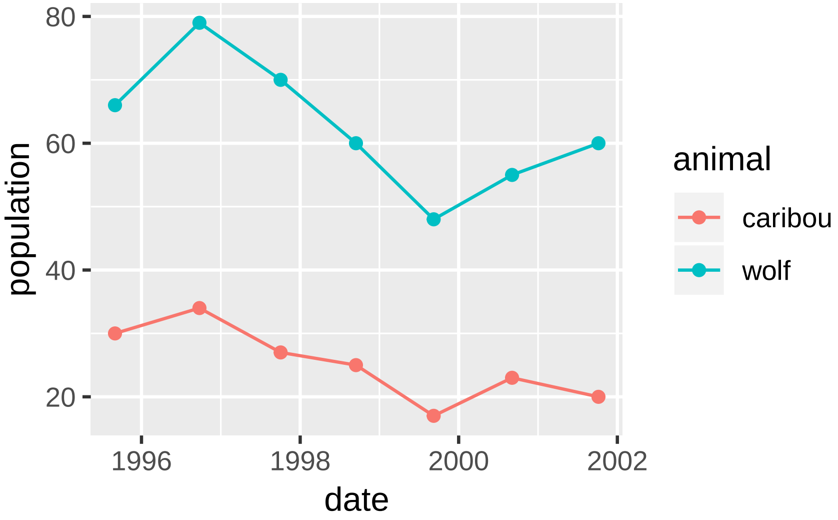
I used an ordinary `geom_line` this time, to connect neighbouring years, as is often done with a time series. The overall trend is downward, though the 1999 value might be a low from which the population is recovering.

(g) The caribou and wolf populations over time are really “time series”. See if you can make a plot of *both* the caribou and wolf populations against time. You can make two *y*-axes, one for caribou and one for wolf; this will probably require some research on your part to figure out.

Solution

The obvious starting point is to note that both the `caribou` and `wolf` columns are animal populations, just of different animals. One way of plotting both populations is to `gather` them up into one column, and then plot them against time, with the two animals distinguished by colour:

```
denali %>% gather(animal, population, caribou:wolf) %>%
    ggplot(aes(x = date, y = population, colour = animal)) +
    geom_point() + geom_line()
```



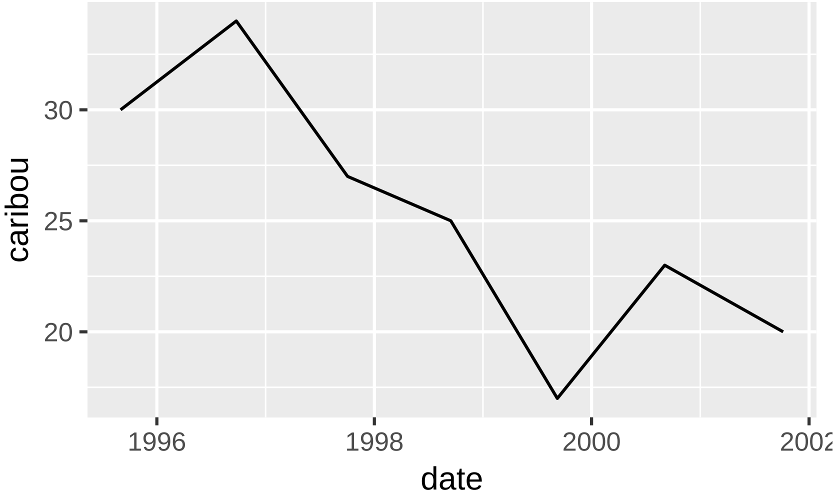
This is not quite the story, though, because the caribou and wolf populations are on different scales. The caribou population is numbered in hundreds, while the wolf population is an actual count.

The surveys are late in the year, so the one that is nearly in 1996 is actually the 1995 survey.

What would be nice would be to have a secondary *y*-axis, so that there were two *y*-scales, one for each animal. This is very easy to manipulate, though (you can change either scale and get a very different-looking graph), so we ought to be careful.

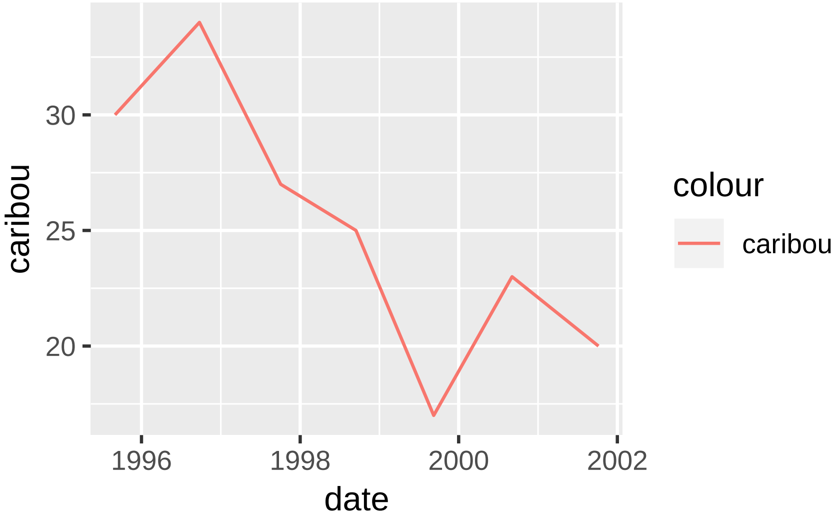
All right, so let's put the caribou on the left:

```
ggplot(denali, aes(x = date, y = caribou)) + geom_line()
```



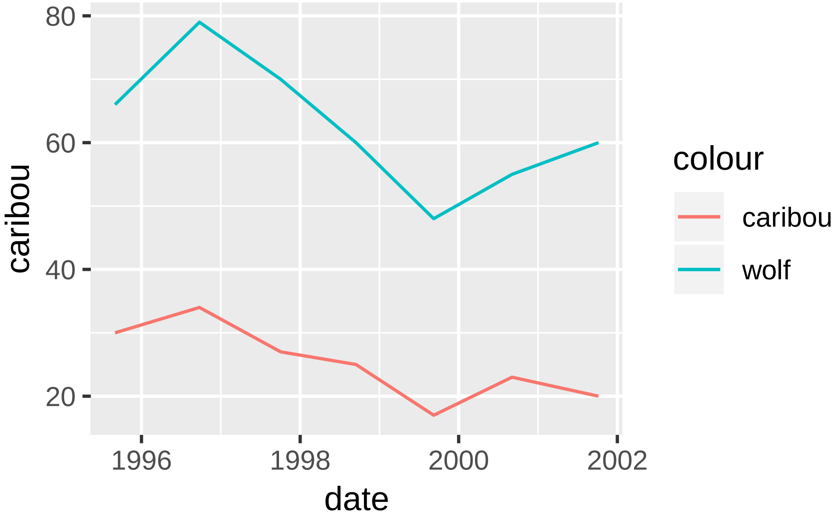
Or we can add a `colour` aesthetic to distinguish the caribou from the wolf populations, that we're going to add in a moment. This looks rather odd at first:

```
ggplot(denali, aes(x = date, y = caribou, colour = "caribou")) +
    geom_line()
```



Now we think about adding the wolf numbers. This is done by adding a second `geom_line`, overriding the `y` and the `colour` to specify that this is wolf now:

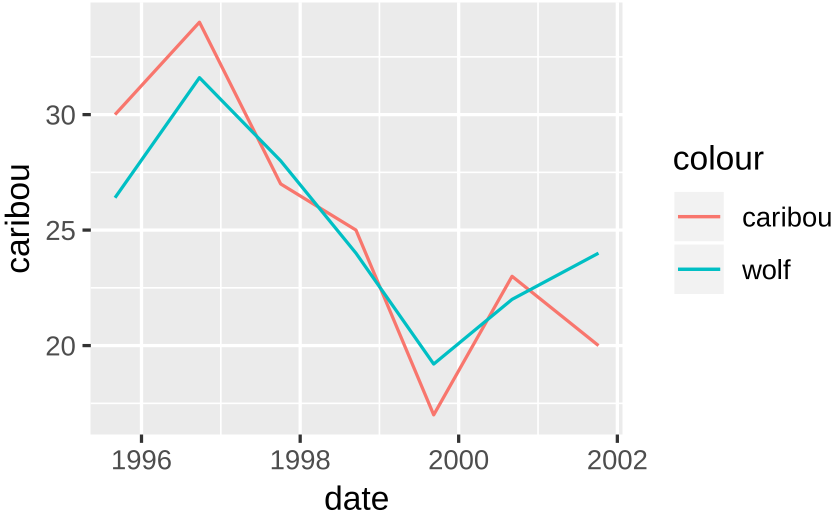
```
ggplot(denali, aes(x = date, y = caribou, colour = "caribou")) +
    geom_line() + geom_line(aes(y = wolf, colour = "wolf"))
```



What has happened is that we get lines of different colour for each animal, with a legend. So far so good. The problem is that the wolf numbers are about 2.5 times bigger than the caribou numbers, so that we don't get a good sense of how they go up and down together. If we divided the wolf numbers by 2.5, we would see this better:

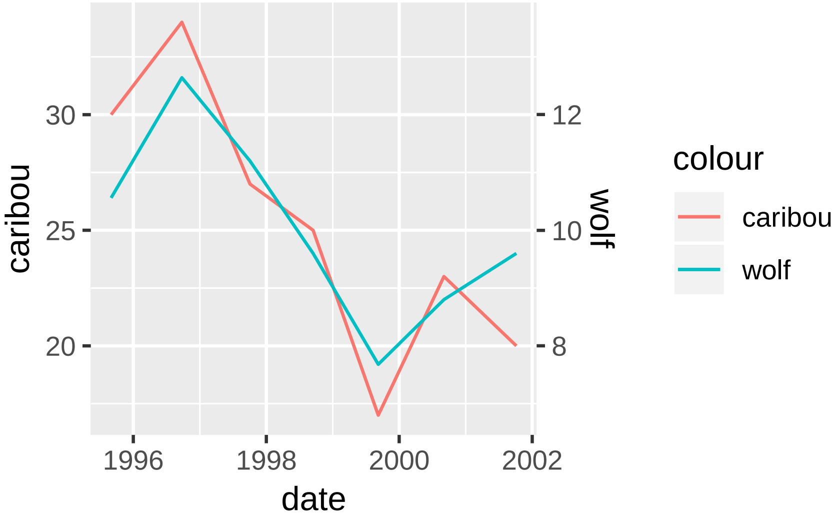
Which means, if you stop to think about it, that there are *actually* about 40 times more caribou than wolves.

```
ggplot(denali, aes(x = date, y = caribou, colour = "caribou")) +
    geom_line() + geom_line(aes(y = wolf/2.5,
    colour = "wolf"))
```



Now we get to the secondary *y*-axis. We want to label this `wolf` and have it reflect that we actually made the graph by dividing the wolf values by 2.5:

```
ggplot(denali, aes(x = date, y = caribou, colour = "caribou")) +
    geom_line() + geom_line(aes(y = wolf/2.5,
    colour = "wolf")) + scale_y_continuous(sec.axis = sec_axis(~./2.5,
    name = "wolf"))
```



Woo, and, very possibly, hoo. I got most of these ideas from link.

Now we see how the populations vary over time, and also that they vary together.

This is about the only double-*y*-axis setup that I like, with scales chosen so that both the series vary about the same amount. By "discreetly" changing the wolf scale, you could make it look as if one population was much bigger than the other, or varied much more than the other. Lies and statistics.

In my opinion, too many people just plot series against time, possibly with a second y-axis. . Variables that vary together, like the wolf and caribou populations here, ought to be plotted *against each other* on a scatterplot, possibly with the time points labelled.

And all too often with Excel (spit)

The ambitious among you may like to compare the graphs here with other predator-prey relationships. If you are of a mathematical bent, you might look into the Lotka-Volterra equations, which is a system of two differential equations describing how changes in one population cause changes in the other population.

15
Functions

```
library(tidyverse)
```

```
## -- Attaching packages ---- tidyverse 1.2.1 --
```

```
## v ggplot2 3.0.0     v purrr   0.2.5
## v tibble  1.4.2     v dplyr   0.7.6
## v tidyr   0.8.1     v stringr 1.3.1
## v readr   1.1.1     v forcats 0.3.0
```

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

15.1 Making some R functions

Let's write some simple R functions to convert temperatures, and later to play with text.

(a) A temperature in Celsius is converted to one in Kelvin by adding 273.15. (A temperature of −273.15 Celsius, 0 Kelvin, is the "absolute zero" temperature that nothing can be colder than.) Write a function called `c_to_k` that converts an input Celsius temperature to one in Kelvin, and test that it works.

Solution

This is mostly an exercise in structuring your function correctly. Let's call the input `C` (uppercase C, since lowercase c has a special meaning to R):

```
c_to_k = function(C) {
    C + 273.15
}
c_to_k(0)
```

```
## [1] 273.15
```

```
c_to_k(20)
```

```
## [1] 293.15
```

This is the simplest way to do it: the last line of the function, if calculated but not saved, is the value that gets returned to the outside world. The checks suggest that it worked.

If you're used to Python or similar, you might prefer to calculate the value to be returned and then return it. You can do that in R too:

```
c_to_k = function(C) {
    K = C + 273.15
    return(K)
}
c_to_k(0)
```

```
## [1] 273.15
```

```
c_to_k(20)
```

```
## [1] 293.15
```

That works just as well, and for the rest of this question, you can go either way.

R style is to use the last line of the function for the return value, unless you are jumping out of the function before the end, in which case use *return*.

(b) Write a function to convert a Fahrenheit temperature to Celsius. The way you do that is to subtract 32 and then multiply by 5/9.

Solution

On the model of the previous one, we should call this `f_to_c`. I'm going to return the last line, but you can save the calculated value and return that instead:

```
f_to_c = function(F) {
    (F - 32) * 5/9
}
f_to_c(32)
```

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

```
f_to_c(50)
```

```
## [1] 10
```

```
f_to_c(68)
```

```
## [1] 20
```

Americans are very good at saying things like "temperatures in the 50s", which don't mean much to me, so I like to have benchmarks to work with: these are the Fahrenheit versions of 0, 10, and 20 Celsius.

Thus "in the 50s" means "between about 10 and 15 Celsius".

(c) *Using the functions you already wrote*, write a function to convert an input Fahrenheit temperature to Kelvin.

Solution

This implies that you can piggy-back on the functions you just wrote, which goes as below. First you convert the Fahrenheit to Celsius, and then you convert *that* to Kelvin. (This is less error-prone than trying to use algebra to get a formula for this conversion and then implementing that):

```
f_to_k = function(F) {
    C = f_to_c(F)
    K = c_to_k(C)
    return(K)
}
f_to_k(32)
```

```
## [1] 273.15
```

```
f_to_k(68)
```

```
## [1] 293.15
```

These check because in Celsius they are 0 and 20 and we found the Kelvin equivalents of those to be these values earlier.

I wrote this one with a `return` because I thought it made the structure clearer: run one function, save the result, run another function, save the result, then return what you've got.

(d) Rewrite your Fahrenheit-to-Celsius convertor to take a suitable default value and check that it works as a default.

Solution

You can choose any default you like. I'll take a default of 68 (what I would call "a nice day"):

```
f_to_c = function(F = 68) {
    (F - 32) * 5/9
}
f_to_c(68)
```

```
## [1] 20
```

```
f_to_c()
```

```
## [1] 20
```

The change is in the top line of the function. You see the result: if we run it without an input, we get the same answer as if the input had been 68.

(e) What happens if you feed your Fahrenheit-to-Celsius convertor a *vector* of Fahrenheit temperatures? What if you use it in a `mutate`?

Solution
Try it and see:

```
temps = seq(30, 80, 10)
temps
```

```
## [1] 30 40 50 60 70 80
```

```
f_to_c(temps)
```

```
## [1] -1.111111  4.444444 10.000000 15.555556
## [5] 21.111111 26.666667
```

Each of the Fahrenheit temperatures gets converted into a Celsius one. This is perhaps more useful in a data frame, thus:

```
tibble(temps = seq(30, 80, 10)) %>% mutate(celsius = f_to_c(temps))
```

```
## # A tibble: 6 x 2
##   temps celsius
##   <dbl>   <dbl>
## 1    30   -1.11
## 2    40    4.44
## 3    50   10
## 4    60   15.6
## 5    70   21.1
## 6    80   26.7
```

All the temperatures are side-by-side with their equivalents.
Here's another way to do the above:

```
temps = seq(30, 80, 10)
temps %>% enframe(value = "fahrenheit") %>% mutate(celsius = f_to_c(temps))
```

```
## # A tibble: 6 x 3
##    name fahrenheit celsius
##   <int>      <dbl>   <dbl>
## 1     1         30   -1.11
## 2     2          40    4.44
## 3     3          50   10
## 4     4          60   15.6
## 5     5          70   21.1
## 6     6          80   26.7
```

enframe creates a two-column data frame out of a vector (like temps). A vector can have "names", in which case they'll be used as the name column; the values will go in a column called value unless you rename it, as I did.

(f) Write another function called wrap that takes two arguments: a piece of text called text, which defaults to hello, and another piece of text called outside, which defaults to *. The function returns text with the text outside placed before and after, so that calling the function with the defaults should return *hello*. To do this, you can use str_c from stringr (loaded with the tidyverse) which places its text arguments side by side and glues them together into one piece of text. Test your function briefly.

Solution
This:

```
wrap = function(text = "hello", outside = "*") {
    str_c(outside, text, outside)
}
```

I can run this with the defaults:

```
wrap()
```

```
## [1] "*hello*"
```

or with text of my choosing:

```
wrap("goodbye", "_")
```

```
## [1] "_goodbye_"
```

I think that's what I meant by "test briefly".

(g) What happens if you want to change the default outside but use the default for text? How do you make sure that happens? Explore.

Solution
The obvious thing is this, which doesn't work:

```
wrap("!")
```

```
## [1] "*!*"
```

This takes `text` to be `!`, and `outside` to be the default. How do we get `outside` to be `!` instead? The key is to specify the input by name:

```
wrap(outside = "!")
```

```
## [1] "!hello!"
```

This correctly uses the default for `text`.

If you specify inputs without names, they are taken to be in the order that they appear in the function definition. As soon as they get out of order, which typically happens by using the default for something early in the list, as we did here for `text`, you have to specify names for anything that comes after that. These are the names you put on the function's top line.

You can always use names:

```
wrap(text = "thing", outside = "**")
```

```
## [1] "**thing**"
```

and if you use names, they don't even have to be in order:

```
wrap(outside = "!?", text = "fred")
```

```
## [1] "!?fred!?"
```

(h) What happens if you feed your function `wrap` a vector for either of its arguments? What about if you use it in a `mutate`?

Solution

Let's try:

```
mytext = c("a", "b", "c")
wrap(text = mytext)
```

```
## [1] "*a*" "*b*" "*c*"
```

```
myout = c("*", "!")
wrap(outside = myout)
```

```
## [1] "*hello*" "!hello!"
```

If one of the inputs is a vector, the other one gets "recycled" as many times as the vector is long. What if they're both vectors?

```
mytext2 = c("a", "b", "c", "d")
wrap(mytext2, myout)
```

```
## [1] "*a*" "!b!" "*c*" "!d!"
```

This uses the two inputs in parallel, repeating the short one as needed. But this, though it works, gives a warning:

```
wrap(mytext, myout)
```

```
## Warning in stri_c(..., sep = sep, collapse =
## collapse, ignore_null = TRUE): longer object
## length is not a multiple of shorter object
## length
```

```
## [1] "*a*" "!b!" "*c*"
```

This is because the shorter vector (of length 2 here) doesn't go evenly into the longer one (length 3). It gives a warning because this is probably not what you wanted.

The `mutate` thing is easier, because all the columns in a data frame have to be the same length. `LETTERS` is a vector with the uppercase letters in it:

```
tibble(mytext = LETTERS[1:6], myout = c("*", "**",
    "!", "!!", "_", "__")) %>% mutate(newthing = wrap(mytext,
    myout))
```

```
## # A tibble: 6 x 3
##   mytext myout newthing
##   <chr>  <chr> <chr>
## 1 A      *     *A*
## 2 B      **    **B**
## 3 C      !     !C!
## 4 D      !!    !!D!!
## 5 E      _     _E_
## 6 F      __    __F__
```

15.2 *The Collatz sequence*

The Collatz sequence is a sequence of integers $x_1, x_2, \ldots$ defined in a deceptively simple way: if x_n is the current term of the sequence, then x_{n+1} is defined as $x_n/2$ if x_n is even, and $3x_n + 1$ if x_n is odd. We are interested in understanding how this sequence behaves; for example, what happens to it as n gets large, for different choices of the first term x_1? We will explore this numerically with R; the ambitious among you might like to look into the mathematics of it.

(a) What happens to the sequence when it reaches 4? What would be a sensible way of defining where it ends? Explain briefly.

Solution

When the sequence reaches 4 (that is, when its current term is 4), the next term is 2 and the one after that is 1. Then the following term is 4 again ($(3 \times 1) + 1$) and then it repeats indefinitely, $4, 2, 1, 4, 2, 1, \ldots$. I think a sensible way to define where the sequence ends is to say "when it reaches 1", since if you start at 2 you'll never reach 4 (so "when it reaches 4" won't work), and it seems at least plausible that it will hit the cycle 4, 2, 1 sometime.

(b) Write an R function called `is_odd` that returns `TRUE` if its input is an odd number and `FALSE` if it is even (you can assume that the input is an integer and not a decimal number). To do *that*, you can use the function `%%` where `a %% b` is the remainder when `a` is divided by `b`. To think about oddness or evenness, consider the remainder when you divide by 2.

Solution

Let's try this out. For example, 5 is odd and 6 is even, so

```
5%%2
```

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

```
6%%2
```

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

When a number is odd, its remainder on dividing by 2 is 1, and when even, the remainder is 0. There is an additional shortcut here in that 1 is the numeric value of `TRUE` and 0 of `FALSE`, so all we have to do is calculate the remainder on dividing by 2, turn it into a `logical`, and return it:

```
is_odd = function(x) {
    r = x%%2
    as.logical(r)
}
```

You probably haven't seen `as.logical` before, but it's the same idea as `as.numeric`: turn something that looks like a `TRUE` or `FALSE` into something that actually *is*.

We should test it:

```
is_odd(19)
```

```
## [1] TRUE
```

```
is_odd(12)
```

```
## [1] FALSE
```

```
is_odd(0)
```

```
## [1] FALSE
```

0 is usually considered an even number, so this is good.

(c) Write an R function called `hotpo1` that takes an integer as input and returns the next number in the Collatz sequence. To do this, use the function you just wrote that determines whether a number is even or odd.

Hotpo is short for half or triple-plus-one.

Solution

The logic is "if the input is odd, return 3 times it plus 1, otherwise return half of it". The R structure is an `if-then-else`:

```
hotpo1 = function(x) {
    if (is_odd(x))
        3 * x + 1 else x/2
}
```

In R, the condition that is tested goes in brackets, and then if the value-if-true and the value-if-false are single statements, you just type them. (If they are more complicated than that, you put them in curly brackets.) Now you see the value of writing `is_odd` earlier; this code almost looks like the English-language description of the sequence. If we had not written `is_odd` before, the condition would have looked something like

```
if (x%%2 == 1) 3 * x + 1 else x/2
```

which would have been a lot harder to read.

All right, let's try that out:

```
hotpo1(4)
```

```
## [1] 2
```

```
hotpo1(7)
```

```
## [1] 22
```

```
hotpo1(24)
```

```
## [1] 12
```

That looks all right so far.

(d) Now write a function hotpo that will return the whole Collatz sequence for an input x_1. For this, assume that you will eventually get to 1.

Solution

This is a loop, but not a for loop (or something that we could do with a map), because we don't know how many times we have to go around. This is the kind of thing that we should use a while loop for: "keep going while a condition is true". In this case, we should keep going if we haven't reached 1 yet. If we haven't reached 1, we should generate the next value of the sequence and glue it onto what we have so far. To initialize the sequence, we start with the input value. There is an R trick to glue a value onto the sequence, which is to use c with a vector and a value, and save it back into the vector:

```
hotpo = function(x) {
    sequence = x
    term = x
    while (term > 1) {
        term = hotpo1(term)
        sequence = c(sequence, term)
    }
    sequence
}
```

I use term to hold the current term of the sequence, and overwrite it with the next one (since I don't need the old one any more).

Does it work?

```
hotpo(4)
```

```
## [1] 4 2 1
```

```
hotpo(12)
```

```
##  [1] 12  6  3 10  5 16  8  4  2  1
```

```
hotpo(97)
```

```
##   [1]   97  292  146   73  220  110   55  166
##   [9]   83  250  125  376  188   94   47  142
##  [17]   71  214  107  322  161  484  242  121
##  [25]  364  182   91  274  137  412  206  103
##  [33]  310  155  466  233  700  350  175  526
##  [41]  263  790  395 1186  593 1780  890  445
##  [49] 1336  668  334  167  502  251  754  377
##  [57] 1132  566  283  850  425 1276  638  319
##  [65]  958  479 1438  719 2158 1079 3238 1619
##  [73] 4858 2429 7288 3644 1822  911 2734 1367
##  [81] 4102 2051 6154 3077 9232 4616 2308 1154
##  [89]  577 1732  866  433 1300  650  325  976
##  [97]  488  244  122   61  184   92   46   23
## [105]   70   35  106   53  160   80   40   20
## [113]   10    5   16    8    4    2    1
```

97 is a wild ride, but it does eventually get to 1.

Extra: where I originally saw this, which was "Metamagical Themas" by Douglas Hofstadter, he was illustrating the programming language Lisp and the process of recursion, whereby you define a function in terms of itself. This one is a natural for that, because the Collatz sequence starting at x is x along with the Collatz sequence starting at the next term. For example, if you start at 12, the next term is 6, so that the Collatz sequence starting at 12 is 12 followed by the Collatz sequence starting at 6. There is no dependence any further back. You can do recursion in R also; there is no problem with a function calling itself:

```
hotpo_rec = function(x) {
    if (x == 1)
        1 else c(x, hotpo_rec(hotpo1(x)))
}
```

Recursive functions have two parts: a "base case" that says how you know you are done (the 1 here), and a "recursion" that says how you move to a simpler case, here working out the next term, getting the whole sequence for that, and gluing the input onto the front. It seems paradoxical that you define a function in terms of itself, but what you are doing is calling a simpler sequence, in this case one that is length one shorter than the sequence for the original input. Thus, we hope, we will eventually reach 1.

Nobody knows whether you *always* get to 1, but also nobody has ever found a case where you don't. Collatz's conjecture, that you will get to 1 eventually, is known to be true for all starting x_1 up to some absurdly large number, but not for *all* starting points.

Does it work?

```
hotpo_rec(12)
```

```
##  [1] 12  6  3 10  5 16  8  4  2  1
```

```
hotpo_rec(97)
```

```
##   [1]   97  292  146   73  220  110   55  166
##   [9]   83  250  125  376  188   94   47  142
##  [17]   71  214  107  322  161  484  242  121
##  [25]  364  182   91  274  137  412  206  103
##  [33]  310  155  466  233  700  350  175  526
##  [41]  263  790  395 1186  593 1780  890  445
##  [49] 1336  668  334  167  502  251  754  377
##  [57] 1132  566  283  850  425 1276  638  319
##  [65]  958  479 1438  719 2158 1079 3238 1619
##  [73] 4858 2429 7288 3644 1822  911 2734 1367
##  [81] 4102 2051 6154 3077 9232 4616 2308 1154
##  [89]  577 1732  866  433 1300  650  325  976
##  [97]  488  244  122   61  184   92   46   23
## [105]   70   35  106   53  160   80   40   20
## [113]   10    5   16    8    4    2    1
```

It does.

Recursive functions are often simple to understand, but they are not always very efficient. They can take a lot of memory, because they have to handle the intermediate calls to the function, which they have to save to use later (in the case of `hotpo_rec(97)` there are a lot of those). Recursive functions are often paired with a technique called "memoization", where each time you calculate the function's value, you *save* it in another array. The first thing you do in the recursive function is to check whether you already have the answer, in which case you just look it up and return it. It was a lot of work here to calculate the sequence from 97, but if we had saved the results, we would already have the answers for 292, 146, 73, 220 and so on, and getting those later would be a table lookup rather than another recursive calculation.

(e) Write two (very small) functions that take an entire sequence as input and return (i) the length of the sequence and (ii) the maximum value it attains.

Solution

These are both one-liners. Call the input whatever you like:

```
hotpo_len = function(sequence) length(sequence)
hotpo_max = function(sequence) max(sequence)
```

Because they are one-liners, you don't even need the curly brackets, although there's no problem if they are there.

Testing:

```
hotpo_len(hotpo(12))
```

```
## [1] 10
```

```
hotpo_max(hotpo(97))
```

```
## [1] 9232
```

This checks with what we had before.

(f) Make a data frame consisting of the values 11 through 20, and, using `tidyverse` ideas, obtain a data frame containing the Collatz sequences starting at each of those values, along with their lengths and their maximum values. Which sequence is longest? Which one goes up highest?

Solution

This one uses `map` ideas: an actual `map` for the sequence, and `map_dbl` for the length and maximum value, since these are both actually integers but the calculation in our functions actually uses decimals. Thus, a pipeline:

I should have been more careful in my functions to make sure everything was integers, and, in particular, to do integer division by 2 because I knew that this division was going to come out even.

```
tibble(x = 11:20) %>% mutate(sequence = map(x,
    ~hotpo(.))) %>% mutate(length = map_dbl(sequence,
    ~hotpo_len(.))) %>% mutate(high = map_dbl(sequence,
    ~hotpo_max(.)))
```

```
## # A tibble: 10 x 4
##        x sequence   length  high
##    <int> <list>      <dbl> <dbl>
##  1    11 <dbl [15]>     15    52
##  2    12 <dbl [10]>     10    16
##  3    13 <dbl [10]>     10    40
##  4    14 <dbl [18]>     18    52
##  5    15 <dbl [18]>     18   160
##  6    16 <dbl [5]>       5    16
##  7    17 <dbl [13]>     13    52
##  8    18 <dbl [21]>     21    52
##  9    19 <dbl [21]>     21    88
## 10    20 <dbl [8]>       8    20
```

First, we obtain a list-column containing the sequences, then two ordinary columns of their lengths and their maximum values. The `map` is the same each time: for each of the first thing, run the function on *it*, where "it" is represented by the dot.

The sequences for 18 and 19 are the longest, but the sequence for 15 goes up the highest.