Data Science for Biological, Medical and Health Research: Notes for 432

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Contents

Introduction

These Notes provide a series of examples using R to work through issues that are likely to come up in PQHS/CRSP/MPHP 432.

While these Notes share some of the features of a textbook, they are neither comprehensive nor completely original. The main purpose is to give students in 432 a set of common materials on which to draw during the course. In class, we will sometimes:

- reiterate points made in this document,
- amplify what is here,
- simplify the presentation of things done here,
- use new examples to show some of the same techniques,
- refer to issues not mentioned in this document,

but what we don't (always) do is follow these notes very precisely. We assume instead that you will read the materials and try to learn from them, just as you will attend classes and try to learn from them. We welcome feedback of all kinds on this document or anything else. Just email us at `431-help at case dot edu`, or submit a pull request. Note that we still use `431-help` even though we're now in 432.

What you will mostly find are brief explanations of a key idea or summary, accompanied (most of the time) by R code and a demonstration of the results of applying that code.

Everything you see here is available to you as HTML or PDF. You will also have access to the R Markdown files, which contain the code which generates everything in the document, including all of the R results. We will demonstrate the use of R Markdown (this document is generated with the additional help of an R package called bookdown) and R Studio (the "program" which we use to interface with the R language) in class.

To download the data and R code related to these notes, visit the Data and Code section of the 432 course website.

R Packages used in these notes

Here, we'll load in the packages used in these notes.

```r
library(tableone)
library(skimr)
library(broom)
library(magrittr)
library(tidyverse)
```

Data used in these notes

Here, we'll load in the data sets used in these notes.

```
fakestroke <- read.csv("data/fakestroke.csv") %>% tbl_df
bloodbrain <- read.csv("data/bloodbrain.csv") %>% tbl_df
smartcle1 <- read.csv("data/smartcle1.csv") %>% tbl_df
```

Chapter 1

Building Table 1

Many scientific articles involve direct comparison of results from various exposures, perhaps treatments. In 431, we studied numerous methods, including various sorts of hypothesis tests, confidence intervals, and descriptive summaries, which can help us to understand and compare outcomes in such a setting. One common approach is to present what's often called Table 1. Table 1 provides a summary of the characteristics of a sample, or of groups of samples, which is most commonly used to help understand the nature of the data being compared.

1.1 Two examples from the *New England Journal of Medicine*

1.1.1 A simple Table 1

Table 1 is especially common in the context of clinical research. Consider the excerpt below, from a January 2015 article in the *New England Journal of Medicine* (Tolaney et al., 2015).

Table 1. Baseline Characteristics of the Patients.*

Characteristic	Patients (N=406)
	no. (%)
Age group	
<50 yr	132 (32.5)
50–59 yr	137 (33.7)
60–69 yr	96 (23.6)
≥70 yr	41 (10.1)
Sex	
Female	405 (99.8)
Male	1 (0.2)
Race†	
White	351 (86.5)
Black	28 (6.9)
Asian	11 (2.7)
Other	16 (3.9)

This (partial) table reports baseline characteristics on age group, sex and race, describing 406 patients with

HER2-positive[1] invasive breast cancer that began the protocol therapy. Age, sex and race (along with severity of illness) are the most commonly identified characteristics in a Table 1.

In addition to the measures shown in this excerpt, the full Table also includes detailed information on the primary tumor for each patient, including its size, nodal status and histologic grade. Footnotes tell us that the percentages shown are subject to rounding, and may not total 100, and that the race information was self-reported.

1.1.2 A group comparison

A more typical Table 1 involves a group comparison, for example in this excerpt from Roy et al. (2008). This Table 1 describes a multi-center randomized clinical trial comparing two different approaches to caring for patients with heart failure and atrial fibrillation[2].

Table 1. Baseline Characteristics of the Patients.*

Variable	Rhythm-Control Group (N=682)	Rate-Control Group (N=694)
Male sex (%)	78	85
Age (yr)	66±11	67±11
Body-mass index†	27.8±5.4	28.0±5.1
Nonwhite race (%)‡	16	13
NYHA class III or IV (%)		
At baseline	32	31
During previous 6 mo	76	76
Predominant cardiac diagnosis (%)§		
Coronary artery disease	48	48
Valvular heart disease	5	5
Nonischemic cardiomyopathy	36	39
Congenital heart disease	1	1
Hypertensive heart disease	10	7

The article provides percentages, means and standard deviations across groups, but note that it does not provide p values for the comparison of baseline characteristics. This is a common feature of NEJM reports on randomized clinical trials, where we anticipate that the two groups will be well matched at baseline. Note that the patients in this study were *randomly* assigned to either the rhythm-control group or to the rate-control group, using blocked randomizations stratified by study center.

1.2 The MR CLEAN trial

Berkhemer et al. (2015) reported on the MR CLEAN trial, involving 500 patients with acute ischemic stroke caused by a proximal intracranial arterial occlusion. The trial was conducted at 16 medical centers in the Netherlands, where 233 were randomly assigned to the intervention (intraarterial treatment plus usual care) and 267 to control (usual care alone.) The primary outcome was the modified Rankin scale score at 90 days; this categorical scale measures functional outcome, with scores ranging from 0 (no symptoms) to 6 (death). The fundamental conclusion of Berkhemer et al. (2015) was that in patients with acute ischemic stroke

[1] HER2 = human epidermal growth factor receptor type 2. Over-expression of this occurs in 15-20% of invasive breast cancers, and has been associated with poor outcomes.

[2] The complete Table 1 appears on pages 2668-2669 of Roy et al. (2008), but I have only reproduced the first page and the footnote in this excerpt.

caused by a proximal intracranial occlusion of the anterior circulation, intraarterial treatment administered within 6 hours after stroke onset was effective and safe.

Here's the Table 1 from Berkhemer et al. (2015).

Table 1. Baseline Characteristics of the 500 Patients.*

Characteristic	Intervention (N=233)	Control (N=267)
Age — yr		
Median	65.8	65.7
Interquartile range	54.5–76.0	55.5–76.4
Male sex — no. (%)	135 (57.9)	157 (58.8)
NIHSS score†		
Median (interquartile range)	17 (14–21)	18 (14–22)
Range	3–30	4–38
Location of stroke in left hemisphere — no. (%)	116 (49.8)	153 (57.3)
History of ischemic stroke — no. (%)	29 (12.4)	25 (9.4)
Atrial fibrillation — no. (%)	66 (28.3)	69 (25.8)
Diabetes mellitus — no. (%)	34 (14.6)	34 (12.7)
Prestroke modified Rankin scale score — no. (%)‡		
0	190 (81.5)	214 (80.1)
1	21 (9.0)	29 (10.9)
2	12 (5.2)	13 (4.9)
>2	10 (4.3)	11 (4.1)
Systolic blood pressure — mm Hg§	146±26.0	145±24.4
Treatment with IV alteplase — no. (%)	203 (87.1)	242 (90.6)
Time from stroke onset to start of IV alteplase — min		
Median	85	87
Interquartile range	67–110	65–116
ASPECTS — median (interquartile range)¶	9 (7–10)	9 (8–10)
Intracranial arterial occlusion — no./total no. (%)‖		
Intracranial ICA	1/233 (0.4)	3/266 (1.1)
ICA with involvement of the M1 middle cerebral artery segment	59/233 (25.3)	75/266 (28.2)
M1 middle cerebral artery segment	154/233 (66.1)	165/266 (62.0)
M2 middle cerebral artery segment	18/233 (7.7)	21/266 (7.9)
A1 or A2 anterior cerebral artery segment	1/233 (0.4)	2/266 (0.8)
Extracranial ICA occlusion — no./total no. (%)‖**	75/233 (32.2)	70/266 (26.3)
Time from stroke onset to randomization — min††		
Median	204	196
Interquartile range	152–251	149–266
Time from stroke onset to groin puncture — min		
Median	260	NA
Interquartile range	210–313	

The Table was accompanied by the following notes.

* The intervention group was assigned to intraarterial treatment plus usual care, and the control group was assigned to usual care alone. Plus–minus values are means ±SD. ICA denotes internal carotid artery, IV intravenous, and NA not applicable.
† Scores on the National Institutes of Health Stroke Scale (NIHSS) range from 0 to 42, with higher scores indicating more severe neurologic deficits. The NIHSS is a 15-item scale, and values for 30 of the 7500 items were missing (0.4%). The highest number of missing items for a single patient was 6.
‡ Scores on the modified Rankin scale of functional disability range from 0 (no symptoms) to 6 (death). A score of 2 or less indicates functional independence.
§ Data on systolic blood pressure at baseline were missing for one patient assigned to the control group.
¶ The Alberta Stroke Program Early Computed Tomography Score (ASPECTS) is a measure of the extent of stroke. Scores ranges from 0 to 10, with higher scores indicating fewer early ischemic changes. Scores were not available for four patients assigned to the control group: noncontrast computed tomography was not performed in one patient, and three patients had strokes in the territory of the anterior cerebral artery.
‖ Vessel imaging was not performed in one patient in the control group, so the level of occlusion was not known.
** Extracranial ICA occlusions were reported by local investigators.
†† Data were missing for two patients in the intervention group.

1.3 Simulated `fakestroke` data

Consider the simulated data, available on the Data and Code page of our course website in the `fakestroke.csv` file, which I built to let us mirror the Table 1 for MR CLEAN (Berkhemer et al., 2015). The `fakestroke.csv` file contains the following 18 variables for 500 patients.

Variable	Description
`studyid`	Study ID # (z001 through z500)
`trt`	Treatment group (Intervention or Control)
`age`	Age in years
`sex`	Male or Female
`nihss`	NIH Stroke Scale Score (can range from 0-42; higher scores indicate more severe neurological deficits)
`location`	Stroke Location - Left or Right Hemisphere
`hx.isch`	History of Ischemic Stroke (Yes/No)
`afib`	Atrial Fibrillation (1 = Yes, 0 = No)
`dm`	Diabetes Mellitus (1 = Yes, 0 = No)
`mrankin`	Pre-stroke modified Rankin scale score (0, 1, 2 or > 2) indicating functional disability - complete range is 0 (no symptoms) to 6 (death)
`sbp`	Systolic blood pressure, in mm Hg
`iv.altep`	Treatment with IV alteplase (Yes/No)
`time.iv`	Time from stroke onset to start of IV alteplase (minutes) if iv.altep=Yes
`aspects`	Alberta Stroke Program Early Computed Tomography score, which measures extent of stroke from 0 - 10; higher scores indicate fewer early ischemic changes
`ia.occlus`	Intracranial arterial occlusion, based on vessel imaging - five categories[3]
`extra.ica`	Extracranial ICA occlusion (1 = Yes, 0 = No)
`time.rand`	Time from stroke onset to study randomization, in minutes
`time.punc`	Time from stroke onset to groin puncture, in minutes (only if Intervention)

Here's a quick look at the simulated data in `fakestroke`.

[3] The five categories are Intracranial ICA, ICA with involvement of the M1 middle cerebral artery segment, M1 middle cerebral artery segment, M2 middle cerebral artery segment, A1 or A2 anterior cerebral artery segment

```r
fakestroke
```

```
# A tibble: 500 x 18
   studyid trt        age sex   nihss location hx.isch  afib    dm mrankin
   <fct>   <fct>    <dbl> <fct> <int> <fct>    <fct>   <int> <int> <fct>
 1 z001    Control   53.0 Male     21 Right    No          0     0 2
 2 z002    Interve~  51.0 Male     23 Left     No          1     0 0
 3 z003    Control   68.0 Fema~    11 Right    No          0     0 0
 4 z004    Control   28.0 Male     22 Left     No          0     0 0
 5 z005    Control   91.0 Male     24 Right    No          0     0 0
 6 z006    Control   34.0 Fema~    18 Left     No          0     0 2
 7 z007    Interve~  75.0 Male     25 Right    No          0     0 0
 8 z008    Control   89.0 Fema~    18 Right    No          0     0 0
 9 z009    Control   75.0 Male     25 Left     No          1     0 2
10 z010    Interve~  26.0 Fema~    27 Right    No          0     0 0
# ... with 490 more rows, and 8 more variables: sbp <int>, iv.altep <fct>,
#   time.iv <int>, aspects <int>, ia.occlus <fct>, extra.ica <int>,
#   time.rand <int>, time.punc <int>
```

1.4 Building Table 1 for `fakestroke`: Attempt 1

Our goal, then, is to take the data in `fakestroke.csv` and use it to generate a Table 1 for the study that compares the 233 patients in the Intervention group to the 267 patients in the Control group, on all of the other variables (except study ID #) available. I'll use the `tableone` package of functions available in R to help me complete this task. We'll make a first attempt, using the `CreateTableOne` function in the `tableone` package. To use the function, we'll need to specify:

- the `vars` or variables we want to place in the rows of our Table 1 (which will include just about everything in the `fakestroke` data except the `studyid` code and the `trt` variable for which we have other plans, and the `time.punc` which applies only to subjects in the Intervention group.)
  - A useful trick here is to use the `dput` function, specifically something like `dput(names(fakestroke))` can be used to generate a list of all of the variables included in the `fakestroke` tibble, and then this can be copied and pasted into the `vars` specification, saving some typing.
- the `strata` which indicates the levels want to use in the columns of our Table 1 (for us, that's `trt`)

```r
fs.vars <- c("age", "sex", "nihss", "location",
          "hx.isch", "afib", "dm", "mrankin", "sbp",
          "iv.altep", "time.iv", "aspects",
          "ia.occlus", "extra.ica", "time.rand")

fs.trt <- c("trt")

att1 <- CreateTableOne(data = fakestroke,
                       vars = fs.vars,
                       strata = fs.trt)
print(att1)
```

```
                       Stratified by trt
                        Control        Intervention   p      test
  n                       267            233
  age (mean (sd))       65.38 (16.10)  63.93 (18.09)   0.343
  sex = Male (%)          157 (58.8)     135 (57.9)    0.917
  nihss (mean (sd))     18.08 (4.32)   17.97 (5.04)    0.787
  location = Right (%)    114 (42.7)     117 (50.2)    0.111
```

```
  hx.isch = Yes (%)         25 ( 9.4)      29 (12.4)   0.335
  afib (mean (sd))        0.26 (0.44)    0.28 (0.45)   0.534
  dm (mean (sd))          0.13 (0.33)    0.12 (0.33)   0.923
  mrankin (%)                                          0.922
     > 2                    11 ( 4.1)      10 ( 4.3)
     0                     214 (80.1)     190 (81.5)
     1                      29 (10.9)      21 ( 9.0)
     2                      13 ( 4.9)      12 ( 5.2)
  sbp (mean (sd))       145.00 (24.40) 146.03 (26.00)  0.647
  iv.altep = Yes (%)       242 (90.6)     203 (87.1)   0.267
  time.iv (mean (sd))    87.96 (26.01)  98.22 (45.48)  0.003
  aspects (mean (sd))     8.65 (1.47)    8.35 (1.64)   0.033
  ia.occlus (%)                                        0.795
     A1 or A2                2 ( 0.8)       1 ( 0.4)
     ICA with M1            75 (28.2)      59 (25.3)
     Intracranial ICA        3 ( 1.1)       1 ( 0.4)
     M1                    165 (62.0)     154 (66.1)
     M2                     21 ( 7.9)      18 ( 7.7)
  extra.ica (mean (sd))   0.26 (0.44)    0.32 (0.47)   0.150
  time.rand (mean (sd)) 213.88 (70.29) 202.51 (57.33)  0.051
```

1.4.1 Some of this is very useful, and other parts need to be fixed.

1. The 1/0 variables (`afib`, `dm`, `extra.ica`) might be better if they were treated as the factors they are, and reported as the Yes/No variables are reported, with counts and percentages rather than with means and standard deviations.
2. In some cases, we may prefer to re-order the levels of the categorical (factor) variables, particularly the `mrankin` variable, but also the `ia.occlus` variable. It would also be more typical to put the Intervention group to the left and the Control group to the right, so we may need to adjust our `trt` variable's levels accordingly.
3. For each of the quantitative variables (`age`, `nihss`, `sbp`, `time.iv`, `aspects`, `extra.ica`, `time.rand` and `time.punc`) we should make a decision whether a summary with mean and standard deviation is appropriate, or whether we should instead summarize with, say, the median and quartiles. A mean and standard deviation really only yields an appropriate summary when the data are least approximately Normally distributed. This will make the *p* values a bit more reasonable, too. The `test` column in the first attempt will soon have something useful to tell us.
4. If we'd left in the `time.punc` variable, we'd get some warnings, having to do with the fact that `time.punc` is only relevant to patients in the Intervention group.

1.4.2 `fakestroke` Cleaning Up Categorical Variables

Let's specify each of the categorical variables as categorical explicitly. This helps the `CreateTableOne` function treat them appropriately, and display them with counts and percentages. This includes all of the 1/0, Yes/No and multi-categorical variables.

```r
fs.factorvars <- c("sex", "location", "hx.isch", "afib", "dm",
                   "mrankin", "iv.altep", "ia.occlus", "extra.ica")
```

Then we simply add a `factorVars = fs.factorvars` call to the `CreateTableOne` function.

We also want to re-order some of those categorical variables, so that the levels are more useful to us. Specifically, we want to:

- place Intervention before Control in the `trt` variable,
- reorder the `mrankin` scale as 0, 1, 2, > 2, and

- rearrange the `ia.occlus` variable to the order[4] presented in Berkhemer et al. (2015).

To accomplish this, we'll use the `fct_relevel` function from the `forcats` package (loaded with the rest of the core `tidyverse` packages) to reorder our levels manually.

```
fakestroke <- fakestroke %>%
    mutate(trt = fct_relevel(trt, "Intervention", "Control"),
           mrankin = fct_relevel(mrankin, "0", "1", "2", "> 2"),
           ia.occlus = fct_relevel(ia.occlus, "Intracranial ICA",
                                   "ICA with M1", "M1", "M2",
                                   "A1 or A2")
           )
```

1.5 fakestroke Table 1: Attempt 2

```
att2 <- CreateTableOne(data = fakestroke,
                       vars = fs.vars,
                       factorVars = fs.factorvars,
                       strata = fs.trt)
print(att2)
```

```
                       Stratified by trt
                        Intervention   Control        p      test
  n                        233            267
  age (mean (sd))        63.93 (18.09)  65.38 (16.10)  0.343
  sex = Male (%)           135 (57.9)     157 (58.8)   0.917
  nihss (mean (sd))      17.97 (5.04)   18.08 (4.32)   0.787
  location = Right (%)     117 (50.2)     114 (42.7)   0.111
  hx.isch = Yes (%)         29 (12.4)      25 ( 9.4)   0.335
  afib = 1 (%)              66 (28.3)      69 (25.8)   0.601
  dm = 1 (%)                29 (12.4)      34 (12.7)   1.000
  mrankin (%)                                          0.922
     0                     190 (81.5)     214 (80.1)
     1                      21 ( 9.0)      29 (10.9)
     2                      12 ( 5.2)      13 ( 4.9)
     > 2                    10 ( 4.3)      11 ( 4.1)
  sbp (mean (sd))       146.03 (26.00) 145.00 (24.40)  0.647
  iv.altep = Yes (%)       203 (87.1)     242 (90.6)   0.267
  time.iv (mean (sd))    98.22 (45.48)  87.96 (26.01)  0.003
  aspects (mean (sd))     8.35 (1.64)    8.65 (1.47)   0.033
  ia.occlus (%)                                        0.795
     Intracranial ICA        1 ( 0.4)       3 ( 1.1)
     ICA with M1            59 (25.3)      75 (28.2)
     M1                    154 (66.1)     165 (62.0)
     M2                     18 ( 7.7)      21 ( 7.9)
     A1 or A2                1 ( 0.4)       2 ( 0.8)
  extra.ica = 1 (%)         75 (32.2)      70 (26.3)   0.179
  time.rand (mean (sd)) 202.51 (57.33) 213.88 (70.29)  0.051
```

The categorical data presentation looks much improved.

[4] We might also have considered reordering the `ia.occlus` factor by its frequency, using the `fct_infreq` function

1.5.1 What summaries should we show?

Now, we'll move on to the issue of making a decision about what type of summary to show for the quantitative variables. Since the `fakestroke` data are just simulated and only match the summary statistics of the original results, not the details, we'll adopt the decisions made by Berkhemer et al. (2015), which were to use medians and interquartile ranges to summarize the distributions of all of the continuous variables **except** systolic blood pressure.

- Specifying certain quantitative variables as *non-normal* causes R to show them with medians and the 25th and 75th percentiles, rather than means and standard deviations, and also causes those variables to be tested using non-parametric tests, like the Wilcoxon signed rank test, rather than the t test. The `test` column indicates this with the word `nonnorm`.
  - In real data situations, what should we do? The answer is to look at the data. I would not make the decision as to which approach to take without first plotting (perhaps in a histogram or a Normal Q-Q plot) the observed distributions in each of the two samples, so that I could make a sound decision about whether Normality was a reasonable assumption. If the means and medians are meaningfully different from each other, this is especially important.
  - To be honest, though, if the variable in question is a relatively unimportant covariate and the p values for the two approaches are nearly the same, I'm not sure that further investigation is especially important,
- Specifying *exact* tests for certain categorical variables (we'll try this for the `location` and `mrankin` variables) can be done, and these changes will be noted in the `test` column, as well.
  - In real data situations, I would rarely be concerned about this issue, and often choose Pearson (approximate) options across the board. This is reasonable so long as the number of subjects falling in each category is reasonably large, say above 10. If not, then an exact test may be an improvement.

To accomplish the Table 1, then, we need to specify which variables should be treated as non-Normal in the `print` statement - notice that we don't need to redo the `CreateTableOne` for this change.

```r
print(att2,
      nonnormal = c("age", "nihss", "time.iv", "aspects", "time.rand"),
      exact = c("location", "mrankin"))
```

```
                          Stratified by trt
                           Intervention          Control
  n                           233                  267
  age (median [IQR])        65.80 [54.50, 76.00]   65.70 [55.75, 76.20]
  sex = Male (%)              135 (57.9)           157 (58.8)
  nihss (median [IQR])      17.00 [14.00, 21.00]   18.00 [14.00, 22.00]
  location = Right (%)        117 (50.2)           114 (42.7)
  hx.isch = Yes (%)            29 (12.4)            25 ( 9.4)
  afib = 1 (%)                 66 (28.3)            69 (25.8)
  dm = 1 (%)                   29 (12.4)            34 (12.7)
  mrankin (%)
     0                        190 (81.5)           214 (80.1)
     1                         21 ( 9.0)            29 (10.9)
     2                         12 ( 5.2)            13 ( 4.9)
     > 2                       10 ( 4.3)            11 ( 4.1)
  sbp (mean (sd))          146.03 (26.00)       145.00 (24.40)
  iv.altep = Yes (%)          203 (87.1)           242 (90.6)
  time.iv (median [IQR])    85.00 [67.00, 110.00]  87.00 [65.00, 116.00]
  aspects (median [IQR])     9.00 [7.00, 10.00]     9.00 [8.00, 10.00]
  ia.occlus (%)
     Intracranial ICA           1 ( 0.4)             3 ( 1.1)
     ICA with M1               59 (25.3)            75 (28.2)
```

```
     M1                        154 (66.1)            165 (62.0)
     M2                         18 ( 7.7)             21 ( 7.9)
     A1 or A2                    1 ( 0.4)              2 ( 0.8)
  extra.ica = 1 (%)             75 (32.2)             70 (26.3)
  time.rand (median [IQR]) 204.00 [152.00, 249.50] 196.00 [149.00, 266.00]
                          Stratified by trt
                           p      test
  n
  age (median [IQR])        0.579 nonnorm
  sex = Male (%)            0.917
  nihss (median [IQR])      0.453 nonnorm
  location = Right (%)      0.106 exact
  hx.isch = Yes (%)         0.335
  afib = 1 (%)              0.601
  dm = 1 (%)                1.000
  mrankin (%)               0.917 exact
     0
     1
     2
     > 2
  sbp (mean (sd))           0.647
  iv.altep = Yes (%)        0.267
  time.iv (median [IQR])    0.596 nonnorm
  aspects (median [IQR])    0.075 nonnorm
  ia.occlus (%)             0.795
     Intracranial ICA
     ICA with M1
     M1
     M2
     A1 or A2
  extra.ica = 1 (%)         0.179
  time.rand (median [IQR])  0.251 nonnorm
```

1.6 Obtaining a more detailed Summary

If this was a real data set, we'd want to get a more detailed description of the data to make decisions about things like potentially collapsing categories of a variable, or whether or not a normal distribution was useful for a particular continuous variable, etc. You can do this with the `summary` command applied to a created Table 1, which shows, among other things, the effect of changing from normal to non-normal *p* values for continuous variables, and from approximate to "exact" *p* values for categorical factors.

Again, as noted above, in a real data situation, we'd want to plot the quantitative variables (within each group) to make a smart decision about whether a t test or Wilcoxon approach is more appropriate.

Note in the summary below that we have some missing values here. Often, we'll present this information within the Table 1, as well.

```r
summary(att2)
```

```
     ### Summary of continuous variables ###

trt: Intervention
            n miss p.miss mean sd median p25 p75 min max  skew  kurt
```

```
age       233    0    0.0   64 18     66  54  76  23  96 -0.34 -0.52
nihss     233    0    0.0   18  5     17  14  21  10  28  0.48 -0.74
sbp       233    0    0.0  146 26    146 129 164  78 214 -0.07 -0.22
time.iv   233   30   12.9   98 45     85  67 110  42 218  1.03  0.08
aspects   233    0    0.0    8  2      9   7  10   5  10 -0.56 -0.98
time.rand 233    2    0.9  203 57    204 152 250 100 300  0.01 -1.16
--------------------------------------------------------
trt: Control
            n miss p.miss mean sd median p25 p75 min max   skew  kurt
age       267    0    0.0   65 16     66  56  76  24  94 -0.296 -0.28
nihss     267    0    0.0   18  4     18  14  22  11  25  0.017 -1.24
sbp       267    1    0.4  145 24    145 128 161  82 231  0.156  0.08
time.iv   267   25    9.4   88 26     87  65 116  44 130  0.001 -1.32
aspects   267    4    1.5    9  1      9   8  10   5  10 -1.071  0.36
time.rand 267    0    0.0  214 70    196 149 266 120 360  0.508 -0.93

p-values
              pNormal pNonNormal
age       0.342813660 0.57856976
nihss     0.787487252 0.45311695
sbp       0.647157646 0.51346132
time.iv   0.003073372 0.59641104
aspects   0.032662901 0.07464683
time.rand 0.050803672 0.25134327

Standardize mean differences
              1 vs 2
age       0.08478764
nihss     0.02405390
sbp       0.04100833
time.iv   0.27691223
aspects   0.19210662
time.rand 0.17720957

=======================================================================================

     ### Summary of categorical variables ###

trt: Intervention
       var   n miss p.miss           level freq percent cum.percent
       sex 233    0    0.0          Female   98    42.1        42.1
                                      Male  135    57.9       100.0

  location 233    0    0.0            Left  116    49.8        49.8
                                     Right  117    50.2       100.0

   hx.isch 233    0    0.0              No  204    87.6        87.6
                                       Yes   29    12.4       100.0

      afib 233    0    0.0               0  167    71.7        71.7
                                         1   66    28.3       100.0

        dm 233    0    0.0               0  204    87.6        87.6
                                         1   29    12.4       100.0
```

```
   mrankin 233    0    0.0                 0  190    81.5         81.5
                                           1   21     9.0         90.6
                                           2   12     5.2         95.7
                                         > 2   10     4.3        100.0

  iv.altep 233    0    0.0                No   30    12.9         12.9
                                         Yes  203    87.1        100.0

 ia.occlus 233    0    0.0 Intracranial ICA    1     0.4          0.4
                                ICA with M1   59    25.3         25.8
                                         M1  154    66.1         91.8
                                         M2   18     7.7         99.6
                                   A1 or A2    1     0.4        100.0

 extra.ica 233    0    0.0                 0  158    67.8         67.8
                                           1   75    32.2        100.0

--------------------------------------------------------
trt: Control
       var   n miss p.miss            level freq percent cum.percent
       sex 267    0    0.0           Female  110    41.2         41.2
                                       Male  157    58.8        100.0

  location 267    0    0.0             Left  153    57.3         57.3
                                      Right  114    42.7        100.0

   hx.isch 267    0    0.0               No  242    90.6         90.6
                                        Yes   25     9.4        100.0

      afib 267    0    0.0                0  198    74.2         74.2
                                          1   69    25.8        100.0

        dm 267    0    0.0                0  233    87.3         87.3
                                          1   34    12.7        100.0

   mrankin 267    0    0.0                0  214    80.1         80.1
                                          1   29    10.9         91.0
                                          2   13     4.9         95.9
                                        > 2   11     4.1        100.0

  iv.altep 267    0    0.0               No   25     9.4          9.4
                                        Yes  242    90.6        100.0

 ia.occlus 267    1    0.4 Intracranial ICA    3     1.1          1.1
                                ICA with M1   75    28.2         29.3
                                         M1  165    62.0         91.4
                                         M2   21     7.9         99.2
                                   A1 or A2    2     0.8        100.0

 extra.ica 267    1    0.4                0  196    73.7         73.7
                                          1   70    26.3        100.0
```

```
p-values
             pApprox    pExact
sex        0.9171387 0.8561188
location   0.1113553 0.1056020
hx.isch    0.3352617 0.3124683
afib       0.6009691 0.5460206
dm         1.0000000 1.0000000
mrankin    0.9224798 0.9173657
iv.altep   0.2674968 0.2518374
ia.occlus  0.7945580 0.8189090
extra.ica  0.1793385 0.1667574

Standardize mean differences
                1 vs 2
sex        0.017479025
location   0.151168444
hx.isch    0.099032275
afib       0.055906317
dm         0.008673478
mrankin    0.062543164
iv.altep   0.111897009
ia.occlus  0.117394890
extra.ica  0.129370206
```

In this case, I have simulated the data to mirror the results in the published Table 1 for this study. In no way have I captured the full range of the real data, or any of the relationships in that data, so it's more important here to see what's available in the analysis, rather than to interpret it closely in the clinical context.

1.7 Exporting the Completed Table 1 from R to Excel or Word

Once you've built the table and are generally satisfied with it, you'll probably want to be able to drop it into Excel or Word for final cleanup.

1.7.1 Approach A: Save and open in Excel

One option is to **save the Table 1** to a `.csv` file, which you can then open directly in Excel. This is the approach I generally use. Note the addition of some `quote`, `noSpaces` and `printToggle` selections here.

```r
fs.table1save <- print(att2,
      nonnormal = c("age", "nihss", "time.iv", "aspects", "time.rand"),
      exact = c("location", "mrankin"),
      quote = FALSE, noSpaces = TRUE, printToggle = FALSE)

write.csv(fs.table1save, file = "fs-table1.csv")
```

When I then open the `fs-table1.csv` file in Excel, it looks like this:

	A	B	C	D	E
1		Intervention	Control	p	test
2	n	233	267		
3	age (median [IQR])	65.80 [54.50, 76.00]	65.70 [55.75, 76.20]	0.579	nonnorm
4	sex = Male (%)	135 (57.9)	157 (58.8)	0.917	
5	nihss (median [IQR])	17.00 [14.00, 21.00]	18.00 [14.00, 22.00]	0.453	nonnorm
6	location = Right (%)	117 (50.2)	114 (42.7)	0.111	
7	hx.isch = Yes (%)	29 (12.4)	25 (9.4)	0.335	
8	afib = 1 (%)	66 (28.3)	69 (25.8)	0.601	
9	dm = 1 (%)	29 (12.4)	34 (12.7)	1	
10	mrankin (%)			0.922	
11	0	190 (81.5)	214 (80.1)		
12	1	21 (9.0)	29 (10.9)		
13	2	12 (5.2)	13 (4.9)		
14	>2	10 (4.3)	11 (4.1)		
15	sbp (mean (sd))	146.03 (26.00)	145.00 (24.40)	0.647	
16	iv.altep = Yes (%)	203 (87.1)	242 (90.6)	0.267	
17	time.iv (median [IQR])	85.00 [67.00, 110.00]	87.00 [65.00, 116.00]	0.596	nonnorm
18	aspects (median [IQR])	9.00 [7.00, 10.00]	9.00 [8.00, 10.00]	0.075	nonnorm
19	ia.occlus (%)			0.795	
20	Intracranial ICA	1 (0.4)	3 (1.1)		
21	ICA with M1	59 (25.3)	75 (28.2)		
22	M1	154 (66.1)	165 (62.0)		
23	M2	18 (7.7)	21 (7.9)		
24	A1 or A2	1 (0.4)	2 (0.8)		
25	extra.ica = 1 (%)	75 (32.2)	70 (26.3)	0.179	
26	time.rand (median [IQR])	204.00 [152.00, 249.50]	196.00 [149.00, 266.00]	0.251	nonnorm
27	time.punc (median [IQR])	260.00 [212.00, 313.00]	NA [NA, NA]	NA	nonnorm
28					

And from here, I can either drop it directly into Word, or present it as is, or start tweaking it to meet formatting needs.

1.7.2 Approach B: Produce the Table so you can cut and paste it

```
print(att2,
      nonnormal = c("age", "nihss", "time.iv", "aspects", "time.rand"),
      exact = c("location", "mrankin"),
      quote = TRUE, noSpaces = TRUE)
```

This will look like a mess by itself, but if you:

1. copy and paste that mess into Excel
2. select Text to Columns from the Data menu
3. select Delimited, then Space and select Treat consecutive delimiters as one

you should get something usable again.

Or, in Word,

1. insert the text

2. select the text with your mouse
3. select Insert … Table … Convert Text to Table
4. place a quotation mark in the "Other" area under Separate text at …

After dropping blank columns, the result looks pretty good.

1.8 A Controlled Biological Experiment - The Blood-Brain Barrier

My source for the data and the following explanatory paragraph is page 307 from Ramsey and Schafer (2002). The original data come from Barnett et al. (1995).

> The human brain (and that of rats, coincidentally) is protected from the bacteria and toxins that course through the bloodstream by something called the blood-brain barrier. After a method of disrupting the barrier was developed, researchers tested this new mechanism, as follows. A series of 34 rats were inoculated with human lung cancer cells to induce brain tumors. After 9-11 days they were infused with either the barrier disruption (BD) solution or, as a control, a normal saline (NS) solution. Fifteen minutes later, the rats received a standard dose of a particular therapeutic antibody (L6-F(ab')2. The key measure of the effectiveness of transmission across the brain-blood barrier is the ratio of the antibody concentration in the brain tumor to the antibody concentration in normal tissue outside the brain. The rats were then sacrificed, and the amounts of antibody in the brain tumor and in normal tissue from the liver were measured. The study's primary objective is to determine whether the antibody concentration in the tumor increased when the blood-barrier disruption infusion was given, and if so, by how much?

1.9 The `bloodbrain.csv` file

Consider the data, available on the Data and Code page of our course website in the `bloodbrain.csv` file, which includes the following variables:

Variable	Description
`case`	identification number for the rat (1 - 34)
`brain`	an outcome: Brain tumor antibody count (per gram)
`liver`	an outcome: Liver antibody count (per gram)
`tlratio`	an outcome: tumor / liver concentration ratio
`solution`	the treatment: BD (barrier disruption) or NS (normal saline)
`sactime`	a design variable: Sacrifice time (hours; either 0.5, 3, 24 or 72)
`postin`	covariate: Days post-inoculation of lung cancer cells (9, 10 or 11)
`sex`	covariate: M or F
`wt.init`	covariate: Initial weight (grams)
`wt.loss`	covariate: Weight loss (grams)
`wt.tumor`	covariate: Tumor weight (10^{-4} grams)

And here's what the data look like in R.

```
bloodbrain
```

```
# A tibble: 34 x 11
    case  brain   liver tlratio solution sactime postin sex   wt.init
   <int>  <int>   <int>   <dbl> <fct>      <dbl>  <int> <fct>   <int>
 1     1  41081 1456164  0.0282 BD         0.500     10 F         239
```

```
 2      2  44286 1602171  0.0276 BD         0.500      10 F          225
 3      3 102926 1601936  0.0642 BD         0.500      10 F          224
 4      4  25927 1776411  0.0146 BD         0.500      10 F          184
 5      5  42643 1351184  0.0316 BD         0.500      10 F          250
 6      6  31342 1790863  0.0175 NS         0.500      10 F          196
 7      7  22815 1633386  0.0140 NS         0.500      10 F          200
 8      8  16629 1618757  0.0103 NS         0.500      10 F          273
 9      9  22315 1567602  0.0142 NS         0.500      10 F          216
10     10  77961 1060057  0.0735 BD         3.00       10 F          267
# ... with 24 more rows, and 2 more variables: wt.loss <dbl>, wt.tumor
#   <int>
```

1.10 A Table 1 for bloodbrain

Barnett et al. (1995) did not provide a Table 1 for these data, so let's build one to compare the two `solutions` (`BD` vs. `NS`) on the covariates and outcomes, plus the natural logarithm of the tumor/liver concentration ratio (`tlratio`). We'll opt to treat the sacrifice time (`sactime`) and the days post-inoculation of lung cancer cells (`postin`) as categorical rather than quantitative variables.

```r
bloodbrain <- bloodbrain %>%
    mutate(logTL = log(tlratio))

dput(names(bloodbrain))
```

```
c("case", "brain", "liver", "tlratio", "solution", "sactime",
"postin", "sex", "wt.init", "wt.loss", "wt.tumor", "logTL")
```

OK - there's the list of variables we'll need. I'll put the outcomes at the bottom of the table.

```r
bb.vars <- c("sactime", "postin", "sex", "wt.init", "wt.loss",
             "wt.tumor", "brain", "liver", "tlratio", "logTL")

bb.factors <- c("sactime", "sex", "postin")

bb.att1 <- CreateTableOne(data = bloodbrain,
                          vars = bb.vars,
                          factorVars = bb.factors,
                          strata = c("solution"))
summary(bb.att1)
```

```
     ### Summary of continuous variables ###

solution: BD
          n miss p.miss   mean    sd median    p25   p75    min   max
wt.init   17    0      0    243 3e+01  2e+02  2e+02 3e+02  2e+02 3e+02
wt.loss   17    0      0      3 5e+00  4e+00  1e+00 6e+00 -5e+00 1e+01
wt.tumor  17    0      0    157 8e+01  2e+02  1e+02 2e+02  2e+01 4e+02
brain     17    0      0  56043 3e+04  5e+04  4e+04 8e+04  6e+03 1e+05
liver     17    0      0 672577 7e+05  6e+05  2e+04 1e+06  2e+03 2e+06
tlratio   17    0      0      2 3e+00  1e-01  6e-02 3e+00  1e-02 9e+00
logTL     17    0      0     -1 2e+00 -2e+00 -3e+00 1e+00 -4e+00 2e+00
          skew kurt
wt.init  -0.39  0.7
wt.loss  -0.10  0.2
```

```
wt.tumor  0.53  1.0
brain     0.29 -0.6
liver     0.35 -1.7
tlratio   1.58  1.7
logTL     0.08 -1.7
-------------------------------------------------------
solution: NS
          n miss p.miss   mean    sd median    p25    p75    min   max
wt.init  17    0      0    240 3e+01  2e+02  2e+02  3e+02  2e+02 3e+02
wt.loss  17    0      0      4 4e+00  3e+00  2e+00  7e+00 -4e+00 1e+01
wt.tumor 17    0      0    209 1e+02  2e+02  2e+02  3e+02  3e+01 5e+02
brain    17    0      0  23887 1e+04  2e+04  1e+04  3e+04  1e+03 5e+04
liver    17    0      0 664975 7e+05  7e+05  2e+04  1e+06  9e+02 2e+06
tlratio  17    0      0      1 2e+00  5e-02  3e-02  9e-01  1e-02 7e+00
logTL    17    0      0     -2 2e+00 -3e+00 -3e+00 -7e-02 -5e+00 2e+00
          skew  kurt
wt.init   0.33 -0.48
wt.loss  -0.09  0.08
wt.tumor  0.63  0.77
brain     0.30 -0.35
liver     0.40 -1.56
tlratio   2.27  4.84
logTL     0.27 -1.61

p-values
             pNormal  pNonNormal
wt.init  0.807308940 0.641940278
wt.loss  0.683756156 0.876749808
wt.tumor 0.151510151 0.190482094
brain    0.001027678 0.002579901
liver    0.974853609 0.904045603
tlratio  0.320501715 0.221425879
logTL    0.351633525 0.221425879

Standardize mean differences
             1 vs 2
wt.init  0.08435244
wt.loss  0.14099823
wt.tumor 0.50397184
brain    1.23884159
liver    0.01089667
tlratio  0.34611465
logTL    0.32420504

=======================================================================================

     ### Summary of categorical variables ###

solution: BD
     var  n miss p.miss level freq percent cum.percent
 sactime 17    0    0.0   0.5    5    29.4        29.4
                            3    4    23.5        52.9
                           24    4    23.5        76.5
                           72    4    23.5       100.0
```

```
  postin 17    0    0.0     9    1     5.9         5.9
                           10   14    82.4        88.2
                           11    2    11.8       100.0

     sex 17    0    0.0     F   13    76.5        76.5
                            M    4    23.5       100.0

--------------------------------------------------------
solution: NS
     var  n miss p.miss level freq percent cum.percent
 sactime 17    0    0.0   0.5    4    23.5        23.5
                            3    5    29.4        52.9
                           24    4    23.5        76.5
                           72    4    23.5       100.0

  postin 17    0    0.0     9    2    11.8        11.8
                           10   13    76.5        88.2
                           11    2    11.8       100.0

     sex 17    0    0.0     F   13    76.5        76.5
                            M    4    23.5       100.0


p-values
          pApprox pExact
sactime 0.9739246      1
postin  0.8309504      1
sex     1.0000000      1

Standardize mean differences
           1 vs 2
sactime 0.1622214
postin  0.2098877
sex     0.0000000
```

Note that, in this particular case, the decisions we make about normality vs. non-normality (for quantitative variables) and the decisions we make about approximate vs. exact testing (for categorical variables) won't actually change the implications of the *p* values. Each approach gives similar results for each variable. Of course, that's not always true.

1.10.1 Generate final Table 1 for `bloodbrain`

I'll choose to treat `tlratio` and its logarithm as non-Normal, but otherwise, use t tests, but admittedly, that's an arbitrary decision, really.

```r
print(bb.att1, nonnormal = c("tlratio", "logTL"))
```

```
                        Stratified by solution
                         BD                      NS
  n                            17                      17
  sactime (%)
     0.5                        5 (29.4)                4 (23.5)
     3                          4 (23.5)                5 (29.4)
     24                         4 (23.5)                4 (23.5)
```

```
    72                           4 (23.5)                 4 (23.5)
  postin (%)
    9                            1 ( 5.9)                 2 (11.8)
    10                          14 (82.4)                13 (76.5)
    11                           2 (11.8)                 2 (11.8)
  sex = M (%)                    4 (23.5)                 4 (23.5)
  wt.init (mean (sd))       242.82 (27.23)           240.47 (28.54)
  wt.loss (mean (sd))         3.34 (4.68)              3.94 (3.88)
  wt.tumor (mean (sd))      157.29 (84.00)           208.53 (116.68)
  brain (mean (sd))       56043.41 (33675.40)      23887.18 (14610.53)
  liver (mean (sd))      672577.35 (694479.58)    664975.47 (700773.13)
  tlratio (median [IQR])      0.12 [0.06, 2.84]        0.05 [0.03, 0.94]
  logTL (median [IQR])       -2.10 [-2.74, 1.04]      -2.95 [-3.41, -0.07]
                        Stratified by solution
                         p      test
  n
  sactime (%)             0.974
    0.5
    3
    24
    72
  postin (%)              0.831
    9
    10
    11
  sex = M (%)             1.000
  wt.init (mean (sd))     0.807
  wt.loss (mean (sd))     0.684
  wt.tumor (mean (sd))    0.152
  brain (mean (sd))       0.001
  liver (mean (sd))       0.975
  tlratio (median [IQR])  0.221 nonnorm
  logTL (median [IQR])    0.221 nonnorm
```

Or, we can get an Excel-readable version, using

```
bb.t1 <- print(bb.att1, nonnormal = c("tlratio", "logTL"), quote = FALSE,
               noSpaces = TRUE, printToggle = FALSE)

write.csv(bb.t1, file = "bb-table1.csv")
```

which, when dropped into Excel, will look like this:

	A	B	C	D	E
1		BD	NS	p	test
2	n	17	17		
3	sex = M (%)	4 (23.5)	4 (23.5)	1	
4	sactime (%)			0.974	
5	0.5	5 (29.4)	4 (23.5)		
6	3	4 (23.5)	5 (29.4)		
7	24	4 (23.5)	4 (23.5)		
8	72	4 (23.5)	4 (23.5)		
9	postin (%)			0.831	
10	9	1 (5.9)	2 (11.8)		
11	10	14 (82.4)	13 (76.5)		
12	11	2 (11.8)	2 (11.8)		
13	wt.init (mean (sd))	242.82 (27.23)	240.47 (28.54)	0.807	
14	wt.loss (mean (sd))	3.34 (4.68)	3.94 (3.88)	0.684	
15	wt.tumor (mean (sd))	157.29 (84.00)	208.53 (116.68)	0.152	
16	brain (mean (sd))	56043.41 (33675.40)	23887.18 (14610.53)	0.001	
17	liver (mean (sd))	672577.35 (694479.58)	664975.47 (700773.13)	0.975	
18	tlratio (median [IQR])	0.12 [0.06, 2.84]	0.05 [0.03, 0.94]	0.221	nonnorm
19	logTL (median [IQR])	-2.10 [-2.74, 1.04]	-2.95 [-3.41, -0.07]	0.221	nonnorm
20					

One thing I would definitely clean up here, in practice, is to change the presentation of the p value for `sex` from 1 to > 0.99, or just omit it altogether. I'd also drop the `computer-ese` where possible, add units for the measures, round **a lot**, identify the outcomes carefully, and use notes to indicate deviations from the main approach.

1.10.2 A More Finished Version (after Cleanup in Word)

Table 1. Comparing Rats Receiving BD to those Receiving NS on Available Covariates and Design Variables, and Key Outcomes

	Barrier Disruption (BD: treatment)	Normal Saline (NS: control)	p
# of Rats	17	17	
Sex = Male	4 (23.5)	4 (23.5)	-
Sacrifice Time (hours)			0.97
0.5	5 (29.4)	4 (23.5)	
3	4 (23.5)	5 (29.4)	
24	4 (23.5)	4 (23.5)	
72	4 (23.5)	4 (23.5)	
Days post-inoculation of lung cancer cells			0.83
9	1 (5.9)	2 (11.8)	
10	14 (82.4)	13 (76.5)	
11	2 (11.8)	2 (11.8)	
Initial Weight (g)	243 (27)	240 (29)	0.81
Weight Loss (g)	3.3 (4.7)	3.9 (3.9)	0.68
Tumor Weight (10^{-4} g)	157.3 (84.0)	208.5 (116.7)	0.15
Key Outcomes: mean (sd) unless otherwise indicated			
Brain Tumor Antibody Count (per g)	56,043 (33,675)	23,887 (14,611)	0.001
Liver Antibody Count (per g)	672,577 (694,480)	664,975 (700,773)	0.98
Tumor/Liver Ratio (median [Q25, Q75])	0.12 [0.06, 2.84]	0.05 [0.03, 0.94]	0.22
Natural Log of Tumor/Liver Ratio (median [Q25, Q75])	-2.10 [-2.74, 1.04]	-2.95 [-3.41, -0.07]	0.22

Table 1 Notes:

- Categorical variables are summarized with counts, percentages and p values based on approximate chi-square tests.
- Continuous variables, unless otherwise indicated, are summarized with means, standard deviations and p values based on t tests.
- The Tumor / Liver ratio and its natural logarithm are summarized with the median and quartiles and a p value from a non-parametric (Wilcoxon signed rank) test.

Chapter 2

Linear Regression on a small SMART data set

2.1 BRFSS and SMART

The Centers for Disease Control analyzes Behavioral Risk Factor Surveillance System (BRFSS) survey data for specific metropolitan and micropolitan statistical areas (MMSAs) in a program called the Selected Metropolitan/Micropolitan Area Risk Trends of BRFSS (SMART BRFSS.)

In this work, we will focus on data from the 2016 SMART, and in particular on data from the Cleveland-Elyria, OH, Metropolitan Statistical Area. The purpose of this survey is to provide localized health information that can help public health practitioners identify local emerging health problems, plan and evaluate local responses, and efficiently allocate resources to specific needs.

2.1.1 Key resources

- the full data are available in the form of the 2016 SMART BRFSS MMSA Data, found in a zipped SAS Transport Format file. The data were released in August 2017.
- the MMSA Variable Layout PDF which simply lists the variables included in the data file
- the Calculated Variables PDF which describes the risk factors by data variable names - there is also an online summary matrix of these calculated variables, as well.
- the lengthy 2016 Survey Questions PDF which lists all questions asked as part of the BRFSS in 2016
- the enormous Codebook for the 2016 BRFSS Survey PDF which identifies the variables by name for us.

Later this term, we'll use all of those resources to help construct a more complete data set than we'll study today. I'll also demonstrate how I built the `smartcle1` data set that we'll use in this Chapter.

2.2 The `smartcle1` data: Cookbook

The `smartcle1.csv` data file available on the Data and Code page of our website describes information on 11 variables for 1036 respondents to the BRFSS 2016, who live in the Cleveland-Elyria, OH, Metropolitan Statistical Area. The variables in the `smartcle1.csv` file are listed below, along with (in some cases) the BRFSS items that generate these responses.

Variable	Description
`SEQNO`	respondent identification number (all begin with 2016)

Variable	Description
`physhealth`	Now thinking about your physical health, which includes physical illness and injury, for how many days during the past 30 days was your physical health not good?
`menthealth`	Now thinking about your mental health, which includes stress, depression, and problems with emotions, for how many days during the past 30 days was your mental health not good?
`poorhealth`	During the past 30 days, for about how many days did poor physical or mental health keep you from doing your usual activities, such as self-care, work, or recreation?
`genhealth`	Would you say that in general, your health is … (five categories: Excellent, Very Good, Good, Fair or Poor)
`bmi`	Body mass index, in kg/m^2
`female`	Sex, 1 = female, 0 = male
`internet30`	Have you used the internet in the past 30 days? (1 = yes, 0 = no)
`exerany`	During the past month, other than your regular job, did you participate in any physical activities or exercises such as running, calisthenics, golf, gardening, or walking for exercise? (1 = yes, 0 = no)
`sleephrs`	On average, how many hours of sleep do you get in a 24-hour period?
`alcdays`	How many days during the past 30 days did you have at least one drink of any alcoholic beverage such as beer, wine, a malt beverage or liquor?

```
str(smartcle1)
```

```
Classes 'tbl_df', 'tbl' and 'data.frame':   1036 obs. of  11 variables:
 $ SEQNO     : num  2.02e+09 2.02e+09 2.02e+09 2.02e+09 2.02e+09 ...
 $ physhealth: int  0 0 1 0 5 4 2 2 0 0 ...
 $ menthealth: int  0 0 5 0 0 18 0 3 0 0 ...
 $ poorhealth: int  NA NA 0 NA 0 6 0 0 NA NA ...
 $ genhealth : Factor w/ 5 levels "1_Excellent",..: 2 1 2 3 1 2 3 3 2 3 ...
 $ bmi       : num  26.7 23.7 26.9 21.7 24.1 ...
 $ female    : int  1 0 0 1 0 0 1 1 0 0 ...
 $ internet30: int  1 1 1 1 1 1 1 1 1 1 ...
 $ exerany   : int  1 1 0 1 1 1 1 1 1 0 ...
 $ sleephrs  : int  6 6 8 9 7 5 9 7 7 7 ...
 $ alcdays   : int  1 4 4 3 2 28 4 2 4 25 ...
```

2.3 `smartcle2`: Omitting Missing Observations: Complete-Case Analyses

For the purpose of fitting our first few models, we will eliminate the missingness problem, and look only at the *complete cases* in our `smartcle1` data.

To inspect the missingness in our data, we might consider using the `skim` function from the `skimr` package. We'll exclude the respondent identifier code (`SEQNO`) from this summary as uninteresting.

```
smartcle1 %>%
    skim(-SEQNO)
```

```
Skim summary statistics
 n obs: 1036
 n variables: 11
```

```
Variable type: factor
  variable missing complete    n n_unique
 genhealth       3     1033 1036        5
                             top_counts ordered
 2_V: 350, 3_G: 344, 1_E: 173, 4_F: 122   FALSE

Variable type: integer
   variable missing complete    n mean   sd p0 p25 median p75 p100
    alcdays      46      990 1036 4.65 8.05  0   0      1   4   30
    exerany       3     1033 1036 0.76 0.43  0   1      1   1    1
     female       0     1036 1036 0.6  0.49  0   0      1   1    1
 internet30       6     1030 1036 0.81 0.39  0   1      1   1    1
 menthealth      11     1025 1036 2.72 6.82  0   0      0   2   30
 physhealth      17     1019 1036 3.97 8.67  0   0      0   2   30
 poorhealth     543      493 1036 4.07 8.09  0   0      0   3   30
   sleephrs       8     1028 1036 7.02 1.53  1   6      7   8   20

Variable type: numeric
 variable missing complete    n  mean   sd    p0  p25 median   p75  p100
      bmi      84      952 1036 27.89 6.47 12.71 23.7   26.68 30.53 66.06
```

Now, we'll create a new tibble called `smartcle2` which contains every variable except `poorhealth`, and which includes all respondents with complete data on the variables (other than `poorhealth`). We'll store those observations with complete data in the `smartcle2` tibble.

```
smartcle2 <- smartcle1 %>%
    select(-poorhealth) %>%
    filter(complete.cases(.))

smartcle2
```

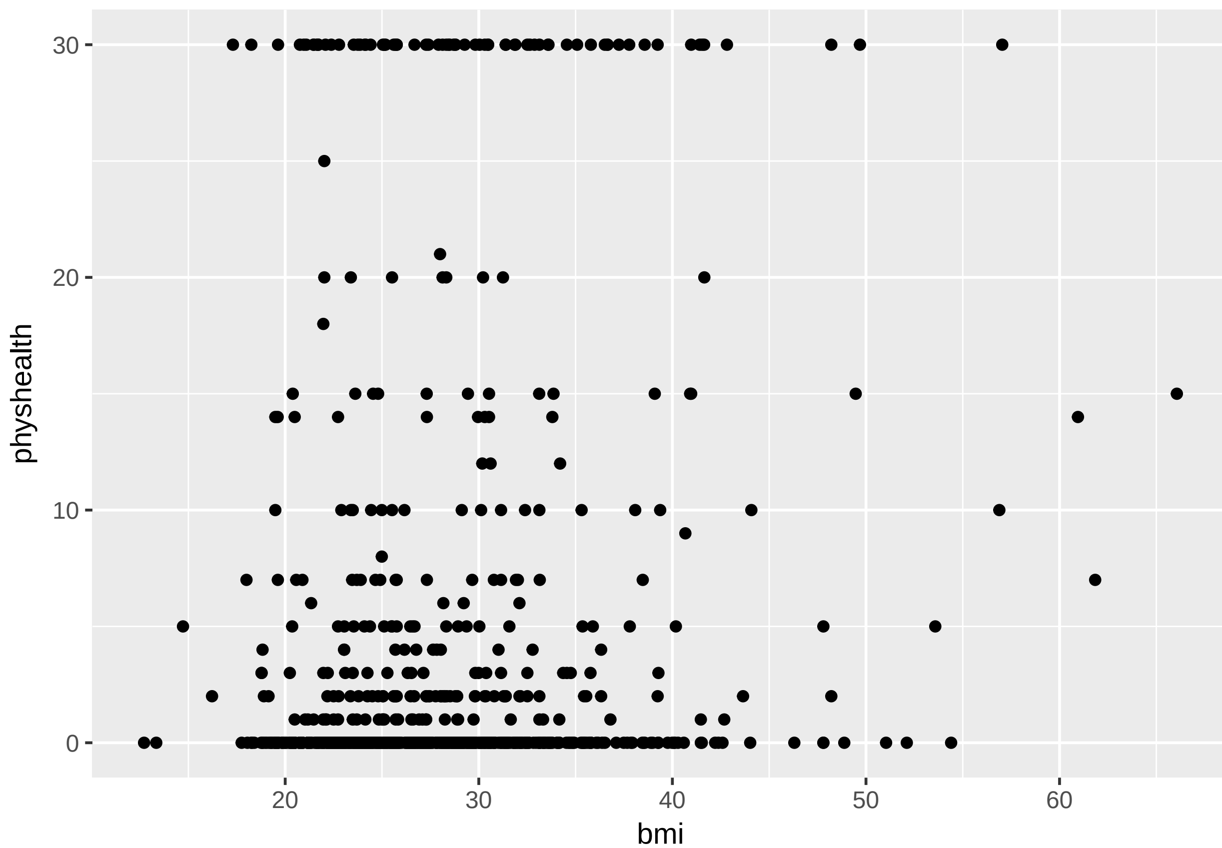
```
# A tibble: 896 x 10
     SEQNO physhealth menthealth genhealth   bmi female internet30 exerany
     <dbl>      <int>      <int> <fct>     <dbl>  <int>      <int>   <int>
 1  2.02e9          0          0 2_VeryGo~  26.7      1          1       1
 2  2.02e9          0          0 1_Excell~  23.7      0          1       1
 3  2.02e9          1          5 2_VeryGo~  26.9      0          1       0
 4  2.02e9          0          0 3_Good     21.7      1          1       1
 5  2.02e9          5          0 1_Excell~  24.1      0          1       1
 6  2.02e9          4         18 2_VeryGo~  27.6      0          1       1
 7  2.02e9          2          0 3_Good     25.7      1          1       1
 8  2.02e9          2          3 3_Good     28.5      1          1       1
 9  2.02e9          0          0 2_VeryGo~  28.6      0          1       1
10  2.02e9          0          0 3_Good     23.1      0          1       0
# ... with 886 more rows, and 2 more variables: sleephrs <int>, alcdays
#   <int>
```

Note that there are only 896 respondents with **complete** data on the 10 variables (excluding `poorhealth`) in the `smartcle2` tibble, as compared to our original `smartcle1` data which described 1036 respondents and 11 variables, but with lots of missing data.

2.4 Can we use bmi to predict physhealth?

We'll start with an effort to predict `physhealth` using `bmi`. A natural graph would be a scatterplot.

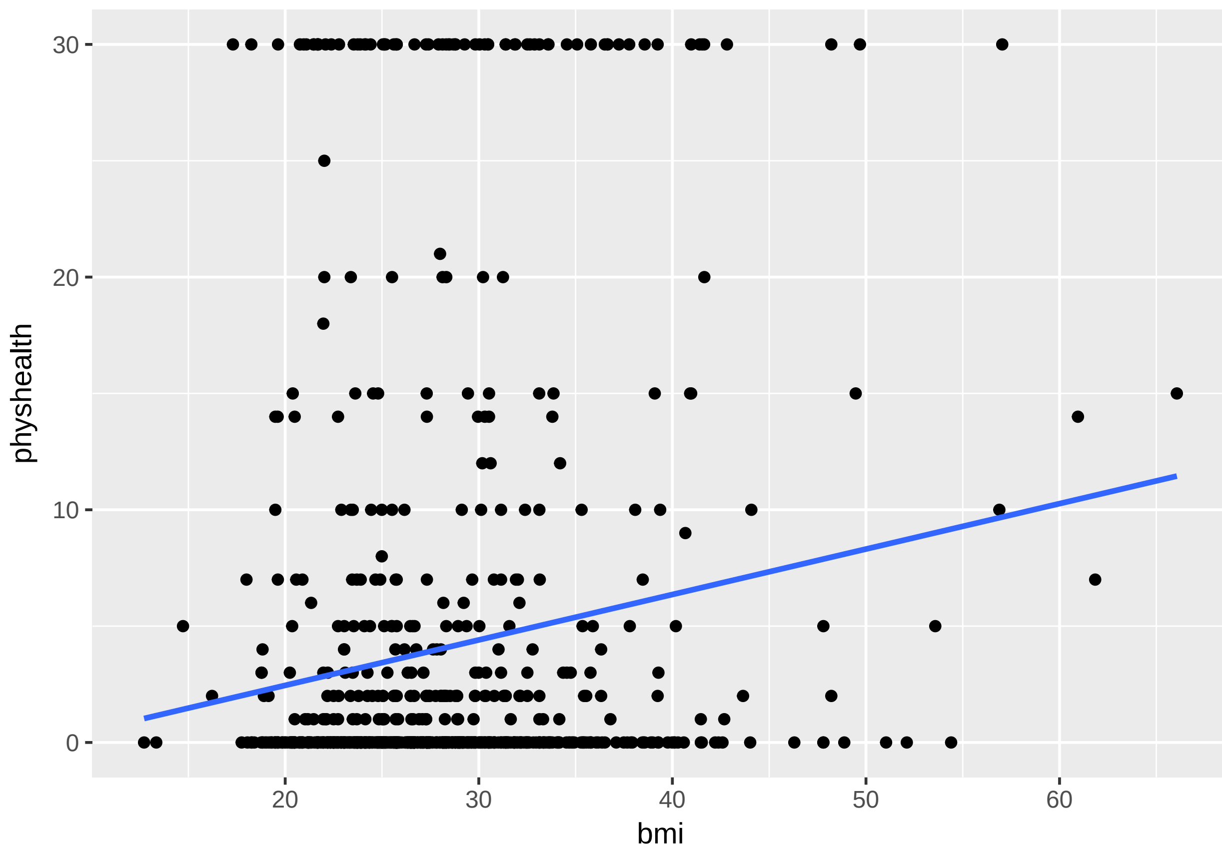
```r
ggplot(data = smartcle2, aes(x = bmi, y = physhealth)) +
    geom_point()
```



A good question to ask ourselves here might be: "In what BMI range can we make a reasonable prediction of `physhealth`?"

Now, we might take the plot above and add a simple linear model …

```r
ggplot(data = smartcle2, aes(x = bmi, y = physhealth)) +
    geom_point() +
    geom_smooth(method = "lm", se = FALSE)
```



which shows the same least squares regression model that we can fit with the `lm` command.

2.4.0.1 Fitting a Simple Regression Model

```r
model_A <- lm(physhealth ~ bmi, data = smartcle2)

model_A
```

```

Call:
lm(formula = physhealth ~ bmi, data = smartcle2)

Coefficients:
(Intercept)          bmi
    -1.4514       0.1953
```

```r
summary(model_A)
```

```

Call:
lm(formula = physhealth ~ bmi, data = smartcle2)

Residuals:
   Min     1Q Median     3Q    Max
-9.171 -4.057 -3.193 -1.576 28.073
```

```
Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -1.45143    1.29185  -1.124    0.262
bmi          0.19527    0.04521   4.319 1.74e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 8.556 on 894 degrees of freedom
Multiple R-squared:  0.02044,   Adjusted R-squared:  0.01934
F-statistic: 18.65 on 1 and 894 DF,  p-value: 1.742e-05
```

```r
confint(model_A, level = 0.95)
```

```
                 2.5 %    97.5 %
(Intercept) -3.9868457 1.0839862
bmi          0.1065409 0.2840068
```

The model coefficients can be obtained by printing the model object, and the `summary` function provides several useful descriptions of the model's residuals, its statistical significance, and quality of fit.

2.4.1 Model Summary for a Simple (One-Predictor) Regression

The fitted model predicts `physhealth` with the equation -1.45 + 0.195*`bmi`, as we can read off from the model coefficients.

Each of the 896 respondents included in the `smartcle2` data makes a contribution to this model.

2.4.1.1 Residuals

Suppose Harry is one of the people in that group, and Harry's data is `bmi` = 20, and `physhealth` = 3.

- Harry's *observed* value of `physhealth` is just the value we have in the data for them, in this case, observed `physhealth` = 3 for Harry.
- Harry's *fitted* or *predicted* `physhealth` value is the result of calculating -1.45 + 0.195*`bmi` for Harry. So, if Harry's BMI was 20, then Harry's predicted `physhealth` value is -1.45 + (0.195*20) = 2.45.
- The *residual* for Harry is then his *observed* outcome minus his *fitted* outcome, so Harry has a residual of 3 - 2.45 = 0.55.
- Graphically, a residual represents vertical distance between the observed point and the fitted regression line.
- Points above the regression line will have positive residuals, and points below the regression line will have negative residuals. Points on the line have zero residuals.

The residuals are summarized at the top of the `summary` output for linear model.

- The mean residual will always be zero in an ordinary least squares model, but a five number summary of the residuals is provided by the summary, as is an estimated standard deviation of the residuals (called here the Residual standard error.)
- In the `smartcle2` data, the minimum residual was -9.17, so for one subject, the observed value was 9.17 days smaller than the predicted value. This means that the prediction was 9.17 days too large for that subject.
- Similarly, the maximum residual was 28.07 days, so for one subject the prediction was 28.07 days too small. Not a strong performance.
- In a least squares model, the residuals are assumed to follow a Normal distribution, with mean zero, and standard deviation (for the `smartcle2` data) of about 8.6 days. Thus, by the definition of a Normal distribution, we'd expect
- about 68% of the residuals to be between -8.6 and +8.6 days,

- about 95% of the residuals to be between -17.2 and +17.2 days,
- about all (99.7%) of the residuals to be between -25.8 and +25.8 days.

2.4.1.2 Coefficients section

The `summary` for a linear model shows Estimates, Standard Errors, t values and *p* values for each coefficient fit.

- The Estimates are the point estimates of the intercept and slope of `bmi` in our model.
- In this case, our estimated slope is 0.195, which implies that if Harry's BMI is 20 and Sally's BMI is 21, we predict that Sally's `physhealth` will be 0.195 days larger than Harry's.
- The Standard Errors are also provided for each estimate. We can create rough 95% confidence intervals by adding and subtracting two standard errors from each coefficient, or we can get a slightly more accurate answer with the `confint` function.
- Here, the 95% confidence interval for the slope of `bmi` is estimated to be (0.11, 0.28). This is a good measure of the uncertainty in the slope that is captured by our model. We are 95% confident in the process of building this interval, but this doesn't mean we're 95% sure that the true slope is actually in that interval.

Also available are a *t* value (just the Estimate divided by the Standard Error) and the appropriate *p* value for testing the null hypothesis that the true value of the coefficient is 0 against a two-tailed alternative.

- If a slope coefficient is statistically significantly different from 0, this implies that 0 will not be part of the uncertainty interval obtained through `confint`.
- If the slope was zero, it would suggest that `bmi` would add no predictive value to the model. But that's unlikely here.

If the `bmi` slope coefficient is associated with a small *p* value, as in the case of our `model_A`, it suggests that the model including `bmi` is statistically significantly better at predicting `physhealth` than the model without `bmi`.

- Without `bmi` our `model_A` would become an *intercept-only* model, in this case, which would predict the mean `physhealth` for everyone, regardless of any other information.

2.4.1.3 Model Fit Summaries

The `summary` of a linear model also displays:

- The residual standard error and associated degrees of freedom for the residuals.
- For a simple (one-predictor) least regression like this, the residual degrees of freedom will be the sample size minus 2.
- The multiple R-squared (or coefficient of determination)
- This is interpreted as the proportion of variation in the outcome (`physhealth`) accounted for by the model, and will always fall between 0 and 1 as a result.
- Our model_A accounts for a mere 2% of the variation in `physhealth`.
- The Adjusted R-squared value "adjusts" for the size of our model in terms of the number of coefficients included in the model.
- The adjusted R-squared will always be less than the Multiple R-squared.
- We still hope to find models with relatively large adjusted R^2 values.
- In particular, we hope to find models where the adjusted R^2 isn't substantially less than the Multiple R-squared.
- The adjusted R-squared is usually a better estimate of likely performance of our model in new data than is the Multiple R-squared.
- The adjusted R-squared result is no longer interpretable as a proportion of anything - in fact, it can fall below 0.

- We can obtain the adjusted R^2 from the raw R^2, the number of observations N and the number of predictors p included in the model, as follows:

$$R^2_{adj} = 1 - \frac{(1 - R^2)(N - 1)}{N - p - 1},$$

- The F statistic and p value from a global ANOVA test of the model.
  - Obtaining a statistically significant result here is usually pretty straightforward, since the comparison is between our model, and a model which simply predicts the mean value of the outcome for everyone.
  - In a simple (one-predictor) linear regression like this, the t statistic for the slope is just the square root of the F statistic, and the resulting p values for the slope's t test and for the global F test will be identical.
- To see the complete ANOVA F test for this model, we can run `anova(model_A)`.

```
anova(model_A)
```

```
Analysis of Variance Table

Response: physhealth
           Df Sum Sq Mean Sq F value    Pr(>F)
bmi         1   1366  1365.5  18.655 1.742e-05 ***
Residuals 894  65441    73.2
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

2.4.2 Using the `broom` package

The `broom` package has three functions of particular use in a linear regression model:

- `tidy` builds a data frame/tibble containing information about the coefficients in the model, their standard errors, t statistics and p values.

```
tidy(model_A)
```

```
         term   estimate  std.error statistic      p.value
1 (Intercept) -1.4514298 1.29185199 -1.123526 2.615156e-01
2         bmi  0.1952739 0.04521145  4.319125 1.741859e-05
```

- `glance` builds a data frame/tibble containing summary statistics about the model, including
- the (raw) multiple R^2 and adjusted R^2
- `sigma` which is the residual standard error
- the F `statistic`, `p.value` model `df` and `df.residual` associated with the global ANOVA test, plus
- several statistics that will be useful in comparing models down the line:
- the model's log likelihood function value, `logLik`
- the model's Akaike's Information Criterion value, `AIC`
- the model's Bayesian Information Criterion value, `BIC`
- and the model's `deviance` statistic

```
glance(model_A)
```

```
   r.squared adj.r.squared    sigma statistic      p.value df    logLik
1 0.02044019    0.01934449 8.555737  18.65484 1.741859e-05  2 -3193.723
       AIC     BIC deviance df.residual
1 6393.446 6407.84 65441.36         894
```

- `augment` builds a data frame/tibble which adds fitted values, residuals and other diagnostic summaries that describe each observation to the original data used to fit the model, and this includes

- `.fitted` and `.resid`, the fitted and residual values, in addition to
- `.hat`, the leverage value for this observation
- `.cooksd`, the Cook's distance measure of *influence* for this observation
- `.stdresid`, the standardized residual (think of this as a z-score - a measure of the residual divided by its associated standard deviation `.sigma`)
- and `se.fit` which will help us generate prediction intervals for the model downstream

Note that each of the new columns begins with `.` to avoid overwriting any data.

```r
augment(model_A)
```

```
    physhealth   bmi   .fitted   .se.fit       .resid        .hat   .sigma
1            0 26.69  3.760430 0.2907252 -3.76043009 0.001154651 8.559600
2            0 23.70  3.176561 0.3422908 -3.17656119 0.001600574 8.559865
3            1 26.92  3.805343 0.2890054 -2.80534308 0.001141030 8.560010
4            0 21.66  2.778202 0.4005101 -2.77820248 0.002191352 8.560020
5            5 24.09  3.252718 0.3329154  1.74728200 0.001514095 8.560326
6            4 27.64  3.945940 0.2860087  0.05405972 0.001117490 8.560526
7            2 25.71  3.569062 0.3019825 -1.56906169 0.001245801 8.560365
8            2 28.52  4.117781 0.2873552 -2.11778129 0.001128037 8.560232
9            0 28.63  4.139261 0.2879099 -4.13926142 0.001132396 8.559404
10           0 23.10  3.059397 0.3579331 -3.05939686 0.001750205 8.559913
11           0 26.60  3.742855 0.2914965 -3.74285544 0.001160785 8.559608
12          30 20.76  2.602456 0.4299951 27.39754402 0.002525877 8.511164
13           0 21.66  2.778202 0.4005101 -2.77820248 0.002191352 8.560020
14           3 32.51  4.896924 0.3546724 -1.89692407 0.001718462 8.560290
15           0 32.60  4.914499 0.3570966 -4.91449872 0.001742034 8.558943
16           0 18.27  2.116224 0.5195177 -2.11622402 0.003687108 8.560232
17           0 21.20  2.688376 0.4153437 -2.68837649 0.002356680 8.560052
18           0 33.13  5.017994 0.3719552 -5.01799388 0.001890021 8.558876
19           3 27.14  3.848303 0.2877025 -0.84830334 0.001130765 8.560479
20           0 13.34  1.153524 0.7162199 -1.15352380 0.007007739 8.560438
21           0 26.60  3.742855 0.2914965 -3.74285544 0.001160785 8.559608
22           0 36.37  5.650681 0.4791047 -5.65068125 0.003135784 8.558431
23           0 27.32  3.883453 0.2868888 -3.88345263 0.001124378 8.559538
24           1 21.03  2.655180 0.4209535 -1.65517993 0.002420770 8.560346
25           0 28.04  4.024050 0.2859361 -4.02404983 0.001116923 8.559465
26           0 26.68  3.758477 0.2908082 -3.75847735 0.001155310 8.559601
27           1 21.17  2.682518 0.4163289 -1.68251827 0.002367872 8.560340
28           6 32.10  4.816862 0.3440220  1.18313822 0.001616805 8.560434
29           0 21.19  2.686424 0.4156719 -2.68642375 0.002360405 8.560053
30           0 27.09  3.838540 0.2879690 -3.83853964 0.001132861 8.559561
31           0 27.32  3.883453 0.2868888 -3.88345263 0.001124378 8.559538
32           0 31.41  4.682123 0.3276877 -4.68212280 0.001466917 8.559090
33           0 12.71  1.030501 0.7424237 -1.03050125 0.007529893 8.560456
34           0 31.83  4.764138 0.3373811 -4.76413783 0.001554986 8.559039
35           0 18.96  2.250963 0.4937660 -2.25096300 0.003330639 8.560193
36           0 25.90  3.606164 0.2993209 -3.60616373 0.001223937 8.559674
37           0 37.86  5.941639 0.5346811 -5.94163933 0.003905483 8.558207
38           0 23.92  3.219521 0.3369208 -3.21952144 0.001550746 8.559847
39           2 28.04  4.024050 0.2859361 -2.02404983 0.001116923 8.560258
40           0 24.11  3.256623 0.3324527 -3.25662348 0.001509889 8.559831
41           0 20.32  2.516535 0.4450535 -2.51653548 0.002705887 8.560110
42           3 30.38  4.480991 0.3076073 -1.48099071 0.001292642 8.560382
43           0 28.63  4.139261 0.2879099 -4.13926142 0.001132396 8.559404
```

44	1	22.50	2.942233	0.3748880	-1.94223253	0.001919943	8.560279
45	0	25.67	3.561251	0.3025709	-3.56125073	0.001250661	8.559695
46	0	26.31	3.686226	0.2943507	-3.68622602	0.001183628	8.559636
47	0	30.48	4.500518	0.3093068	-4.50051809	0.001306965	8.559199
48	30	40.97	6.548941	0.6578200	23.45105891	0.005911522	8.524265
49	0	26.66	3.754572	0.2909762	-3.75457187	0.001156645	8.559603
50	0	18.76	2.211908	0.5011666	-2.21190822	0.003431227	8.560205
51	0	29.44	4.297433	0.2945592	-4.29743326	0.001185306	8.559316
52	0	22.35	2.912941	0.3793115	-2.91294145	0.001965518	8.559970
53	0	29.15	4.240804	0.2916680	-4.24080383	0.001162152	8.559348
54	0	20.37	2.526299	0.4433231	-2.52629917	0.002684887	8.560107
55	0	28.79	4.170505	0.2888677	-4.17050524	0.001139943	8.559387
56	14	33.80	5.148827	0.3920310	8.85117262	0.002099549	8.555389
57	0	19.29	2.315403	0.4816776	-2.31540338	0.003169553	8.560174
58	2	22.18	2.879745	0.3844078	-0.87974489	0.002018690	8.560475
59	2	25.61	3.549534	0.3034716	-1.54953430	0.001258118	8.560369
60	2	25.05	3.440181	0.3128889	-1.44018093	0.001337413	8.560390
61	0	33.66	5.121489	0.3877264	-5.12148903	0.002053695	8.558807
62	0	25.83	3.592495	0.3002756	-3.59249455	0.001231758	8.559681
63	3	21.97	2.838737	0.3908203	0.16126262	0.002086601	8.560524
64	0	25.76	3.578825	0.3012606	-3.57882538	0.001239852	8.559687
65	30	25.18	3.465567	0.3105443	26.53443347	0.001317444	8.514289
66	0	28.47	4.108018	0.2871312	-4.10801760	0.001126279	8.559421
67	0	31.50	4.699697	0.3296968	-4.69969745	0.001484960	8.559079
68	30	31.39	4.678217	0.3272465	25.32178268	0.001462969	8.518423
69	0	19.49	2.354458	0.4744297	-2.35445816	0.003074886	8.560162
70	1	27.28	3.875642	0.2870499	-2.87564168	0.001125641	8.559984
71	0	29.16	4.242757	0.2917584	-4.24275657	0.001162872	8.559347
72	0	32.18	4.832484	0.3460479	-4.83248369	0.001635903	8.558996
73	0	22.50	2.942233	0.3748880	-2.94223253	0.001919943	8.559958
74	0	40.09	6.377100	0.6222261	-6.37710008	0.005289098	8.557851
75	0	44.02	7.144526	0.7843095	-7.14452643	0.008403499	8.557158
76	0	24.19	3.272245	0.3306201	-3.27224539	0.001493289	8.559824
77	0	34.10	5.207410	0.4014359	-5.20740954	0.002201494	8.558748
78	7	32.02	4.801240	0.3420223	2.19876013	0.001598064	8.560209
79	15	27.31	3.881500	0.2869280	11.11850010	0.001124685	8.552427
80	0	19.88	2.430615	0.4604790	-2.43061497	0.002896709	8.560138
81	0	23.56	3.149223	0.3458137	-3.14922285	0.001633689	8.559876
82	0	23.60	3.157034	0.3447990	-3.15703380	0.001624116	8.559873
83	3	39.28	6.218928	0.5899372	-3.21892824	0.004754411	8.559845
84	0	20.49	2.549732	0.4391899	-2.54973204	0.002635056	8.560099
85	0	24.16	3.266387	0.3313039	-3.26638717	0.001499472	8.559827
86	0	42.21	6.791081	0.7087322	-6.79108070	0.006861980	8.557488
87	0	27.47	3.912744	0.2863856	-3.91274372	0.001120437	8.559523
88	0	28.35	4.084585	0.2866656	-4.08458473	0.001122629	8.559433
89	2	26.66	3.754572	0.2909762	-1.75457187	0.001156645	8.560324
90	0	27.01	3.822918	0.2884316	-3.82291773	0.001136504	8.559569
91	0	24.79	3.389410	0.3178525	-3.38940972	0.001380182	8.559773
92	0	25.76	3.578825	0.3012606	-3.57882538	0.001239852	8.559687
93	0	24.91	3.412843	0.3155169	-3.41284258	0.001359973	8.559763
94	0	24.33	3.299584	0.3274846	-3.29958373	0.001465099	8.559813
95	0	31.01	4.604013	0.3192334	-4.60401325	0.001392201	8.559137
96	1	31.65	4.728989	0.3331288	-3.72898853	0.001516036	8.559615
97	2	27.46	3.910791	0.2864142	-1.91079098	0.001120661	8.560287

98	0	27.38	3.895169	0.2866684	-3.89516907	0.001122651	8.559532
99	1	22.73	2.987146	0.3682447	-1.98714553	0.001852500	8.560267
100	30	25.61	3.549534	0.3034716	26.45046570	0.001258118	8.514585
101	0	22.49	2.940280	0.3751807	-2.94027980	0.001922942	8.559959
102	0	26.49	3.721375	0.2925132	-3.72137531	0.001168897	8.559619
103	0	54.40	9.171469	1.2332475	-9.17146930	0.020777134	8.554906
104	30	22.08	2.860218	0.3874456	27.13978250	0.002050721	8.512114
105	2	31.39	4.678217	0.3272465	-2.67821732	0.001462969	8.560056
106	0	27.47	3.912744	0.2863856	-3.91274372	0.001120437	8.559523
107	25	22.02	2.848501	0.3892821	22.15149893	0.002070208	8.528305
108	1	33.13	5.017994	0.3719552	-4.01799388	0.001890021	8.559468
109	0	26.51	3.725281	0.2923223	-3.72528079	0.001167372	8.559617
110	7	25.71	3.569062	0.3019825	3.43093831	0.001245801	8.559755
111	0	27.31	3.881500	0.2869280	-3.88149990	0.001124685	8.559539
112	0	21.66	2.778202	0.4005101	-2.77820248	0.002191352	8.560020
113	0	35.36	5.453455	0.4432954	-5.45345463	0.002684550	8.558575
114	2	24.25	3.283962	0.3292651	-1.28396182	0.001481073	8.560418
115	0	21.16	2.680566	0.4166577	-2.68056554	0.002371614	8.560055
116	15	23.62	3.160939	0.3442940	11.83906072	0.001619363	8.551338
117	0	25.03	3.436275	0.3132578	-3.43627545	0.001340569	8.559752
118	0	26.87	3.795579	0.2893483	-3.79557939	0.001143739	8.559582
119	30	25.05	3.440181	0.3128889	26.55981907	0.001337413	8.514200
120	0	27.40	3.899075	0.2866006	-3.89907454	0.001122120	8.559530
121	0	29.02	4.215418	0.2905548	-4.21541823	0.001153297	8.559362
122	0	19.32	2.321262	0.4805865	-2.32126160	0.003155211	8.560172
123	30	17.30	1.926808	0.5566620	28.07319164	0.004233195	8.508602
124	0	27.83	3.983042	0.2858316	-3.98304231	0.001116106	8.559487
125	0	29.73	4.354063	0.2979997	-4.35406268	0.001213157	8.559284
126	0	21.34	2.715715	0.4107744	-2.71571483	0.002305111	8.560042
127	0	27.77	3.971326	0.2858596	-3.97132588	0.001116326	8.559493
128	0	26.31	3.686226	0.2943507	-3.68622602	0.001183628	8.559636
129	2	31.39	4.678217	0.3272465	-2.67821732	0.001462969	8.560056
130	0	32.51	4.896924	0.3546724	-4.89692407	0.001718462	8.558955
131	30	34.55	5.295283	0.4159739	24.70471722	0.002363836	8.520418
132	0	25.11	3.451897	0.3117952	-3.45189736	0.001328079	8.559745
133	14	19.61	2.377891	0.4701109	11.62210898	0.003019157	8.551660
134	0	22.50	2.942233	0.3748880	-2.94223253	0.001919943	8.559958
135	15	24.80	3.391362	0.3176549	11.60863754	0.001378467	8.551695
136	0	24.66	3.364024	0.3204671	-3.36402411	0.001402982	8.559785
137	0	34.70	5.324574	0.4209268	-5.32457387	0.002420463	8.558667
138	5	26.68	3.758477	0.2908082	1.24152265	0.001155310	8.560425
139	15	24.54	3.340591	0.3229568	11.65940875	0.001424866	8.551617
140	0	28.93	4.197844	0.2898514	-4.19784358	0.001147720	8.559372
141	0	29.82	4.371637	0.2991762	-4.37163733	0.001222755	8.559274
142	0	31.99	4.795382	0.3412793	-4.79538165	0.001591128	8.559019
143	4	27.83	3.983042	0.2858316	0.01695769	0.001116106	8.560526
144	2	28.25	4.065057	0.2863555	-2.06505734	0.001120202	8.560247
145	1	20.49	2.549732	0.4391899	-1.54973204	0.002635056	8.560368
146	3	26.33	3.690131	0.2941359	-0.69013149	0.001181902	8.560495
147	30	23.87	3.209758	0.3381230	26.79024225	0.001561833	8.513379
148	0	30.78	4.559100	0.3147401	-4.55910026	0.001353285	8.559164
149	5	25.76	3.578825	0.3012606	1.42117462	0.001239852	8.560394
150	5	23.54	3.145317	0.3463235	1.85468263	0.001638510	8.560300
151	0	42.38	6.824277	0.7157721	-6.82427726	0.006998979	8.557458

152	30	33.60	5.109773	0.3858987	24.89022740	0.002034379	8.519826
153	10	23.39	3.116026	0.3501976	6.88397371	0.001675373	8.557420
154	0	28.25	4.065057	0.2863555	-4.06505734	0.001120202	8.559444
155	4	18.83	2.225577	0.4985703	1.77442260	0.003395767	8.560319
156	7	18.00	2.063500	0.5297538	4.93649992	0.003833834	8.558926
157	0	29.49	4.307197	0.2951137	-4.30719695	0.001189773	8.559311
158	30	30.04	4.414598	0.3022636	25.58540241	0.001248122	8.517549
159	0	25.40	3.508527	0.3067922	-3.50852679	0.001285801	8.559720
160	2	28.04	4.024050	0.2859361	-2.02404983	0.001116923	8.560258
161	2	31.32	4.664548	0.3257171	-2.66454815	0.001449327	8.560061
162	0	24.92	3.414795	0.3153257	-3.41479532	0.001358325	8.559762
163	5	35.89	5.556950	0.4618697	-0.55694978	0.002914232	8.560505
164	2	28.25	4.065057	0.2863555	-2.06505734	0.001120202	8.560247
165	30	39.24	6.211117	0.5883558	23.78888272	0.004728956	8.523255
166	0	32.44	4.883255	0.3528079	-4.88325490	0.001700441	8.558963
167	2	29.80	4.367732	0.2989104	-2.36773186	0.001220583	8.560159
168	0	23.82	3.199994	0.3393361	-3.19999406	0.001573060	8.559855
169	0	23.92	3.219521	0.3369208	-3.21952144	0.001550746	8.559847
170	0	23.54	3.145317	0.3463235	-3.14531737	0.001638510	8.559878
171	0	27.14	3.848303	0.2877025	-3.84830334	0.001130765	8.559556
172	7	33.15	5.021899	0.3725345	1.97810065	0.001895912	8.560269
173	10	19.49	2.354458	0.4744297	7.64554184	0.003074886	8.556690
174	30	32.51	4.896924	0.3546724	25.10307593	0.001718462	8.519138
175	0	25.73	3.572967	0.3016919	-3.57296717	0.001243404	8.559690
176	30	26.68	3.758477	0.2908082	26.24152265	0.001155310	8.515315
177	0	23.90	3.215616	0.3374004	-3.21561597	0.001555164	8.559848
178	3	18.78	2.215814	0.5004241	0.78418630	0.003421068	8.560485
179	0	32.10	4.816862	0.3440220	-4.81686178	0.001616805	8.559006
180	30	30.31	4.467322	0.3064517	25.53267847	0.001282949	8.517725
181	30	36.51	5.678020	0.4841993	24.32198041	0.003202827	8.521622
182	0	23.99	3.233191	0.3352560	-3.23319061	0.001535459	8.559841
183	0	24.84	3.399173	0.3168701	-3.39917341	0.001371664	8.559769
184	0	23.04	3.047680	0.3595725	-3.04768043	0.001766274	8.559917
185	0	22.73	2.987146	0.3682447	-2.98714553	0.001852500	8.559941
186	0	25.83	3.592495	0.3002756	-3.59249455	0.001231758	8.559681
187	0	31.47	4.693839	0.3290229	-4.69383924	0.001478895	8.559083
188	0	29.62	4.332583	0.2966312	-4.33258256	0.001202040	8.559296
189	10	33.13	5.017994	0.3719552	4.98200612	0.001890021	8.558899
190	0	25.71	3.569062	0.3019825	-3.56906169	0.001245801	8.559692
191	0	29.23	4.256426	0.2924097	-4.25642574	0.001168070	8.559339
192	0	33.66	5.121489	0.3877264	-5.12148903	0.002053695	8.558807
193	0	29.99	4.404834	0.3015359	-4.40483389	0.001242119	8.559255
194	0	26.66	3.754572	0.2909762	-3.75457187	0.001156645	8.559603
195	0	26.51	3.725281	0.2923223	-3.72528079	0.001167372	8.559617
196	0	38.51	6.068567	0.5597375	-6.06856735	0.004280101	8.558106
197	0	22.28	2.899272	0.3813995	-2.89927228	0.001987217	8.559975
198	0	22.89	3.018389	0.3637271	-3.01838935	0.001807326	8.559929
199	0	31.84	4.766091	0.3376215	-4.76609057	0.001557203	8.559038
200	0	22.18	2.879745	0.3844078	-2.87974489	0.002018690	8.559982
201	2	30.31	4.467322	0.3064517	-2.46732153	0.001282949	8.560127
202	14	30.53	4.510282	0.3101777	9.48971821	0.001314336	8.554626
203	0	25.20	3.469472	0.3101919	-3.46947201	0.001314456	8.559737
204	0	34.93	5.369487	0.4286186	-5.36948686	0.002509732	8.558635
205	0	23.19	3.076972	0.3554987	-3.07697151	0.001726479	8.559905

206	1	26.52	3.727234	0.2922279	-2.72723353	0.001166617	8.560039
207	3	18.78	2.215814	0.5004241	0.78418630	0.003421068	8.560485
208	0	28.93	4.197844	0.2898514	-4.19784358	0.001147720	8.559372
209	0	25.80	3.586636	0.3006941	-3.58663634	0.001235193	8.559683
210	0	24.11	3.256623	0.3324527	-3.25662348	0.001509889	8.559831
211	0	23.03	3.045728	0.3598470	-3.04572769	0.001768972	8.559918
212	30	33.13	5.017994	0.3719552	24.98200612	0.001890021	8.519530
213	0	30.21	4.447794	0.3048503	-4.44779415	0.001269575	8.559230
214	0	25.27	3.483141	0.3089761	-3.48314118	0.001304172	8.559731
215	0	24.88	3.406984	0.3160937	-3.40698437	0.001364950	8.559766
216	0	28.27	4.068963	0.2864118	-4.06896282	0.001120643	8.559442
217	30	21.66	2.778202	0.4005101	27.22179752	0.002191352	8.511813
218	8	24.99	3.428464	0.3140022	4.57153551	0.001346948	8.559157
219	0	25.67	3.561251	0.3025709	-3.56125073	0.001250661	8.559695
220	14	20.49	2.549732	0.4391899	11.45026796	0.002635056	8.551924
221	2	27.77	3.971326	0.2858596	-1.97132588	0.001116326	8.560271
222	30	22.78	2.996909	0.3668236	27.00309078	0.001838230	8.512612
223	2	27.29	3.877594	0.2870085	-1.87759442	0.001125317	8.560295
224	0	25.61	3.549534	0.3034716	-3.54953430	0.001258118	8.559701
225	0	30.77	4.557148	0.3145510	-4.55714752	0.001351660	8.559166
226	0	24.75	3.381599	0.3186477	-3.38159876	0.001387097	8.559777
227	0	23.32	3.102357	0.3520357	-3.10235712	0.001693006	8.559895
228	0	21.34	2.715715	0.4107744	-2.71571483	0.002305111	8.560042
229	0	17.75	2.014682	0.5393048	-2.01468161	0.003973321	8.560259
230	30	20.96	2.641511	0.4232824	27.35848924	0.002447629	8.511309
231	0	25.49	3.526101	0.3053373	-3.52610143	0.001273635	8.559712
232	2	27.42	3.902980	0.2865356	-1.90298002	0.001121611	8.560289
233	10	32.39	4.873491	0.3514874	5.12650880	0.001687737	8.558804
234	0	29.03	4.217371	0.2906364	-4.21737097	0.001153945	8.559361
235	30	35.08	5.398778	0.4336959	24.60122206	0.002569542	8.520746
236	0	30.53	4.510282	0.3101777	-4.51028179	0.001314336	8.559193
237	4	26.16	3.656935	0.2960441	0.34306507	0.001197286	8.560518
238	2	32.14	4.824673	0.3450317	-2.82467273	0.001626309	8.560003
239	0	31.83	4.764138	0.3373811	-4.76413783	0.001554986	8.559039
240	0	25.61	3.549534	0.3034716	-3.54953430	0.001258118	8.559701
241	0	41.47	6.646578	0.6782514	-6.64657803	0.006284439	8.557618
242	30	28.44	4.102159	0.2870052	25.89784062	0.001125291	8.516495
243	0	23.92	3.219521	0.3369208	-3.21952144	0.001550746	8.559847
244	0	24.14	3.262482	0.3317621	-3.26248170	0.001503622	8.559829
245	0	25.76	3.578825	0.3012606	-3.57882538	0.001239852	8.559687
246	0	37.10	5.793231	0.5059756	-5.79323118	0.003497393	8.558323
247	0	23.74	3.184372	0.3412992	-3.18437214	0.001591313	8.559861
248	0	32.20	4.836389	0.3465584	-4.83638917	0.001640733	8.558993
249	0	22.33	2.909036	0.3799065	-2.90903597	0.001971690	8.559971
250	0	27.31	3.881500	0.2869280	-3.88149990	0.001124685	8.559539
251	0	21.86	2.817257	0.3942288	-2.81725725	0.002123156	8.560006
252	0	35.68	5.515942	0.4544498	-5.51594227	0.002821350	8.558530
253	7	61.84	10.624307	1.5624078	-3.62430696	0.033348321	8.559637
254	0	24.38	3.309347	0.3263872	-3.30934743	0.001455296	8.559808
255	2	29.82	4.371637	0.2991762	-2.37163733	0.001222755	8.560157
256	0	28.13	4.041624	0.2860773	-4.04162448	0.001118026	8.559456
257	0	36.16	5.609674	0.4715190	-5.60967373	0.003037272	8.558461
258	2	24.50	3.332780	0.3238027	-1.33278029	0.001432340	8.560409
259	0	32.58	4.910593	0.3565553	-4.91059324	0.001736757	8.558946

260	0	26.66	3.754572	0.2909762	-3.75457187	0.001156645	8.559603
261	0	26.31	3.686226	0.2943507	-3.68622602	0.001183628	8.559636
262	0	18.83	2.225577	0.4985703	-2.22557740	0.003395767	8.560201
263	20	25.52	3.531960	0.3048629	16.46804035	0.001269680	8.542747
264	0	29.02	4.215418	0.2905548	-4.21541823	0.001153297	8.559362
265	30	23.75	3.186325	0.3410523	26.81367512	0.001589012	8.513295
266	0	21.97	2.838737	0.3908203	-2.83873738	0.002086601	8.559998
267	30	24.16	3.266387	0.3313039	26.73361283	0.001499472	8.513582
268	0	21.60	2.766486	0.4024150	-2.76648604	0.002212246	8.560024
269	0	24.99	3.428464	0.3140022	-3.42846449	0.001346948	8.559756
270	0	24.25	3.283962	0.3292651	-3.28396182	0.001481073	8.559819
271	5	29.37	4.283764	0.2938104	0.71623591	0.001179287	8.560492
272	0	29.45	4.299386	0.2946688	-4.29938600	0.001186188	8.559315
273	0	32.82	4.957459	0.3631462	-4.95745897	0.001801558	8.558915
274	0	38.57	6.080284	0.5620716	-6.08028378	0.004315870	8.558097
275	0	31.39	4.678217	0.3272465	-4.67821732	0.001462969	8.559092
276	0	20.24	2.500914	0.4478319	-2.50091357	0.002739778	8.560116
277	6	28.17	4.049435	0.2861587	1.95056457	0.001118662	8.560277
278	0	25.16	3.461661	0.3108989	-3.46166105	0.001320455	8.559741
279	0	29.16	4.242757	0.2917584	-4.24275657	0.001162872	8.559347
280	9	40.67	6.490359	0.6456307	2.50964107	0.005694473	8.560111
281	0	19.25	2.307592	0.4831344	-2.30759242	0.003188755	8.560176
282	0	21.22	2.692282	0.4146882	-2.69228197	0.002349246	8.560051
283	0	23.63	3.162892	0.3440422	-3.16289202	0.001616995	8.559870
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493	0	35.44	5.469077	0.4460661	-5.46907654	0.002718214	8.558564
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505	0	29.80	4.367732	0.2989104	-4.36773186	0.001220583	8.559276
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703	0	20.09	2.471622	0.4530734	-2.47162248	0.002804286	8.560125
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705	0	20.24	2.500914	0.4478319	-2.50091357	0.002739778	8.560116
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487 1.084428e-04 -0.400763212
488 1.169386e-04 -0.313906324
489 4.224208e-06 -0.085049147
490 5.157437e-03  3.035729092
491 1.180325e-04 -0.353078884
492 1.085457e-04 -0.415133074
493 5.583815e-04 -0.640099735
494 1.098147e-04 -0.429050048
495 1.176888e-04 -0.294077190
496 1.097515e-04 -0.428593698
```

```
497 4.867124e-05 -0.217646698
498 1.327388e-02  2.844228866
499 5.206681e-03  3.020690137
500 1.135229e-04 -0.347867707
501 1.101823e-04 -0.376135850
502 5.926616e-03  3.090040050
503 1.139637e-04 -0.344220629
504 5.055996e-06  0.093810407
505 1.594392e-04 -0.510815146
506 1.124292e-04 -0.356757808
507 2.866015e-03  1.363235922
508 9.441877e-03 -1.028757783
509 1.088070e-04 -0.392553234
510 1.265499e-03 -0.728375324
511 4.473895e-04  0.470271047
512 4.586549e-03  0.799439607
513 1.089856e-04 -0.421748909
514 1.085157e-04 -0.414448720
515 1.140996e-04 -0.343080932
516 2.355806e-02  2.739491532
517 1.978999e-02  3.265573492
518 1.831097e-04 -0.527511410
519 1.384653e-04 -0.490928459
520 1.163244e-04 -0.321883546
521 1.105962e-04 -0.372259963
522 4.143882e-04 -0.610464237
523 1.107012e-04 -0.434526564
524 1.089521e-04 -0.390272846
525 1.117331e-04 -0.439547227
526 1.160862e-04 -0.454155831
527 1.144211e-04 -0.340345687
528 8.619400e-03  2.912597090
529 2.072913e-05  0.040510302
530 3.790786e-06 -0.053071352
531 3.637463e-04  0.756469100
532 1.084167e-04 -0.411483276
533 2.141573e-04 -0.544675193
534 2.388394e-02  2.736651204
535 1.101823e-04 -0.376135850
536 1.873825e-05  0.171694532
537 5.383472e-04 -0.636421595
538 8.336158e-07  0.033298662
539 1.357396e-04 -0.487729402
540 2.779162e-04 -0.571243859
541 1.095440e-04 -0.382748026
542 1.141674e-04 -0.250766746
543 5.407772e-05 -0.280609446
544 1.544943e-04 -0.506699660
545 2.709635e-04 -0.568723202
546 1.160862e-04 -0.454155831
547 1.102773e-04 -0.375223863
548 1.393251e-03 -0.739704081
549 1.116784e-04 -0.362912829
550 1.521453e-04 -0.504642117
```

```
551 1.173388e-04 -0.278805816
552 1.109167e-04 -0.435667579
553 1.173111e-04 -0.307524573
554 6.393903e-03  3.104560286
555 1.160862e-04 -0.454155831
556 2.203035e-04 -0.547651347
557 1.128510e-04 -0.353338476
558 5.160296e-03  3.031395946
559 1.710098e-04 -0.519505190
560 1.160862e-04 -0.454155831
561 1.277648e-04 -0.476991805
562 5.583815e-04 -0.640099735
563 1.091859e-05  0.111177564
564 1.116301e-04 -0.439090782
565 1.106364e-02  3.184257033
566 1.104966e-04 -0.433385575
567 1.488938e-04 -0.501670343
568 5.819932e-03  2.982345372
569 4.794971e-02  2.560475747
570 1.109611e-04 -0.435895785
571 8.546740e-05 -0.268591767
572 8.244227e-03 -1.003396229
573 1.493432e-03 -0.748032788
574 7.476393e-05  0.364469016
575 1.159740e-04 -0.325758232
576 8.097828e-03  3.141367190
577 1.264331e-04 -0.474936026
578 1.148122e-04 -0.336926680
579 1.133279e-04 -0.349463328
580 1.072688e-03 -0.709435838
581 1.600094e-04 -0.511272456
582 1.194388e-03 -0.721674557
583 5.312406e-03 -0.927008660
584 9.119430e-04 -0.691441251
585 1.092550e-04 -0.386168314
586 1.086142e-04 -0.416501806
587 3.247376e-04  0.511654187
588 6.026447e-04  0.816523962
589 9.884695e-05 -0.338885652
590 1.251610e-04 -0.472880358
591 1.113790e-04 -0.365420519
592 5.926616e-03  3.090040050
593 4.887773e-04 -0.626769794
594 1.106717e-04 -0.371575999
595 1.128510e-04 -0.353338476
596 2.413609e-02  2.734467032
597 2.099385e-06 -0.056735056
598 4.700615e-04  0.440942149
599 1.159740e-04 -0.325758232
600 1.087386e-04 -0.418554963
601 1.486504e-04 -0.501441756
602 1.357396e-04 -0.487729402
603 1.175452e-04 -0.283592469
604 1.098030e-05  0.111406154
```

```
605 1.160013e-04 -0.453927536
606 3.752429e-05 -0.255890699
607 1.092550e-04 -0.386168314
608 2.714387e-04 -0.493683061
609 1.254386e-04 -0.473337164
610 1.151328e-02  3.189641160
611 1.087386e-04 -0.418554963
612 1.701345e-02  2.801804446
613 2.586757e-05  0.110013775
614 1.168120e-04 -0.315729683
615 1.159740e-04 -0.325758232
616 2.266893e-04 -0.550627838
617 6.518371e-06  0.107739487
618 1.112369e-04 -0.437265044
619 4.312844e-02  2.592210199
620 1.328261e-04 -0.484073692
621 2.435058e-05  0.204137497
622 1.753371e-04 -0.522478675
623 1.173267e-04 -0.278577878
624 1.173388e-04 -0.278805816
625 1.678603e-05 -0.164299960
626 1.112369e-04 -0.437265044
627 8.777901e-04 -0.687291462
628 1.296352e-04 -0.479733019
629 1.154539e-04 -0.331000514
630 1.143946e-04 -0.340573623
631 2.918278e-03  0.990697799
632 5.759574e-05 -0.192090634
633 1.616209e-06  0.050856571
634 1.087540e-04 -0.418783096
635 2.906739e-03  0.991824154
636 1.172495e-04 -0.277210240
637 1.780973e-04 -0.524308660
638 3.764570e-04 -0.601054177
639 5.273160e-05 -0.264639348
640 2.594226e-04 -0.564369955
641 2.104465e-03  1.818679608
642 1.133279e-04 -0.349463328
643 8.026831e-05 -0.264240863
644 1.136433e-04 -0.446850946
645 1.090804e-04 -0.388448583
646 2.238930e-03 -0.473507276
647 1.085530e-04 -0.397570332
648 1.086455e-04 -0.395517841
649 1.277648e-04 -0.476991805
650 1.092550e-04 -0.386168314
651 1.083800e-04 -0.403728161
652 3.676638e-05 -0.253834766
653 1.176321e-04 -0.298407738
654 1.737668e-03 -0.690096696
655 4.697105e-05 -0.203731101
656 2.715886e-05 -0.219578024
657 1.089832e-04 -0.389816776
658 1.446597e-04 -0.497556024
```

```
659 3.339690e-05 -0.243784480
660 1.250233e-04 -0.472651957
661 9.295904e-04  1.251664898
662 1.142742e-04 -0.448905325
663 4.422552e-09 -0.002812530
664 1.267239e-04 -0.475392856
665 1.167955e-04 -0.315957603
666 4.038638e-04 -0.607939177
667 1.251610e-04 -0.472880358
668 1.176374e-04 -0.287011444
669 3.459839e-04 -0.592795069
670 1.386016e-03 -0.662059282
671 9.936949e-05  0.400117207
672 1.176453e-04 -0.297723970
673 3.301470e-04 -0.588208008
674 2.179882e-05  0.181063504
675 1.498767e-04 -0.502584706
676 2.246986e-04 -0.549711958
677 1.937868e-03 -0.780468665
678 1.753371e-04 -0.522478675
679 1.137113e-04 -0.447079206
680 2.849576e-05  0.197748502
681 1.159308e-04 -0.326214079
682 5.254843e-04  0.419329417
683 1.435951e-02  2.831165717
684 1.860800e-04 -0.529341713
685 1.145685e-04 -0.449818412
686 4.232459e-08 -0.006948427
687 3.617459e-04 -0.597153655
688 6.103371e-05 -0.299769152
689 2.078594e-07 -0.015856693
690 1.403072e-04 -0.492985152
691 1.151328e-02  3.189641160
692 1.175452e-04 -0.283592469
693 5.074655e-04  0.874157118
694 1.129072e-04 -0.352882571
695 3.525343e-04 -0.594630158
696 1.174301e-04 -0.457580416
697 1.118712e-04 -0.361317054
698 1.544943e-04 -0.506699660
699 1.827807e-05 -0.162735539
700 1.167865e-04 -0.455982242
701 1.538348e-02  2.819451192
702 1.116301e-04 -0.439090782
703 1.176741e-04 -0.289290735
704 4.951052e-04  0.883950956
705 1.176931e-04 -0.292709639
706 1.171497e-04 -0.275614650
707 8.181615e-07 -0.033214246
708 1.540366e-03  1.288383423
709 1.322772e-06 -0.028010398
710 7.983795e-04  1.114900992
711 1.231694e-04 -0.469454489
712 1.138817e-04 -0.344904451
```

```
713 1.087386e-04 -0.418554963
714 1.147608e-04 -0.337382544
715 1.128510e-04 -0.353338476
716 3.157456e-03 -0.701385866
717 1.277648e-04 -0.476991805
718 1.169674e-04 -0.456438857
719 1.119544e-04 -0.360633157
720 1.296352e-04 -0.479733019
721 2.174373e-04 -0.546277696
722 2.824462e-04 -0.572848051
723 9.904479e-04  1.226851515
724 1.135813e-04 -0.247574890
725 1.084637e-04 -0.413080036
726 1.337139e-04 -0.485216061
727 1.384653e-04 -0.490928459
728 1.433158e-04 -0.496184697
729 6.031459e-04 -0.647918146
730 1.087386e-04 -0.418554963
731 1.101192e-04 -0.431103673
732 1.124854e-04 -0.356301892
733 1.574765e-04 -0.509214615
734 1.277648e-04 -0.476991805
735 1.116301e-04 -0.439090782
736 1.176670e-04 -0.296356431
737 2.720528e-02  2.708738921
738 3.247828e-04 -0.586602757
739 7.555278e-03  2.933668535
740 2.798270e-04  0.627936230
741 1.150649e-04 -0.334647369
742 1.270483e-04  0.425273627
743 1.156733e-04 -0.260569709
744 1.176670e-04 -0.296356431
745 1.114602e-04 -0.364736599
746 1.175244e-04 -0.457808731
747 2.367551e-05 -0.201084851
748 1.125067e-04 -0.442742465
749 1.136339e-04 -0.346955930
750 1.104227e-04 -0.373855898
751 1.142742e-04 -0.448905325
752 3.419530e-04 -0.591648216
753 1.124573e-04 -0.356529850
754 2.835558e-04 -0.426216514
755 1.446597e-04 -0.497556024
756 2.082453e-04 -0.541699370
757 1.083592e-04 -0.407377510
758 1.176842e-04 -0.294760964
759 1.526067e-04  0.442665579
760 2.407412e-04 -0.556810869
761 1.106717e-04 -0.371575999
762 1.085921e-04 -0.396658107
763 5.447043e-05  0.277045550
764 1.831097e-04 -0.527511410
765 1.083917e-04 -0.410342759
766 3.928006e-03  0.424087107
```

```
767 1.671851e-04 -0.516760698
768 1.105711e-04 -0.372487952
769 5.195938e-05 -0.254601706
770 2.423699e-04 -0.557497965
771 1.110202e-02  3.184725014
772 4.751948e-04  0.333794732
773 1.106717e-04 -0.371575999
774 1.868265e-07  0.013612723
775 1.092277e-04 -0.424258565
776 4.838918e-05 -0.215137376
777 1.129634e-04 -0.352426667
778 5.840995e-05  0.311044131
779 2.501529e-04 -0.560704659
780 2.193425e-04 -0.547193456
781 1.251610e-04 -0.472880358
782 2.907762e-03  0.421598532
783 1.086662e-04 -0.417414311
784 1.109283e-04 -0.369296150
785 2.082453e-04 -0.541699370
786 1.353638e-04 -0.487272418
787 1.198584e-04  0.419554651
788 1.831097e-04 -0.527511410
789 1.174440e-04 -0.304561613
790 1.088715e-04 -0.420380053
791 6.045086e-04 -0.648148148
792 5.522307e-05  0.285487168
793 1.289711e-03  1.168034134
794 2.317459e-03  1.795304578
795 2.407412e-04 -0.556810869
796 1.171036e-04 -0.274930821
797 1.101913e-04 -0.431560045
798 3.506013e-06 -0.070875110
799 1.632646e-03 -0.758913611
800 1.125978e-04 -0.355390065
801 3.209976e-05 -0.239445039
802 1.176321e-04 -0.298407738
803 1.110329e-04 -0.368384225
804 2.204866e-03  1.986182082
805 1.083739e-04 -0.404184319
806 4.687109e-06  0.058413618
807 1.151043e-04 -0.451416359
808 7.070589e-03  3.121198785
809 1.116301e-04 -0.439090782
810 5.782723e-04 -0.493366028
811 2.071720e-05 -0.181452868
812 1.176321e-04 -0.298407738
813 1.212162e-04 -0.465800558
814 1.702060e-04  0.452739160
815 1.187035e-04 -0.460548612
816 5.978905e-05 -0.320772934
817 1.600094e-04 -0.511272456
818 3.298315e-04  0.741825741
819 1.111649e-04 -0.367244329
820 6.437610e-04 -0.654589379
```

```
821 1.084041e-04 -0.402359707
822 1.084366e-04 -0.400991280
823 1.265361e-05  0.147478063
824 7.204473e-05 -0.358446693
825 1.690773e-04 -0.518132913
826 8.035317e-05 -0.373980686
827 6.045086e-04 -0.648148148
828 1.096055e-04 -0.382063986
829 5.819932e-03  2.982345372
830 1.084848e-04 -0.399394817
831 9.344773e-05 -0.392263011
832 1.138817e-04 -0.344904451
833 5.445025e-05 -0.284488169
834 2.082453e-04 -0.541699370
835 4.820432e-04 -0.625391352
836 5.499194e-03  2.997292527
837 1.147866e-04 -0.337154612
838 1.357396e-04 -0.487729402
839 1.173388e-04 -0.278805816
840 1.153345e-04 -0.332140151
841 7.809845e-03  2.928282258
842 1.174709e-04 -0.303877851
843 4.655777e-04 -0.621945661
844 1.105962e-04 -0.372259963
845 1.092550e-04 -0.386168314
846 3.513911e-04  0.519000011
847 1.147608e-04 -0.337382544
848 1.575201e-05 -0.160415957
849 1.171497e-04 -0.275614650
850 5.312406e-03 -0.927008660
851 2.304966e-05 -0.108901027
852 1.174709e-04 -0.303877851
853 1.138817e-04 -0.344904451
854 4.527800e-04 -0.619189532
855 1.656387e-04 -0.515617233
856 1.179754e-02  2.863313153
857 4.067084e-04 -0.608627799
858 1.086683e-04 -0.395061740
859 1.126124e-04 -0.242786908
860 2.594226e-04 -0.564369955
861 1.277648e-04 -0.476991805
862 1.083630e-04 -0.405324727
863 1.176374e-04 -0.287011444
864 1.946783e-03  1.861933362
865 7.817944e-04  1.122869490
866 1.176670e-04 -0.296356431
867 1.378671e-04 -0.490242922
868 7.877879e-04  1.183093863
869 1.125656e-04 -0.442970704
870 1.091833e-04 -0.387080414
871 3.642998e-04 -0.597841931
872 1.143680e-04 -0.340801559
873 1.116301e-04 -0.439090782
874 1.165345e-04 -0.268092375
```

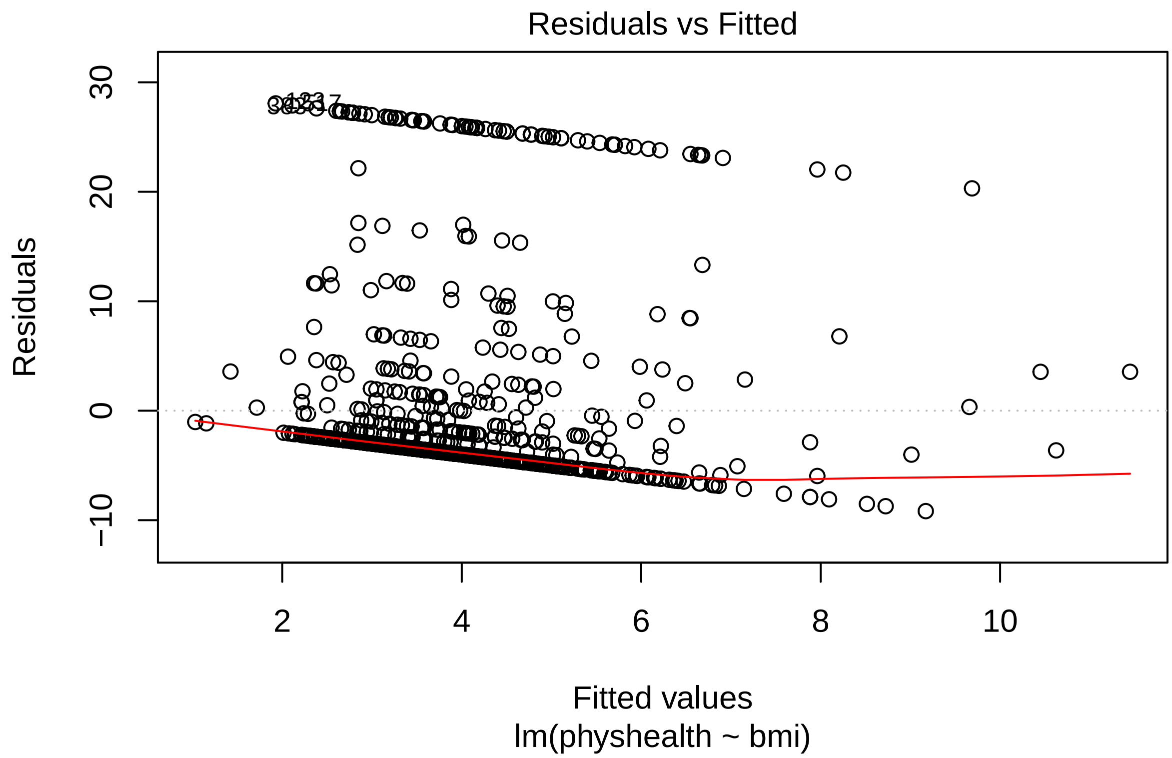
```
875 1.115689e-04 -0.363824710
876 1.122890e-04 -0.357897605
877 1.167865e-04 -0.455982242
878 1.105711e-04 -0.372487952
879 5.159031e-05 -0.249811147
880 1.176321e-04 -0.298407738
881 1.087540e-04 -0.418783096
882 1.084041e-04 -0.402359707
883 7.185837e-05 -0.163448352
884 4.153578e-04 -0.610693803
885 1.124292e-04 -0.356757808
886 1.260025e-04 -0.474250791
887 3.427553e-04 -0.591877582
888 1.147866e-04 -0.337154612
889 1.264331e-04 -0.474936026
890 1.544943e-04 -0.506699660
891 5.145751e-05  0.235481940
892 1.153345e-04 -0.332140151
893 1.086942e-04 -0.417870569
894 1.167865e-04 -0.455982242
895 1.518893e-04 -0.504413510
896 2.583775e-05 -0.190808690
```

For more on the `broom` package, you may want to look at this vignette.

2.4.3 How does the model do? (Residuals vs. Fitted Values)

- Remember that the R^2 value was about 2%.

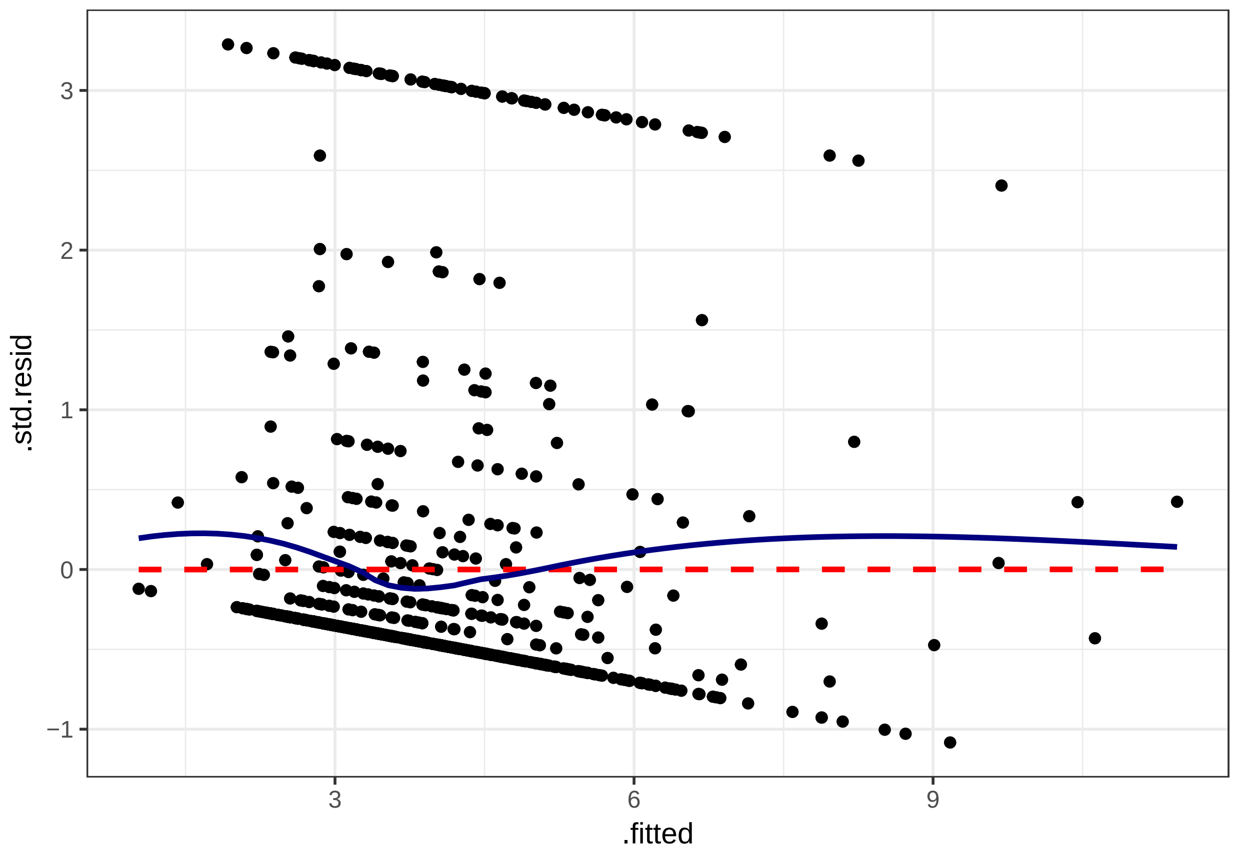
```
plot(model_A, which = 1)
```



This is a plot of residuals vs. fitted values. The goal here is for this plot to look like a random scatter of points, perhaps like a “fuzzy football”, and that’s **not** what we have. Why?

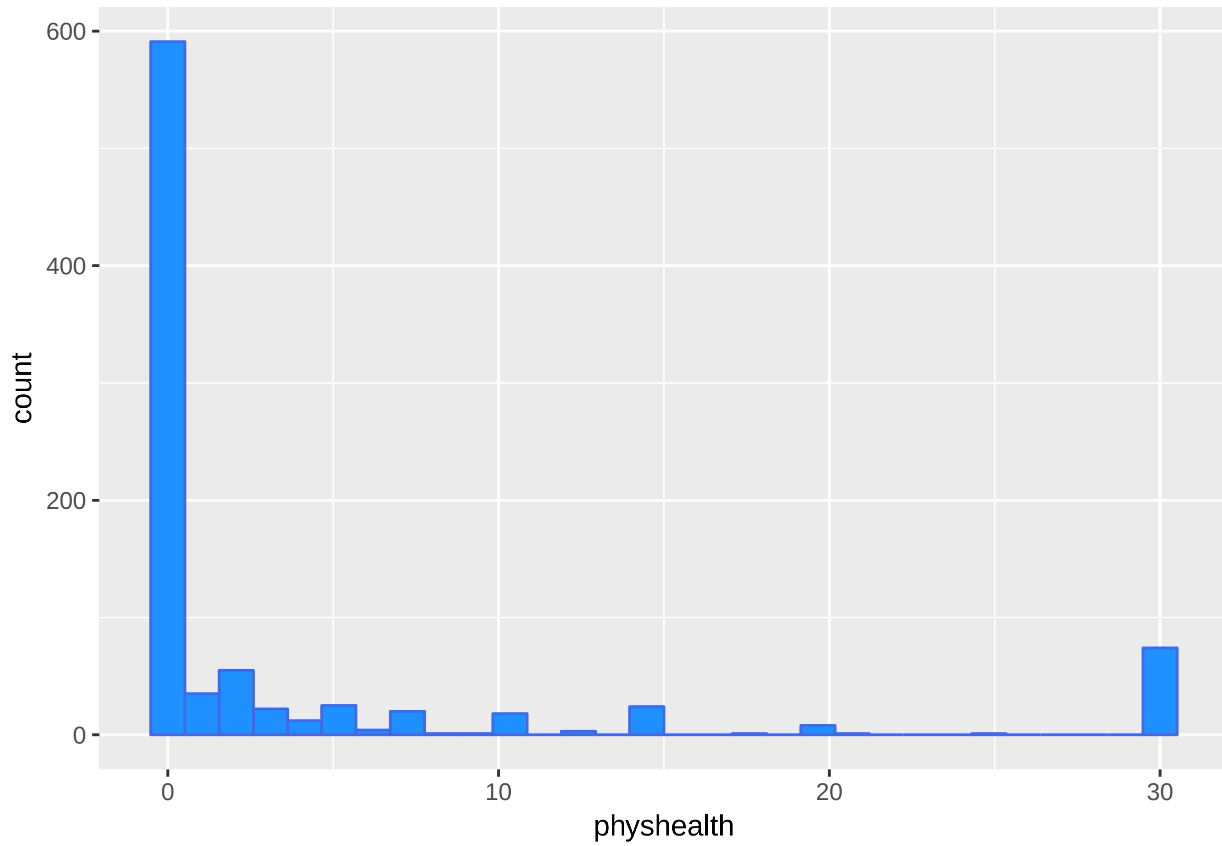
If you prefer, here’s a `ggplot2` version of a similar plot, now looking at standardized residuals instead of raw residuals, and adding a loess smooth and a linear fit to the result.

```
ggplot(augment(model_A), aes(x = .fitted, y = .std.resid)) +
    geom_point() +
    geom_smooth(method = "lm", se = FALSE, col = "red", linetype = "dashed") +
    geom_smooth(method = "loess", se = FALSE, col = "navy") +
    theme_bw()
```



The problem we're having here becomes, I think, a little more obvious if we look at what we're predicting. Does `physhealth` look like a good candidate for a linear model?

```
ggplot(smartcle2, aes(x = physhealth)) +
geom_histogram(bins = 30, fill = "dodgerblue", color = "royalblue")
```



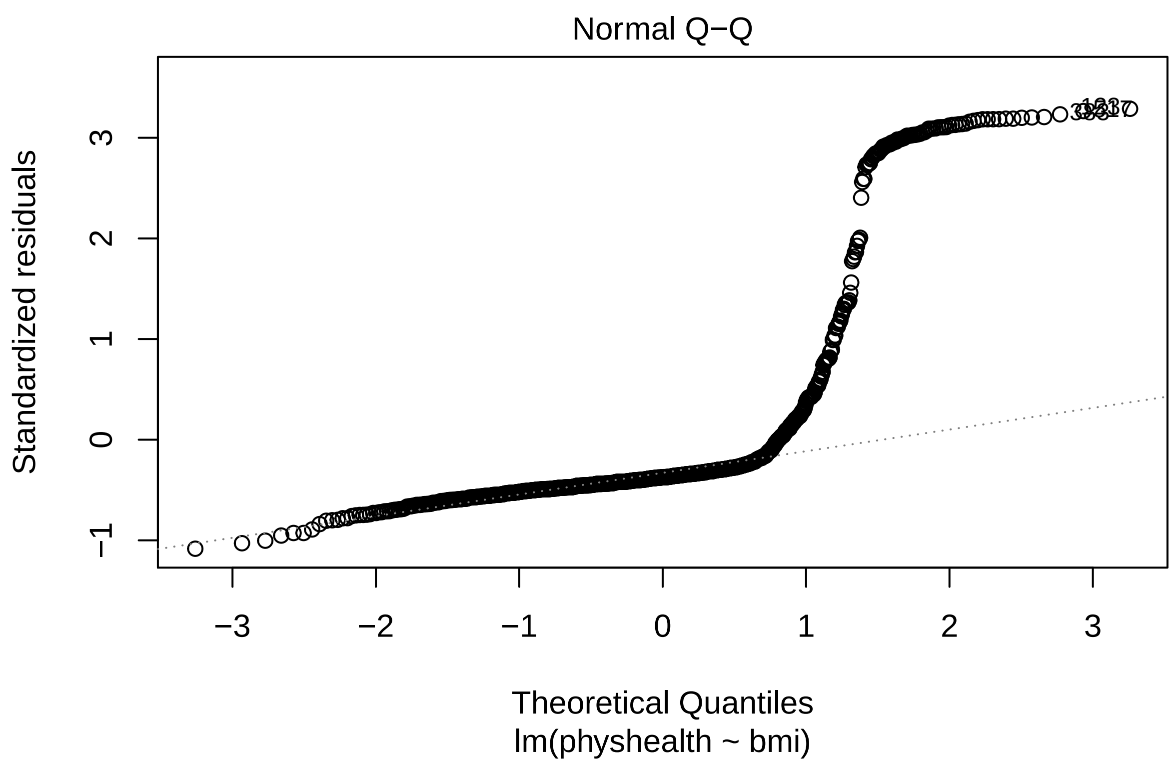

```
smartcle2 %>% count(physhealth == 0, physhealth == 30)
```

```
# A tibble: 3 x 3
  `physhealth == 0` `physhealth == 30`     n
  <lgl>             <lgl>              <int>
1 F                 F                    231
2 F                 T                     74
3 T                 F                    591
```

No matter what model we fit, if we are predicting `physhealth`, and most of the data are values of 0 and 30, we have limited variation in our outcome, and so our linear model will be somewhat questionable just on that basis.

A normal Q-Q plot of the standardized residuals for our `model_A` shows this problem, too.

```
plot(model_A, which = 2)
```



We're going to need a method to deal with this sort of outcome, that has both a floor and a ceiling. We'll get there eventually, but linear regression alone doesn't look promising.

All right, so that didn't go anywhere great. Let's try again, with a new outcome.

2.5 A New Small Study

We'll begin by investigating the problem of predicting `bmi`, at first with just three regerssion inputs: `sex`, `exerany` and `sleephrs`, in our new `smartcle2` data set.

- The outcome of interest is `bmi`.
- Inputs to the regression model are:
  - `female` = 1 if the subject is female, and 0 if they are male
  - `exerany` = 1 if the subject exercised in the past 30 days, and 0 if they didn't
  - `sleephrs` = hours slept in a typical 24-hour period (treated as quantitative)

2.5.1 Counting as exploratory data analysis

Counting things can be amazingly useful.

2.5.1.1 How many respondents had exercised in the past 30 days? Did this vary by sex?

```
smartcle2 %>% count(female, exerany) %>% mutate(percent = 100*n / sum(n))
```

```
# A tibble: 4 x 4
  female exerany     n percent
   <int>   <int> <int>   <dbl>
1      0       0    64    7.14
2      0       1   308   34.4
3      1       0   145   16.2
4      1       1   379   42.3
```

so we know now that 42.3% of the subjects in our data were women who exercised. Suppose that instead we want to find the percentage of exercisers within each sex…

```
smartcle2 %>%
    count(female, exerany) %>%
    group_by(female) %>%
    mutate(prob = 100*n / sum(n))
```

```
# A tibble: 4 x 4
# Groups: female [2]
  female exerany     n  prob
   <int>   <int> <int> <dbl>
1      0       0    64  17.2
2      0       1   308  82.8
3      1       0   145  27.7
4      1       1   379  72.3
```

and now we know that 82.8% of the males exercised at least once in the last 30 days, as compared to 72.3% of the females.

2.5.1.2 What's the distribution of `sleephrs`?

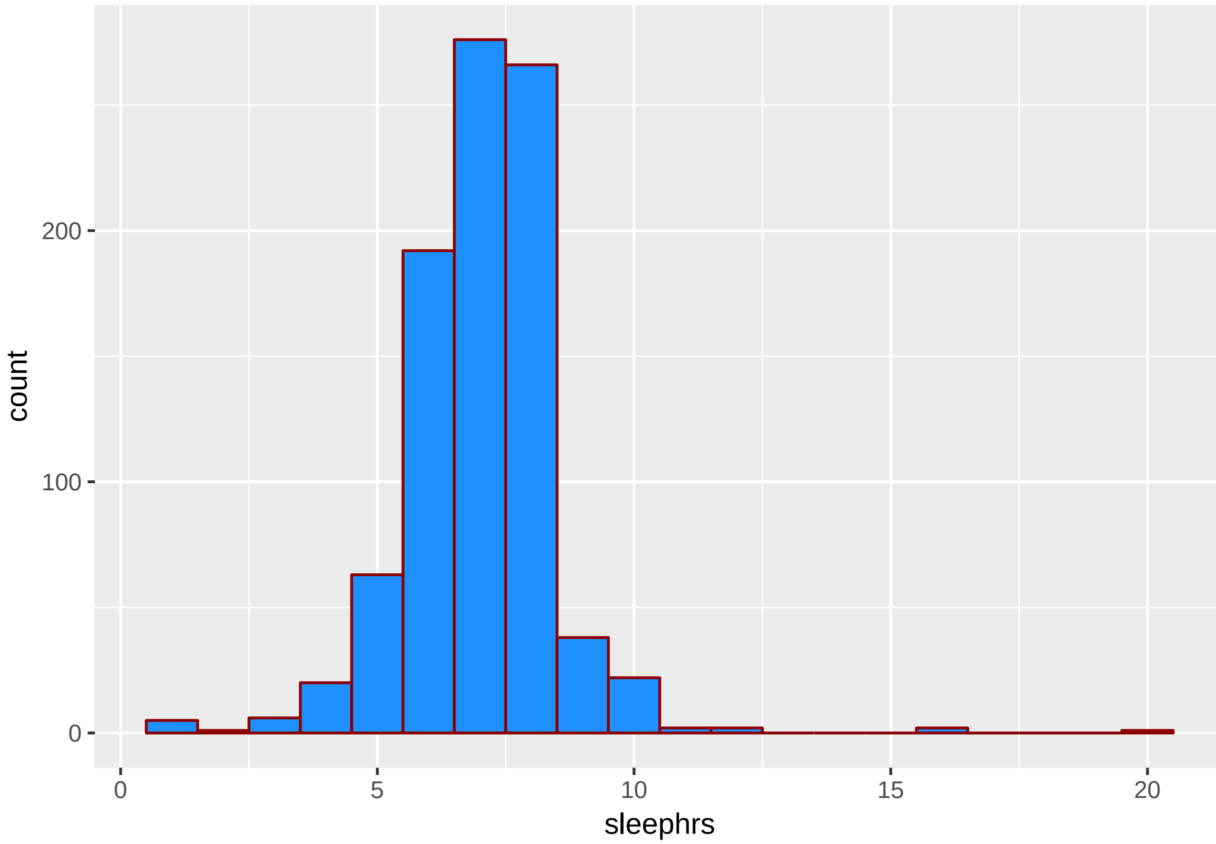
We can count quantitative variables with discrete sets of possible values, like `sleephrs`, which is captured as an integer (that must fall between 0 and 24.)

```
smartcle2 %>% count(sleephrs)
```

```
# A tibble: 14 x 2
   sleephrs     n
      <int> <int>
 1        1     5
 2        2     1
 3        3     6
 4        4    20
 5        5    63
 6        6   192
 7        7   276
 8        8   266
 9        9    38
10       10    22
11       11     2
12       12     2
13       16     2
14       20     1
```

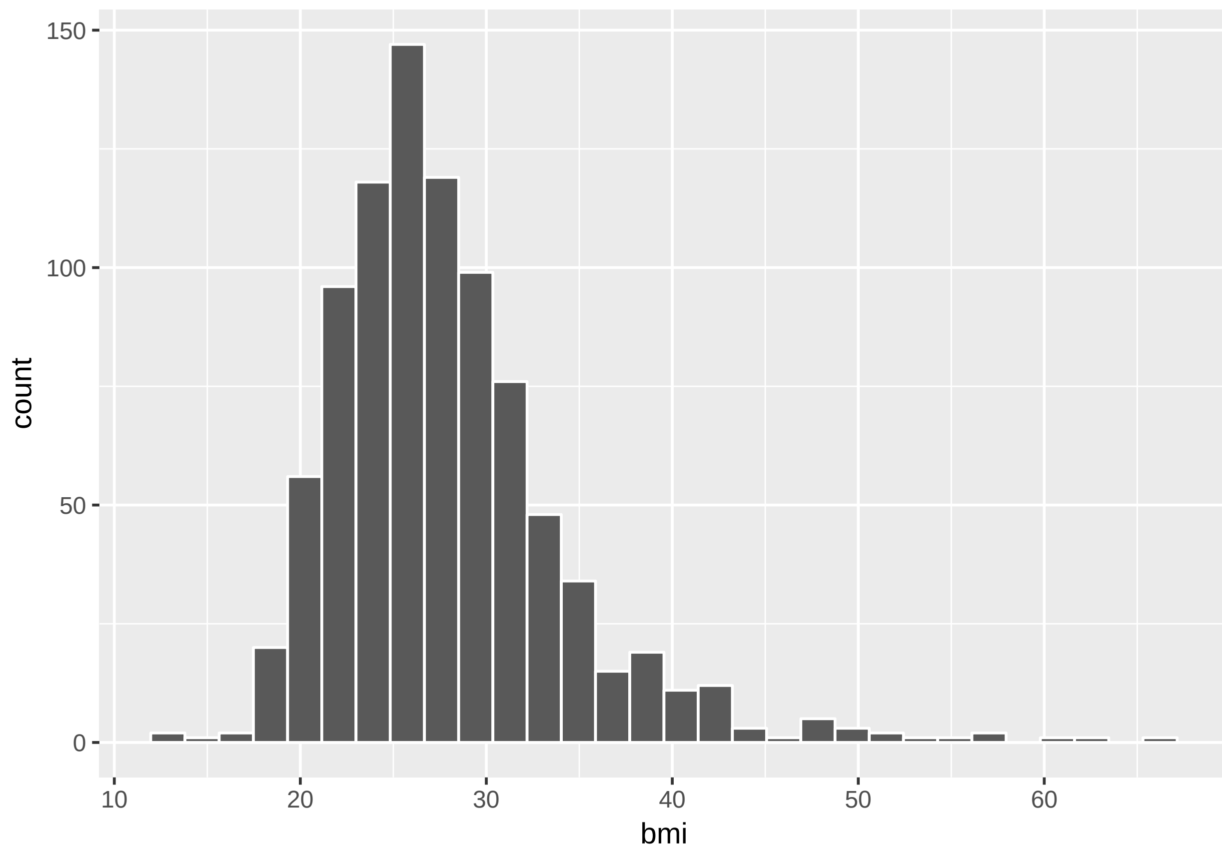
Of course, a natural summary of a quantitative variable like this would be graphical.

```
ggplot(smartcle2, aes(sleephrs)) +
    geom_histogram(binwidth = 1, fill = "dodgerblue", col = "darkred")
```



2.5.1.3 What's the distribution of BMI?

```
ggplot(smartcle2, aes(bmi)) +
    geom_histogram(bins = 30, col = "white")
```



2.5.1.4 How many of the respondents have a BMI below 30?

```
smartcle2 %>% count(bmi < 30) %>% mutate(proportion = n / sum(n))
```

```
# A tibble: 2 x 3
  `bmi < 30`     n proportion
  <lgl>      <int>      <dbl>
1 F            253      0.282
2 T            643      0.718
```

2.5.1.5 How many of the respondents who have a BMI < 30 exercised?

```
smartcle2 %>% count(exerany, bmi < 30) %>%
    group_by(exerany) %>%
    mutate(percent = 100*n/sum(n))
```

```
# A tibble: 4 x 4
# Groups: exerany [2]
  exerany `bmi < 30`     n percent
    <int> <lgl>      <int>   <dbl>
1       0 F             88    42.1
2       0 T            121    57.9
3       1 F            165    24.0
4       1 T            522    76.0
```

2.5.1.6 Is obesity associated with sex, in these data?

```
smartcle2 %>% count(female, bmi < 30) %>%
    group_by(female) %>%
    mutate(percent = 100*n/sum(n))
```

```
# A tibble: 4 x 4
# Groups: female [2]
  female `bmi < 30`     n percent
   <int> <lgl>      <int>   <dbl>
1      0 F            105    28.2
2      0 T            267    71.8
3      1 F            148    28.2
4      1 T            376    71.8
```

2.5.1.7 Comparing `sleephrs` summaries by obesity status

Can we compare the `sleephrs` means, medians and 75th percentiles for respondents whose BMI is below 30 to the respondents whose BMI is not?

```
smartcle2 %>%
    group_by(bmi < 30) %>%
    summarize(mean(sleephrs), median(sleephrs),
              q75 = quantile(sleephrs, 0.75))
```

```
# A tibble: 2 x 4
  `bmi < 30` `mean(sleephrs)` `median(sleephrs)`   q75
  <lgl>                 <dbl>              <int> <dbl>
1 F                      6.93                  7  8.00
2 T                      7.06                  7  8.00
```

2.5.1.8 The `skim` function within a pipe

The **skim** function works within pipes and with the other `tidyverse` functions.

```
skim_with(numeric = list(hist = NULL), integer = list(hist = NULL))
## above line eliminates the sparkline histograms
## it can be commented out when working in the console,
## but I need it to produce the Notes without errors right now

smartcle2 %>%
    group_by(exerany) %>%
    skim(bmi, sleephrs)
```

```
Skim summary statistics
 n obs: 896
 n variables: 10
 group variables: exerany

Variable type: integer
 exerany variable missing complete   n mean   sd p0 p25 median p75 p100
       0 sleephrs       0      209 209 7    1.85  1   6      7   8   20
       1 sleephrs       0      687 687 7.03 1.34  1   6      7   8   16
```

```
Variable type: numeric
 exerany variable missing complete   n  mean   sd    p0   p25 median   p75
       0      bmi       0      209 209 29.57 7.46 18    24.11  28.49 33.13
       1      bmi       0      687 687 27.35 5.84 12.71 23.7   26.52 29.81
  p100
 66.06
 60.95
```

2.5.1.9 The usual summary for a data frame

Of course, we can use the usual `summary` to get some basic information about the data, too.

```
summary(smartcle2)
```

```
     SEQNO              physhealth       menthealth           genhealth
 Min.   :2.016e+09   Min.   : 0.00   Min.   : 0.000   1_Excellent:155
 1st Qu.:2.016e+09   1st Qu.: 0.00   1st Qu.: 0.000   2_VeryGood :306
 Median :2.016e+09   Median : 0.00   Median : 0.000   3_Good     :295
 Mean   :2.016e+09   Mean   : 3.99   Mean   : 2.693   4_Fair     :102
 3rd Qu.:2.016e+09   3rd Qu.: 2.00   3rd Qu.: 2.000   5_Poor     : 38
 Max.   :2.016e+09   Max.   :30.00   Max.   :30.000
      bmi            female         internet30        exerany
 Min.   :12.71   Min.   :0.0000   Min.   :0.0000   Min.   :0.0000
 1st Qu.:23.70   1st Qu.:0.0000   1st Qu.:1.0000   1st Qu.:1.0000
 Median :26.80   Median :1.0000   Median :1.0000   Median :1.0000
 Mean   :27.87   Mean   :0.5848   Mean   :0.8147   Mean   :0.7667
 3rd Qu.:30.53   3rd Qu.:1.0000   3rd Qu.:1.0000   3rd Qu.:1.0000
 Max.   :66.06   Max.   :1.0000   Max.   :1.0000   Max.   :1.0000
    sleephrs          alcdays
 Min.   : 1.000   Min.   : 0.000
 1st Qu.: 6.000   1st Qu.: 0.000
 Median : 7.000   Median : 1.000
 Mean   : 7.022   Mean   : 4.834
 3rd Qu.: 8.000   3rd Qu.: 5.000
 Max.   :20.000   Max.   :30.000
```

2.5.1.10 The `describe` function in `Hmisc`

Or we can use the `describe` function from the `Hmisc` package.

```
Hmisc::describe(smartcle2)
```

```
smartcle2

 10  Variables      896  Observations
---------------------------------------------------------------------------
SEQNO
        n  missing distinct     Info     Mean      Gmd      .05
      896        0      896        1 2.016e+09    345.7 2.016e+09
      .10      .25      .50      .75      .90      .95
2.016e+09 2.016e+09 2.016e+09 2.016e+09 2.016e+09 2.016e+09

lowest : 2016000001 2016000002 2016000003 2016000004 2016000005
highest: 2016001031 2016001032 2016001033 2016001034 2016001036
---------------------------------------------------------------------------
```

```
physhealth
       n  missing distinct     Info     Mean      Gmd      .05      .10
     896        0       19    0.712     3.99    6.664        0        0
     .25      .50      .75      .90      .95
       0        0        2       15       30

Value          0     1     2     3     4     5     6     7     8     9
Frequency    591    35    55    22    12    25     4    20     1     1
Proportion 0.660 0.039 0.061 0.025 0.013 0.028 0.004 0.022 0.001 0.001

Value         10    12    14    15    18    20    21    25    30
Frequency     18     3    10    14     1     8     1     1    74
Proportion 0.020 0.003 0.011 0.016 0.001 0.009 0.001 0.001 0.083
---------------------------------------------------------------------------
menthealth
       n  missing distinct     Info     Mean      Gmd      .05      .10
     896        0       17    0.645    2.693    4.652        0        0
     .25      .50      .75      .90      .95
       0        0        2        8       20

Value          0     1     2     3     4     5     6     7     8    10
Frequency    634    25    56    27    15    30     4    13     4    18
Proportion 0.708 0.028 0.062 0.030 0.017 0.033 0.004 0.015 0.004 0.020

Value         14    15    18    20    23    29    30
Frequency      2    20     1     9     1     1    36
Proportion 0.002 0.022 0.001 0.010 0.001 0.001 0.040
---------------------------------------------------------------------------
genhealth
       n  missing distinct
     896        0        5

Value      1_Excellent  2_VeryGood      3_Good      4_Fair      5_Poor
Frequency          155         306         295         102          38
Proportion       0.173       0.342       0.329       0.114       0.042
---------------------------------------------------------------------------
bmi
       n  missing distinct     Info     Mean      Gmd      .05      .10
     896        0      467        1    27.87    6.572    20.06    21.23
     .25      .50      .75      .90      .95
   23.70    26.80    30.53    35.36    39.30

lowest : 12.71 13.34 14.72 16.22 17.30, highest: 56.89 57.04 60.95 61.84 66.06
---------------------------------------------------------------------------
female
       n  missing distinct     Info      Sum     Mean      Gmd
     896        0        2    0.728      524   0.5848   0.4862

---------------------------------------------------------------------------
internet30
       n  missing distinct     Info      Sum     Mean      Gmd
     896        0        2    0.453      730   0.8147   0.3022

---------------------------------------------------------------------------
```

```
exerany
       n  missing distinct     Info      Sum     Mean      Gmd
     896        0        2    0.537      687   0.7667   0.3581

---------------------------------------------------------------------------
sleephrs
       n  missing distinct     Info     Mean      Gmd      .05      .10
     896        0       14    0.934    7.022    1.477        5        5
     .25      .50      .75      .90      .95
       6        7        8        8        9

Value          1     2     3     4     5     6     7     8     9    10
Frequency      5     1     6    20    63   192   276   266    38    22
Proportion 0.006 0.001 0.007 0.022 0.070 0.214 0.308 0.297 0.042 0.025

Value         11    12    16    20
Frequency      2     2     2     1
Proportion 0.002 0.002 0.002 0.001
---------------------------------------------------------------------------
alcdays
       n  missing distinct     Info     Mean      Gmd      .05      .10
     896        0       22    0.909    4.834    7.189        0        0
     .25      .50      .75      .90      .95
       0        1        5       17       30

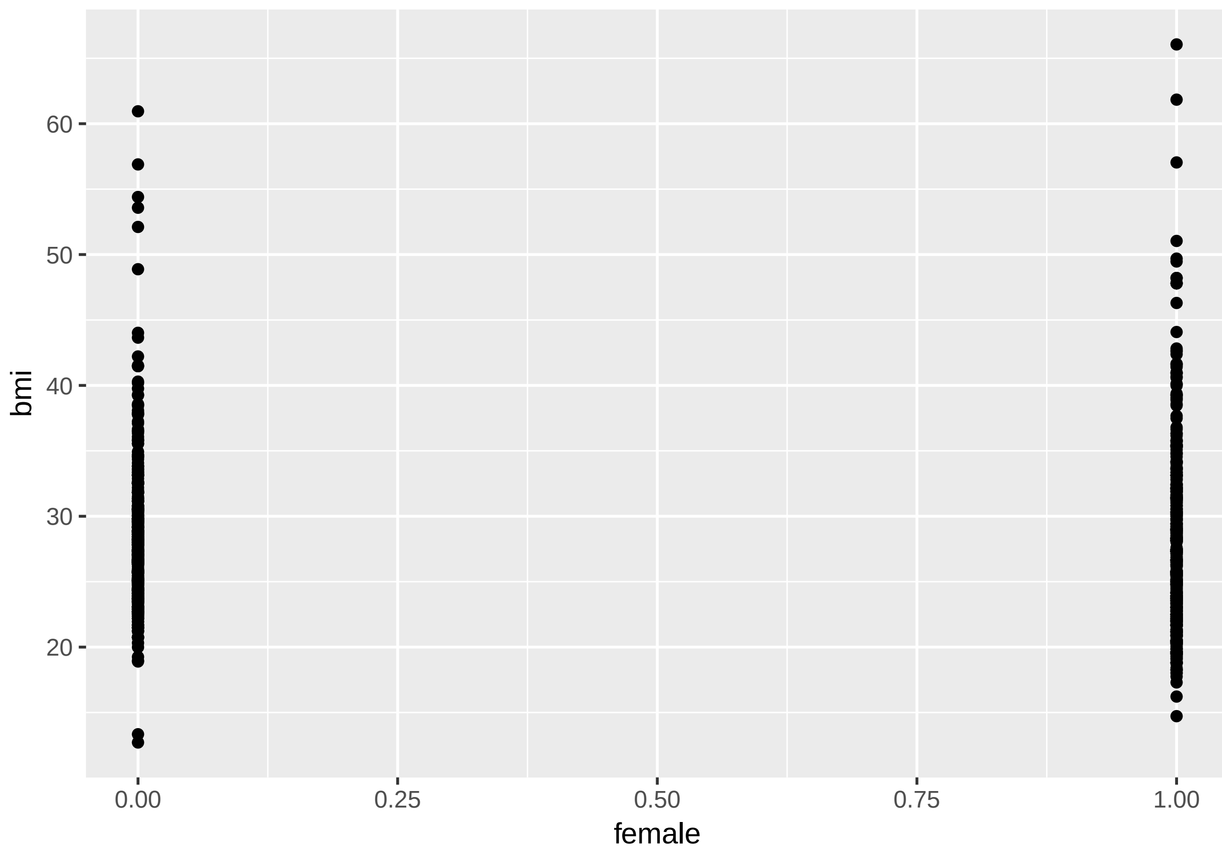
lowest :  0  1  2  3  4, highest: 25 26 27 28 30
---------------------------------------------------------------------------
```

2.6 Predicting `bmi`

2.6.1 Does `female` predict `bmi` well?

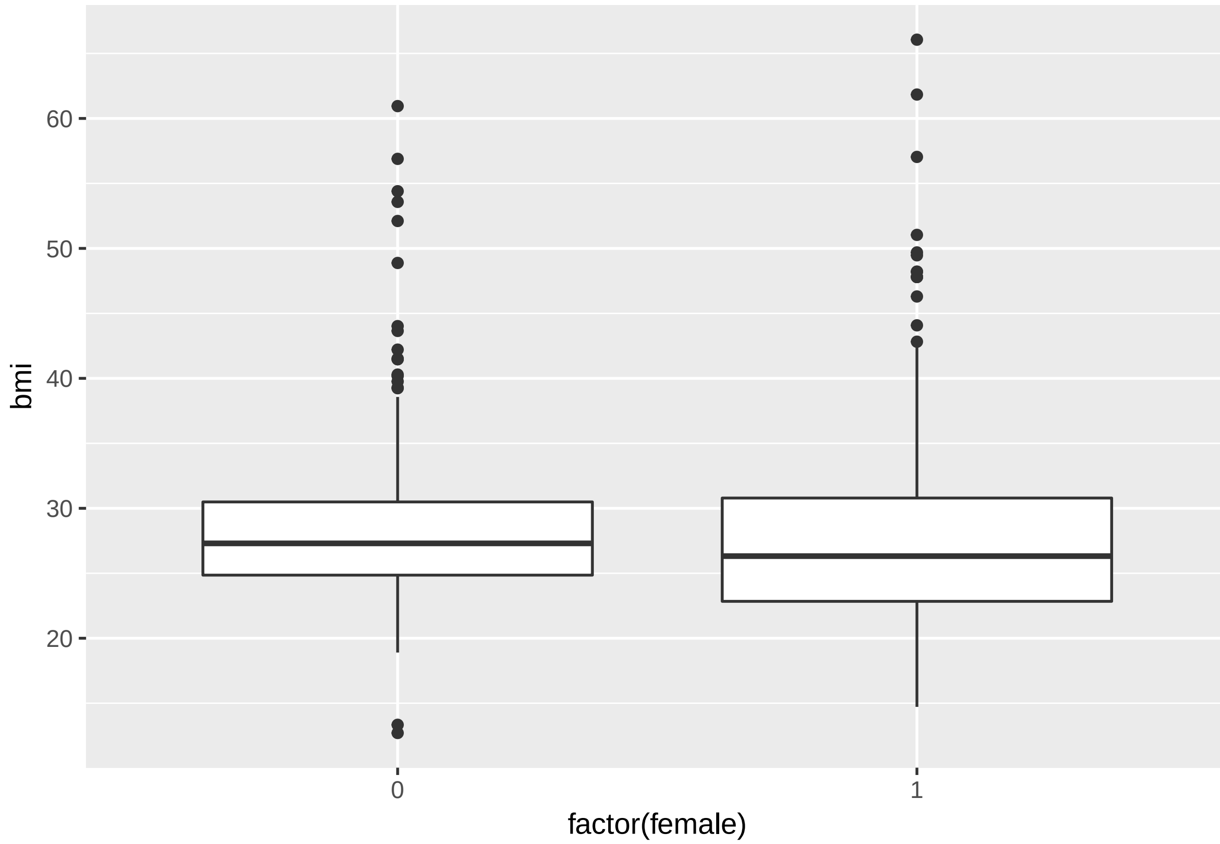
2.6.1.1 Graphical Assessment

```r
ggplot(smartcle2, aes(x = female, y = bmi)) +
    geom_point()
```



Not so helpful. We should probably specify that `female` is a factor, and try another plotting approach.

```
ggplot(smartcle2, aes(x = factor(female), y = bmi)) +
    geom_boxplot()
```



The median BMI looks a little higher for males. Let's see if a model reflects that.

2.6.1.2 Model c2_m1: A simple t-test model

```
c2_m1 <- lm(bmi ~ female, data = smartcle2)
c2_m1
```

```
Call:
lm(formula = bmi ~ female, data = smartcle2)

Coefficients:
(Intercept)       female
    28.3600      -0.8457
```

```
summary(c2_m1)
```

```
Call:
lm(formula = bmi ~ female, data = smartcle2)

Residuals:
    Min      1Q  Median      3Q     Max
-15.650  -4.129  -1.080   2.727  38.546

Coefficients:
```

```
            Estimate Std. Error t value Pr(>|t|)
(Intercept)  28.3600     0.3274  86.613   <2e-16 ***
female       -0.8457     0.4282  -1.975   0.0485 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.315 on 894 degrees of freedom
Multiple R-squared:  0.004345,  Adjusted R-squared:  0.003231
F-statistic: 3.902 on 1 and 894 DF,  p-value: 0.04855
```

```r
confint(c2_m1)
```

```
                2.5 %      97.5 %
(Intercept) 27.717372 29.00262801
female      -1.686052 -0.00539878
```

The model suggests, based on these 896 subjects, that

- our best prediction for males is BMI = 28.36 kg/m^2, and
- our best prediction for females is BMI = 28.36 - 0.85 = 27.51 kg/m^2.
- the mean difference between females and males is -0.85 kg/m^2 in BMI
- a 95% confidence (uncertainty) interval for that mean female - male difference in BMI ranges from -1.69 to -0.01
- the model accounts for 0.4% of the variation in BMI, so that knowing the respondent's sex does very little to reduce the size of the prediction errors as compared to an intercept only model that would predict the overall mean (regardless of sex) for all subjects.
- the model makes some enormous errors, with one subject being predicted to have a BMI 38 points lower than his/her actual BMI.

Note that this simple regression model just gives us the t-test.

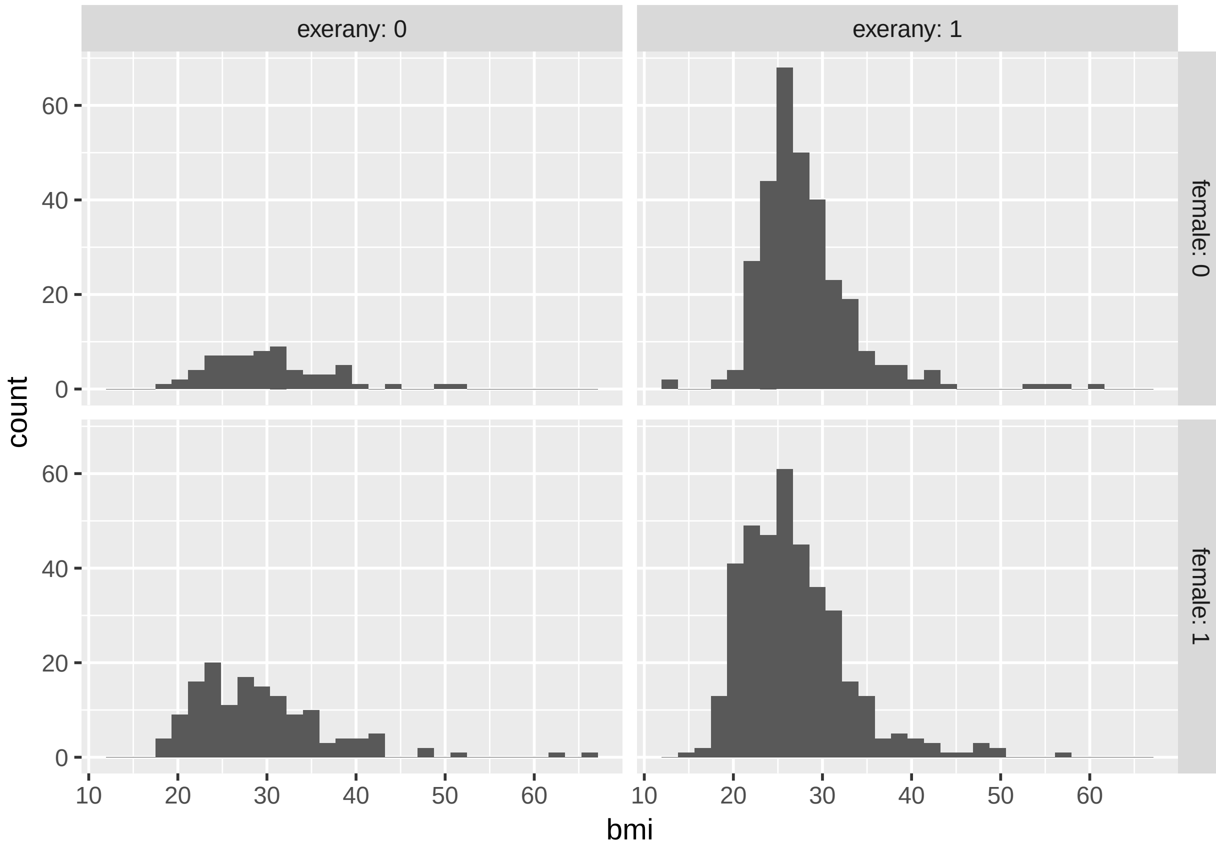
```r
t.test(bmi ~ female, var.equal = TRUE, data = smartcle2)
```

```

    Two Sample t-test

data:  bmi by female
t = 1.9752, df = 894, p-value = 0.04855
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 0.00539878 1.68605160
sample estimates:
mean in group 0 mean in group 1
       28.36000        27.51427
```

2.7 m2: Adding another predictor (two-way ANOVA without interaction)

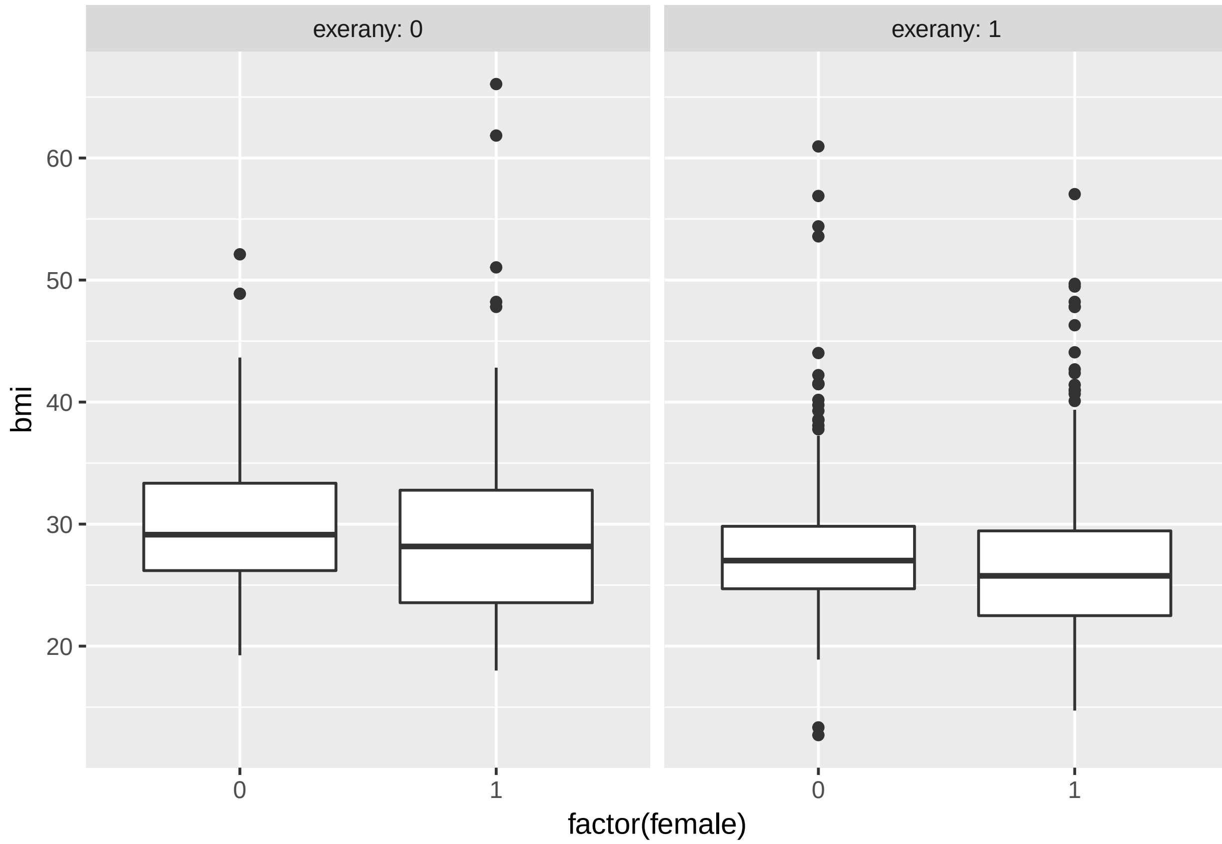
When we add in the information about `exerany` to our original model, we might first picture the data. We could look at separate histograms,

```r
ggplot(smartcle2, aes(x = bmi)) +
    geom_histogram(bins = 30) +
    facet_grid(female ~ exerany, labeller = label_both)
```

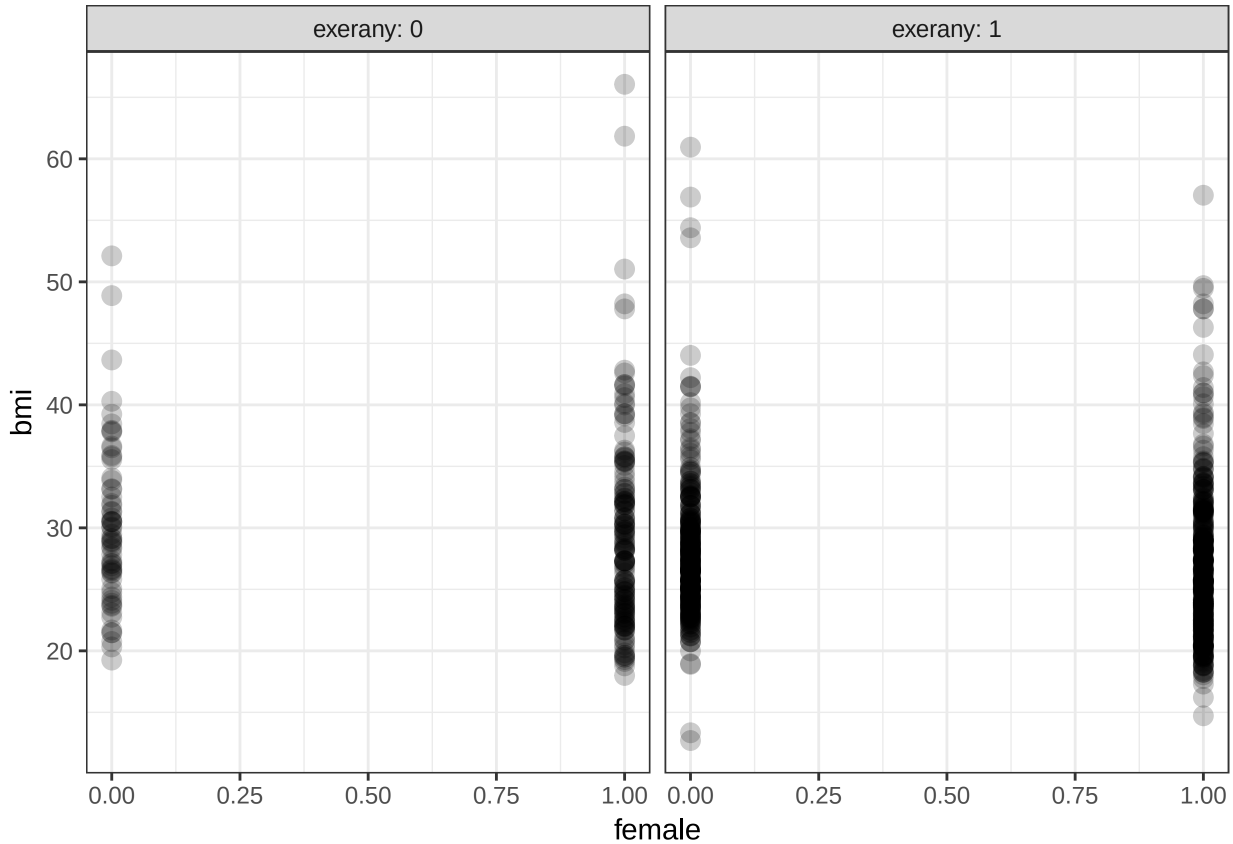


or maybe boxplots?

```
ggplot(smartcle2, aes(x = factor(female), y = bmi)) +
    geom_boxplot() +
    facet_wrap(~ exerany, labeller = label_both)
```




```
ggplot(smartcle2, aes(x = female, y = bmi))+
    geom_point(size = 3, alpha = 0.2) +
    theme_bw() +
    facet_wrap(~ exerany, labeller = label_both)
```



OK. Let's try fitting a model.

```
c2_m2 <- lm(bmi ~ female + exerany, data = smartcle2)
c2_m2
```

```
Call:
lm(formula = bmi ~ female + exerany, data = smartcle2)

Coefficients:
(Intercept)       female      exerany
     30.334       -1.095       -2.384
```

This new model predicts only four predicted values:

- `bmi` = 30.334 if the subject is male and did not exercise (so `female` = 0 and `exerany` = 0)
- `bmi` = 30.334 - 1.095 = 29.239 if the subject is female and did not exercise (`female` = 1 and `exerany` = 0)
- `bmi` = 30.334 - 2.384 = 27.950 if the subject is male and exercised (so `female` = 0 and `exerany` = 1), and, finally
- `bmi` = 30.334 - 1.095 - 2.384 = 26.855 if the subject is female and exercised (so both `female` and `exerany` = 1).

For those who did not exercise, the model is:

- `bmi` = 30.334 - 1.095 `female`

and for those who did exercise, the model is:

- `bmi` = 27.95 - 1.095 `female`

Only the intercept of the `bmi-female` model changes depending on `exerany`.

```
summary(c2_m2)
```

```

Call:
lm(formula = bmi ~ female + exerany, data = smartcle2)

Residuals:
    Min      1Q  Median      3Q     Max 
-15.240  -4.091  -1.095   2.602  36.822 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept)  30.3335     0.5231   57.99  < 2e-16 ***
female       -1.0952     0.4262   -2.57   0.0103 *  
exerany      -2.3836     0.4965   -4.80 1.86e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.239 on 893 degrees of freedom
Multiple R-squared:  0.02939,	Adjusted R-squared:  0.02722 
F-statistic: 13.52 on 2 and 893 DF,  p-value: 1.641e-06
```

```
confint(c2_m2)
```

```
                2.5 %     97.5 %
(Intercept) 29.306846 31.3602182
female      -1.931629 -0.2588299
exerany     -3.358156 -1.4090777
```

The slopes of both `female` and `exerany` have confidence intervals that are completely below zero, indicating that both `female` sex and `exerany` appear to be associated with reductions in `bmi`.

The R^2 value suggests that just under 3% of the variation in `bmi` is accounted for by this ANOVA model.

In fact, this regression (on two binary indicator variables) is simply a two-way ANOVA model without an interaction term.

```
anova(c2_m2)
```

```
Analysis of Variance Table

Response: bmi
           Df Sum Sq Mean Sq F value    Pr(>F)    
female      1    156  155.61  3.9977   0.04586 *  
exerany     1    897  896.93 23.0435 1.856e-06 ***
Residuals 893  34759   38.92                      
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

2.8 m3: Adding the interaction term (Two-way ANOVA with interaction)

Suppose we want to let the effect of `female` vary depending on the `exerany` status. Then we need to incorporate an interaction term in our model.

```r
c2_m3 <- lm(bmi ~ female * exerany, data = smartcle2)
c2_m3
```

```

Call:
lm(formula = bmi ~ female * exerany, data = smartcle2)

Coefficients:
   (Intercept)          female         exerany  female:exerany
       30.1359         -0.8104         -2.1450         -0.3592
```

So, for example, for a male who exercises, this model predicts

- `bmi` = 30.136 - 0.810 (0) - 2.145 (1) - 0.359 (0)(1) = 30.136 - 2.145 = 27.991

And for a female who exercises, the model predicts

- `bmi` = 30.136 - 0.810 (1) - 2.145 (1) - 0.359 (1)(1) = 30.136 - 0.810 - 2.145 - 0.359 = 26.822

For those who did not exercise, the model is:

- `bmi` = 30.136 - 0.81 `female`

But for those who did exercise, the model is:

- `bmi` = (30.136 - 2.145) + (-0.810 + (-0.359)) `female`, or „,
- `bmi` = 27.991 - 1.169 `female`

Now, both the slope and the intercept of the `bmi-female` model change depending on `exerany`.

```r
summary(c2_m3)
```

```

Call:
lm(formula = bmi ~ female * exerany, data = smartcle2)

Residuals:
    Min      1Q  Median      3Q     Max
-15.281  -4.101  -1.061   2.566  36.734

Coefficients:
               Estimate Std. Error t value Pr(>|t|)
(Intercept)     30.1359     0.7802  38.624   <2e-16 ***
female          -0.8104     0.9367  -0.865   0.3872
exerany         -2.1450     0.8575  -2.501   0.0125 *
female:exerany  -0.3592     1.0520  -0.341   0.7328
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.242 on 892 degrees of freedom
Multiple R-squared:  0.02952,	Adjusted R-squared:  0.02625
F-statistic: 9.044 on 3 and 892 DF,  p-value: 6.669e-06
```

```r
confint(c2_m3)
```

```
                   2.5 %     97.5 %
(Intercept)    28.604610 31.6672650
female         -2.648893  1.0280526
exerany        -3.827886 -0.4620407
female:exerany -2.423994  1.7055248
```

In fact, this regression (on two binary indicator variables and a product term) is simply a two-way ANOVA model with an interaction term.

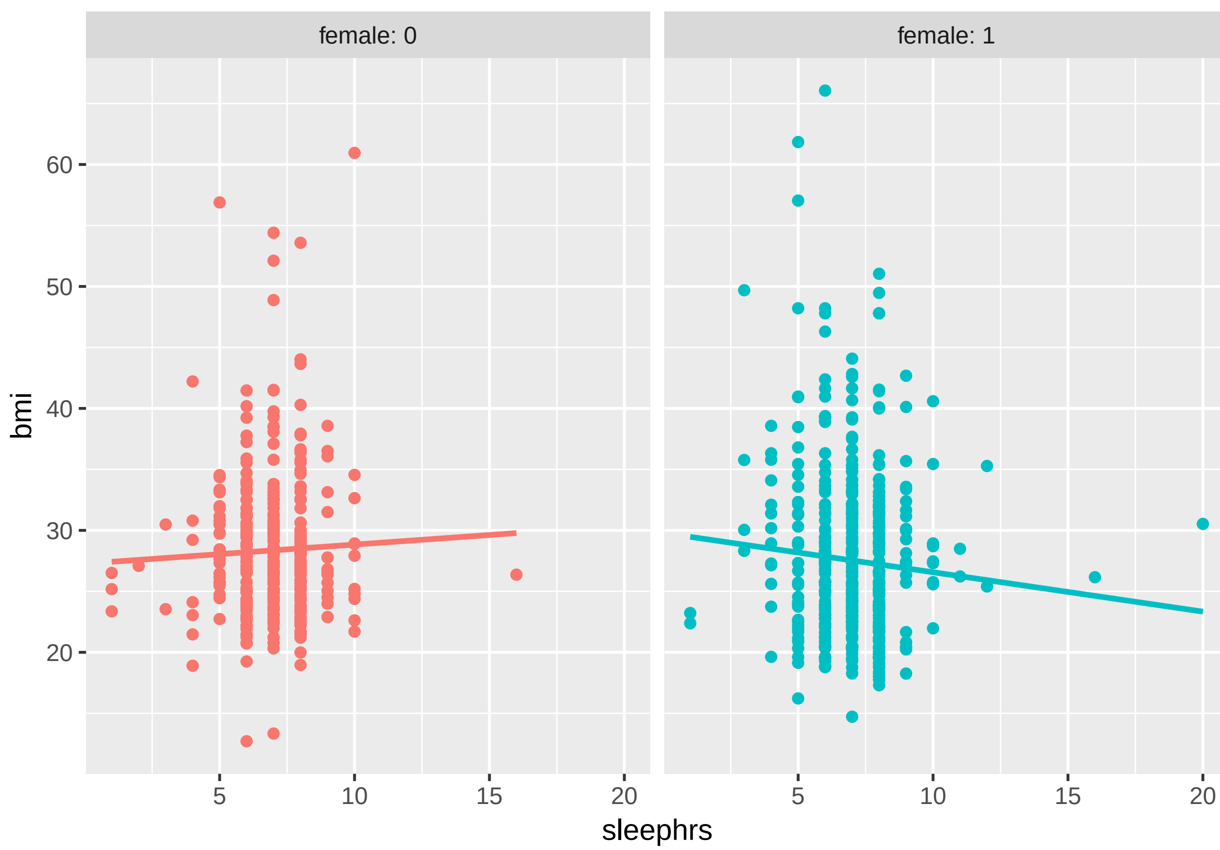
```
anova(c2_m3)
```

```
Analysis of Variance Table

Response: bmi
                Df Sum Sq Mean Sq F value    Pr(>F)
female           1    156  155.61  3.9938   0.04597 *
exerany          1    897  896.93 23.0207 1.878e-06 ***
female:exerany   1      5    4.54  0.1166   0.73283
Residuals      892  34754   38.96
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The interaction term doesn't change very much here. Its uncertainty interval includes zero, and the overall model still accounts for just under 3% of the variation in `bmi`.

2.9 m4: Using `female` and `sleephrs` in a model for `bmi`

```
ggplot(smartcle2, aes(x = sleephrs, y = bmi, color = factor(female))) +
    geom_point() +
    guides(col = FALSE) +
    geom_smooth(method = "lm", se = FALSE) +
    facet_wrap(~ female, labeller = label_both)
```



Does the difference in slopes of `bmi` and `sleephrs` for males and females appear to be substantial and important?

```
c2_m4 <- lm(bmi ~ female * sleephrs, data = smartcle2)

summary(c2_m4)
```

```

Call:
lm(formula = bmi ~ female * sleephrs, data = smartcle2)

Residuals:
    Min      1Q  Median      3Q     Max 
-15.498  -4.179  -1.035   2.830  38.204 

Coefficients:
                Estimate Std. Error t value Pr(>|t|)    
(Intercept)      27.2661     1.6320  16.707   <2e-16 ***
female            2.5263     2.0975   1.204    0.229    
sleephrs          0.1569     0.2294   0.684    0.494    
female:sleephrs  -0.4797     0.2931  -1.636    0.102    
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.31 on 892 degrees of freedom
Multiple R-squared:  0.008341,  Adjusted R-squared:  0.005006 
F-statistic: 2.501 on 3 and 892 DF,  p-value: 0.05818
```

Does it seem as though the addition of `sleephrs` has improved our model substantially over a model with `female` alone (which, you recall, was `c2_m1`)?

Since the `c2_m4` model contains the `c2_m1` model's predictors as a subset and the outcome is the same for each model, we consider the models *nested* and have some extra tools available to compare them.

- I might start by looking at the basic summaries for each model.

```
glance(c2_m4)
```

```
    r.squared adj.r.squared    sigma statistic    p.value df    logLik
1 0.008341404   0.005006229 6.309685   2.50104 0.05818038  4 -2919.873
       AIC      BIC deviance df.residual
1 5849.747 5873.736 35512.42         892
```

```
glance(c2_m1)
```

```
    r.squared adj.r.squared   sigma statistic    p.value df    logLik
1 0.004345169   0.003231461 6.31531  3.901534 0.04854928  2 -2921.675
      AIC      BIC deviance df.residual
1 5849.35 5863.744 35655.53         894
```

- The R^2 is twice as large for the model with `sleephrs`, but still very tiny.
- The *p* value for the global ANOVA test is actually less significant in `c2_m4` than in `c2_m1`.
- Smaller AIC and smaller BIC statistics are more desirable. Here, there's little to choose from, but `c2_m1` is a little better on each standard.
- We might also consider a significance test by looking at an ANOVA model comparison. This is only appropriate because `c2_m1` is nested in `c2_m4`.

```
anova(c2_m4, c2_m1)
```

```
Analysis of Variance Table
```

```
Model 1: bmi ~ female * sleephrs
Model 2: bmi ~ female
  Res.Df   RSS Df Sum of Sq      F Pr(>F)
1    892 35512
2    894 35656 -2   -143.11 1.7973 0.1663
```

The addition of the `sleephrs` term picked up 143 in the sum of squares column, at a cost of two degrees of freedom, yielding a *p* value of 0.166, suggesting that this isn't a significant improvement over the model that just did a t-test on `female`.

2.10 m5: What if we add more variables?

We can boost our R^2 a bit, to over 5%, by adding in two new variables, related to whether or not the subject (in the past 30 days) used the internet, and on how many days the subject drank alcoholic beverages.

```
c2_m5 <- lm(bmi ~ female + exerany + sleephrs + internet30 + alcdays,
         data = smartcle2)
summary(c2_m5)
```

```

Call:
lm(formula = bmi ~ female + exerany + sleephrs + internet30 + 
    alcdays, data = smartcle2)

Residuals:
    Min      1Q  Median      3Q     Max 
-16.147  -3.997  -0.856   2.487  35.965 

Coefficients:
            Estimate Std. Error t value Pr(>|t|)    
(Intercept) 30.84066    1.18458  26.035  < 2e-16 ***
female      -1.28801    0.42805  -3.009   0.0027 ** 
exerany     -2.42161    0.49853  -4.858 1.40e-06 ***
sleephrs    -0.14118    0.13988  -1.009   0.3131    
internet30   1.38916    0.54252   2.561   0.0106 *  
alcdays     -0.10460    0.02595  -4.030 6.04e-05 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 6.174 on 890 degrees of freedom
Multiple R-squared:  0.05258,	Adjusted R-squared:  0.04726 
F-statistic: 9.879 on 5 and 890 DF,  p-value: 3.304e-09
```

2.11 m6: Would adding self-reported health help?

And we can do even a bit better than that by adding in a multi-categorical measure: self-reported general health.

```
c2_m6 <- lm(bmi ~ female + exerany + sleephrs + internet30 + alcdays + genhealth,
         data = smartcle2)
summary(c2_m6)
```

```
Call:
lm(formula = bmi ~ female + exerany + sleephrs + internet30 +
    alcdays + genhealth, data = smartcle2)

Residuals:
    Min      1Q  Median      3Q     Max
-16.331  -3.813  -0.838   2.679  34.166

Coefficients:
                    Estimate Std. Error t value Pr(>|t|)
(Intercept)         26.49498    1.31121  20.206  < 2e-16 ***
female              -0.85520    0.41969  -2.038 0.041879 *
exerany             -1.61968    0.50541  -3.205 0.001400 **
sleephrs            -0.12719    0.13613  -0.934 0.350368
internet30           2.02498    0.53898   3.757 0.000183 ***
alcdays             -0.08431    0.02537  -3.324 0.000925 ***
genhealth2_VeryGood  2.10537    0.59408   3.544 0.000415 ***
genhealth3_Good      4.08245    0.60739   6.721 3.22e-11 ***
genhealth4_Fair      4.99213    0.80178   6.226 7.37e-10 ***
genhealth5_Poor      3.11025    1.12614   2.762 0.005866 **
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 5.993 on 886 degrees of freedom
Multiple R-squared:  0.1115,    Adjusted R-squared:  0.1024
F-statistic: 12.35 on 9 and 886 DF,  p-value: < 2.2e-16
```

2.12 m7: What if we added days of work missed?

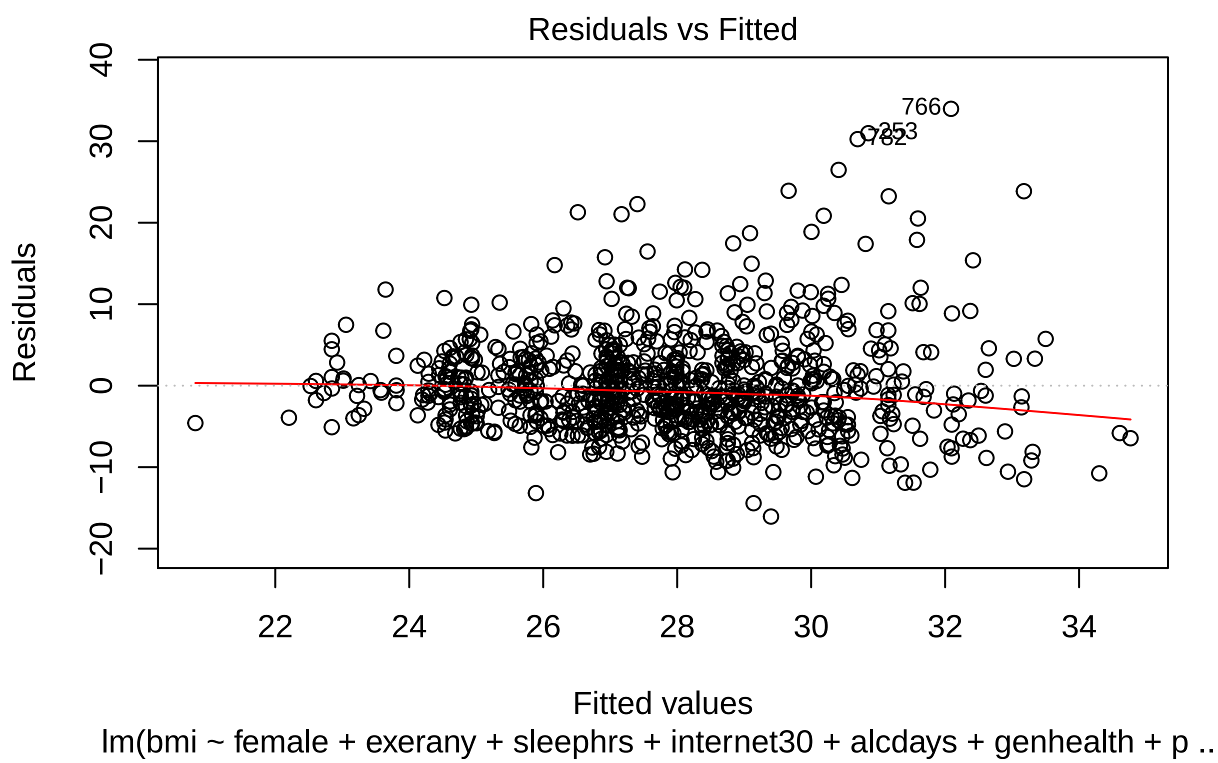
```r
c2_m7 <- lm(bmi ~ female + exerany + sleephrs + internet30 + alcdays +
                genhealth + physhealth + menthealth,
        data = smartcle2)
summary(c2_m7)
```

```
Call:
lm(formula = bmi ~ female + exerany + sleephrs + internet30 +
    alcdays + genhealth + physhealth + menthealth, data = smartcle2)

Residuals:
    Min      1Q  Median      3Q     Max
-16.060  -3.804  -0.890   2.794  33.972

Coefficients:
                    Estimate Std. Error t value Pr(>|t|)
(Intercept)         25.88208    1.31854  19.629  < 2e-16 ***
female              -0.96435    0.41908  -2.301 0.021616 *
exerany             -1.43171    0.50635  -2.828 0.004797 **
sleephrs            -0.08033    0.13624  -0.590 0.555583
internet30           2.00267    0.53759   3.725 0.000207 ***
alcdays             -0.07997    0.02528  -3.163 0.001614 **
```

```
genhealth2_VeryGood  2.09533    0.59238   3.537 0.000425 ***
genhealth3_Good      3.90949    0.60788   6.431 2.07e-10 ***
genhealth4_Fair      4.27152    0.83986   5.086 4.47e-07 ***
genhealth5_Poor      1.26021    1.31556   0.958 0.338361
physhealth           0.06088    0.03005   2.026 0.043064 *
menthealth           0.06636    0.03177   2.089 0.037021 *
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 5.964 on 884 degrees of freedom
Multiple R-squared:  0.1219,    Adjusted R-squared:  0.111
F-statistic: 11.16 on 11 and 884 DF,  p-value: < 2.2e-16
```

How do the assumptions behind this model look?

```
plot(c2_m7, which = 1)
```



2.13 Next Up

- Would stepwise regression help us build a better model?
  - Is there another, better, approach for variable selection?
- How should we validate this model?
  - Is breaking into training and test samples our best option?
- How should we think about potential transformations of these predictors?
  - What's a Spearman rho-squared plot, and how might it help us decide how to spend degrees of freedom on non-linear terms better?

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