

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

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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.

```
library(tableone)
library(skimr)
library(ggbridges)
library(magrittr)
library(arm)
library(rms)
library(leaps)
library(lars)
library(simputation)
library(modelr)
library(broom)
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
bonding <- read.csv("data/bonding.csv") %>% tbl_df
cortisol <- read.csv("data/cortisol.csv") %>% tbl_df
emphysema <- read.csv("data/emphysema.csv") %>% tbl_df
prost <- read.csv("data/prost.csv") %>% tbl_df
maleptsd <- read.csv("data/maleptsd.csv") %>% tbl_df
```


Special Functions used in these notes

```
specify_decimal <- function(x, k) format(round(x, k), nsmall=k)
```


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-positive¹ 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 fibrillation².

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

¹HER2 = 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.

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

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

³The 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

```
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   Interv~  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   Interv~  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  Interv~  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`)

```
fs.vars <- c("age", "sex", "nihss", "location",
            "hx.isch", "afib", "dm", "mrainkin", "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		p	test
	Control 267	Intervention 233		
n				
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.

```
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 order⁴ 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	
mrain (mean (sd))			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.

⁴We 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 `mrarkin` 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.

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

	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)
mrarkin (%)		
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.

```
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 within our `data` subfolder (note that the `data` folder must already exist), 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.

```
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 = "data/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	mrarkin (%)			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

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



```
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.

```
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 placed in a data subfolder, using

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

write.csv(bb.t1, file = "data/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. We will discuss methods for imputing missing data later in these Notes.

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.

```
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
```

```
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 Summarizing the `smartcle2` data numerically

2.4.1 The New Toy: The `skim` function

```
skim(smartcle2, -SEQNO)
```

Skim summary statistics

n obs: 896

n variables: 10

Variable type: factor

variable	missing	complete	n	n_unique
genhealth	0	896	896	5

top_counts ordered

2_V: 306, 3_G: 295, 1_E: 155, 4_F: 102 FALSE

Variable type: integer

variable	missing	complete	n	mean	sd	p0	p25	median	p75	p100
alcdays	0	896	896	4.83	8.14	0	0	1	5	30
exerany	0	896	896	0.77	0.42	0	1	1	1	1
female	0	896	896	0.58	0.49	0	0	1	1	1
internet30	0	896	896	0.81	0.39	0	1	1	1	1
menthealth	0	896	896	2.69	6.72	0	0	0	2	30
physhealth	0	896	896	3.99	8.64	0	0	0	2	30
sleephrs	0	896	896	7.02	1.48	1	6	7	8	20

Variable type: numeric

variable	missing	complete	n	mean	sd	p0	p25	median	p75	p100
bmi	0	896	896	27.87	6.33	12.71	23.7	26.8	30.53	66.06

2.4.2 The usual summary for a data frame

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

```
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

2.4.3 The describe function in Hmisc

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

```
Hmisc::describe(select(smartcle2, bmi, genhealth, female))
```

```
select(smartcle2, bmi, genhealth, female)
```

```
3 Variables      896 Observations
-----
```

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
-----
```

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

```
-----
```

female	n	missing	distinct	Info	Sum	Mean	Gmd
	896	0	2	0.728	524	0.5848	0.4862

```
-----
```

2.5 Counting as exploratory data analysis

Counting things can be amazingly useful.

2.5.1 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.

2.5.2 What's the distribution of sleephrs?

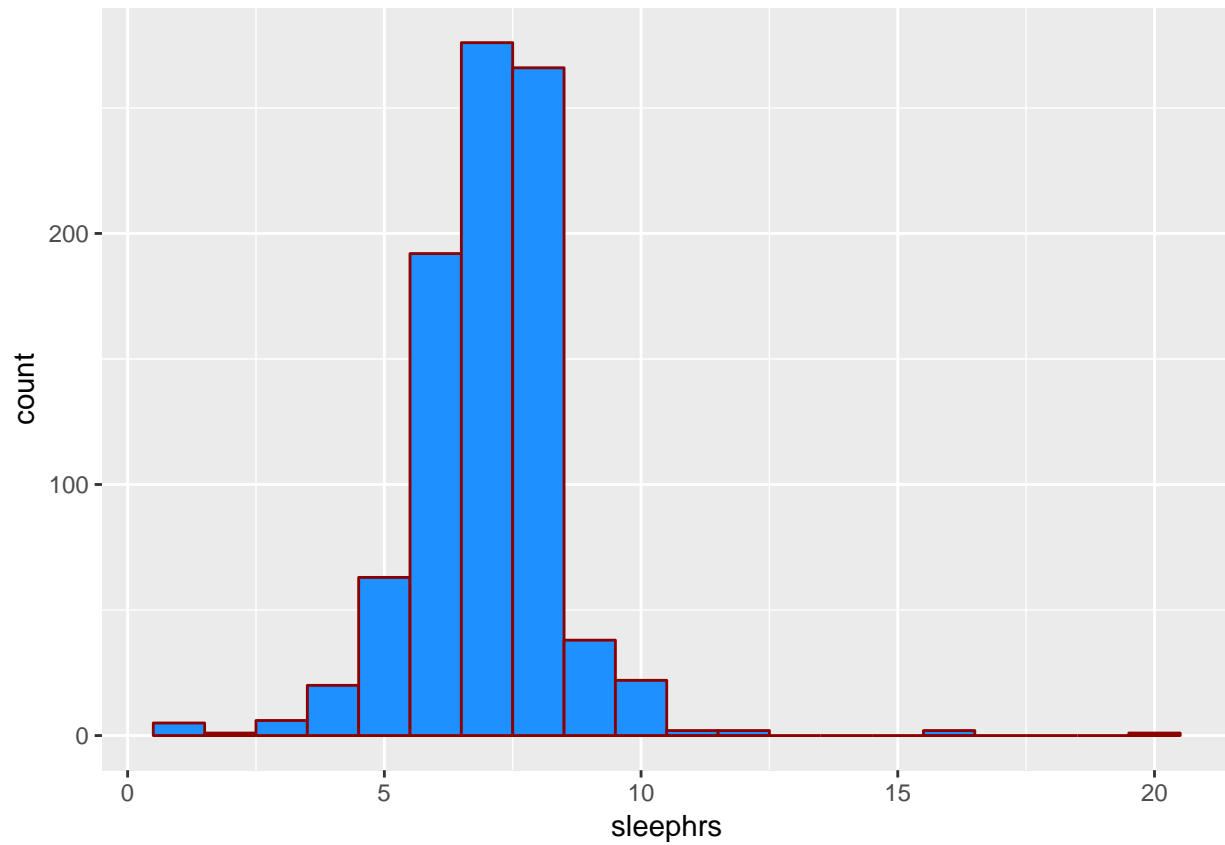
We can count quantitative variables with discrete sets of possible values, like `sleephrs`, which is captured as an integer (that must fall between 0 and 24.)

```
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
```

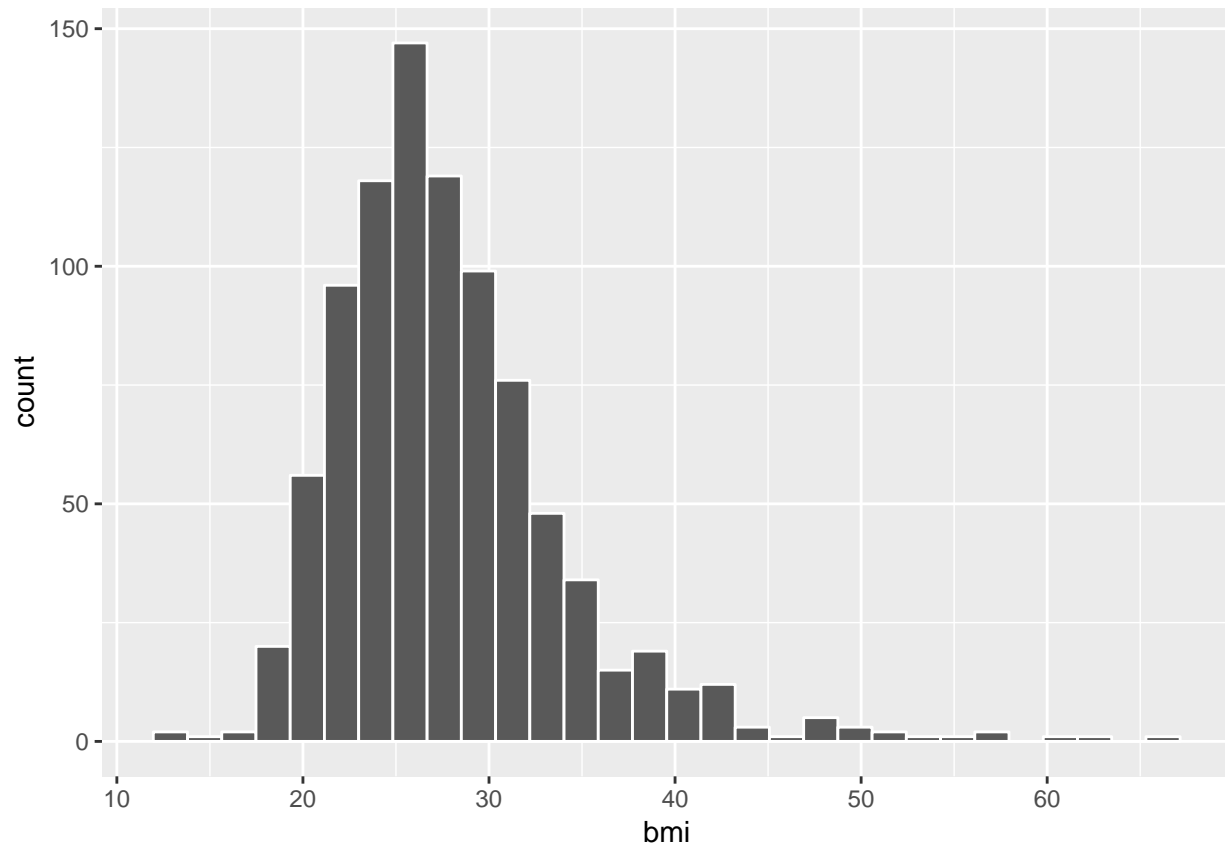
Of course, a natural summary of a quantitative variable like this would be graphical.

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

2.5.3 What's the distribution of BMI?

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



2.5.4 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
```

2.5.5 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
```

2.5.6 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
```

2.5.7 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
```

2.5.8 The skim function within a pipe

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

```
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

2.6 First Modeling Attempt: Can bmi predict physhealth?

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

```
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 ...

```
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.

2.6.1 Fitting a Simple Regression Model

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

```
model_A
```

Call:

```
lm(formula = physhealth ~ bmi, data = smartcle2)
```

Coefficients:

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

```
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

```
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.

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

The fitted model predicts `physhealth` with the equation $-1.45 + 0.195 \cdot \text{bmi}$, 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.

2.6.2.1 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 $-1.45 + 0.195 \cdot \text{bmi}$ 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.

2.6.2.2 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.

2.6.2.3 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:

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

- 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

2.6.3 Using the broom package

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

2.6.3.1 The tidy function

`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

2.6.3.2 The glance function

`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

```

2.6.3.3 The augment function

`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
- `.cooks`, 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.

```
head(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
      .cooks .std.resid
1 1.117852e-04 -0.439775451
2 1.106717e-04 -0.371575999
3 6.147744e-05 -0.328077528
4 1.160381e-04 -0.325074461
5 3.167016e-05  0.204378225
6 2.235722e-08  0.006322069

```

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

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

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

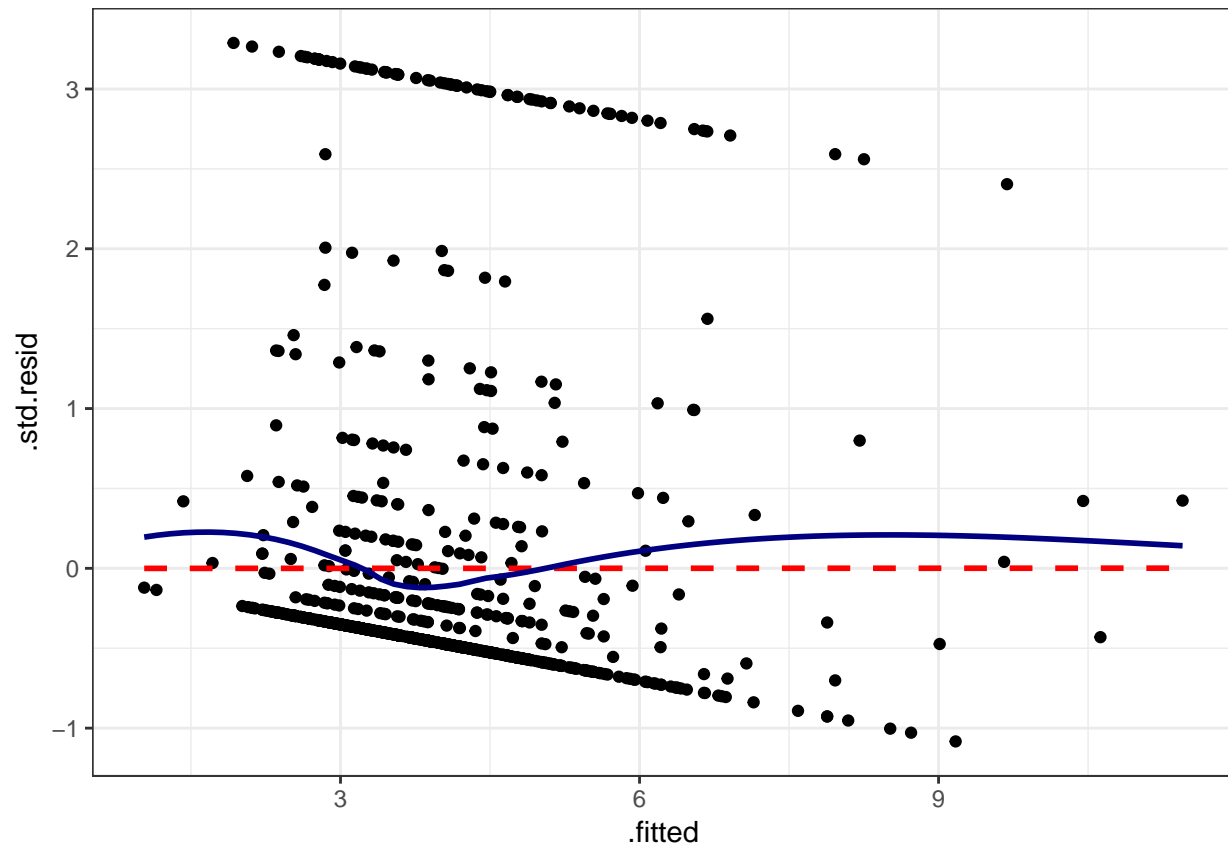
```
plot(model_A, which = 1)
```



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.

2.7 A New Small Study: Predicting BMI

We’ll begin by investigating the problem of predicting `bmi`, at first with just three regression 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)

2.7.1 Does female predict bmi well?

2.7.1.1 Graphical Assessment

```
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.

2.8 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

```

```
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 $\text{BMI} = 28.36 \text{ kg/m}^2$, and
- our best prediction for females is $\text{BMI} = 28.36 - 0.85 = 27.51 \text{ kg/m}^2$.
- 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.

```
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

```

2.9 c2_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,

```

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:

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

For those who did not exercise, the model is:

- $\text{bmi} = 30.334 - 1.095 \text{ female}$

and for those who did exercise, the model is:

- $\text{bmi} = 27.95 - 1.095 \text{ female}$

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

2.10 c2_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.

```
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

- $\text{bmi} = 30.136 - 0.810 (0) - 2.145 (1) - 0.359 (0)(1) = 30.136 - 2.145 = 27.991$

And for a female who exercises, the model predicts

- $\text{bmi} = 30.136 - 0.810 (1) - 2.145 (1) - 0.359 (1)(1) = 30.136 - 0.810 - 2.145 - 0.359 = 26.822$

For those who did not exercise, the model is:

- $\text{bmi} = 30.136 - 0.81 \text{ female}$

But for those who did exercise, the model is:

- $\text{bmi} = (30.136 - 2.145) + (-0.810 + (-0.359)) \text{ female}$, or ,,
- $\text{bmi} = 27.991 - 1.169 \text{ female}$

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

```
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

```
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

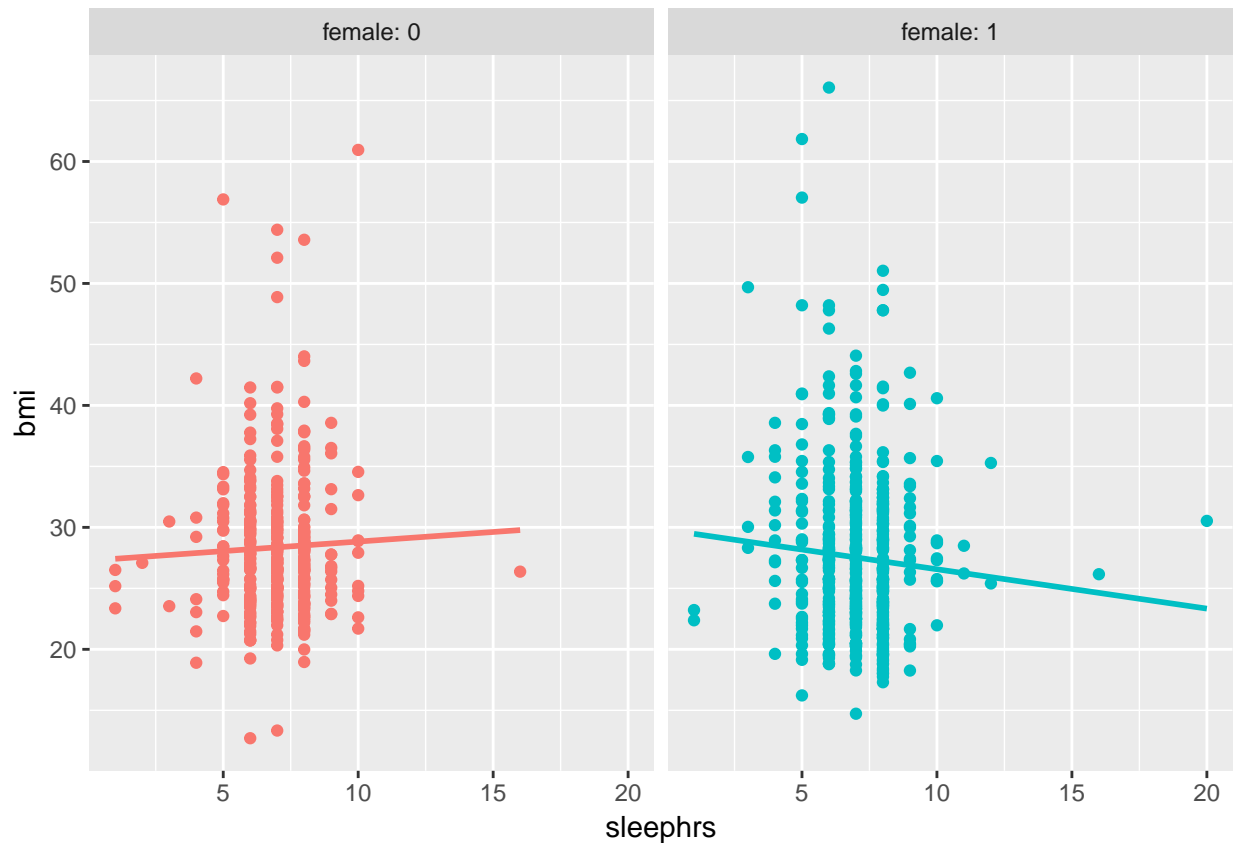
	Df	Sum Sq	Mean Sq	F value	Pr(>F)
female	1	156	155.61	3.9938	0.04597 *
exerany	1	897	896.93	23.0207	1.878e-06 ***
female:exerany	1	5	4.54	0.1166	0.73283
Residuals	892	34754	38.96		

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.

2.11 c2_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 = smartc1e2)
summary(c2_m4)
```

Call:

```
lm(formula = bmi ~ female * sleephrs, data = smartc1e2)
```

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`.

2.12 Making Predictions with a Linear Regression Model

Recall model 4, which yields predictions for body mass index on the basis of the main effects of sex (`female`) and hours of sleep (`sleephrs`) and their interaction.

```
c2_m4
```

Call:

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

Coefficients:

(Intercept)	female	sleephrs	female:sleephrs
27.2661	2.5263	0.1569	-0.4797

2.12.1 Fitting an Individual Prediction and 95% Prediction Interval

What do we predict for the `bmi` of a subject who is `female` and gets 8 hours of sleep per night?

```

c2_new1 <- data_frame(female = 1, sleephrs = 8)
predict(c2_m4, newdata = c2_new1, interval = "prediction", level = 0.95)

```

	fit	lwr	upr
1	27.21065	14.8107	39.6106

The predicted `bmi` for this new subject is 27.61. The prediction interval shows the bounds of a 95% uncertainty interval for a predicted `bmi` for an individual female subject who gets 8 hours of sleep on average per evening. From the `predict` function applied to a linear model, we can get the prediction intervals for any new data points in this manner.

2.12.2 Confidence Interval for an Average Prediction

- What do we predict for the **average body mass index of a population of subjects** who are female and sleep for 8 hours?

```
predict(c2_m4, newdata = c2_new1, interval = "confidence", level = 0.95)
```

	fit	lwr	upr
1	27.21065	26.57328	27.84801

- How does this result compare to the prediction interval?

2.12.3 Fitting Multiple Individual Predictions to New Data

- How does our prediction change for a respondent if they instead get 7, or 9 hours of sleep? What if they are male, instead of female?

```
c2_new2 <- data_frame(subjectid = 1001:1006, female = c(1, 1, 1, 0, 0, 0), sleephrs = c(7, 8, 9, 7, 8, 9))
pred2 <- predict(c2_m4, newdata = c2_new2, interval = "prediction", level = 0.95) %>% tbl_df()

result2 <- bind_cols(c2_new2, pred2)
result2
```

```
# A tibble: 6 x 6
  subjectid female sleephrs   fit   lwr   upr
    <int>   <dbl>   <dbl> <dbl> <dbl> <dbl>
1     1001     1.00     7.00  27.5  15.1  39.9
2     1002     1.00     8.00  27.2  14.8  39.6
3     1003     1.00     9.00  26.9  14.5  39.3
4     1004     0.00     7.00  28.4  16.0  40.8
5     1005     0.00     8.00  28.5  16.1  40.9
6     1006     0.00     9.00  28.7  16.2  41.1
```

The `result2` tibble contains predictions for each scenario.

- Which has a bigger impact on these predictions and prediction intervals? A one category change in `female` or a one hour change in `sleephrs`?

2.12.4 Simulation to represent predictive uncertainty in Model 4

Suppose we want to predict the `bmi` of a female subject who sleeps for eight hours per night. As we have seen, we can do this automatically for a linear model like this one, using the `predict` function applied to the linear model, but a simulation prediction can also be done. Recall the detail of `c2_m4`:

```
c2_m4
```

Call:

```
lm(formula = bmi ~ female * sleephrs, data = smartc1e2)
```

Coefficients:

(Intercept)	female	sleephrs	female:sleephrs
27.2661	2.5263	0.1569	-0.4797

```
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			

We see that the residual standard error for our `bmi` predictions with this model is 6.31.

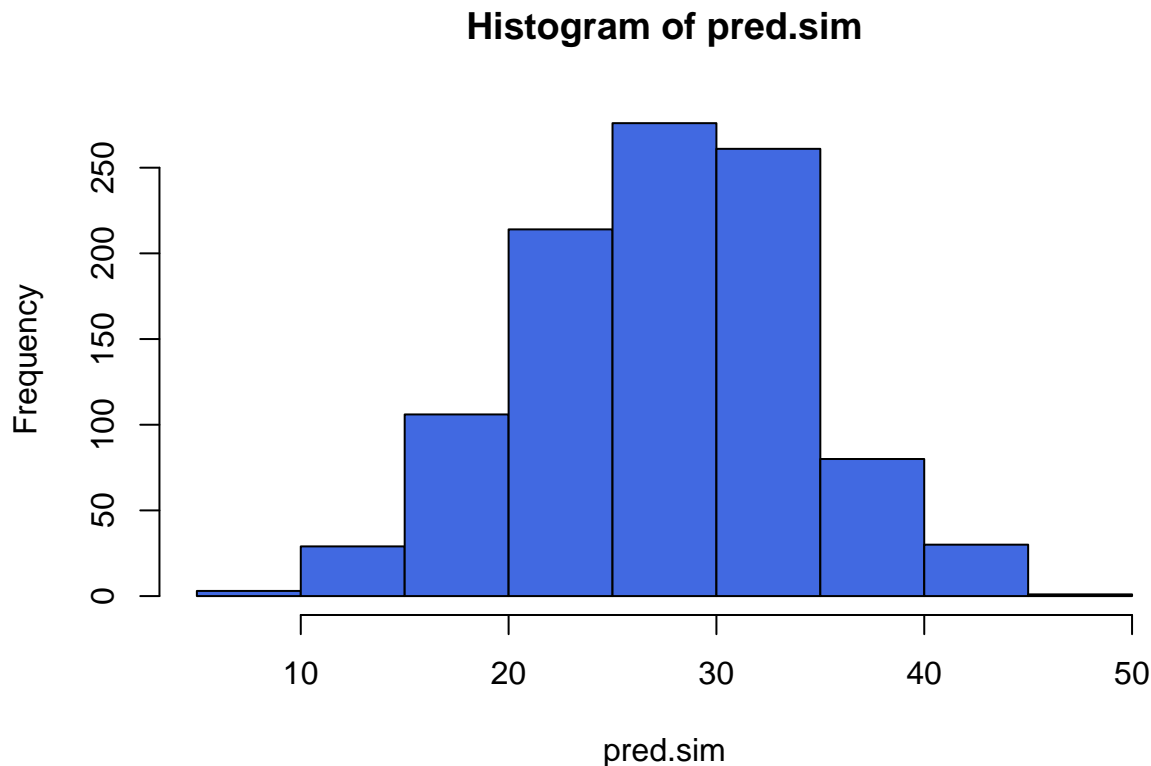
For a female respondent sleeping eight hours, recall that our point estimate (predicted value) of `bmi` is 27.21

```
predict(c2_m4, newdata = c2_new1, interval = "prediction", level = 0.95)
```

	fit	lwr	upr
1	27.21065	14.8107	39.6106

The standard deviation is 6.31, so we could summarize the predictive distribution with a command that tells R to draw 1000 random numbers from a normal distribution with mean 27.21 and standard deviation 6.31. Let's summarize that and get a quick picture.

```
set.seed(432094)
pred.sim <- rnorm(1000, 27.21, 6.31)
hist(pred.sim, col = "royalblue")
```



```
mean(pred.sim)
```

```
[1] 27.41856
```

```
quantile(pred.sim, c(0.025, 0.975))
```

```
      2.5%      97.5%
14.48487 40.16778
```

How do these results compare to the prediction interval of (14.81, 39.61) that we generated earlier?

2.13 Centering the model

Our model `c2_m4` has four predictors (the constant, `sleephrs`, `female` and their interaction) but just two inputs (`female` and `sleephrs`.) If we **center** the quantitative input `sleephrs` before building the model, we get a more interpretable interaction term.

```
smartcle2_c <- smartcle2 %>%
  mutate(sleephrs_c = sleephrs - mean(sleephrs))
```

```
c2_m4_c <- lm(bmi ~ female * sleephrs_c, data = smartcle2_c)
summary(c2_m4_c)
```

Call:

```
lm(formula = bmi ~ female * sleephrs_c, data = smartcle2_c)
```

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)	28.3681	0.3274	86.658	<2e-16 ***
female	-0.8420	0.4280	-1.967	0.0495 *
sleephrs_c	0.1569	0.2294	0.684	0.4940
female:sleephrs_c	-0.4797	0.2931	-1.636	0.1021

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

What has changed as compared to the original c2_m4?

- Our original model was $\text{bmi} = 27.26 + 2.53 \text{ female} + 0.16 \text{ sleephrs} - 0.48 \text{ female} \times \text{sleephrs}$
- Our new model is $\text{bmi} = 28.37 - 0.84 \text{ female} + 0.16 \text{ centered sleephrs} - 0.48 \text{ female} \times \text{centered sleephrs}$.

So our new model on centered data is:

- $28.37 + 0.16 \text{ centered sleephrs}_c$ for male subjects, and
- $(28.37 - 0.84) + (0.16 - 0.48) \text{ centered sleephrs}_c$, or $27.53 - 0.32 \text{ centered sleephrs}_c$ for female subjects.

In our new (centered `sleephrs_c`) model,

- the main effect of `female` now corresponds to a predictive difference (female - male) in `bmi` with `sleephrs` at its mean value, 7.02 hours,
- the intercept term is now the predicted `bmi` for a male respondent who sleeps an average number of hours, and
- the product term corresponds to the change in the slope of centered `sleephrs_c` on `bmi` for a female rather than a male subject, while
- the residual standard deviation and the R-squared values remain unchanged from the model before centering.

2.13.1 Plot of Model 4 on Centered `sleephrs`: `c2_m4_c`

```
ggplot(smartcle2_c, aes(x = sleephrs_c, y = bmi, group = female, col = factor(female))) +
  geom_point(alpha = 0.5, size = 2) +
  geom_smooth(method = "lm", se = FALSE) +
  guides(color = FALSE) +
  labs(x = "Sleep Hours, centered", y = "Body Mass Index",
```

```
title = "Model `c2_m4` on centered data") +
facet_wrap(~ female, labeller = label_both)
```



2.14 Rescaling an input by subtracting the mean and dividing by 2 standard deviations

Centering helped us interpret the main effects in the regression, but it still leaves a scaling problem.

- The `female` coefficient estimate is much larger than that of `sleephrs`, but this is misleading, considering that we are comparing the complete change in one variable (sex = female or not) to a 1-hour change in average sleep.
- Gelman and Hill (2007) recommend all continuous predictors be scaled by dividing by 2 standard deviations, so that:
 - a 1-unit change in the rescaled predictor corresponds to a change from 1 standard deviation below the mean, to 1 standard deviation above.
 - an unscaled binary (1/0) predictor with 50% probability of occurring will be exactly comparable to a rescaled continuous predictor done in this way.

```
smartcle2_rescale <- smartcle2 %>%
  mutate(sleephrs_z = (sleephrs - mean(sleephrs))/(2*sd(sleephrs)))
```

2.14.1 Refitting model `c2_m4` to the rescaled data

```
c2_m4_z <- lm(bmi ~ female * sleephrs_z, data = smartcle2_rescale)
summary(c2_m4_z)
```

Call:

```
lm(formula = bmi ~ female * sleephrs_z, data = smartcle2_rescale)
```

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)	28.3681	0.3274	86.658	<2e-16 ***
female	-0.8420	0.4280	-1.967	0.0495 *
sleephrs_z	0.4637	0.6778	0.684	0.4940
female:sleephrs_z	-1.4173	0.8661	-1.636	0.1021

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

2.14.2 Interpreting the model on rescaled data

What has changed as compared to the original `c2_m4`?

- Our original model was $\text{bmi} = 27.26 + 2.53 \text{ female} + 0.16 \text{ sleephrs} - 0.48 \text{ female} \times \text{sleephrs}$
- Our model on centered `sleephrs` was $\text{bmi} = 28.37 - 0.84 \text{ female} + 0.16 \text{ centered sleephrs}_c - 0.48 \text{ female} \times \text{centered sleephrs}_c$.
- Our new model on rescaled `sleephrs` is $\text{bmi} = 28.37 - 0.84 \text{ female} + 0.46 \text{ rescaled sleephrs}_z - 1.42 \text{ female} \times \text{rescaled sleephrs}_z$.

So our rescaled model is:

- $28.37 + 0.46 \text{ rescaled sleephrs}_z$ for male subjects, and
- $(28.37 - 0.84) + (0.46 - 1.42) \text{ rescaled sleephrs}_z$, or $27.53 - 0.96 \text{ rescaled sleephrs}_z$ for female subjects.

In this new rescaled (`sleephrs_z`) model, then,

- the main effect of `female`, -0.84, still corresponds to a predictive difference (female - male) in `bmi` with `sleephrs` at its mean value, 7.02 hours,
- the intercept term is still the predicted `bmi` for a male respondent who sleeps an average number of hours, and
- the residual standard deviation and the R-squared values remain unchanged,

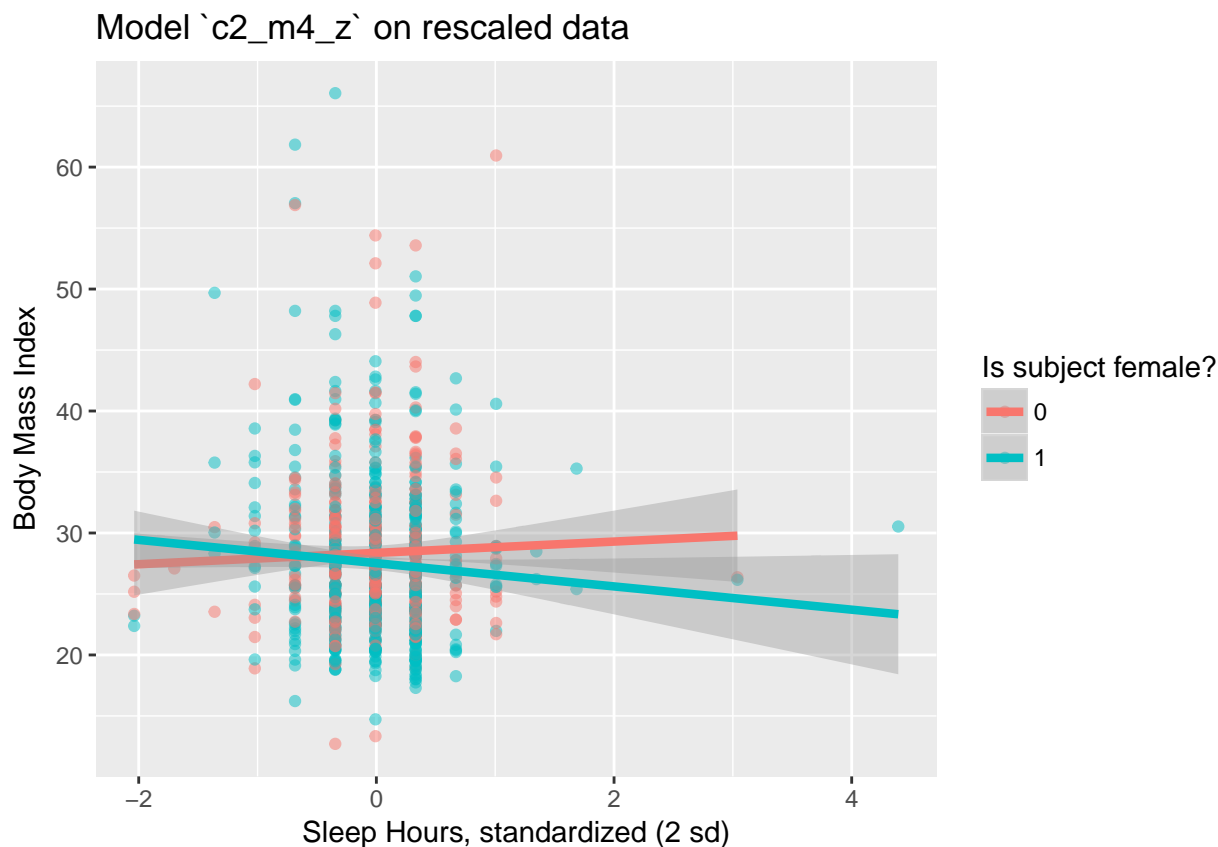
as before, but now we also have that:

- the coefficient of `sleephrs_z` indicates the predictive difference in `bmi` associated with a change in `sleephrs` of 2 standard deviations (from one standard deviation below the mean of 7.02 to one standard deviation above 7.02.)

- Since the standard deviation of `sleephrs` is 1.48, this corresponds to a change from 5.54 hours per night to 8.50 hours per night.
- the coefficient of the product term (-1.42) corresponds to the change in the coefficient of `sleephrs_z` for females as compared to males.

2.14.3 Plot of model on rescaled data

```
ggplot(smartcle2_rescale, aes(x = sleephrs_z, y = bmi,
                             group = female, col = factor(female))) +
  geom_point(alpha = 0.5) +
  geom_smooth(method = "lm", size = 1.5) +
  scale_color_discrete(name = "Is subject female?") +
  labs(x = "Sleep Hours, standardized (2 sd)", y = "Body Mass Index",
       title = "Model `c2_m4_z` on rescaled data")
```



2.15 c2_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

1. Here's the ANOVA for this model. What can we study with this?

```
anova(c2_m5)
```

Analysis of Variance Table

Response: bmi

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
female	1	156	155.61	4.0818	0.04365 *
exerany	1	897	896.93	23.5283	1.453e-06 ***
sleephrs	1	33	32.90	0.8631	0.35313
internet30	1	178	178.33	4.6779	0.03082 *
alcdays	1	619	619.26	16.2443	6.044e-05 ***
Residuals	890	33928	38.12		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

2. Consider the revised output below. Now what can we study?

```
anova(lm(bmi ~ exerany + internet30 + alcdays + female + sleephrs,
    data = smartcle2))
```

Analysis of Variance Table

Response: bmi

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
exerany	1	795	795.46	20.8664	5.618e-06 ***
internet30	1	212	211.95	5.5599	0.0185925 *
alcdays	1	486	486.03	12.7496	0.0003752 ***
female	1	351	350.75	9.2010	0.0024891 **
sleephrs	1	39	38.83	1.0186	0.3131176
Residuals	890	33928	38.12		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

3. What does the output below let us conclude?

```
anova(lm(bmi ~ exerany + internet30 + alcdays + female + sleephrs,
        data = smartcle2),
      lm(bmi ~ exerany + female + alcdays,
        data = smartcle2))
```

Analysis of Variance Table

Model 1: bmi ~ exerany + internet30 + alcdays + female + sleephrs

Model 2: bmi ~ exerany + female + alcdays

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	890	33928				
2	892	34221	-2	-293.2	3.8456	0.02173 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

4. What does it mean for the models to be “nested”?

2.16 c2_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 **

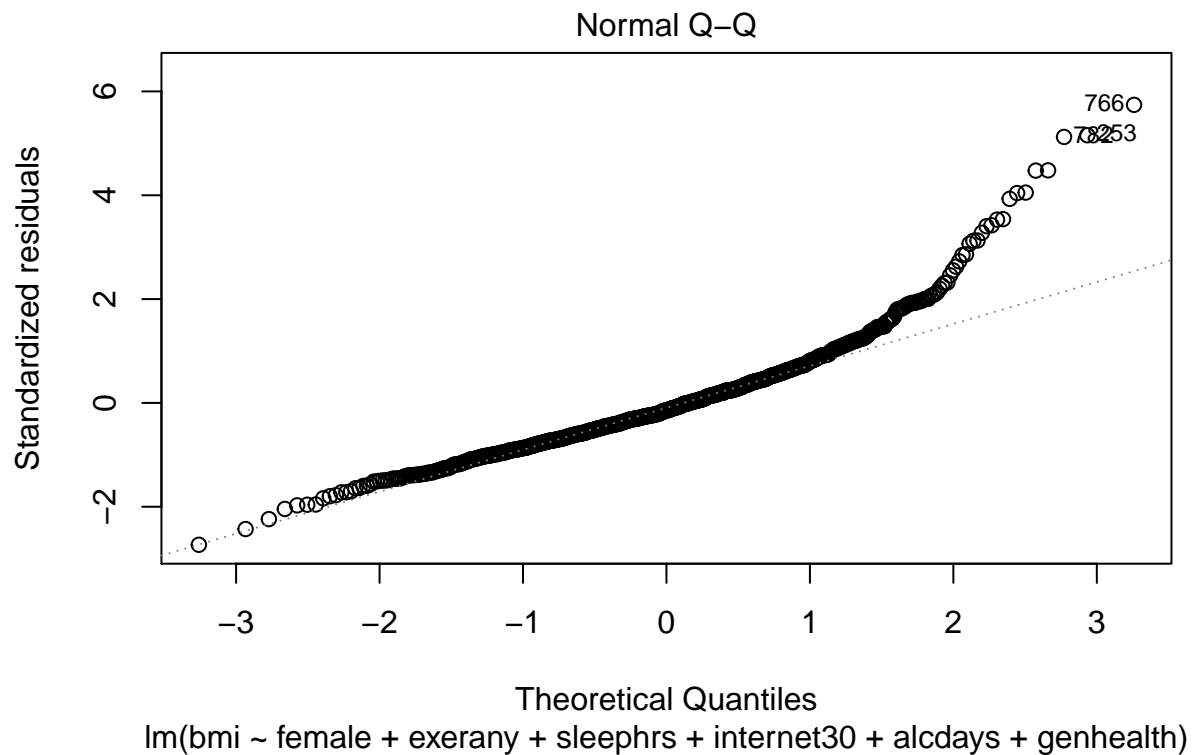
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

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

1. If Harry and Marty have the same values of `female`, `exerany`, `sleephrs`, `internet30` and `alcdays`, but Harry rates his health as Good, and Marty rates his as Fair, then what is the difference in the predictions? Who is predicted to have a larger BMI, and by how much?
2. What does this normal probability plot of the residuals suggest?

```
plot(c2_m6, which = 2)
```



2.17 c2_m7: What if we added the menthealth variable?

```
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

2.18 Key Regression Assumptions for Building Effective Prediction Models

1. Validity - the data you are analyzing should map to the research question you are trying to answer.
 - The outcome should accurately reflect the phenomenon of interest.
 - The model should include all relevant predictors. (It can be difficult to decide which predictors are necessary, and what to do with predictors that have large standard errors.)
 - The model should generalize to all of the cases to which it will be applied.
 - Can the available data answer our question reliably?
2. Additivity and linearity - most important assumption of a regression model is that its deterministic component is a linear function of the predictors. We often think about transformations in this setting.
3. Independence of errors - errors from the prediction line are independent of each other
4. Equal variance of errors - if this is violated, we can more efficiently estimate parameters using *weighted least squares* approaches, where each point is weighted inversely proportional to its variance, but this doesn't affect the coefficients much, if at all.
5. Normality of errors - not generally important for estimating the regression line

2.18.1 Checking Assumptions in model c2_m7

1. How does the assumption of linearity behind this model look?

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



We see no strong signs of serious non-linearity here. There's no obvious curve in the plot, for example.

2. What can we conclude from the plot below?

```
plot(c2_m7, which = 5)
```



`lm(bmi ~ female + exerany + sleephrs + internet30 + alcdays + genhealth + p ...`

This plot can help us identify points with large standardized residuals, large leverage values, and large influence on the model (as indicated by large values of Cook's distance.) In this case, I see no signs of any points used in the model with especially large influence, although there are some poorly fitted points (with especially large standardized residuals.)

Chapter 3

Analysis of Variance

3.1 The bonding data: A Designed Dental Experiment

The `bonding` data describe a designed experiment into the properties of four different resin types (`resin = A, B, C, D`) and two different curing light sources (`light = Halogen, LED`) as they relate to the resulting bonding strength (measured in MPa¹) on the surface of teeth. The source is Kim (2014).

The experiment involved making measurements of bonding strength under a total of 80 experimental setups, or runs, with 10 runs completed at each of the eight combinations of a light source and a resin type. The data are gathered in the `bonding.csv` file.

```
bonding

# A tibble: 80 x 4
  run_ID light  resin strength
  <fct>  <fct>  <fct>    <dbl>
1 R101   LED    B        12.8
2 R102   Halogen B        22.2
3 R103   Halogen B        24.6
4 R104   LED    A        17.0
5 R105   LED    C        32.2
6 R106   Halogen B        27.1
7 R107   LED    A        23.4
8 R108   Halogen A        23.5
9 R109   Halogen D        37.3
10 R110  Halogen A        19.7
# ... with 70 more rows
```

3.2 A One-Factor Analysis of Variance

Suppose we are interested in the distribution of the `strength` values for the four different types of `resin`.

```
bonding %>% group_by(resin) %>% summarize(n = n(), mean(strength), median(strength))
```

```
# A tibble: 4 x 4
  resin      n `mean(strength)` `median(strength)`
  <fct> <int>         <dbl>         <dbl>
1 A         20         18.4         18.0
```

¹The MPa is defined as the failure load (in Newtons) divided by the entire bonded area, in mm².

2	B	20	22.2	22.7
3	C	20	25.2	25.7
4	D	20	32.1	35.3

I'd begin serious work with a plot.

3.2.1 Look at the Data!

```
ggplot(bonding, aes(x = resin, y = strength)) +  
  geom_boxplot()
```



Another good plot for this purpose is a ridgeline plot.

```
ggplot(bonding, aes(x = strength, y = resin, fill = resin)) +  
  geom_density_ridges2() +  
  guides(fill = FALSE)
```

Picking joint bandwidth of 3.09



3.2.2 Table of Summary Statistics

With the small size of this experiment ($n = 20$ for each `resin` type), graphical summaries may not perform as well as they often do. We'll also produce a quick table of summary statistics for `strength` within each `resin` type, with the `skim()` function.

```
bonding %>% group_by(resin) %>% skim(strength)
```

Skim summary statistics

```
n obs: 80
n variables: 4
group variables: resin
```

Variable type: numeric

resin	variable	missing	complete	n	mean	sd	p0	p25	median	p75
A	strength	0	20	20	18.41	4.81	9.3	15.73	17.95	20.4
B	strength	0	20	20	22.23	6.75	11.8	18.45	22.7	25.75
C	strength	0	20	20	25.16	6.33	14.5	20.65	25.7	30.7
D	strength	0	20	20	32.08	9.74	17.3	21.82	35.3	40.15

```
p100
28
35.2
34.5
47.2
```

Since the means and medians are fairly close, and the distributions (with the possible exception of **resin D**) are reasonably well approximated by the Normal, I'll fit an ANOVA model.

```
anova(lm(strength ~ resin, data = bonding))
```

Analysis of Variance Table

```
Response: strength
      Df Sum Sq Mean Sq F value    Pr(>F)
resin    3 1999.7   666.57   13.107 5.52e-07 ***
Residuals 76 3865.2    50.86
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

It appears that the **resin** types have a significant association with mean **strength** of the bonds. Can we identify which **resin** types have generally higher or lower **strength**?

```
TukeyHSD(aov(lm(strength ~ resin, data = bonding)))
```

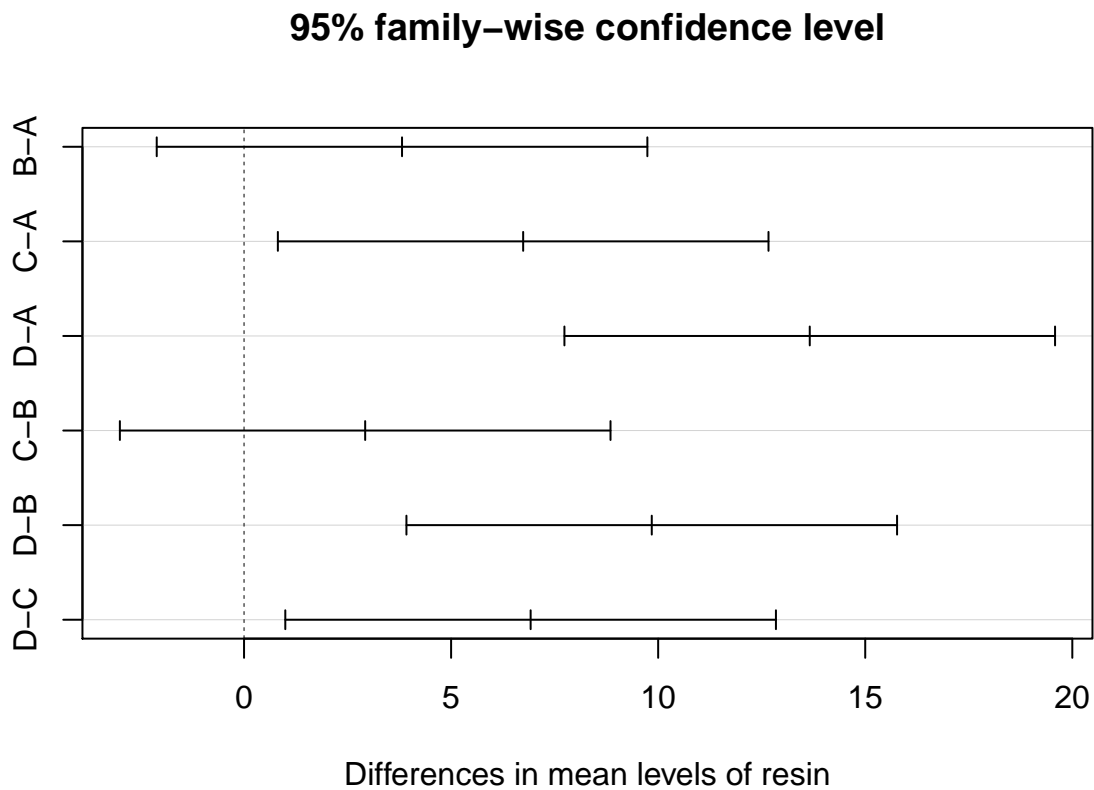
```
Tukey multiple comparisons of means
95% family-wise confidence level
```

```
Fit: aov(formula = lm(strength ~ resin, data = bonding))
```

```
$resin
      diff      lwr      upr    p adj
B-A  3.815 -2.1088676  9.738868 0.3351635
C-A  6.740  0.8161324 12.663868 0.0193344
D-A 13.660  7.7361324 19.583868 0.0000003
C-B  2.925 -2.9988676  8.848868 0.5676635
D-B  9.845  3.9211324 15.768868 0.0002276
D-C  6.920  0.9961324 12.843868 0.0154615
```

Based on these confidence intervals (which have a family-wise 95% confidence level), we see that D is associated with significantly larger mean **strength** than A or B or C, and that C is also associated with significantly larger mean **strength** than A. This may be easier to see in a plot of these confidence intervals.

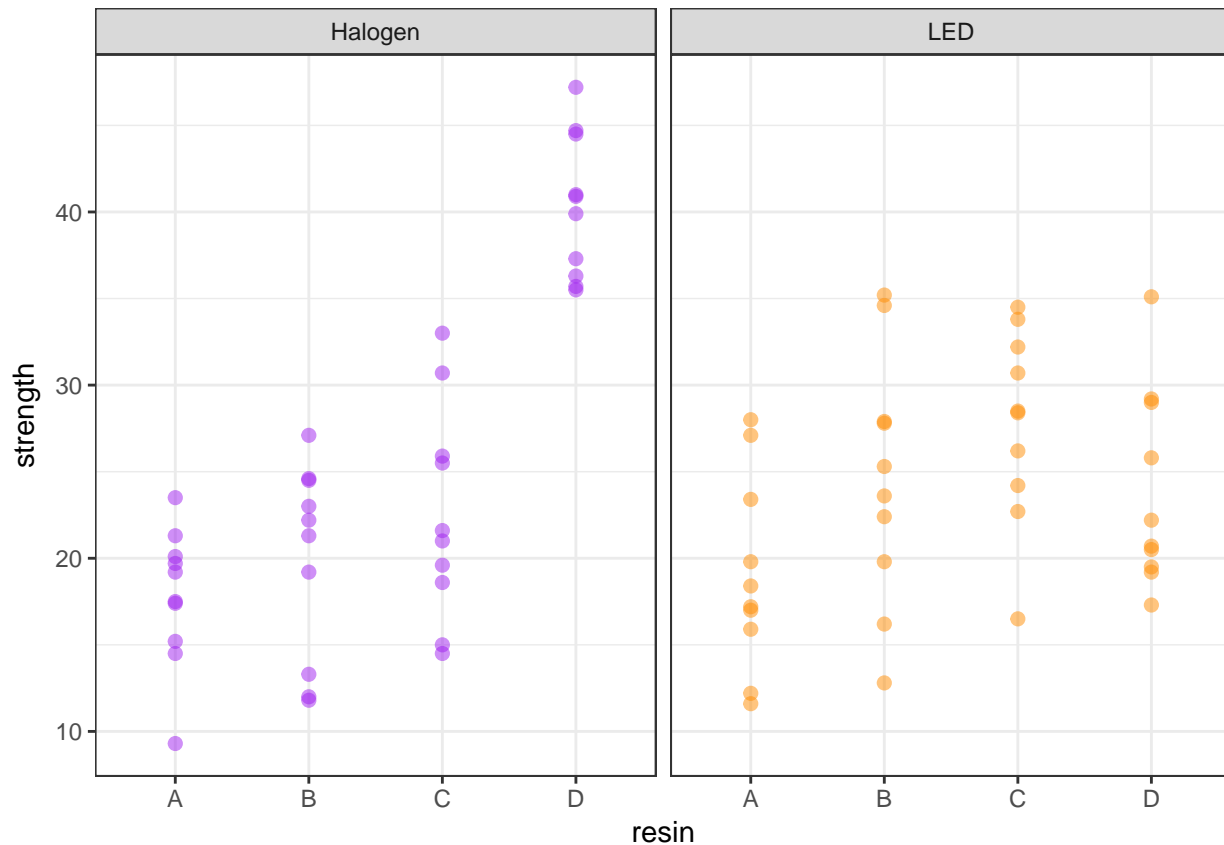
```
plot(TukeyHSD(aov(lm(strength ~ resin, data = bonding))))
```

3.3 A Two-Way ANOVA: Looking at Two Factors

Now, we'll now add consideration of the `light` source into our study. We can look at the distribution of the `strength` values at the combinations of both `light` and `resin`, with a plot like this one...

```
ggplot(bonding, aes(x = resin, y = strength, color = light)) +
  geom_point(size = 2, alpha = 0.5) +
  facet_wrap(~ light) +
  guides(color = FALSE) +
  scale_color_manual(values = c("purple", "darkorange")) +
  theme_bw()
```



3.4 A Means Plot (with standard deviations) to check for interaction

Sometimes, we'll instead look at a plot simply of the means (and, often, the standard deviations) of **strength** at each combination of **light** and **resin**. We'll start by building up a data set with the summaries we want to plot.

```
bond.sum <- bonding %>%
  group_by(resin, light) %>%
  summarize(mean.str = mean(strength), sd.str = sd(strength))
```

```
bond.sum
```

```
# A tibble: 8 x 4
# Groups:   resin [?]
  resin light  mean.str sd.str
  <fct> <fct>    <dbl> <dbl>
1 A     Halogen    17.8  4.02
2 A     LED       19.1  5.63
3 B     Halogen    19.9  5.62
4 B     LED       24.6  7.25
5 C     Halogen    22.5  6.19
6 C     LED       27.8  5.56
7 D     Halogen    40.3  4.15
8 D     LED       23.8  5.70
```

Now, we'll use this new data set to plot the means and standard deviations of **strength** at each combination of **resin** and **light**.

```
## The error bars will overlap unless we adjust the position.
pd <- position_dodge(0.2) # move them .1 to the left and right

ggplot(bond.sum, aes(x = resin, y = mean.str, col = light)) +
  geom_errorbar(aes(ymin = mean.str - sd.str,
                    ymax = mean.str + sd.str),
               width = 0.2, position = pd) +
  geom_point(size = 2, position = pd) +
  geom_line(aes(group = light), position = pd) +
  scale_color_manual(values = c("purple", "darkorange")) +
  theme_bw() +
  labs(y = "Bonding Strength (MPa)", x = "Resin Type",
       title = "Observed Means (+/- SD) of Bonding Strength")
```



Is there evidence of a meaningful interaction between the resin type and the **light** source on the bonding strength in this plot?

- Sure. A meaningful interaction just means that the strength associated with different **resin** types depends on the **light** source.
 - With LED **light**, it appears that **resin C** leads to the strongest bonding strength.
 - With Halogen **light**, though, it seems that **resin D** is substantially stronger.
- Note that the lines we see here connecting the **light** sources aren't in parallel (as they would be if we had zero interaction between **resin** and **light**), but rather, they cross.

3.4.1 Skimming the data after grouping by resin and light

We might want to look at a numerical summary of the `strengths` within these groups, too.

```
bonding %>%
  group_by(resin, light) %>%
  skim(strength)
```

Skim summary statistics

```
n obs: 80
n variables: 4
group variables: resin, light
```

Variable type: numeric

resin	light	variable	missing	complete	n	mean	sd	p0	p25	median
A	Halogen	strength	0	10	10	17.77	4.02	9.3	15.75	18.35
A	LED	strength	0	10	10	19.06	5.63	11.6	16.18	17.8
B	Halogen	strength	0	10	10	19.9	5.62	11.8	14.78	21.75
B	LED	strength	0	10	10	24.56	7.25	12.8	20.45	24.45
C	Halogen	strength	0	10	10	22.54	6.19	14.5	18.85	21.3
C	LED	strength	0	10	10	27.77	5.56	16.5	24.7	28.45
D	Halogen	strength	0	10	10	40.3	4.15	35.5	36.55	40.4
D	LED	strength	0	10	10	23.85	5.7	17.3	19.75	21.45

p75	p100
20	23.5
22.5	28
24.12	27.1
27.87	35.2
25.8	33
31.83	34.5
43.62	47.2
28.2	35.1

3.5 Fitting the Two-Way ANOVA model with Interaction

```
c3_m1 <- lm(strength ~ resin * light, data = bonding)
summary(c3_m1)
```

Call:

```
lm(formula = strength ~ resin * light, data = bonding)
```

Residuals:

Min	1Q	Median	3Q	Max
-11.760	-3.663	-0.320	3.697	11.250

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	17.770	1.771	10.033	2.57e-15 ***
resinB	2.130	2.505	0.850	0.3979
resinC	4.770	2.505	1.904	0.0609 .
resinD	22.530	2.505	8.995	2.13e-13 ***

```

lightLED          1.290      2.505   0.515   0.6081
resinB:lightLED    3.370      3.542   0.951   0.3446
resinC:lightLED    3.940      3.542   1.112   0.2697
resinD:lightLED   -17.740      3.542  -5.008  3.78e-06 ***
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 5.601 on 72 degrees of freedom
Multiple R-squared:  0.6149,    Adjusted R-squared:  0.5775 
F-statistic: 16.42 on 7 and 72 DF,  p-value: 9.801e-13

```

3.5.1 The ANOVA table for our model

In a two-way ANOVA model, we begin by assessing the interaction term. If it's important, then our best model is the model including the interaction. If it's not important, we will often move on to consider a new model, fit without an interaction.

The ANOVA table is especially helpful in this case, because it lets us look specifically at the interaction effect.

```
anova(c3_m1)
```

Analysis of Variance Table

```

Response: strength
      Df Sum Sq Mean Sq F value    Pr(>F)    
resin   3 1999.72  666.57  21.2499 5.792e-10 ***
light   1   34.72   34.72   1.1067  0.2963    
resin:light 3 1571.96  523.99  16.7043 2.457e-08 ***
Residuals 72 2258.52   31.37                      
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

3.5.2 Is the interaction important?

In this case, the interaction:

- is evident in the means plot, and
- is highly statistically significant, and
- accounts for a sizeable fraction (27%) of the overall variation

$$\eta_{interaction}^2 = \frac{SS(\text{resin:light})}{SS(\text{Total})} = \frac{1571.96}{1999.72 + 34.72 + 1571.96 + 2258.52} = 0.268$$

If the interaction were *either* large or significant we would be inclined to keep it in the model. In this case, it's both, so there's no real reason to remove it.

3.5.3 Interpreting the Interaction

Recall the model equation, which is:

```
c3_m1
```

Call:

```
lm(formula = strength ~ resin * light, data = bonding)
```

Coefficients:

(Intercept)	resinB	resinC	resinD
17.77	2.13	4.77	22.53
lightLED	resinB:lightLED	resinC:lightLED	resinD:lightLED
1.29	3.37	3.94	-17.74

so we have:

$$strength = 17.77 + 2.13resinB + 4.77resinC + 22.53resinD + 1.29lightLED + 3.37resinB*lightLED + 3.94resinC*lightLED - 17.74resinD*lightLED$$

So, if `light` = Halogen, our equation is:

$$strength = 17.77 + 2.13resinB + 4.77resinC + 22.53resinD$$

And if `light` = LED, our equation is:

$$strength = 19.06 + 5.50resinB + 8.71resinC + 4.79resinD$$

Note that both the intercept and the slopes change as a result of the interaction. The model yields a different prediction for every possible combination of a `resin` type and a `light` source.

3.6 Comparing Individual Combinations of `resin` and `light`

To make comparisons between individual combinations of a `resin` type and a `light` source, using something like Tukey's HSD approach for multiple comparisons, we first refit the model using the `aov` structure, rather than `lm`.

```
c3m1_aov <- aov(strength ~ resin * light, data = bonding)
```

```
summary(c3m1_aov)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
resin	3	1999.7	666.6	21.250	5.79e-10 ***
light	1	34.7	34.7	1.107	0.296
resin:light	3	1572.0	524.0	16.704	2.46e-08 ***
Residuals	72	2258.5	31.4		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

And now, we can obtain Tukey HSD comparisons (which will maintain an overall 95% family-wise confidence level) across the `resin` types, the `light` sources, and the combinations, with the `TukeyHSD` command. This approach is only completely appropriate if these comparisons are pre-planned, and if the design is balanced (as this is, with the same sample size for each combination of a `light` source and `resin` type.)

```
TukeyHSD(c3m1_aov)
```

```
Tukey multiple comparisons of means
95% family-wise confidence level
```

```
Fit: aov(formula = strength ~ resin * light, data = bonding)
```

```
$resin
```

	diff	lwr	upr	p adj
B-A	3.815	-0.843129	8.473129	0.1461960
C-A	6.740	2.081871	11.398129	0.0016436
D-A	13.660	9.001871	18.318129	0.0000000
C-B	2.925	-1.733129	7.583129	0.3568373
D-B	9.845	5.186871	14.503129	0.0000026
D-C	6.920	2.261871	11.578129	0.0011731

```
$light
```

	diff	lwr	upr	p adj
LED-Halogen	-1.3175	-3.814042	1.179042	0.2963128

```
$`resin:light`
```

	diff	lwr	upr	p adj
B:Halogen-A:Halogen	2.13	-5.68928258	9.949283	0.9893515
C:Halogen-A:Halogen	4.77	-3.04928258	12.589283	0.5525230
D:Halogen-A:Halogen	22.53	14.71071742	30.349283	0.0000000
A:LED-A:Halogen	1.29	-6.52928258	9.109283	0.9995485
B:LED-A:Halogen	6.79	-1.02928258	14.609283	0.1361092
C:LED-A:Halogen	10.00	2.18071742	17.819283	0.0037074
D:LED-A:Halogen	6.08	-1.73928258	13.899283	0.2443200
C:Halogen-B:Halogen	2.64	-5.17928258	10.459283	0.9640100
D:Halogen-B:Halogen	20.40	12.58071742	28.219283	0.0000000
A:LED-B:Halogen	-0.84	-8.65928258	6.979283	0.9999747
B:LED-B:Halogen	4.66	-3.15928258	12.479283	0.5818695
C:LED-B:Halogen	7.87	0.05071742	15.689283	0.0473914
D:LED-B:Halogen	3.95	-3.86928258	11.769283	0.7621860
D:Halogen-C:Halogen	17.76	9.94071742	25.579283	0.0000000
A:LED-C:Halogen	-3.48	-11.29928258	4.339283	0.8591455
B:LED-C:Halogen	2.02	-5.79928258	9.839283	0.9922412
C:LED-C:Halogen	5.23	-2.58928258	13.049283	0.4323859
D:LED-C:Halogen	1.31	-6.50928258	9.129283	0.9995004
A:LED-D:Halogen	-21.24	-29.05928258	-13.420717	0.0000000
B:LED-D:Halogen	-15.74	-23.55928258	-7.920717	0.0000006
C:LED-D:Halogen	-12.53	-20.34928258	-4.710717	0.0001014
D:LED-D:Halogen	-16.45	-24.26928258	-8.630717	0.0000002
B:LED-A:LED	5.50	-2.31928258	13.319283	0.3665620
C:LED-A:LED	8.71	0.89071742	16.529283	0.0185285
D:LED-A:LED	4.79	-3.02928258	12.609283	0.5471915
C:LED-B:LED	3.21	-4.60928258	11.029283	0.9027236
D:LED-B:LED	-0.71	-8.52928258	7.109283	0.9999920
D:LED-C:LED	-3.92	-11.73928258	3.899283	0.7690762

One conclusion from this is that the combination of D and Halogen is significantly stronger than each of the other seven combinations.

3.7 The bonding model without Interaction

It seems incorrect in this situation to fit a model without the interaction term, but we'll do so just so you can see what's involved.

```
c3_m2 <- lm(strength ~ resin + light, data = bonding)
summary(c3_m2)
```

Call:

```
lm(formula = strength ~ resin + light, data = bonding)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-14.1163	-4.9531	0.1187	4.4613	14.4663

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	19.074	1.787	10.676	< 2e-16 ***
resinB	3.815	2.260	1.688	0.09555 .
resinC	6.740	2.260	2.982	0.00386 **
resinD	13.660	2.260	6.044	5.39e-08 ***
lightLED	-1.317	1.598	-0.824	0.41229

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 7.147 on 75 degrees of freedom

Multiple R-squared: 0.3469, Adjusted R-squared: 0.312

F-statistic: 9.958 on 4 and 75 DF, p-value: 1.616e-06

In the no-interaction model, if light = Halogen, our equation is:

$$strength = 19.07 + 3.82resinB + 6.74resinC + 13.66resinD$$

And if light = LED, our equation is:

$$strength = 17.75 + 3.82resinB + 6.74resinC + 13.66resinD$$

So, in the no-interaction model, only the intercept changes.

```
anova(c3_m2)
```

Analysis of Variance Table

Response: strength

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
resin	3	1999.7	666.57	13.0514	6.036e-07 ***
light	1	34.7	34.72	0.6797	0.4123
Residuals	75	3830.5	51.07		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

And, it appears, if we ignore the interaction, then resin type has a significant impact on strength but light source doesn't. This is clearer when we look at boxplots of the separated light and resin groups.

```
p1 <- ggplot(bonding, aes(x = light, y = strength)) +
  geom_boxplot()
p2 <- ggplot(bonding, aes(x = resin, y = strength)) +
  geom_boxplot()
```



```
gridExtra::grid.arrange(p1, p2, nrow = 1)
```



3.8 cortisol: A Hypothetical Clinical Trial

156 adults who complained of problems with a high-stress lifestyle were enrolled in a hypothetical clinical trial of the effectiveness of a behavioral intervention designed to help reduce stress levels, as measured by salivary cortisol.

The subjects were randomly assigned to one of three intervention groups (usual care, low dose, and high dose.) The “low dose” subjects received a one-week intervention with a follow-up at week 5. The “high dose” subjects received a more intensive three-week intervention, with follow up at week 5.

Since cortisol levels rise and fall with circadian rhythms, the cortisol measurements were taken just after rising for all subjects. These measurements were taken at baseline, and again at five weeks. The difference (baseline - week 5) in cortisol level (in micrograms / l) serves as the primary outcome.

3.8.1 Codebook and Raw Data for cortisol

The data are gathered in the `cortisol` data set. Included are:

Variable	Description
<code>subject</code>	subject identification code
<code>interv</code>	intervention group (UC = usual care, Low, High)
<code>waist</code>	waist circumference at baseline (in inches)

Variable	Description
sex	male or female
cort.1	salivary cortisol level (microg/l) week 1
cort.5	salivary cortisol level (microg/l) week 5

```
cortisol

# A tibble: 156 x 6
  subject interv waist sex   cort.1 cort.5
    <int> <fct>   <dbl> <fct> <dbl> <dbl>
1     1001 UC      48.3 M      13.4  13.3
2     1002 Low     58.3 M      17.8  16.6
3     1003 High    43.0 M      14.4  12.7
4     1004 Low     44.9 M       9.00  9.80
5     1005 High    46.1 M      14.2  14.2
6     1006 UC      41.3 M      14.8  15.1
7     1007 Low     51.0 F      13.7  16.0
8     1008 UC      42.0 F      17.3  18.7
9     1009 Low     24.7 F      15.3  15.8
10    1010 Low     59.4 M      12.4  11.7
# ... with 146 more rows
```

3.9 Creating a factor combining sex and waist

Next, we'll put the `waist` and `sex` data in the `cortisol` example together. We want to build a second categorical variable (called `fat_est`) combining this information, to indicate “healthy” vs. “unhealthy” levels of fat around the waist.

- Male subjects whose waist circumference is 40 inches or more, and
- Female subjects whose waist circumference is 35 inches or more, will fall in the “unhealthy” group.

```
cortisol <- cortisol %>%
  mutate(
    fat_est = factor(case_when(
      sex == "M" & waist >= 40 ~ "unhealthy",
      sex == "F" & waist >= 35 ~ "unhealthy",
      TRUE ~ "healthy")),
    cort_diff = cort.1 - cort.5)

summary(cortisol)
```

subject	interv	waist	sex	cort.1
Min. :1001	High:53	Min. :20.80	F:83	Min. : 6.000
1st Qu.:1040	Low :52	1st Qu.:33.27	M:73	1st Qu.: 9.675
Median :1078	UC :51	Median :40.35		Median :12.400
Mean :1078		Mean :40.42		Mean :12.686
3rd Qu.:1117		3rd Qu.:47.77		3rd Qu.:16.025
Max. :1156		Max. :59.90		Max. :19.000
cort.5	fat_est	cort_diff		
Min. : 4.2	healthy : 56	Min. : -2.3000		
1st Qu.: 9.6	unhealthy:100	1st Qu.: -0.5000		
Median :12.6		Median : 0.2000		
Mean :12.4		Mean : 0.2821		

3rd Qu.:15.7	3rd Qu.: 1.2000
Max. :19.7	Max. : 2.0000

3.10 A Means Plot for the cortisol trial (with standard errors)

Again, we'll start by building up a data set with the summaries we want to plot.

```
cort.sum <- cortisol %>%
  group_by(interv, fat_est) %>%
  summarize(mean.cort = mean(cort_diff),
            se.cort = sd(cort_diff)/sqrt(n()))

cort.sum
```

```
# A tibble: 6 x 4
# Groups:   interv [?]
  interv fat_est mean.cort se.cort
  <fct>  <fct>      <dbl>  <dbl>
1 High   healthy     0.695  0.217
2 High   unhealthy   0.352  0.150
3 Low    healthy     0.500  0.182
4 Low    unhealthy   0.327  0.190
5 UC     healthy     0.347  0.225
6 UC     unhealthy   -0.226  0.155
```

Now, we'll use this new data set to plot the means and standard errors.

```
## The error bars will overlap unless we adjust the position.
pd <- position_dodge(0.2) # move them .1 to the left and right

ggplot(cort.sum, aes(x = interv, y = mean.cort, col = fat_est)) +
  geom_errorbar(aes(ymin = mean.cort - se.cort,
                  ymax = mean.cort + se.cort),
              width = 0.2, position = pd) +
  geom_point(size = 2, position = pd) +
  geom_line(aes(group = fat_est), position = pd) +
  scale_color_manual(values = c("royalblue", "darkred")) +
  theme_bw() +
  labs(y = "Salivary Cortisol Level", x = "Intervention Group",
       title = "Observed Means (+/- SE) of Salivary Cortisol")
```



3.11 A Two-Way ANOVA model for cortisol with Interaction

```
c3_m3 <- lm(cort_diff ~ interv * fat_est, data = cortisol)
anova(c3_m3)
```

Analysis of Variance Table

Response: cort_diff

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
interv	2	7.847	3.9235	4.4698	0.01301 *
fat_est	1	4.614	4.6139	5.2564	0.02326 *
interv:fat_est	2	0.943	0.4715	0.5371	0.58554
Residuals	150	131.666	0.8778		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Does it seem like we need the interaction term in this case?

```
summary(c3_m3)
```

Call:

```
lm(formula = cort_diff ~ interv * fat_est, data = cortisol)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-2.62727	-0.75702	0.08636	0.84848	2.12647

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	0.6950	0.2095	3.317	0.00114 **
intervLow	-0.1950	0.3001	-0.650	0.51689
intervUC	-0.3479	0.3091	-1.126	0.26206
fat_estunhealthy	-0.3435	0.2655	-1.294	0.19774
intervLow:fat_estunhealthy	0.1708	0.3785	0.451	0.65256
intervUC:fat_estunhealthy	-0.2300	0.3846	-0.598	0.55068

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.9369 on 150 degrees of freedom
Multiple R-squared: 0.0924, Adjusted R-squared: 0.06214
F-statistic: 3.054 on 5 and 150 DF, p-value: 0.01179

How do you reconcile the apparent difference in significance levels between this regression summary and the ANOVA table above?

3.12 A Two-Way ANOVA model for cortisol without Interaction

3.12.1 The Graph

```
p1 <- ggplot(cortisol, aes(x = interv, y = cort_diff)) +
  geom_boxplot()
p2 <- ggplot(cortisol, aes(x = fat_est, y = cort_diff)) +
  geom_boxplot()

gridExtra::grid.arrange(p1, p2, nrow = 1)
```



3.12.2 The ANOVA Model

```
c3_m4 <- lm(cort_diff ~ interv + fat_est, data = cortisol)
anova(c3_m4)
```

Analysis of Variance Table

```
Response: cort_diff
      Df Sum Sq Mean Sq F value Pr(>F)
interv  2  7.847   3.9235   4.4972 0.01266 *
fat_est  1  4.614   4.6139   5.2886 0.02283 *
Residuals 152 132.609   0.8724
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

How do these results compare to those we saw in the model with interaction?

3.12.3 The Regression Summary

```
summary(c3_m4)
```

Call:

```
lm(formula = cort_diff ~ interv + fat_est, data = cortisol)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-2.55929	-0.74527	0.05457	0.86456	2.05489

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)	
(Intercept)	0.70452	0.16093	4.378	2.22e-05	***
intervLow	-0.08645	0.18232	-0.474	0.63606	
intervUC	-0.50063	0.18334	-2.731	0.00707	**
fat_estunhealthy	-0.35878	0.15601	-2.300	0.02283	*

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.934 on 152 degrees of freedom

Multiple R-squared: 0.0859, Adjusted R-squared: 0.06785

F-statistic: 4.761 on 3 and 152 DF, p-value: 0.00335

3.12.4 Tukey HSD Comparisons

Without the interaction term, we can make direct comparisons between levels of the intervention, and between levels of the `fat_est` variable. This is probably best done here in a Tukey HSD comparison.

```
TukeyHSD(aov(cort_diff ~ interv + fat_est, data = cortisol))
```

```
Tukey multiple comparisons of means
 95% family-wise confidence level
```

```
Fit: aov(formula = cort_diff ~ interv + fat_est, data = cortisol)
```

```
$interv
```

	diff	lwr	upr	p adj
Low-High	-0.09074746	-0.5222655	0.34077063	0.8724916
UC-High	-0.51642619	-0.9500745	-0.08277793	0.0150150
UC-Low	-0.42567873	-0.8613670	0.01000948	0.0570728

```
$fat_est
```

	diff	lwr	upr	p adj
unhealthy-healthy	-0.3582443	-0.6662455	-0.05024305	0.0229266

What conclusions can we draw, at a 5% significance level?

Chapter 4

Analysis of Covariance

4.1 An Emphysema Study

My source for this example is Riffenburgh (2006), section 18.4. Serum theophylline levels (in mg/dl) were measured in 16 patients with emphysema at baseline, then 5 days later (at the end of a course of antibiotics) and then at 10 days after baseline. Clinicians anticipate that the antibiotic will increase the theophylline level. The data are stored in the `emphysema.csv` data file, and note that the age for patient 5 is not available.

4.1.1 Codebook

Variable	Description
<code>patient</code>	ID code
<code>age</code>	patient's age in years
<code>sex</code>	patient's sex (F or M)
<code>st_base</code>	patient's serum theophylline at baseline (mg/dl)
<code>st_day5</code>	patient's serum theophylline at day 5 (mg/dl)
<code>st_day10</code>	patient's serum theophylline at day 10 (mg/dl)

We're going to look at the change from baseline to day 5 as our outcome of interest, since the clinical expectation is that the antibiotic (azithromycin) will increase theophylline levels.

```
emphysema <- emphysema %>%  
  mutate(st_delta = st_day5 - st_base)
```

emphysema

A tibble: 16 x 7

	patient	age	sex	st_base	st_day5	st_day10	st_delta
	<int>	<int>	<fct>	<dbl>	<dbl>	<dbl>	<dbl>
1	1	61	F	14.1	2.30	10.3	-11.8
2	2	70	F	7.20	5.40	7.30	- 1.80
3	3	65	M	14.2	11.9	11.3	- 2.30
4	4	65	M	10.3	10.7	13.8	0.400
5	5	NA	M	9.90	10.7	11.7	0.800
6	6	76	M	5.20	6.80	4.20	1.60
7	7	72	M	10.4	14.6	14.1	4.20
8	8	69	F	10.5	7.20	5.40	- 3.30

9	9	66 M	5.00	5.00	5.10	0
10	10	62 M	8.60	8.10	7.40	- 0.500
11	11	65 F	16.6	14.9	13.0	- 1.70
12	12	71 M	16.4	18.6	17.1	2.20
13	13	51 F	12.2	11.0	12.3	- 1.20
14	14	71 M	6.60	3.70	4.50	- 2.90
15	15	64 F	15.4	15.2	13.6	- 0.200
16	16	50 M	10.2	10.8	11.2	0.600

4.2 Does sex affect the mean change in theophylline?

```
emphysema %>% skim(st_delta)
```

Skim summary statistics

n obs: 16

n variables: 7

Variable type: numeric

variable	missing	complete	n	mean	sd	p0	p25	median	p75	p100
st_delta	0	16	16	-0.99	3.48	-11.8	-1.92	-0.35	0.65	4.2

```
emphysema %>% group_by(sex) %>% skim(st_delta)
```

Skim summary statistics

n obs: 16

n variables: 7

group variables: sex

Variable type: numeric

sex	variable	missing	complete	n	mean	sd	p0	p25	median	p75	p100
F	st_delta	0	6	6	-3.33	4.27	-11.8	-2.92	-1.75	-1.32	-0.2
M	st_delta	0	10	10	0.41	2.07	-2.9	-0.38	0.5	1.4	4.2

Overall, the mean change in theophylline during the course of the antibiotic is -0.99, but this is -3.33 for female patients and 0.41 for male patients.

A one-way ANOVA model looks like this:

```
anova(lm(st_delta ~ sex, data = emphysema))
```

Analysis of Variance Table

Response: st_delta

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
sex	1	52.547	52.547	5.6789	0.03189 *
Residuals	14	129.542	9.253		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

The ANOVA F test finds a statistically significant difference between the mean `st_delta` among males and the mean `st_delta` among females. But is there more to the story?

4.3 Is there an association between age and sex in this study?

```
emphysema %>% group_by(sex) %>% skim(age)
```

Skim summary statistics

```
n obs: 16
n variables: 7
group variables: sex
```

Variable type: integer

sex	variable	missing	complete	n	mean	sd	p0	p25	median	p75	p100
F	age	0	6	6	63.33	6.89	51	61.75	64.5	68	70
M	age	1	9	10	66.44	7.57	50	65	66	71	76

But we note that the male patients are also older than the female patients, on average (mean age for males is 66.4, for females 63.3)

- Does the fact that male patients are older affect change in theophylline level?
- And how should we deal with the one missing `age` value (in a male patient)?

4.4 Adding a quantitative covariate, age, to the model

We could fit an ANOVA model to predict `st_delta` using `sex` and `age` directly, but only if we categorized `age` into two or more groups. Because `age` is not categorical, we cannot include it in an ANOVA. But if `age` is an influence, and we don't adjust for it, it may well bias the outcome of our initial ANOVA. With a quantitative variable like `age`, we will need a method called ANCOVA, for **analysis of covariance**.

4.4.1 The ANCOVA model

ANCOVA in this case is just an ANOVA model with our outcome (`st_delta`) adjusted for a continuous covariate, called `age`. For the moment, we'll ignore the one subject with missing `age` and simply fit the regression model with `sex` and `age`.

```
summary(lm(st_delta ~ sex + age, data = emphysema))
```

Call:

```
lm(formula = st_delta ~ sex + age, data = emphysema)
```

Residuals:

Min	1Q	Median	3Q	Max
-8.3352	-0.4789	0.6948	1.5580	3.5202

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	-6.90266	7.92948	-0.871	0.4011
sexM	3.52466	1.75815	2.005	0.0681
age	0.05636	0.12343	0.457	0.6561

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.255 on 12 degrees of freedom
(1 observation deleted due to missingness)

Multiple R-squared: 0.2882, Adjusted R-squared: 0.1696
 F-statistic: 2.43 on 2 and 12 DF, p-value: 0.13

This model assumes that the slope of the regression line between `st_delta` and `age` is the same for both sexes.

Note that the model yields $\text{st_delta} = -6.9 + 3.52(\text{sex} = \text{male}) + 0.056 \text{ age}$, or

- $\text{st_delta} = -6.9 + 0.056 \text{ age}$ for female patients, and
- $\text{st_delta} = (-6.9 + 3.52) + 0.056 \text{ age} = -3.38 + 0.056 \text{ age}$ for male patients.

Note that we can test this assumption of equal slopes by fitting an alternative model (with a product term between `sex` and `age`) that doesn't require the assumption, and we'll do that later.

4.4.2 The ANCOVA Table

First, though, we'll look at the ANCOVA table.

```
anova(lm(st_delta ~ sex + age, data = emphysema))
```

Analysis of Variance Table

Response: st_delta

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
sex	1	49.284	49.284	4.6507	0.05203
age	1	2.209	2.209	0.2085	0.65612
Residuals	12	127.164	10.597		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

When we tested `sex` without accounting for `age`, we found a p value of 0.032, which is less than our usual cutpoint of 0.05. But when we adjusted for `age`, we find that `sex` loses significance, even though `age` is not a significant influence on `st_delta` by itself, according to the ANCOVA table.

4.5 Rerunning the ANCOVA model after simple imputation

We could have *imputed* the missing `age` value for patient 5, rather than just deleting that patient. Suppose we do the simplest potentially reasonable thing to do: insert the mean `age` in where the NA value currently exists.

```
emph_imp <- replace_na(emphysema, list(age = mean(emphysema$age, na.rm = TRUE)))
```

```
emph_imp
```

A tibble: 16 x 7

	patient	age	sex	st_base	st_day5	st_day10	st_delta
	<int>	<dbl>	<fct>	<dbl>	<dbl>	<dbl>	<dbl>
1	1	61.0	F	14.1	2.30	10.3	-11.8
2	2	70.0	F	7.20	5.40	7.30	- 1.80
3	3	65.0	M	14.2	11.9	11.3	- 2.30
4	4	65.0	M	10.3	10.7	13.8	0.400
5	5	65.2	M	9.90	10.7	11.7	0.800
6	6	76.0	M	5.20	6.80	4.20	1.60
7	7	72.0	M	10.4	14.6	14.1	4.20
8	8	69.0	F	10.5	7.20	5.40	- 3.30
9	9	66.0	M	5.00	5.00	5.10	0

10	10	62.0 M	8.60	8.10	7.40	- 0.500
11	11	65.0 F	16.6	14.9	13.0	- 1.70
12	12	71.0 M	16.4	18.6	17.1	2.20
13	13	51.0 F	12.2	11.0	12.3	- 1.20
14	14	71.0 M	6.60	3.70	4.50	- 2.90
15	15	64.0 F	15.4	15.2	13.6	- 0.200
16	16	50.0 M	10.2	10.8	11.2	0.600

More on simple imputation and missing data is coming soon.

For now, we can rerun the ANCOVA model on this new data set, after imputation...

```
anova(lm(st_delta ~ sex + age, data = emph_imp))
```

Analysis of Variance Table

Response: st_delta

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
sex	1	52.547	52.547	5.3623	0.03755 *
age	1	2.151	2.151	0.2195	0.64721
Residuals	13	127.392	9.799		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

When we do this, we see that now the `sex` variable returns to a p value below 0.05. Our complete case analysis (which omitted patient 5) gives us a different result than the ANCOVA based on the data after mean imputation.

4.6 Looking at a factor-covariate interaction

Let's run a model including the interaction (product) term between `age` and `sex`, which implies that the slope of `age` on our outcome (`st_delta`) depends on the patient's sex. We'll use the imputed data again. Here is the new ANCOVA table, which suggests that the interaction of `age` and `sex` is small (because it accounts for only a small amount of the total Sum of Squares) and not significant ($p = 0.91$).

```
anova(lm(st_delta ~ sex * age, data = emph_imp))
```

Analysis of Variance Table

Response: st_delta

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
sex	1	52.547	52.547	4.9549	0.04594 *
age	1	2.151	2.151	0.2028	0.66051
sex:age	1	0.130	0.130	0.0123	0.91355
Residuals	12	127.261	10.605		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Since the interaction term is neither substantial nor significant, we probably don't need it here. But let's look at its interpretation anyway, just to fix ideas. To do that, we'll need the coefficients from the underlying regression model.

```
tidy(lm(st_delta ~ sex * age, data = emph_imp))
```

	term	estimate	std.error	statistic	p.value
1	(Intercept)	-5.64606742	13.4536974	-0.4196666	0.6821446
2	sexM	1.72031026	16.8389209	0.1021627	0.9203148

```

3      age  0.03651685  0.2113871  0.1727488  0.8657284
4  sexM:age  0.02885946  0.2603044  0.1108681  0.9135536

```

Our ANCOVA model for `st_delta` incorporating the `age` x `sex` product term is $-5.65 + 1.72 (\text{sex} = \text{M}) + 0.037 \text{ age} + 0.029 (\text{sex} = \text{M})(\text{age})$. So that means:

- our model for females is `st_delta` = $-5.65 + 0.037 \text{ age}$
- our model for males is `st_delta` = $(-5.65 + 1.72) + (0.037 + 0.029) \text{ age}$, or $-3.93 + 0.066 \text{ age}$

but, again, our conclusion from the ANCOVA table is that this increase in complexity (letting both the slope and intercept vary by `sex`) doesn't add much in the way of predictive value for our `st_delta` outcome.

4.7 Centering the Covariate to Facilitate ANCOVA Interpretation

When developing an ANCOVA model, we will often **center** or even **center and rescale** the covariate to facilitate interpretation of the product term. In this case, let's center `age` and rescale it by dividing by two standard deviations.

```
emph_imp %>% skim(age)
```

Skim summary statistics

```

n obs: 16
n variables: 7

```

Variable type: numeric

```

variable missing complete  n mean  sd p0  p25 median  p75 p100
age           0         16 16 65.2 6.98 50 63.5  65.1 70.25  76

```

Note that in our imputed data, the mean `age` is 65.2 and the standard deviation of `age` is 7 years.

So we build the rescaled `age` variable that I'll call `age_z`, and then use it to refit our model.

```

emph_imp <- emph_imp %>%
  mutate(age_z = (age - mean(age)) / (2 * sd(age)))

anova(lm(st_delta ~ sex * age_z, data = emph_imp))

```

Analysis of Variance Table

Response: `st_delta`

```

      Df Sum Sq Mean Sq F value Pr(>F)
sex      1  52.547   52.547   4.9549 0.04594 *
age_z     1   2.151    2.151   0.2028 0.66051
sex:age_z  1   0.130    0.130   0.0123 0.91355
Residuals 12 127.261   10.605
---

```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```
tidy(lm(st_delta ~ sex * age_z, data = emph_imp))
```

```

      term      estimate std.error statistic  p.value
1 (Intercept) -3.2651685  1.386802  -2.3544587 0.03641637
2      sexM     3.6019471  1.735706   2.0752055 0.06013138
3      age_z     0.5096337  2.950144   0.1727488 0.86572835
4  sexM:age_z     0.4027661  3.632839   0.1108681 0.91355364

```

Comparing the two models, we have:

- (unscaled): `st_delta` = $-5.65 + 1.72 (\text{sex} = \text{M}) + 0.037 \text{ age} + 0.029 (\text{sex} = \text{M}) \times (\text{age})$

- (rescaled): $\text{st_delta} = -3.27 + 3.60 (\text{sex} = \text{M}) + 0.510 \text{ rescaled age_z} + 0.402 (\text{sex} = \text{M}) \times (\text{rescaled age_z})$

In essence, the rescaled model on `age_z` is:

- $\text{st_delta} = -3.27 + 0.510 \text{ age_z}$ for female subjects, and
- $\text{st_delta} = (-3.27 + 3.60) + (0.510 + 0.402) \text{ age_z} = 0.33 + 0.912 \text{ age_z}$ for male subjects

Interpreting the centered, rescaled model, we have:

- no change in the ANOVA results or R-squared or residual standard deviation compared to the uncentered, unscaled model, but
- the intercept (-3.27) now represents the `st_delta` for a female of average age,
- the `sex` slope (3.60) represents the (male - female) difference in predicted `st_delta` for a person of average age,
- the `age_z` slope (0.510) represents the difference in predicted `st_delta` for a female one standard deviation older than the mean age as compared to a female one standard deviation younger than the mean age, and
- the product term's slope (0.402) represents the male - female difference in the slope of `age_z`, so that if you add the `age_z` slope (0.510) and the interaction slope (0.402) you see the difference in predicted `st_delta` for a male one standard deviation older than the mean age as compared to a male one standard deviation younger than the mean age.

Chapter 5

Missing Data Mechanisms and Single Imputation

Almost all serious statistical analyses have to deal with missing data. Data values that are missing are indicated in R, and to R, by the symbol `NA`.

5.1 A Toy Example

In the following tiny data set called `sbp_example`, we have four variables for a set of 15 subjects. In addition to a subject id, we have:

- the treatment this subject received (A, B or C are the treatments),
- an indicator (1 = yes, 0 = no) of whether the subject has diabetes,
- the subject's systolic blood pressure at baseline
- the subject's systolic blood pressure after the application of the treatment

```
# create some temporary variables

subject <- 101:115
x1 <- c("A", "B", "C", "A", "C", "A", "A", NA, "B", "C", "A", "B", "C", "A", "B")
x2 <- c(1, 0, 0, 1, NA, 1, 0, 1, NA, 1, 0, 0, 1, 1, NA)
x3 <- c(120, 145, 150, NA, 155, NA, 135, NA, 115, 170, 150, 145, 140, 160, 135)
x4 <- c(105, 135, 150, 120, 135, 115, 160, 150, 130, 155, 140, 140, 150, 135, 120)

sbp_example <-
  data.frame(subject, treat = x1, diabetes = x2,
             sbp.before = x3, sbp.after = x4) %>%
  tbl_df

rm(subject, x1, x2, x3, x4) # just cleaning up

sbp_example
```

```
# A tibble: 15 x 5
  subject treat diabetes sbp.before sbp.after
  <int> <fct>    <dbl>    <dbl>    <dbl>
1    101 A      1.00      120      105
2    102 B      0       145      135
```

3	103	C	0	150	150
4	104	A	1.00	NA	120
5	105	C	NA	155	135
6	106	A	1.00	NA	115
7	107	A	0	135	160
8	108	<NA>	1.00	NA	150
9	109	B	NA	115	130
10	110	C	1.00	170	155
11	111	A	0	150	140
12	112	B	0	145	140
13	113	C	1.00	140	150
14	114	A	1.00	160	135
15	115	B	NA	135	120

5.1.1 How many missing values do we have in each column?

```
colSums(is.na(sbp_example))
```

```
subject      treat  diabetes sbp.before  sbp.after
      0          1          3          3          0
```

We are missing one `treat`, 3 `diabetes` and 3 `sbp.before` values.

5.1.2 What is the pattern of missing data?

```
mice::md.pattern(sbp_example)
```

```
subject sbp.after treat diabetes sbp.before
9      1          1     1         1         1 0
3      1          1     1         0         1 1
2      1          1     1         1         0 1
1      1          1     0         1         0 2
      0          0     1         3         3 7
```

We have nine subjects with complete data, three subjects with missing `diabetes` (only), two subjects with missing `sbp.before` (only), and 1 subject with missing `treat` and `sbp.before`.

5.1.3 How can we identify the subjects with missing data?

```
sbp_example %>% filter(!complete.cases())
```

```
# A tibble: 6 x 5
  subject treat diabetes sbp.before sbp.after
  <int> <fct>    <dbl>    <dbl>    <dbl>
1    104 A      1.00      NA      120
2    105 C      NA      155      135
3    106 A      1.00      NA      115
4    108 <NA>    1.00      NA      150
5    109 B      NA      115      130
6    115 B      NA      135      120
```

5.2 Missing-data mechanisms

My source for this description of mechanisms is Chapter 25 of Gelman and Hill (2007), and that chapter is available at this link.

1. **MCAR = Missingness completely at random.** A variable is missing completely at random if the probability of missingness is the same for all units, for example, if for each subject, we decide whether to collect the `diabetes` status by rolling a die and refusing to answer if a “6” shows up. If data are missing completely at random, then throwing out cases with missing data does not bias your inferences.
2. **Missingness that depends only on observed predictors.** A more general assumption, called **missing at random** or **MAR**, is that the probability a variable is missing depends only on available information. Here, we would have to be willing to assume that the probability of nonresponse to `diabetes` depends only on the other, fully recorded variables in the data. It is often reasonable to model this process as a logistic regression, where the outcome variable equals 1 for observed cases and 0 for missing. When an outcome variable is missing at random, it is acceptable to exclude the missing cases (that is, to treat them as NA), as long as the regression controls for all the variables that affect the probability of missingness.
3. **Missingness that depends on unobserved predictors.** Missingness is no longer “at random” if it depends on information that has not been recorded and this information also predicts the missing values. If a particular treatment causes discomfort, a patient is more likely to drop out of the study. This missingness is not at random (unless “discomfort” is measured and observed for all patients). If missingness is not at random, it must be explicitly modeled, or else you must accept some bias in your inferences.
4. **Missingness that depends on the missing value itself.** Finally, a particularly difficult situation arises when the probability of missingness depends on the (potentially missing) variable itself. For example, suppose that people with higher earnings are less likely to reveal them.

Essentially, situations 3 and 4 are referred to collectively as **non-random missingness**, and cause more trouble for us than 1 and 2.

5.3 Options for Dealing with Missingness

There are several available methods for dealing with missing data that are MCAR or MAR, but they basically boil down to:

- Complete Case (or Available Case) analyses
- Single Imputation
- Multiple Imputation

5.4 Complete Case (and Available Case) analyses

In **Complete Case** analyses, rows containing NA values are omitted from the data before analyses commence. This is the default approach for many statistical software packages, and may introduce unpredictable bias and fail to include some useful, often hard-won information.

- A complete case analysis can be appropriate when the number of missing observations is not large, and the missing pattern is either MCAR (missing completely at random) or MAR (missing at random.)
- Two problems arise with complete-case analysis:
 1. If the units with missing values differ systematically from the completely observed cases, this could bias the complete-case analysis.
 2. If many variables are included in a model, there may be very few complete cases, so that most of the data would be discarded for the sake of a straightforward analysis.

- A related approach is *available-case* analysis where different aspects of a problem are studied with different subsets of the data, perhaps identified on the basis of what is missing in them.

5.5 Single Imputation

In **single imputation** analyses, NA values are estimated/replaced *one time* with *one particular data value* for the purpose of obtaining more complete samples, at the expense of creating some potential bias in the eventual conclusions or obtaining slightly *less* accurate estimates than would be available if there were no missing values in the data.

- A single imputation can be just a replacement with the mean or median (for a quantity) or the mode (for a categorical variable.) However, such an approach, though easy to understand, underestimates variance and ignores the relationship of missing values to other variables.
- Single imputation can also be done using a variety of models to try to capture information about the NA values that are available in other variables within the data set.
- The `imputation` package can help us execute single imputations using a wide variety of techniques, within the pipe approach used by the `tidyverse`. Another approach I have used in the past is the `mice` package, which can also perform single imputations.

5.6 Multiple Imputation

Multiple imputation, where NA values are repeatedly estimated/replaced with multiple data values, for the purpose of obtaining more complete samples *and* capturing details of the variation inherent in the fact that the data have missingness, so as to obtain *more* accurate estimates than are possible with single imputation.

- We'll postpone the discussion of multiple imputation for a while.

5.7 Building a Complete Case Analysis

We can drop all of the missing values from a data set with `drop_na` or with `na.omit` or by filtering for `complete.cases`. Any of these approaches produces the same result - a new data set with 9 rows (after dropping the six subjects with any NA values) and 5 columns.

```
cc.1 <- na.omit(sbp_example)
cc.2 <- sbp_example %>% drop_na
cc.3 <- sbp_example %>% filter(complete.cases(.))
```

5.8 Single Imputation with the Mean or Mode

The most straightforward approach to single imputation is to impute a single summary of the variable, such as the mean, median or mode.

```
skim(sbp_example)
```

Skim summary statistics

n obs: 15

n variables: 5

Variable type: factor

variable missing complete n n_unique

top_counts ordered

```
treat      1      14 15      3 A: 6, B: 4, C: 4, NA: 1  FALSE
```

Variable type: integer

```
variable missing complete  n mean  sd  p0  p25 median  p75 p100
subject      0      15 15  108 4.47 101 104.5   108 111.5 115
```

Variable type: numeric

```
variable missing complete  n  mean  sd  p0 p25 median  p75 p100
diabetes      3      12 15   0.58 0.51  0  0      1  1      1
sbp.after     0      15 15  136   15.83 105 125   135 150   160
sbp.before    3      12 15 143.33 15.72 115 135   145 151.25 170
```

Here, suppose we decide to impute

- `sbp.before` with the mean (143.33) among non-missing values,
- `diabetes` with its median (1) among non-missing values, and
- `treat` with its most common value, or mode (A)

```
si.1 <- sbp_example %>%
  replace_na(list(sbp.before = 143.33,
                  diabetes = 1,
                  treat = "A"))
si.1
```

A tibble: 15 x 5

```
subject treat diabetes sbp.before sbp.after
  <int> <fct>   <dbl>      <dbl>      <dbl>
1    101 A      1.00      120      105
2    102 B       0       145      135
3    103 C       0       150      150
4    104 A      1.00      143      120
5    105 C      1.00      155      135
6    106 A      1.00      143      115
7    107 A       0       135      160
8    108 A      1.00      143      150
9    109 B      1.00      115      130
10   110 C      1.00      170      155
11   111 A       0       150      140
12   112 B       0       145      140
13   113 C      1.00      140      150
14   114 A      1.00      160      135
15   115 B      1.00      135      120
```

We could accomplish the same thing with, for example:

```
si.2 <- sbp_example %>%
  replace_na(list(sbp.before = mean(sbp_example$sbp.before, na.rm = TRUE),
                  diabetes = median(sbp_example$diabetes, na.rm = TRUE),
                  treat = "A"))
```

5.9 Doing Single Imputation with `simputation`

Single imputation is a potentially appropriate method when missingness can be assumed to be either completely at random (MCAR) or dependent only on observed predictors (MAR). We'll use the `simputation` package to accomplish it.

- The `simputation` vignette is available at <https://cran.r-project.org/web/packages/simputation/vignettes/intro.html>
- The `simputation` reference manual is available at <https://cran.r-project.org/web/packages/simputation/simputation.pdf>

5.9.1 Mirroring Our Prior Approach (imputing means/medians/modes)

Suppose we want to mirror what we did above, simply impute the mean for `sbp.before` and the median for `diabetes` again.

```
si.3 <- sbp_example %>%
  impute_lm(sbp.before ~ 1) %>%
  impute_median(diabetes ~ 1) %>%
  replace_na(list(treat = "A"))
```

```
si.3
```

```
# A tibble: 15 x 5
  subject treat diabetes sbp.before sbp.after
*   <int> <fct>   <dbl>      <dbl>      <dbl>
1     101 A       1.00      120      105
2     102 B       0        145      135
3     103 C       0        150      150
4     104 A       1.00      143      120
5     105 C       1.00      155      135
6     106 A       1.00      143      115
7     107 A       0        135      160
8     108 A       1.00      143      150
9     109 B       1.00      115      130
10    110 C       1.00      170      155
11    111 A       0        150      140
12    112 B       0        145      140
13    113 C       1.00      140      150
14    114 A       1.00      160      135
15    115 B       1.00      135      120
```

5.9.2 Using a model to impute `sbp.before` and `diabetes`

Suppose we wanted to use:

- a robust linear model to predict `sbp.before` missing values, on the basis of `sbp.after` and `diabetes` status, and
- a predictive mean matching approach to predict `diabetes` status, on the basis of `sbp.after`, and
- a decision tree approach to predict `treat` status, using all other variables in the data

```
set.seed(50001)
```

```
imp.4 <- sbp_example %>%
  impute_rlm(sbp.before ~ sbp.after + diabetes) %>%
  impute_pmm(diabetes ~ sbp.after) %>%
  impute_cart(treat ~ .)
```

```
imp.4
```

```
# A tibble: 15 x 5
```

	subject	treat	diabetes	sbp.before	sbp.after
*	<int>	<fct>	<dbl>	<dbl>	<dbl>
1	101	A	1.00	120	105
2	102	B	0	145	135
3	103	C	0	150	150
4	104	A	1.00	139	120
5	105	C	1.00	155	135
6	106	A	1.00	136	115
7	107	A	0	135	160
8	108	A	1.00	155	150
9	109	B	1.00	115	130
10	110	C	1.00	170	155
11	111	A	0	150	140
12	112	B	0	145	140
13	113	C	1.00	140	150
14	114	A	1.00	160	135
15	115	B	1.00	135	120

Details on the many available methods in **simputation** are provided in its manual. These include:

- **impute_cart** uses a Classification and Regression Tree approach for numerical or categorical data. There is also an **impute_rf** command which uses Random Forests for imputation.
- **impute_pmm** is one of several “hot deck” options for imputation, this one is predictive mean matching, which can be used with numeric data (only). Missing values are first imputed using a predictive model. Next, these predictions are replaced with the observed values which are nearest to the prediction. Other imputation options in this group include random hot deck, sequential hot deck and k-nearest neighbor imputation.
- **impute_rlm** is one of several regression imputation methods, including linear models, robust linear models (which use what is called M-estimation to impute numerical variables) and lasso/elastic net/ridge regression models.

simputation can also do EM-based multivariate imputation, and multivariate random forest imputation, as well as many other sorts of approaches.

Chapter 6

A Study of Prostate Cancer

6.1 Data Load and Background

The data in `prost.csv` is derived from Stamey et al. (1989) who examined the relationship between the level of prostate-specific antigen and a number of clinical measures in 97 men who were about to receive a radical prostatectomy. The `prost` data, as I'll name it in R, contains 97 rows and 11 columns.

```
prost
```

```
# A tibble: 97 x 10
  subject  lpsa lcavol lweight  age bph      svi  lcp gleason pgg45
  <int>   <dbl> <dbl>   <dbl> <int> <fct> <int> <dbl> <fct>   <int>
1     1    -0.431 -0.580    2.77   50 Low      0 -1.39 6         0
2     2    -0.163 -0.994    3.32   58 Low      0 -1.39 6         0
3     3    -0.163 -0.511    2.69   74 Low      0 -1.39 7        20
4     4    -0.163 -1.20    3.28   58 Low      0 -1.39 6         0
5     5     0.372  0.751    3.43   62 Low      0 -1.39 6         0
6     6     0.765 -1.05    3.23   50 Low      0 -1.39 6         0
7     7     0.765  0.737    3.47   64 Medium    0 -1.39 6         0
8     8     0.854  0.693    3.54   58 High      0 -1.39 6         0
9     9     1.05  -0.777    3.54   47 Low      0 -1.39 6         0
10    10     1.05   0.223    3.24   63 Low      0 -1.39 6         0
# ... with 87 more rows
```

Note that a related `prost` data frame is also available as part of several R packages, including the `faraway` package, but there is an error in the `lweight` data for subject 32 in those presentations. The value of `lweight` for subject 32 should not be 6.1, corresponding to a prostate that is 449 grams in size, but instead the `lweight` value should be 3.804438, corresponding to a 44.9 gram prostate¹.

I've also changed the `gleason` and `bph` variables from their presentation in other settings, to let me teach some additional details.

6.2 Code Book

Variable	Description
<code>subject</code>	subject number (1 to 97)

¹<https://statweb.stanford.edu/~tibs/ElemStatLearn/> attributes the correction to Professor Stephen W. Link.

Variable	Description
<code>lpsa</code>	$\log(\text{prostate specific antigen in ng/ml})$, our outcome
<code>lcavol</code>	$\log(\text{cancer volume in cm}^3)$
<code>lweight</code>	$\log(\text{prostate weight, in g})$
<code>age</code>	age
<code>bph</code>	benign prostatic hyperplasia amount (Low, Medium, or High)
<code>svi</code>	seminal vesicle invasion (1 = yes, 0 = no)
<code>lcp</code>	$\log(\text{capsular penetration, in cm})$
<code>gleason</code>	combined Gleason score (6, 7, or > 7 here)
<code>pgg45</code>	percentage Gleason scores 4 or 5

Notes:

- in general, higher levels of PSA are stronger indicators of prostate cancer. An old standard (established almost exclusively with testing in white males, and definitely flawed) suggested that values below 4 were normal, and above 4 needed further testing. A PSA of 4 corresponds to an `lpsa` of 1.39.
- all logarithms are natural (base e) logarithms, obtained in R with the function `log()`
- all variables other than `subject` and `lpsa` are candidate predictors
- the `gleason` variable captures the highest combined Gleason score [^Scores range (in these data) from 6 (a well-differentiated, or low-grade cancer) to 9 (a high-grade cancer), although the maximum possible score is 10. 6 is the lowest score used for cancerous prostates. As this combination value increases, the rate at which the cancer grows and spreads should increase. This score refers to the combined Gleason grade, which is based on the sum of two areas (each scored 1-5) that make up most of the cancer.] in a biopsy, and higher scores indicate more aggressive cancer cells. It's stored here as 6, 7, or > 7.
- the `pgg45` variable captures the percentage of individual Gleason scores [^The 1-5 scale for individual biopsies are defined so that 1 indicates something that looks like normal prostate tissue, and 5 indicates that the cells and their growth patterns look very abnormal. In this study, the percentage of 4s and 5s shown in the data appears to be based on 5-20 individual scores in most subjects.] that are 4 or 5, on a 1-5 scale, where higher scores indicate more abnormal cells.

6.3 Additions for Later Use

The code below adds to the `prost` tibble:

- a factor version of the `svi` variable, called `svi_f`, with levels No and Yes,
- a factor version of `gleason` called `gleason_f`, with the levels ordered > 7, 7, and finally 6,
- a factor version of `bph` called `bph_f`, with levels ordered Low, Medium, High,
- a centered version of `lcavol` called `lcavol_c`,
- exponentiated `cavol` and `psa` results derived from the natural logarithms `lcavol` and `lpsa`.

```
prost <- prost %>%
  mutate(svi_f = fct_recode(factor(svi), "No" = "0", "Yes" = "1"),
         gleason_f = fct_relevel(gleason, c("> 7", "7", "6")),
         bph_f = fct_relevel(bph, c("Low", "Medium", "High")),
         lcavol_c = lcavol - mean(lcavol),
         cavol = exp(lcavol),
         psa = exp(lpsa))

glimpse(prost)
```

Observations: 97

Variables: 16

\$ subject <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10, 11, 12, 13, 14, 15, 1...

```

$ lpsa      <dbl> -0.4307829, -0.1625189, -0.1625189, -0.1625189, 0.37...
$ lcavol    <dbl> -0.5798185, -0.9942523, -0.5108256, -1.2039728, 0.75...
$ lweight   <dbl> 2.769459, 3.319626, 2.691243, 3.282789, 3.432373, 3....
$ age       <int> 50, 58, 74, 58, 62, 50, 64, 58, 47, 63, 65, 63, 63, ...
$ bph       <fct> Low, Low, Low, Low, Low, Low, Low, Medium, High, Low, Low...
$ svi       <int> 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0...
$ lcp       <dbl> -1.3862944, -1.3862944, -1.3862944, -1.3862944, -1.3...
$ gleason   <fct> 6, 6, 7, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 7, 7, 7, 6, 7, 6...
$ pgg45     <int> 0, 0, 20, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 30, 5, 5, 0, 30...
$ svi_f     <fct> No, No, No, No, No, No, No, No, No, No, No, No, No, No, ...
$ gleason_f <fct> 6, 6, 7, 6, 6, 6, 6, 6, 6, 6, 6, 6, 6, 7, 7, 7, 6, 7, 6...
$ bph_f     <fct> Low, Low, Low, Low, Low, Low, Low, Medium, High, Low, Low...
$ lcavol_c  <dbl> -1.9298281, -2.3442619, -1.8608352, -2.5539824, -0.5...
$ cavol     <dbl> 0.56, 0.37, 0.60, 0.30, 2.12, 0.35, 2.09, 2.00, 0.46...
$ psa       <dbl> 0.65, 0.85, 0.85, 0.85, 1.45, 2.15, 2.15, 2.35, 2.85...

```

6.4 Fitting and Evaluating a Two-Predictor Model

To begin, let's use two predictors (`lcavol` and `svi`) and their interaction in a linear regression model that predicts `lpsa`. I'll call this model `c5_prost_A`

Earlier, we centered the `lcavol` values to facilitate interpretation of the terms. I'll use that centered version (called `lcavol_c`) of the quantitative predictor, and the 1/0 version of the `svi` variable[^]We could certainly use the factor version of `svi` here, but it won't change the model in any meaningful way. There's no distinction in model *fitting* via `lm` between a 0/1 numeric variable and a No/Yes factor variable. The factor version of this information will be useful elsewhere, for instance in plotting the model.]

```

c5_prost_A <- lm(lpsa ~ lcavol_c * svi, data = prost)
summary(c5_prost_A)

```

Call:

```
lm(formula = lpsa ~ lcavol_c * svi, data = prost)
```

Residuals:

```

      Min       1Q   Median       3Q      Max
-1.6305 -0.5007  0.1266  0.4886  1.6847

```

Coefficients:

```

              Estimate Std. Error t value Pr(>|t|)
(Intercept)   2.33134    0.09128  25.540 < 2e-16 ***
lcavol_c       0.58640    0.08207   7.145 1.98e-10 ***
svi            0.60132    0.35833   1.678  0.0967 .
lcavol_c:svi   0.06479    0.26614   0.243  0.8082
---

```

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Residual standard error: 0.7595 on 93 degrees of freedom

Multiple R-squared: 0.5806, Adjusted R-squared: 0.5671

F-statistic: 42.92 on 3 and 93 DF, p-value: < 2.2e-16

6.4.1 Using tidy

It can be very useful to build a data frame of the model's results. We can use the `tidy` function in the `broom` package to do so.

```
tidy(c5_prost_A)
```

	term	estimate	std.error	statistic	p.value
1	(Intercept)	2.33134409	0.09128253	25.5398727	8.246849e-44
2	lcavol_c	0.58639599	0.08206929	7.1451331	1.981492e-10
3	svi	0.60131973	0.35832695	1.6781314	9.667899e-02
4	lcavol_c:svi	0.06479298	0.26614194	0.2434527	8.081909e-01

This makes it much easier to pull out individual elements of the model fit.

For example, to specify the coefficient for `svi`, rounded to three decimal places, I could use `tidy(c5_prost_A) %>% filter(term == "svi") %>% select(estimate) %>% round(., 3)`

- The result is 0.601.
- If you look at the Markdown file, you'll see that the number shown in the bullet point above this one was generated using inline R code, and the function specified above.

6.4.2 Interpretation

1. The intercept, 2.33, for the model is the predicted value of `lpsa` when `lcavol` is at its average and there is no seminal vesicle invasion (e.g. `svi` = 0).
2. The coefficient for `lcavol_c`, 0.59, is the predicted change in `lpsa` associated with a one unit increase in `lcavol` (or `lcavol_c`) when there is no seminal vesicle invasion.
3. The coefficient for `svi`, 0.60, is the predicted change in `lpsa` associated with having no `svi` to having an `svi` while the `lcavol` remains at its average.
4. The coefficient for `lcavol_c:svi`, the product term, which is 0.06, is the difference in the slope of `lcavol_c` for a subject with `svi` as compared to one with no `svi`.

Note: If you look at the R Markdown, you'll notice that in bullet point 3, I didn't use `round` to round off the estimate (as I did in the other three bullets), but instead a special function I specified at the start of the R Markdown file called `specify_decimal()` which uses the `format` function. This forces, in this case, the trailing zero in the two decimal representation of the `svi` coefficient to be shown. The special function, again, is:

```
specify_decimal <- function(x, k) format(round(x, k), nsmall=k)
```

6.5 Exploring Model c5_prost_A

The `glance` function from the `broom` package builds a nice one-row summary for the model.

```
glance(c5_prost_A)
```

	r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik
1	0.5806435	0.5671158	0.7594785	42.92278	1.678836e-17	4	-108.9077
	AIC	BIC	deviance	df.residual			
1	227.8153	240.6889	53.64311	93			

This summary includes, in order,

- the model R^2 , adjusted R^2 and $\hat{\sigma}$, the residual standard deviation,
- the ANOVA F statistic and associated p value,
- the number of degrees of freedom used by the model, and its log-likelihood ratio
- the model's AIC (Akaike Information Criterion) and BIC (Bayesian Information Criterion)

- the model's deviance statistic and residual degrees of freedom

6.5.1 summary for Model `c5_prost_A`

If necessary, we can also run `summary` on this `c5_prost_A` object to pick up some additional summaries. Since the `svi` variable is binary, the interaction term is, too, so the t test here and the F test in the ANOVA yield the same result.

```
summary(c5_prost_A)
```

Call:

```
lm(formula = lpsa ~ lcavol_c * svi, data = prost)
```

Residuals:

	Min	1Q	Median	3Q	Max
	-1.6305	-0.5007	0.1266	0.4886	1.6847

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	2.33134	0.09128	25.540	< 2e-16 ***
lcavol_c	0.58640	0.08207	7.145	1.98e-10 ***
svi	0.60132	0.35833	1.678	0.0967 .
lcavol_c:svi	0.06479	0.26614	0.243	0.8082

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.7595 on 93 degrees of freedom

Multiple R-squared: 0.5806, Adjusted R-squared: 0.5671

F-statistic: 42.92 on 3 and 93 DF, p-value: < 2.2e-16

If you've forgotten the details of the pieces of this summary, review the Part C Notes from 431.

6.5.2 Adjusted R^2

R^2 is greedy.

- R^2 will always suggest that we make our models as big as possible, often including variables of dubious predictive value.
- As a result, there are various methods for penalizing R^2 so that we wind up with smaller models.
- The **adjusted R^2** is often a useful way to compare multiple models for the same response.
 - $R_{adj}^2 = 1 - \frac{(1-R^2)(n-1)}{n-k}$, where n = the number of observations and k is the number of coefficients estimated by the regression (including the intercept and any slopes).
 - So, in this case, $R_{adj}^2 = 1 - \frac{(1-0.5806)(97-1)}{97-4} = 0.5671$
 - The adjusted R^2 value is not, technically, a proportion of anything, but it is comparable across models for the same outcome.
 - The adjusted R^2 will always be less than the (unadjusted) R^2 .

6.5.3 Coefficient Confidence Intervals

Here are the 90% confidence intervals for the coefficients in Model A. Adjust the `level` to get different intervals.

```
confint(c5_prost_A, level = 0.90)
```

```

              5 %      95 %
(Intercept) 2.17968697 2.4830012
lcavol_c     0.45004577 0.7227462
svi          0.00599401 1.1966454
lcavol_c:svi -0.37737623 0.5069622

```

What can we conclude from this about the utility of the interaction term?

6.5.4 ANOVA for Model `c5_prost_A`

The interaction term appears unnecessary. We might wind up fitting the model without it. A complete ANOVA test is available, including a p value, if you want it.

```
anova(c5_prost_A)
```

Analysis of Variance Table

Response: `lpsa`

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
lcavol_c	1	69.003	69.003	119.6289	< 2.2e-16 ***
svi	1	5.237	5.237	9.0801	0.003329 **
lcavol_c:svi	1	0.034	0.034	0.0593	0.808191
Residuals	93	53.643	0.577		

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Note that the `anova` approach for a `lm` object is sequential. The first row shows the impact of `lcavol_c` as compared to a model with no predictors (just an intercept). The second row shows the impact of adding `svi` to a model that already contains `lcavol_c`. The third row shows the impact of adding the interaction (product) term to the model with the two main effects. So the order in which the variables are added to the regression model matters for this ANOVA. The F tests here describe the incremental impact of each covariate in turn.

6.5.5 Residuals, Fitted Values and Standard Errors with `augment`

The `augment` function in the `broom` package builds a data frame including the data used in the model, along with predictions (fitted values), residuals and other useful information.

```
c5_prost_A_frame <- augment(c5_prost_A) %>% tbl_df
skim(c5_prost_A_frame)
```

Skim summary statistics

```
n obs: 97
n variables: 10
```

Variable type: integer

variable	missing	complete	n	mean	sd	p0	p25	median	p75	p100
svi	0	97	97	0.22	0.41	0	0	0	0	1

Variable type: numeric

variable	missing	complete	n	mean	sd	p0	p25	median
.cooksd	0	97	97	0.011	0.02	6.9e-06	0.00078	0.0035
.fitted	0	97	97	2.48	0.88	0.75	1.84	2.4

```

      .hat      0      97 97  0.041  0.041  0.013  0.016  0.025
      .resid    0      97 97 -6.9e-17 0.75  -1.63  -0.5   0.13
      .se.fit   0      97 97  0.14   0.061  0.087  0.095  0.12
      .sigma    0      97 97  0.76   0.0052 0.74   0.76   0.76
      .std.resid 0      97 97  0.0012 1.01  -2.19  -0.69  0.17
      lcavol_c  0      97 97  5.4e-17 1.18  -2.7   -0.84  0.097
      lpsa      0      97 97  2.48   1.15  -0.43   1.73   2.59
      p75 p100
0.01  0.13
3.07  4.54
0.049 0.25
0.49  1.68
0.17  0.38
0.76  0.76
0.65  2.26
0.78  2.47
3.06  5.58

```

Elements shown here include:

- `.fitted` Fitted values of model (or predicted values)
- `.se.fit` Standard errors of fitted values
- `.resid` Residuals (observed - fitted values)
- `.hat` Diagonal of the hat matrix (these indicate *leverage* - points with high leverage indicate unusual combinations of predictors - values more than 2-3 times the mean leverage are worth some study - leverage is always between 0 and 1, and measures the amount by which the predicted value would change if the observation's y value was increased by one unit - a point with leverage 1 would cause the line to follow that point perfectly)
- `.sigma` Estimate of residual standard deviation when corresponding observation is dropped from model
- `.cooks` Cook's distance, which helps identify influential points (values of Cook's d > 0.5 may be influential, values > 1.0 almost certainly are - an influential point changes the fit substantially when it is removed from the data)
- `.std.resid` Standardized residuals (values above 2 in absolute value are worth some study - treat these as normal deviates [Z scores], essentially)

See `?augment.lm` in R for more details.

6.5.6 Making Predictions with `c5_prost_A`

Suppose we want to predict the `lpsa` for a patient with cancer volume equal to this group's mean, for both a patient with and without seminal vesicle invasion, and in each case, we want to use a 90% prediction interval?

```

newdata <- data.frame(lcavol_c = c(0,0), svi = c(0,1))
predict(c5_prost_A, newdata, interval = "prediction", level = 0.90)

```

```

      fit      lwr      upr
1 2.331344 1.060462 3.602226
2 2.932664 1.545742 4.319586

```

Since the predicted value in `fit` refers to the natural logarithm of PSA, to make the predictions in terms of PSA, we would need to exponentiate. The code below will accomplish that task.

```

pred <- predict(c5_prost_A, newdata, interval = "prediction", level = 0.90)
exp(pred)

```

```

      fit      lwr      upr

```

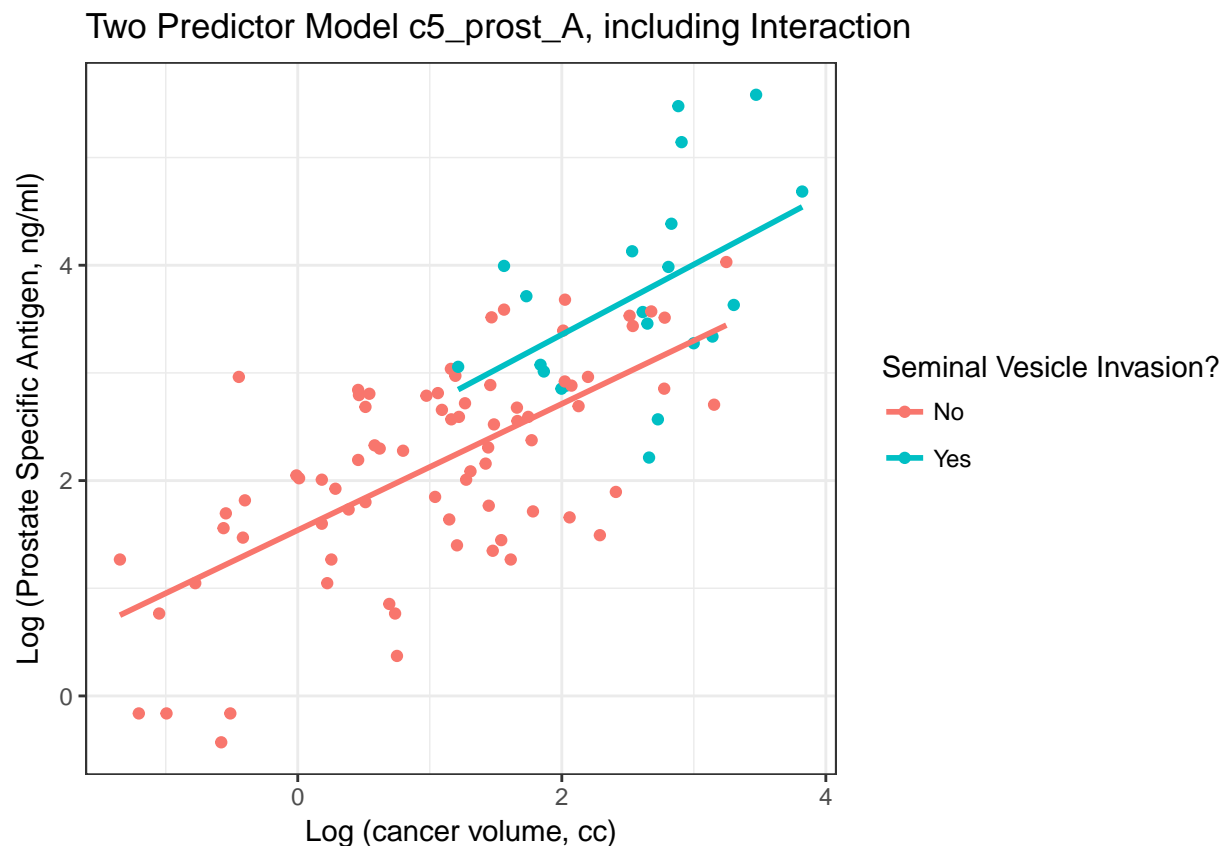
```
1 10.29177 2.887706 36.67978
2 18.77758 4.691450 75.15750
```

6.6 Plotting Model c5_prost_A

6.6.0.1 Plot logs conventionally

Here, we'll use `ggplot2` to plot the logarithms of the variables as they came to us, on a conventional coordinate scale. Note that the lines are nearly parallel. What does this suggest about our Model A?

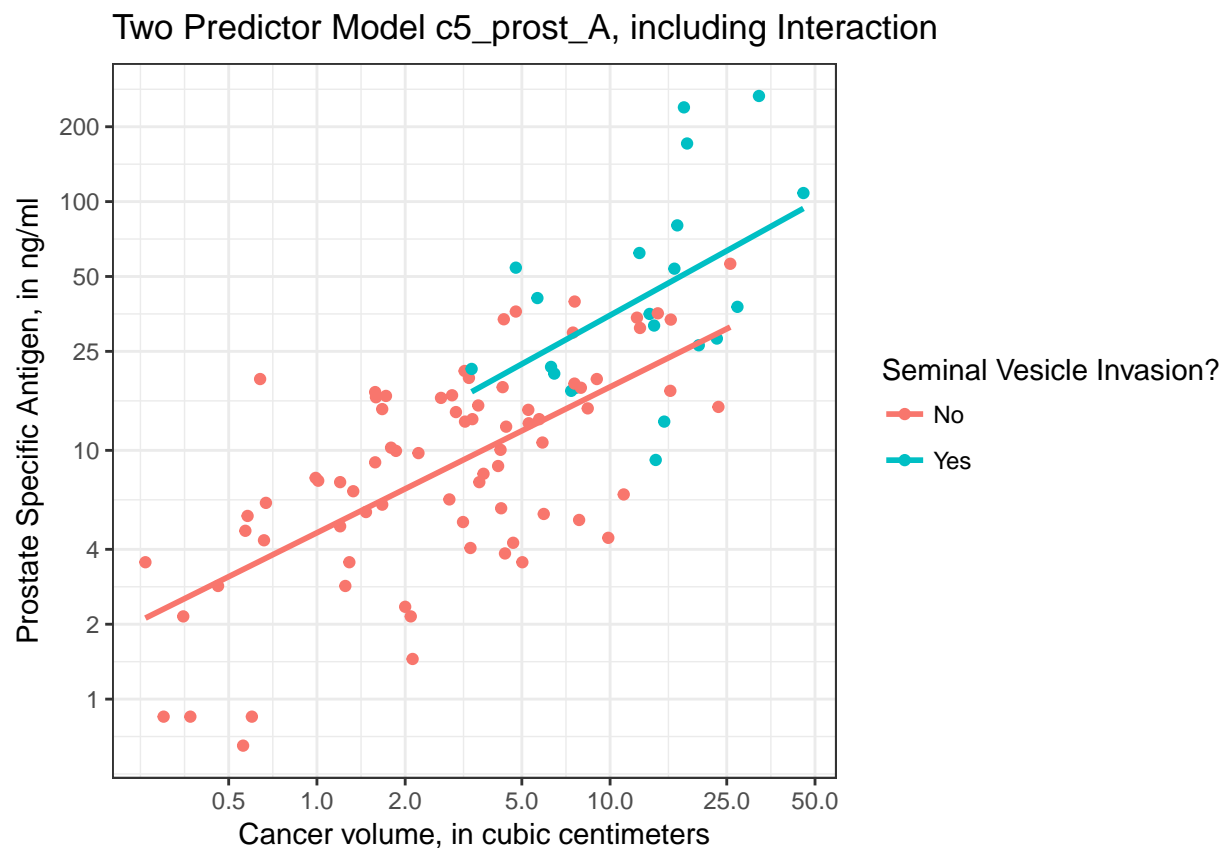
```
ggplot(prost, aes(x = lcavol, y = lpsa, group = svi_f, color = svi_f)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE) +
  scale_color_discrete(name = "Seminal Vesicle Invasion?") +
  theme_bw() +
  labs(x = "Log (cancer volume, cc)",
       y = "Log (Prostate Specific Antigen, ng/ml)",
       title = "Two Predictor Model c5_prost_A, including Interaction")
```



6.6.0.2 Plot on log-log scale

Another approach (which might be easier in some settings) would be to plot the raw values of Cancer Volume and PSA, but use logarithmic axes, again using the natural (base e) logarithm, as follows. If we use the default choice with `trans = "log"`, we'll find a need to select some useful break points for the grid, as I've done in what follows.

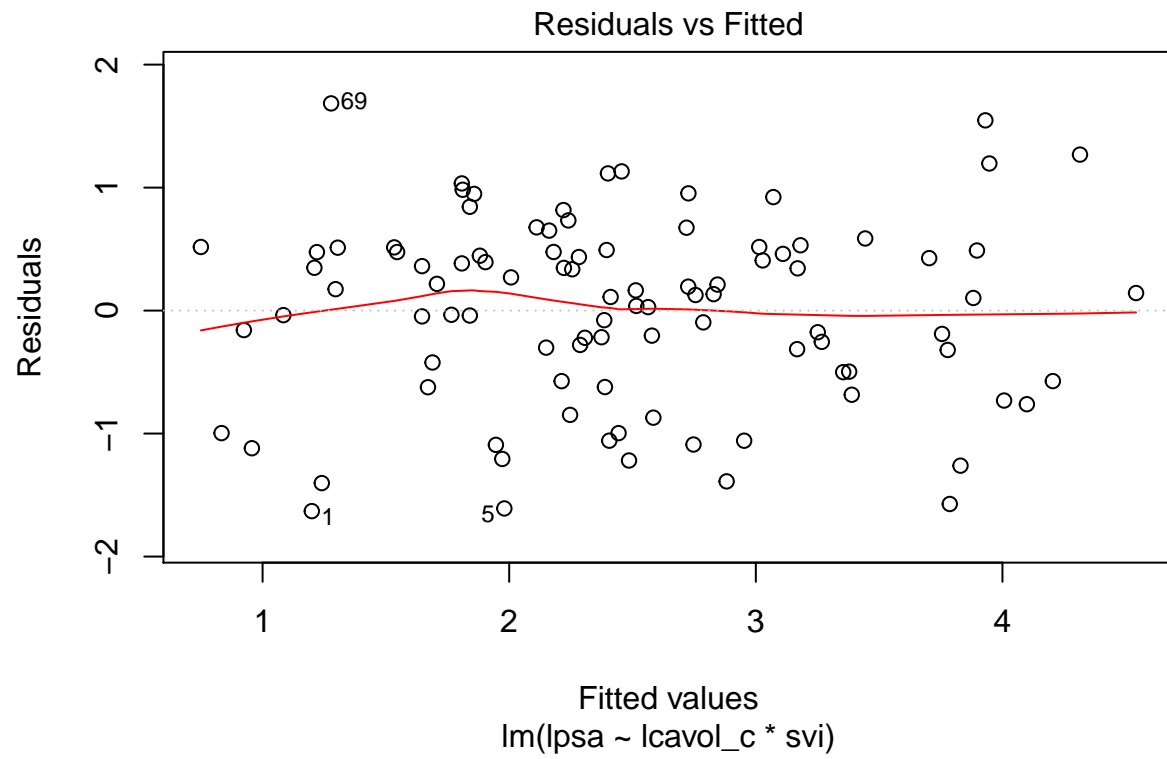

```
ggplot(prost, aes(x = cavol, y = psa, group = svi_f, color = svi_f)) +
  geom_point() +
  geom_smooth(method = "lm", se = FALSE) +
  scale_color_discrete(name = "Seminal Vesicle Invasion?") +
  scale_x_continuous(trans = "log",
                     breaks = c(0.5, 1, 2, 5, 10, 25, 50)) +
  scale_y_continuous(trans = "log",
                     breaks = c(1, 2, 4, 10, 25, 50, 100, 200)) +
  theme_bw() +
  labs(x = "Cancer volume, in cubic centimeters",
       y = "Prostate Specific Antigen, in ng/ml",
       title = "Two Predictor Model c5_prost_A, including Interaction")
```



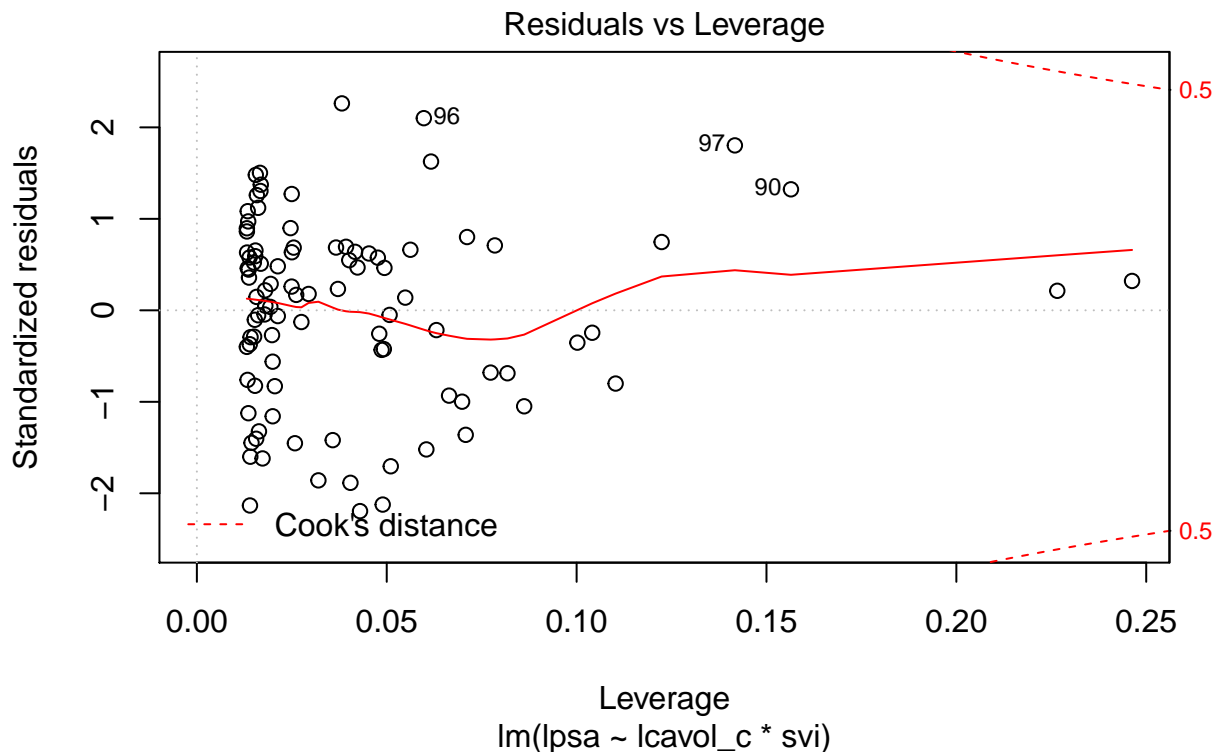
I've used the break point of 4 on the Y axis because of the old rule suggesting further testing for asymptomatic men with PSA of 4 or higher, but the other break points are arbitrary - they seemed to work for me, and used round numbers.

6.6.1 Residual Plots of c5_prost_A

```
plot(c5_prost_A, which = 1)
```



```
plot(c5_prost_A, which = 5)
```



6.7 Cross-Validation of Model `c5_prost_A`

Suppose we want to evaluate whether our model `c5_prost_A` predicts effectively in new data.

One approach (used, for instance, in 431) would be to split our sample into a separate training (perhaps 70% of the data) and test (perhaps 30% of the data) samples, and then:

- 1. fit the model in the training sample,
- 2. use the resulting model to make predictions for `lpsa` in the test sample, and
- 3. evaluate the quality of those predictions, perhaps by comparing the results to what we'd get using a different model.

One problem with this approach is that with a small data set like this, we may be reluctant to cut our sample size for the training or the testing down because we're afraid that our model building and testing will be hampered by a small sample size. A potential solution is the idea of **cross-validation**, which involves partitioning our data into a series of training-test subsets, multiple times, and then combining the results.

The rest of this section is built on some material by David Robinson at <https://rpubs.com/dgrtwo/cv-modelr>.

Suppose that we want to perform what is called *10-crossfold separation*. In words, this approach splits the 97 observations in our `prost` data frame into 10 exclusive partitions of about 90% (so about 87-88 observations) into a training sample, and the remaining 10% (9-10 observations) in a test sample². We then refit a model of interest using the training data, and fit the resulting model on the test data using the `broom` package's `augment` function. This process is then repeated (a total of 10 times) so that each observation is used 9 times in the training sample, and once in the test sample.

²If we did 5-crossfold validation, we'd have 5 partitions into samples of 80% training and 20% test samples.

To code this in R, we'll make use of a few new ideas. Our goal will be to cross-validate model `c5_prost_A`, which, you'll recall, uses `lcavol_c`, `svi` and their interaction, to predict `lpsa` in the `prost` data.

1. First, we set a seed for the validation algorithm, so we can replicate our results down the line.
2. Then we use the `crossv_kfold` function from the `modelr` package to split the `prost` data into ten different partitions, and then use each partition for a split into training and test samples, which the machine indexes with `train` and `test`.
3. Then we use some magic and the `map` function from the `purrr` package (part of the core `tidyverse`) to fit a new `lm(lpsa ~ lcavol_c * svi)` model to each of the training samples generated by `crossv_kfold`.
4. Finally, some additional magic with the `unnest` and `map2` functions applies each of these new models to the appropriate test sample, and generate predictions (`.fitted`) and standard errors for each prediction (`.se.fit`).

```
set.seed(4320308)

prost_models <- prost %>%
  crossv_kfold(k = 10) %>%
  mutate(model = map(train, ~ lm(lpsa ~ lcavol_c * svi, data = .)))

prost_predictions <- prost_models %>%
  unnest(map2(model, test, ~ augment(.x, newdata = .y)))

head(prost_predictions)

# A tibble: 6 x 19
#   .id subject lpsa lcavol lweight age bph svi lcp gleason
#   <chr>   <int> <dbl>   <dbl>   <dbl> <int> <fct> <int> <dbl> <fct>
#1 01         3 -0.163 -0.511    2.69   74 Low    0 -1.39  7
#2 01        12  1.27  -1.35    3.60   63 Medium 0 -1.39  6
#3 01        16  1.45   1.54    3.06   66 Low    0 -1.39  6
#4 01        18  1.49   2.29    3.65   66 Low    0  0.372 6
#5 01        30  1.89   2.41    3.38   65 Low    0  1.62  6
#6 01        34  2.02   0.00995 3.27   54 Low    0 -1.39  6
# ... with 9 more variables: pgg45 <int>, svi_f <fct>, gleason_f <fct>,
#   bph_f <fct>, lcavol_c <dbl>, cavol <dbl>, psa <dbl>, .fitted <dbl>,
#   .se.fit <dbl>
```

The results are a set of predictions based on the splits into training and test groups (remember there are 10 such splits, indexed by `.id`) that describe the complete set of 97 subjects again.

6.7.1 Cross-Validated Summaries of Prediction Quality

Now, we can calculate the root Mean Squared Prediction Error (RMSE) and Mean Absolute Prediction Error (MAE) for this modeling approach (using `lcavol_c` and `svi` to predict `lpsa`) across these observations.

```
prost_predictions %>%
  summarize(RMSE_ourmodel = sqrt(mean((lpsa - .fitted) ^ 2)),
            MAE_ourmodel = mean(abs(lpsa - .fitted)))

# A tibble: 1 x 2
#   RMSE_ourmodel MAE_ourmodel
#   <dbl>         <dbl>
#1    0.783         0.638
```

For now, we'll compare our model to the “intercept only” model that simply predicts the mean `lpsa` across all patients.

```
prost_predictions %>%
  summarize(RMSE_intercept = sqrt(mean((lpsa - mean(lpsa)) ^2)),
            MAE_intercept = mean(abs(lpsa - mean(lpsa))))
```

```
# A tibble: 1 x 2
  RMSE_intercept MAE_intercept
      <dbl>         <dbl>
1         1.15         0.891
```

So our model looks meaningfully better than the “intercept only” model, in that both the RMSE and MAE are much lower (better) with our model.

Another thing we could do with this tibble of predictions we have created is to graph the size of the prediction errors (observed *lpsa* minus predicted values in *.fitted*) that our modeling approach makes.

```
prost_predictions %>%
  mutate(errors = lpsa - .fitted) %>%
  ggplot(., aes(x = errors)) +
  geom_histogram(bins = 30, fill = "darkviolet", col = "yellow") +
  labs(title = "Cross-Validated Errors in Prediction of log(PSA)",
       subtitle = "Using a model (`c5_prostA`) including lcavol_c and svi and their interaction",
       x = "Error in predicting log(PSA)")
```

Cross-Validated Errors in Prediction of log(PSA)

Using a model (*c5_prostA*) including *lcavol_c* and *svi* and their interaction



This suggests that some of our results are off by quite a bit, on the log(PSA) scale, which is summarized for the original data below.

```
prost %>% skim(lpsa)
```

Skim summary statistics

```
n obs: 97
n variables: 16
```

Variable type: numeric

variable	missing	complete	n	mean	sd	p0	p25	median	p75	p100
lpsa	0	97	97	2.48	1.15	-0.43	1.73	2.59	3.06	5.58

If we like, we could transform the predictions and observed values back to the scale of PSA (unlogged) and then calculate and display errors, as follows:

```
prost_predictions %>%
  mutate(err.psa = exp(lpsa) - exp(.fitted)) %>%
  ggplot(., aes(x = err.psa)) +
  geom_histogram(bins = 30, fill = "darkorange", col = "yellow") +
  labs(title = "Cross-Validated Errors in Prediction of PSA",
       subtitle = "Using a model (`c5_prostA`) including lcavol_c and svi and their interaction",
       x = "Error in predicting PSA")
```

Cross-Validated Errors in Prediction of PSA

Using a model (`c5_prostA`) including lcavol_c and svi and their interaction



This suggests that some of our results are off by quite a bit, on the original scale of PSA, which is summarized below.

```
prost %>% mutate(psa = exp(lpsa)) %>% skim(psa)
```

Skim summary statistics

```
n obs: 97
n variables: 16
```

Variable type: numeric

variable	missing	complete	n	mean	sd	p0	p25	median	p75	p100
psa	0	97	97	2.48	1.15	-0.43	1.73	2.59	3.06	5.58

psa	0	97	97	23.74	40.83	0.65	5.65	13.35	21.25	265.85
-----	---	----	----	-------	-------	------	------	-------	-------	--------

We'll return to the notion of cross-validation again, but for now, let's consider the problem of considering adding more predictors to our model, and then making sensible selections as to which predictors actually should be incorporated.

Chapter 7

Stepwise Variable Selection

7.1 Strategy for Model Selection

Ramsey and Schafer (2002) suggest a strategy for dealing with many potential explanatory variables should include the following elements:

1. Identify the key objectives.
2. Screen the available variables, deciding on a list that is sensitive to the objectives and excludes obvious redundancies.
3. Perform exploratory analysis, examining graphical displays and correlation coefficients.
4. Perform transformations, as necessary.
5. Examine a residual plot after fitting a rich model, performing further transformations and considering outliers.
6. Find a suitable subset of the predictors, exerting enough control over any semi-automated selection procedure to be sensitive to the questions of interest.
7. Proceed with the analysis, using the selected explanatory variables.

The Two Key Aspects of Model Selection are:

1. Evaluating each potential subset of predictor variables
2. Deciding on the collection of potential subsets

7.1.1 How Do We Choose Potential Subsets of Predictors?

Choosing potential subsets of predictor variables usually involves either:

1. Stepwise approaches
2. All possible subset (or best possible subset) searches

Note that the use of any variable selection procedure changes the properties of ...

- the estimated coefficients, which are biased, and
- the associated tests and confidence intervals, which are overly optimistic.

Leeb and Potscher (2005) summarize the key issues:

1. Regardless of sample size, the model selection step typically has a dramatic effect on the sampling properties of the estimators that cannot be ignored. In particular, the sampling properties of post-model-selection estimators are typically significantly different from the nominal distributions that arise if a fixed model is supposed.

2. As a consequence, use of inference procedures that do not take into account the model selection step (e.g. using standard t-intervals as if the selected model has been given prior to the statistical analysis) can be highly misleading.

7.2 A “Kitchen Sink” Model (Model `c5_prost_ks`)

Suppose that we now consider a model for the `prost` data we have been working with, which includes main effects (and, in this case, only the main effects) of all eight candidate predictors for `lpsa`, as follows.

```
c5_prost_ks <- lm(lpsa ~ lcavol + lweight + age + bph_f + svi_f +
                  lcp + gleason_f + pgg45, data = prost)
```

```
tidy(c5_prost_ks)
```

	term	estimate	std.error	statistic	p.value
1	(Intercept)	0.169937821	0.931332512	0.1824674	8.556454e-01
2	lcavol	0.544313829	0.087979210	6.1868461	2.010505e-08
3	lweight	0.702237531	0.203013089	3.4590751	8.455164e-04
4	age	-0.023857982	0.011081414	-2.1529727	3.412099e-02
5	bph_fMedium	0.364036274	0.182575941	1.9938896	4.933267e-02
6	bph_fHigh	0.248789989	0.195975792	1.2694935	2.076898e-01
7	svi_fYes	0.710949408	0.241990241	2.9379259	4.240326e-03
8	lcp	-0.119311781	0.089458946	-1.3337043	1.858223e-01
9	gleason_f7	0.220746268	0.343065609	0.6434520	5.216430e-01
10	gleason_f6	-0.053096704	0.430098039	-0.1234526	9.020368e-01
11	pgg45	0.003984574	0.004146495	0.9609499	3.392714e-01

```
glance(c5_prost_ks)
```

	r.squared	adj.r.squared	sigma	statistic	p.value	df	logLik
1	0.6790343	0.6417127	0.6909479	18.19414	2.373796e-17	11	-95.93939

	AIC	BIC	deviance	df.residual
1	215.8788	246.7753	41.05718	86

We’ll often refer to this (all predictors on board) approach as a “kitchen sink” model [This refers to the English idiom “... everything but the kitchen sink” which describes, essentially, everything imaginable. A “kitchen sink regression” is often used as a pejorative term, since no special skill or insight is required to identify it, given a list of potential predictors. For more, yes, there is a Wikipedia page.]

7.3 Sequential Variable Selection: Stepwise Approaches

- Forward Selection
 - We begin with a constant mean and then add potential predictors one at a time according to some criterion (R defaults to minimizing the Akaike Information Criterion) until no further addition significantly improves the fit.
 - Each categorical factor variable is represented in the regression model as a set of indicator variables. In the absence of a good reason to do something else, the set is added to the model as a single unit, and R does this automatically.
- Backwards Elimination
 - Start with the “kitchen sink” model and then delete potential predictors one at a time.
 - Backwards Elimination is less likely than Forward Selection, to omit negatively confounded sets of variables, though all stepwise procedures have problems.
- Stepwise Regression can also be done by combining these methods.

7.3.1 The Big Problems with Stepwise Regression

There is no reason to assume that a single best model can be found.

- The use of forward selection, or backwards elimination, or stepwise regression including both procedures, will NOT always find the same model.
- It also appears to be essentially useless to try different stepwise methods to look for agreement.

Users of stepwise regression frequently place all of their attention on the particular explanatory variables included in the resulting model, when there's **no reason** (in most cases) to assume that model is in any way optimal.

Despite all of its problems, let's use stepwise regression to help predict `lpsa` given a subset of the eight predictors in `c5_prost_ks`.

7.4 Forward Selection with the step function

1. Specify the null model (intercept only)
2. Specify the variables R should consider as predictors (in the scope element of the step function)
3. Specify forward selection only
4. R defaults to using AIC as its stepwise criterion

```
with(prost,
  step(lm(lpsa ~ 1),
    scope=(~ lcavol + lweight + age + bph_f + svi_f +
            lcp + gleason_f + pgg45),
    direction="forward"))
```

Start: AIC=28.84

`lpsa ~ 1`

	Df	Sum of Sq	RSS	AIC
+ lcavol	1	69.003	58.915	-44.366
+ svi_f	1	41.011	86.907	-6.658
+ lcp	1	38.528	89.389	-3.926
+ gleason_f	2	30.121	97.796	6.793
+ lweight	1	24.019	103.899	10.665
+ pgg45	1	22.814	105.103	11.783
+ age	1	3.679	124.239	28.007
<none>			127.918	28.838
+ bph_f	2	4.681	123.237	29.221

Step: AIC=-44.37

`lpsa ~ lcavol`

	Df	Sum of Sq	RSS	AIC
+ lweight	1	7.1726	51.742	-54.958
+ svi_f	1	5.2375	53.677	-51.397
+ bph_f	2	3.2994	55.615	-45.956
+ pgg45	1	1.6980	57.217	-45.203
+ gleason_f	2	2.7834	56.131	-45.061
<none>			58.915	-44.366
+ lcp	1	0.6562	58.259	-43.452
+ age	1	0.0025	58.912	-42.370

Step: AIC=-54.96

lpsa ~ lcavol + lweight

	Df	Sum of Sq	RSS	AIC
+ svi_f	1	5.1737	46.568	-63.177
+ pgg45	1	1.8158	49.926	-56.424
+ gleason_f	2	2.6770	49.065	-56.111
<none>			51.742	-54.958
+ lcp	1	0.8187	50.923	-54.506
+ age	1	0.6456	51.097	-54.176
+ bph_f	2	1.4583	50.284	-53.731

Step: AIC=-63.18

lpsa ~ lcavol + lweight + svi_f

	Df	Sum of Sq	RSS	AIC
<none>			46.568	-63.177
+ gleason_f	2	1.60467	44.964	-62.579
+ age	1	0.62301	45.945	-62.484
+ bph_f	2	1.50046	45.068	-62.354
+ pgg45	1	0.50069	46.068	-62.226
+ lcp	1	0.06937	46.499	-61.322

Call:

```
lm(formula = lpsa ~ lcavol + lweight + svi_f)
```

Coefficients:

(Intercept)	lcavol	lweight	svi_fYes
-0.7772	0.5259	0.6618	0.6657

The resulting model, arrived at after three forward selection steps, includes `lcavol`, `lweight` and `svi_f`.

```
model.fs <- lm(lpsa ~ lcavol + lweight + svi_f,
               data=prost)
summary(model.fs)$adj.r.squared
```

```
[1] 0.6242063
```

```
extractAIC(model.fs)
```

```
[1] 4.00000 -63.17744
```

The adjusted R^2 value for this model is 0.624, and the AIC value used by the stepwise procedure is -63.18, on 4 effective degrees of freedom.

7.5 Backward Elimination using the `step` function

In this case, the backward elimination approach, using reduction in AIC for a criterion, comes to the same conclusion about the “best” model.

```
with(prost,
      step(lm(lpsa ~ lcavol + lweight + age + bph_f +
              svi_f + lcp + gleason_f + pgg45),
            direction="backward"))
```

Start: AIC=-61.4

```
lpsa ~ lcavol + lweight + age + bph_f + svi_f + lcp + gleason_f +
      pgg45
```

	Df	Sum of Sq	RSS	AIC
- gleason_f	2	1.1832	42.240	-62.639
- pgg45	1	0.4409	41.498	-62.359
- lcp	1	0.8492	41.906	-61.409
<none>			41.057	-61.395
- bph_f	2	2.0299	43.087	-60.714
- age	1	2.2129	43.270	-58.303
- svi_f	1	4.1207	45.178	-54.118
- lweight	1	5.7123	46.769	-50.760
- lcavol	1	18.2738	59.331	-27.683

Step: AIC=-62.64

```
lpsa ~ lcavol + lweight + age + bph_f + svi_f + lcp + pgg45
```

	Df	Sum of Sq	RSS	AIC
- lcp	1	0.8470	43.087	-62.713
<none>			42.240	-62.639
- pgg45	1	1.2029	43.443	-61.916
- bph_f	2	2.2515	44.492	-61.602
- age	1	2.0730	44.313	-59.992
- svi_f	1	4.6431	46.884	-54.523
- lweight	1	5.5988	47.839	-52.566
- lcavol	1	21.4956	63.736	-24.736

Step: AIC=-62.71

```
lpsa ~ lcavol + lweight + age + bph_f + svi_f + pgg45
```

	Df	Sum of Sq	RSS	AIC
- pgg45	1	0.5860	43.673	-63.403
<none>			43.087	-62.713
- bph_f	2	2.0214	45.109	-62.266
- age	1	1.7101	44.798	-60.938
- svi_f	1	3.7964	46.884	-56.523
- lweight	1	5.6462	48.734	-52.769
- lcavol	1	22.5152	65.603	-23.936

Step: AIC=-63.4

```
lpsa ~ lcavol + lweight + age + bph_f + svi_f
```

	Df	Sum of Sq	RSS	AIC
<none>			43.673	-63.403
- bph_f	2	2.2720	45.945	-62.484
- age	1	1.3945	45.068	-62.354
- svi_f	1	5.2747	48.948	-54.343
- lweight	1	5.3319	49.005	-54.230
- lcavol	1	25.5538	69.227	-20.720

Call:

```
lm(formula = lpsa ~ lcavol + lweight + age + bph_f + svi_f)
```

Coefficients:

(Intercept)	lcavol	lweight	age	bph_fMedium
0.14329	0.54022	0.67283	-0.01819	0.37607
bph_fHigh	svi_fYes			
0.27216	0.68174			

The backwards elimination approach in this case lands on a model with five inputs (one of which includes two bph indicators,) eliminating only `gleason_f`, `pgg45` and `lcp`.

7.6 Allen-Cady Modified Backward Elimination

Ranking candidate predictors by importance in advance of backwards elimination can help avoid false-positives, while reducing model size. See Vittinghoff et al. (2012), Section 10.3 for more details.

1. First, force into the model any predictors of primary interest, and any confounders necessary for face validity of the final model.
 - “Some variables in the hypothesized causal model may be such well-established causal antecedents of the outcome that it makes sense to include them, essentially to establish the face validity of the model and without regard to the strength or statistical significance of their associations with the primary predictor and outcome ...”
2. Rank the remaining candidate predictors in order of importance.
3. Starting from an initial model with all candidate predictors included, delete predictors in order of ascending importance until the first variable meeting a criterion to stay in the model hits. Then stop.

Only the remaining variable hypothesized to be least important is eligible for removal at each step. When we are willing to do this sorting before collecting (or analyzing) the data, then we can do Allen-Cady backwards elimination using the `drop1` command in R.

7.6.1 Demonstration of the Allen-Cady approach

Suppose, for the moment that we decided to fit a model for the log of `psa` and we decided (before we saw the data) that we would:

```
lcavol + lweight + svi_f + age + bph_f + gleason_f + lcp + pgg45
```

- force the `gleason_f` variable to be in the model, due to prior information about its importance,
- and then rated the importance of the other variables as `lcavol` (most important), then `svi_f` then `age`, and then `bph_f`, then `lweight` and `lcp` followed by `pgg45` (least important)

When we are willing to do this sorting before collecting (or analyzing) the data, then we can do Allen-Cady backwards elimination using the `drop1` command in R.

Step 1. Fit the full model, then see if removing `pgg45` improves AIC...

```
with(prost, drop1(lm(lpsa ~ gleason_f + lcavol + svi_f +
  age + bph_f + lweight + lcp + pgg45),
  scope = (~ pgg45)))
```

Single term deletions

Model:

```
lpsa ~ gleason_f + lcavol + svi_f + age + bph_f + lweight + lcp +
  pgg45
      Df Sum of Sq    RSS    AIC
<none>             41.057 -61.395
pgg45    1    0.44085  41.498 -62.359
```

Since -62.3 is smaller (i.e. more negative) than -61.4, we delete `pgg45` and move on to assess whether we can remove the variable we deemed next least important (`lcp`)

Step 2. Let's see if removing `lcp` from this model improves AIC...

```
with(prost, drop1(lm(lpsa ~ gleason_f + lcavol + svi_f +
  age + bph_f + lweight + lcp),
  scope = (~ lcp)))
```

Single term deletions

Model:

```
lpsa ~ gleason_f + lcavol + svi_f + age + bph_f + lweight + lcp
      Df Sum of Sq    RSS    AIC
<none>          41.498 -62.359
lcp      1    0.56767 42.066 -63.041
```

Again, since -63.0 is smaller than -62.4, we delete `lcp` and next assess whether we should delete `lweight`.

Step 3. Does removing `lweight` from this model improves AIC...

```
with(prost, drop1(lm(lpsa ~ gleason_f + lcavol + svi_f +
  age + bph_f + lweight),
  scope = (~ lweight)))
```

Single term deletions

Model:

```
lpsa ~ gleason_f + lcavol + svi_f + age + bph_f + lweight
      Df Sum of Sq    RSS    AIC
<none>          42.066 -63.041
lweight 1     5.678 47.744 -52.760
```

Since the AIC for the model after the removal of `lweight` is larger (i.e. less negative), we stop, and declare our final model by the Allen-Cady approach to include `gleason_f`, `lcavol`, `svi_f`, `age`, `bph_f` and `lweight`.

7.7 Summarizing the Results

	Method	Suggested Predictors
	Forward selection	<code>lcavol</code> , <code>lweight</code> , <code>svi_f</code>
	Backwards elimination	<code>lcavol</code> , <code>lweight</code> , <code>svi_f</code> , <code>age</code> , <code>bph_f</code>
	Allen-Cady approach	<code>lcavol</code> , <code>lweight</code> , <code>svi_f</code> , <code>age</code> , <code>bph_f</code> , <code>gleason_f</code>

7.7.1 In-Sample Testing and Summaries

Since these models are nested in each other, let's look at the summary statistics (like R^2 , and AIC) and also run an ANOVA-based comparison of these nested models to each other and to the model with the intercept alone, and the kitchen sink model with all available predictors.

```
prost_m_int <- lm(lpsa ~ 1, data = prost)
prost_m_fw <- lm(lpsa ~ lcavol + lweight + svi_f, data = prost)
prost_m_bw <- lm(lpsa ~ lcavol + lweight + svi_f +
  age + bph_f + gleason_f, data = prost)
prost_m_ac <- lm(lpsa ~ lcavol + lweight + svi_f +
  age + bph_f + gleason_f + lcp, data = prost)
```

```
prost_m_ks <- lm(lpsa ~ lcavol + lweight + svi_f +
               age + bph_f + gleason_f + lcp + pgg45, data = prost)
```

7.7.1.1 Model Fit Summaries (in-sample) from glance

Here are the models, at a glance from the broom package.

```
prost_sum <- bind_rows(glance(prost_m_int), glance(prost_m_fw),
                     glance(prost_m_bw), glance(prost_m_ac),
                     glance(prost_m_ks)) %>% round(., 3)
prost_sum$names <- c("intercept", "lcavol + lweight + svi",
                    "... + age + bhp + gleason", "... + lcp", "... + pgg45")
prost_sum <- prost_sum %>%
  select(names, r.squared, adj.r.squared, AIC, BIC, sigma, df, df.residual)

prost_sum
```

	names	r.squared	adj.r.squared	AIC	BIC	sigma
1	intercept	0.000	0.000	306.112	311.261	1.154
2	lcavol + lweight + svi	0.636	0.624	214.097	226.970	0.708
3	... + age + bhp + gleason	0.671	0.641	214.233	239.980	0.691
4	... + lcp	0.676	0.642	214.915	243.237	0.691
5	... + pgg45	0.679	0.642	215.879	246.775	0.691
	df df.residual					
1	1 96					
2	4 93					
3	9 88					
4	10 87					
5	11 86					

From these summaries, it looks like:

- the adjusted R^2 is essentially indistinguishable between the three largest models, but a bit less strong with the three-predictor (4 df) model, and
- the AIC and BIC are (slightly) better (lower) with the three-predictor model (4 df) than any other.

So we might be motivated by these summaries to select any of the three models we're studying closely here.

7.7.1.2 Model Testing via ANOVA (in-sample)

To obtain ANOVA-based test results, we'll run...

```
anova(prost_m_int, prost_m_fw, prost_m_bw, prost_m_ac, prost_m_ks)
```

Analysis of Variance Table

```
Model 1: lpsa ~ 1
Model 2: lpsa ~ lcavol + lweight + svi_f
Model 3: lpsa ~ lcavol + lweight + svi_f + age + bph_f + gleason_f
Model 4: lpsa ~ lcavol + lweight + svi_f + age + bph_f + gleason_f + lcp
Model 5: lpsa ~ lcavol + lweight + svi_f + age + bph_f + gleason_f + lcp +
        pgg45
```

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	96	127.918				
2	93	46.568	3	81.349	56.7991	<2e-16 ***


```

3      88 42.066 5      4.503 1.8863 0.1050
4      87 41.498 1      0.568 1.1891 0.2786
5      86 41.057 1      0.441 0.9234 0.3393
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

```

What conclusions can we draw on the basis of these ANOVA tests?

- There is a statistically significant improvement in predictive value for Model 2 (the forward selection approach) as compared to Model 1 (the intercept only.)
- The ANOVA test comparing Model 5 (kitchen sink) to Model 4 (Allen-Cady result) shows no statistically significant improvement in predictive value.
- Neither does the ANOVA test comparing Model 3 to Model 2 or Model 4 to Model 3.

This suggests that, **if we are willing to let the ANOVA test decide our best model** than that would be the model produced by forward selection, with predictors `lcavol`, `lweight` and `svi_f`. But we haven't validated the models.

1. If the purpose of the model is to predict new data, some sort of out-of-sample or cross-validation approach will be necessary, and
2. Even if our goal isn't prediction but merely description of the current data, we would still want to build diagnostic plots to regression assumptions in each model, and
3. There is no reason to assume in advance that any of these models is in fact correct, or that any one of these stepwise approaches is necessarily better than any other, and
4. The mere act of running a stepwise regression model, as we'll see, can increase the bias in our findings if we accept the results at face value.

So we'll need some ways to validate the results once we complete the selection process.

7.7.2 Validating the Results of the Various Models

We can use a 5-fold cross-validation approach to assess the predictions made by our potential models and then compare them. Let's compare our three models:

- the three predictor model obtained by forward selection, including `lcavol`, `lweight`, and `svi_f`
- the five predictor model obtained by backwards elimination, including `lcavol`, `lweight`, `svi_f`, and also `age`, and `bph_f`
- the six predictor model obtained by the Allen-Cady approach, adding `gleason_f` to the previous model.

Here's the 5-fold validation work (and resulting RMSE and MAE estimates) for the three-predictor model.

```

set.seed(43201012)

prost3_models <- prost %>%
  crossv_kfold(k = 5) %>%
  mutate(model = map(train, ~ lm(lpsa ~ lcavol + lweight +
                                svi_f, data = .)))

prost3_preds <- prost3_models %>%
  unnest(map2(model, test, ~ augment(.x, newdata = .y)))

prost3_preds %>%
  summarize(RMSE_prost3 = sqrt(mean((lpsa - .fitted) ^2)),
            MAE_prost3 = mean(abs(lpsa - .fitted)))

# A tibble: 1 x 2
  RMSE_prost3 MAE_prost3
  <dbl>       <dbl>

```

```
1      0.745      0.587
```

Now, we'll generate the RMSE and MAE estimates for the five-predictor model.

```
set.seed(43206879)

prost5_models <- prost %>%
  crossv_kfold(k = 5) %>%
  mutate(model = map(train, ~ lm(lpsa ~ lcavol + lweight +
                                svi_f + age + bph_f, data = .)))

prost5_preds <- prost5_models %>%
  unnest(map2(model, test, ~ augment(.x, newdata = .y)))

prost5_preds %>%
  summarize(RMSE_prost5 = sqrt(mean((lpsa - .fitted) ^2)),
            MAE_prost5 = mean(abs(lpsa - .fitted)))

# A tibble: 1 x 2
  RMSE_prost5 MAE_prost5
    <dbl>      <dbl>
1      0.750      0.581
```

And at last, we'll generate the RMSE and MAE estimates for the six-predictor model.

```
set.seed(43236198)

prost6_models <- prost %>%
  crossv_kfold(k = 5) %>%
  mutate(model = map(train, ~ lm(lpsa ~ lcavol + lweight +
                                svi_f + age + bph_f + gleason_f, data = .)))

prost6_preds <- prost6_models %>%
  unnest(map2(model, test, ~ augment(.x, newdata = .y)))

prost6_preds %>%
  summarize(RMSE_prost6 = sqrt(mean((lpsa - .fitted) ^2)),
            MAE_prost6 = mean(abs(lpsa - .fitted)))

# A tibble: 1 x 2
  RMSE_prost6 MAE_prost6
    <dbl>      <dbl>
1      0.720      0.551
```

It appears that the six-predictor model does better than either of the other two approaches, with smaller RMSE and MAE. The three-predictor model does slightly better in terms of root mean square prediction error and slightly worse in terms of mean absolute prediction error than the five-predictor model.

OK. A mixed bag, with different conclusions depending on which summary we want to look at. But of course, stepwise regression isn't the only way to do variable selection. Let's consider a broader range of potential predictor sets.

Chapter 8

“Best Subsets” Variable Selection in our Prostate Cancer Study

A second approach to model selection involved fitting all possible subset models and identifying the ones that look best according to some meaningful criterion and ideally one that includes enough variables to model the response appropriately without including lots of redundant or unnecessary terms.

8.1 Four Key Summaries We’ll Use to Evaluate Potential Models

1. Adjusted R^2 , which we try to maximize.
2. Akaike’s Information Criterion (AIC), which we try to minimize, and a Bias-Corrected version of AIC due to Hurwitz and Tsai, which we use when the sample size is small, specifically when the sample size n and the number of predictors being studied k are such that $n/k \leq 40$. We also try to minimize this bias-corrected AIC.
3. Bayesian Information Criterion (BIC), which we also try to minimize.
4. Mallows’ C_p statistic, which we (essentially) try to minimize.

Choosing between AIC and BIC can be challenging.

For model selection purposes, there is no clear choice between AIC and BIC. Given a family of models, including the true model, the probability that BIC will select the correct model approaches one as the sample size n approaches infinity - thus BIC is asymptotically consistent, which AIC is not. [But, for practical purposes,] BIC often chooses models that are too simple [relative to AIC] because of its heavy penalty on complexity.

- Source: Hastie et al. (2001), page 208.

Several useful tools for running “all subsets” or “best subsets” regression comparisons are developed in R’s `leaps` package.

8.2 Using `regsubsets` in the `leaps` package

We can use the `leaps` package to obtain results in the `prost` study from looking at all possible subsets of the candidate predictors.

The `leaps` package isn’t particularly friendly to the tidyverse, and will require us first to identify a set of candidate predictors using `with` and `cbind`, then apply those to a `regsubsets` function, which identifies the set of models.

To start, we’ll ask R to find the one best subset (with 1 predictor variable [in addition to the intercept], then with 2 predictors, and then with each of 3, 4, ... 8 predictor variables) according to an exhaustive search without forcing any of the variables to be in or out. We’d use the `nvmax` command within the `regsubsets` function to limit the number of regression inputs to a maximum.

```
preds <- with(prost,
  cbind(lcavol, lweight, age, bph_f, svi_f, lcp, gleason_f, pgg45))

x1 <- regsubsets(preds, y=prost$lpsa)
rs <- summary(x1)
rs
```

```
Subset selection object
8 Variables (and intercept)
      Forced in Forced out
lcavol      FALSE      FALSE
lweight      FALSE      FALSE
age          FALSE      FALSE
bph_f        FALSE      FALSE
svi_f        FALSE      FALSE
lcp          FALSE      FALSE
gleason_f    FALSE      FALSE
pgg45        FALSE      FALSE
1 subsets of each size up to 8
Selection Algorithm: exhaustive
      lcavol lweight age bph_f svi_f lcp gleason_f pgg45
1 ( 1 ) "*"      "      " " " " " " " " " " "
2 ( 1 ) "*"      "*"      " " " " " " " " " "
3 ( 1 ) "*"      "*"      " " " " "*" " " " "
4 ( 1 ) "*"      "*"      " " "*" "*" "*" " " "
5 ( 1 ) "*"      "*"      "*" "*" "*" "*" " " "
6 ( 1 ) "*"      "*"      "*" "*" "*" "*" " " "*"
7 ( 1 ) "*"      "*"      "*" "*" "*" "*" "*" "*"
8 ( 1 ) "*"      "*"      "*" "*" "*" "*" "*" "*"

```

So...

- the best one-predictor model used `lcavol`
- the best two-predictor model used `lcavol` and `lweight`
- the best three-predictor model used `lcavol`, `lweight` and `svi_f`
- the best four-predictor model added `bph_f`, and
- the best five-predictor model added `age`
- the best six-input model added `gleason_f`,
- the best seven-input model added `lcp`,
- and the eight-input model adds `pgg45`.

All of these “best subsets” are hierarchical, in that each model is a subset of the one below it. This isn’t inevitably true.

- To determine which model is best, we can plot key summaries of model fit (adjusted R^2 , Mallows’ C_p , bias-corrected AIC, and BIC) using either base R plotting techniques (what I’ve done in the past) or `ggplot2` (what I use now.) I’ll show both types of plotting approaches in the next two sections.

8.2.1 Using `which` and `obj`

Let’s see what we’ve fit:

```
rs$obj
```

```
Subset selection object
8 Variables (and intercept)
      Forced in Forced out
lcavol      FALSE      FALSE
lweight     FALSE      FALSE
age         FALSE      FALSE
bph_f       FALSE      FALSE
svi_f       FALSE      FALSE
lcp         FALSE      FALSE
gleason_f   FALSE      FALSE
pgg45       FALSE      FALSE
1 subsets of each size up to 8
Selection Algorithm: exhaustive
```

To see the eight models selected by the system, we use:

```
rs$which
```

```
(Intercept) lcavol lweight age bph_f svi_f lcp gleason_f pgg45
1      TRUE  TRUE  FALSE FALSE FALSE FALSE FALSE      FALSE FALSE
2      TRUE  TRUE   TRUE  FALSE FALSE FALSE FALSE      FALSE FALSE
3      TRUE  TRUE   TRUE  FALSE FALSE  TRUE  FALSE      FALSE FALSE
4      TRUE  TRUE   TRUE  FALSE  TRUE   TRUE  FALSE      FALSE FALSE
5      TRUE  TRUE   TRUE   TRUE  TRUE   TRUE  FALSE      FALSE FALSE
6      TRUE  TRUE   TRUE   TRUE  TRUE   TRUE  FALSE      TRUE  FALSE
7      TRUE  TRUE   TRUE   TRUE  TRUE   TRUE  TRUE      TRUE  FALSE
8      TRUE  TRUE   TRUE   TRUE  TRUE   TRUE  TRUE      TRUE  TRUE
```

We built one subset of each size up to eight predictors, not including the intercept. This means we have models of size $k = 2, 3, 4, 5, 6, 7, 8$ and 9.

The models are:

Size k	Predictors included (besides intercept)
2	lcavol
3	lcavol and lweight
4	add svi_f
5	add bph_f
6	add age
7	add gleason_f
8	add lcp
9	add pgg45

8.3 Calculating bias-corrected AIC

The bias-corrected AIC formula due to Hurwitz and Tsai requires three inputs:

- the residual sum of squares for a model
- the sample size (n) or number of observations used to fit the model
- the number of regression inputs, k , including the intercept, used in the model

So, for a particular model fit to n observations, on k predictors (including the intercept) and a residual sum of squares equal to RSS, we have:

$$AIC_c = n \log\left(\frac{RSS}{n}\right) + 2k + \frac{2k(k+1)}{n-k-1}$$

Note that the corrected AIC_c can be related to the original AIC via:

$$AIC_c = AIC + \frac{2k(k+1)}{n-k-1}$$

8.3.1 Calculation of aic.c in our setting

In our case, we have $n = 97$ observations, and built a series of models with $k = 2:9$ predictors (including the intercept in each case), so we will insert those values into the general formula for bias-corrected AIC which is:

```
aic.c <- n * log( rs$rss / n) + 2 * k +
              (2 * k * (k + 1) / (n - k - 1))
```

We can obtain the residual sum of squares explained by each model by pulling `rss` from the `regsubsets` summary contained here in `rs`.

```
data_frame(k = 2:9, RSS = rs$rss)
```

```
# A tibble: 8 x 2
      k  RSS
  <int> <dbl>
1     2  58.9
2     3  51.7
3     4  46.6
4     5  45.7
5     6  44.6
6     7  43.7
7     8  43.0
8     9  42.8
```

In this case, we have:

```
rs$aic.c <- 97*log(rs$rss / 97) + 2*(2:9) +
            (2 * (2:9) * ((2:9)+1) / (97 - (2:9) - 1))
```

```
round(rs$aic,2) # uncorrected
```

```
[1] -44.24 -54.70 -62.74 -62.29 -62.34 -62.11 -61.17 -59.36
```

```
round(rs$aic.c,2) # bias-corrected
```

```
[1] -44.24 -54.70 -62.74 -62.29 -62.34 -62.11 -61.17 -59.36
```

8.3.2 Building a Tibble containing the necessary information

Again, note the use of `2:9` for the values of k , because we’re fitting one model for each size from 2 through 9.

```
best_mods_1 <- data_frame(
  k = 2:9,
  r2 = rs$rsq,
  adjr2 = rs$adjr2,
  cp = rs$cp,
  aic.c = rs$aic.c,
```

```

    bic = rs$bic
  )

best_mods <- cbind(best_mods_1, rs$which)

best_mods

```

	k	r2	adjr2	cp	aic.c	bic	(Intercept)	lcavol
1	2	0.5394320	0.5345839	28.213914	-44.23838	-66.05416	TRUE	TRUE
2	3	0.5955040	0.5868977	15.456669	-54.70040	-74.07188	TRUE	TRUE
3	4	0.6359499	0.6242063	6.811986	-62.74265	-79.71614	TRUE	TRUE
4	5	0.6425479	0.6270065	7.075509	-62.29223	-76.91557	TRUE	TRUE
5	6	0.6509970	0.6318211	6.851826	-62.33858	-74.66120	TRUE	TRUE
6	7	0.6584484	0.6356783	6.890739	-62.10692	-72.17992	TRUE	TRUE
7	8	0.6634967	0.6370302	7.562119	-61.17338	-69.04961	TRUE	TRUE
8	9	0.6656326	0.6352355	9.000000	-59.35841	-65.09253	TRUE	TRUE

	lweight	age	bph_f	svi_f	lcp	gleason_f	pgg45
1	FALSE	FALSE	FALSE	FALSE	FALSE	FALSE	FALSE
2	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE	FALSE
3	TRUE	FALSE	FALSE	TRUE	FALSE	FALSE	FALSE
4	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE	FALSE
5	TRUE	TRUE	TRUE	TRUE	FALSE	FALSE	FALSE
6	TRUE	TRUE	TRUE	TRUE	FALSE	TRUE	FALSE
7	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	FALSE
8	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE

8.4 Plotting the Best Subsets Results using ggplot2

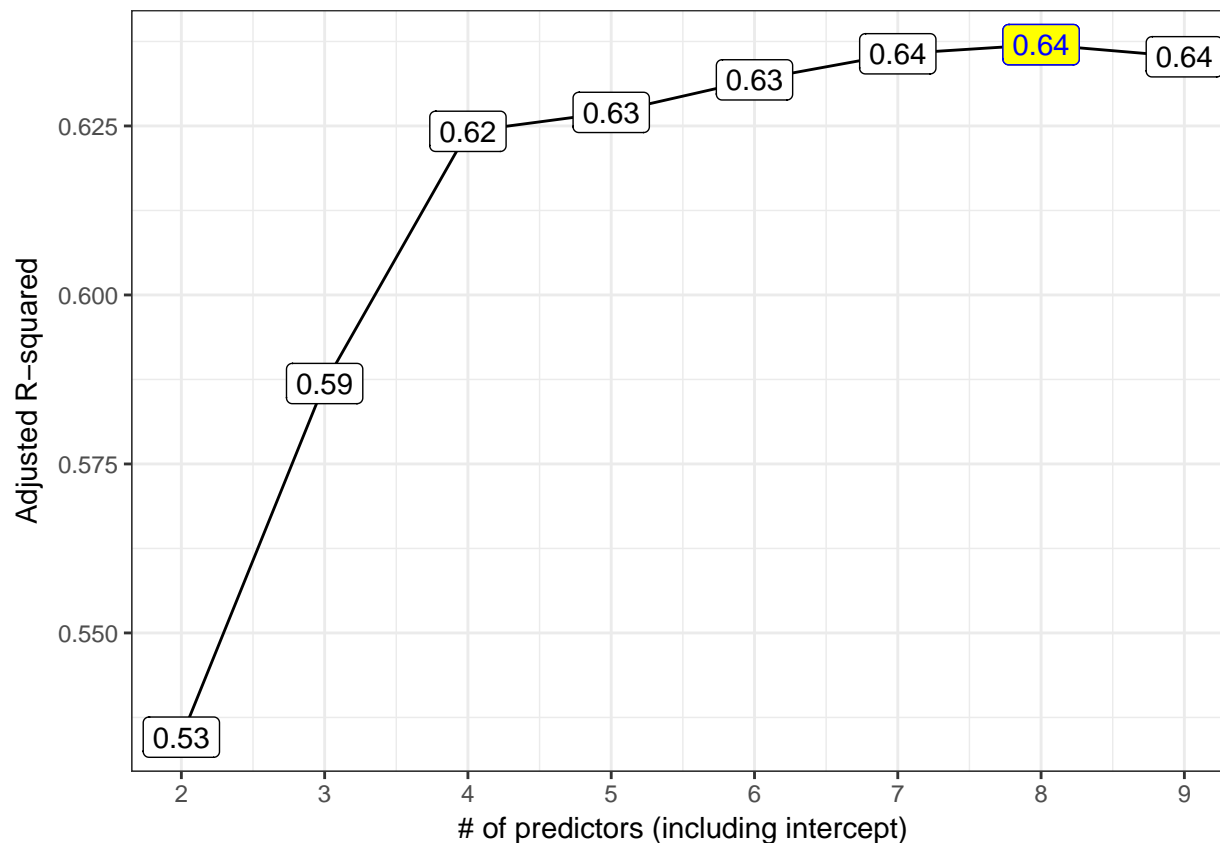
8.4.1 The Adjusted R² Plot

```

p1 <- ggplot(best_mods, aes(x = k, y = adjr2,
                           label = round(adjr2,2))) +
  geom_line() +
  geom_label() +
  geom_label(data = subset(best_mods,
                           adjr2 == max(adjr2)),
            aes(x = k, y = adjr2, label = round(adjr2,2)),
            fill = "yellow", col = "blue") +
  theme_bw() +
  scale_x_continuous(breaks = 2:9) +
  labs(x = "# of predictors (including intercept)",
       y = "Adjusted R-squared")

```

p1



Models 4-9 all look like reasonable choices here. The maximum adjusted R^2 is seen in the model of size 8.

8.4.2 Mallows' C_p

The C_p statistic focuses directly on the tradeoff between **bias** (due to excluding important predictors from the model) and extra **variance** (due to including too many unimportant predictors in the model.)

If N is the sample size, and we select p regression predictors from a set of K (where $p < K$), then the C_p statistic is

$$C_p = \frac{SSE_p}{MSE_K} - N + 2p$$

where:

- SSE_p is the sum of squares for error (residual) in the model with p predictors
- MSE_K is the residual mean square after regression in the model with all K predictors

As it turns out, this is just measuring the particular model's lack of fit, and then adding a penalty for the number of terms in the model (specifically $2p - N$ is the penalty since the lack of fit is measured as $(N - p) \frac{SSE_p}{MSE_K}$).

- If a model has no meaningful lack of fit (i.e. no substantial bias) then the expected value of C_p is roughly p .
- Otherwise, the expectation is p plus a positive bias term.
- In general, we want to see *smaller* values of C_p .
- We usually select a “winning model” by choosing a subset of predictors that have C_p near the value of p .

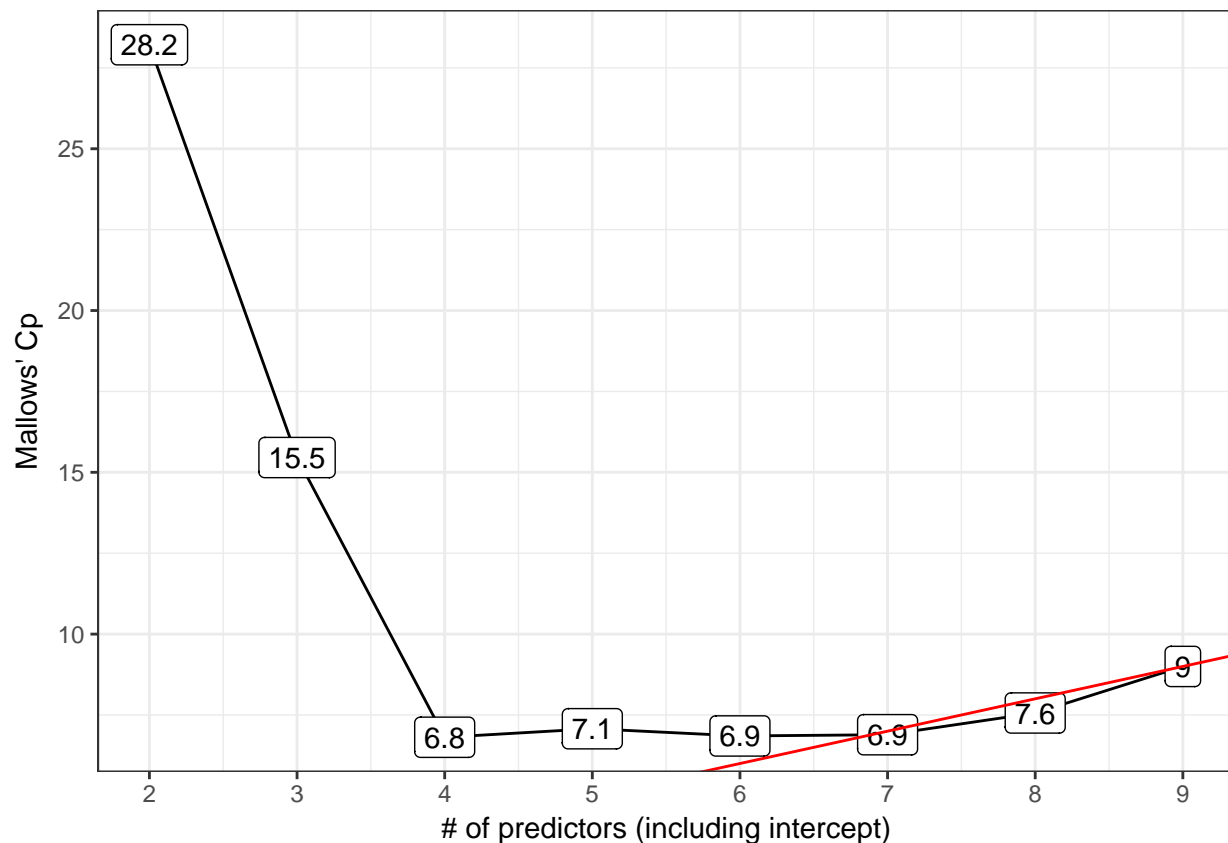
8.4.3 The C_p Plot

The C_p plot is just a scatterplot of C_p on the Y-axis, and p on the X-axis.

Each of the various predictor subsets we will study is represented in a single point. A model without bias should have C_p roughly equal to p , so we'll frequently draw a line at $C_p = p$ to make that clear. We then select our model from among all models with small C_p statistics.

```
p2 <- ggplot(best_mods, aes(x = k, y = cp,
                           label = round(cp,1))) +
  geom_line() +
  geom_label() +
  geom_abline(intercept = 0, slope = 1,
             col = "red") +
  theme_bw() +
  scale_x_continuous(breaks = 2:9) +
  labs(x = "# of predictors (including intercept)",
       y = "Mallows' Cp")
```

p2



- Model 7 looks pretty good, with C_p just barely smaller than the size ($p = 7$) of the model.
- Model 6 is also a possibility, with the difference $C_p - p$ minimized among all models with $C_p \geq p$.

8.4.4 “All Subsets” Regression and Information Criteria

We might consider any of three main information criteria:

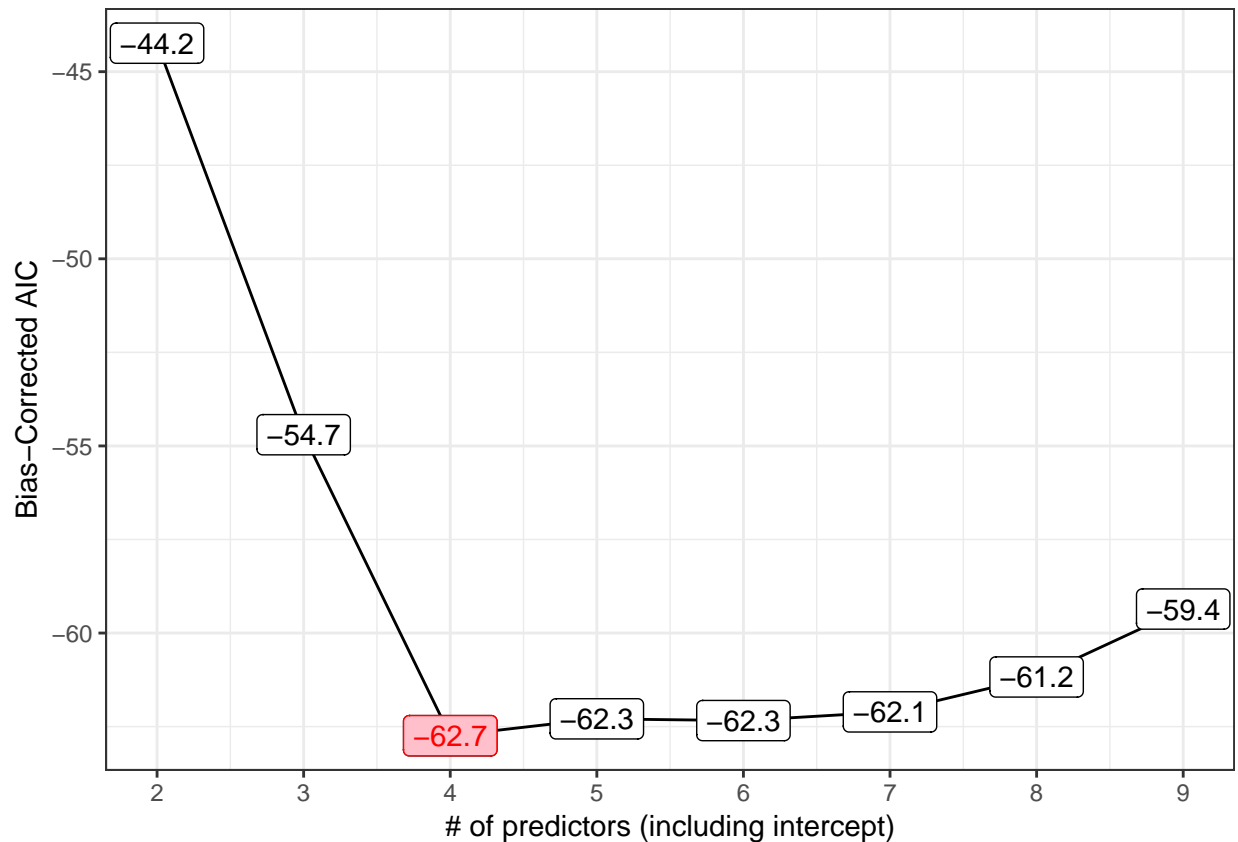
- the Bayesian Information Criterion, called BIC
- the Akaike Information Criterion (used by R’s default stepwise approaches,) called AIC
- a corrected version of AIC due to Hurwitz and Tsai, called AIC_c

Each of these indicates better models by getting smaller. I’ll focus on bias-corrected AIC and on BIC.

8.4.5 The bias-corrected AIC plot

```
p3 <- ggplot(best_mods, aes(x = k, y = aic.c,
                           label = round(aic.c,1))) +
  geom_line() +
  geom_label() +
  geom_label(data = subset(best_mods, aic.c == min(aic.c)),
            aes(x = k, y = aic.c), fill = "pink",
            col = "red") +
  theme_bw() +
  scale_x_continuous(breaks = 2:9) +
  labs(x = "# of predictors (including intercept)",
       y = "Bias-Corrected AIC")
```

p3

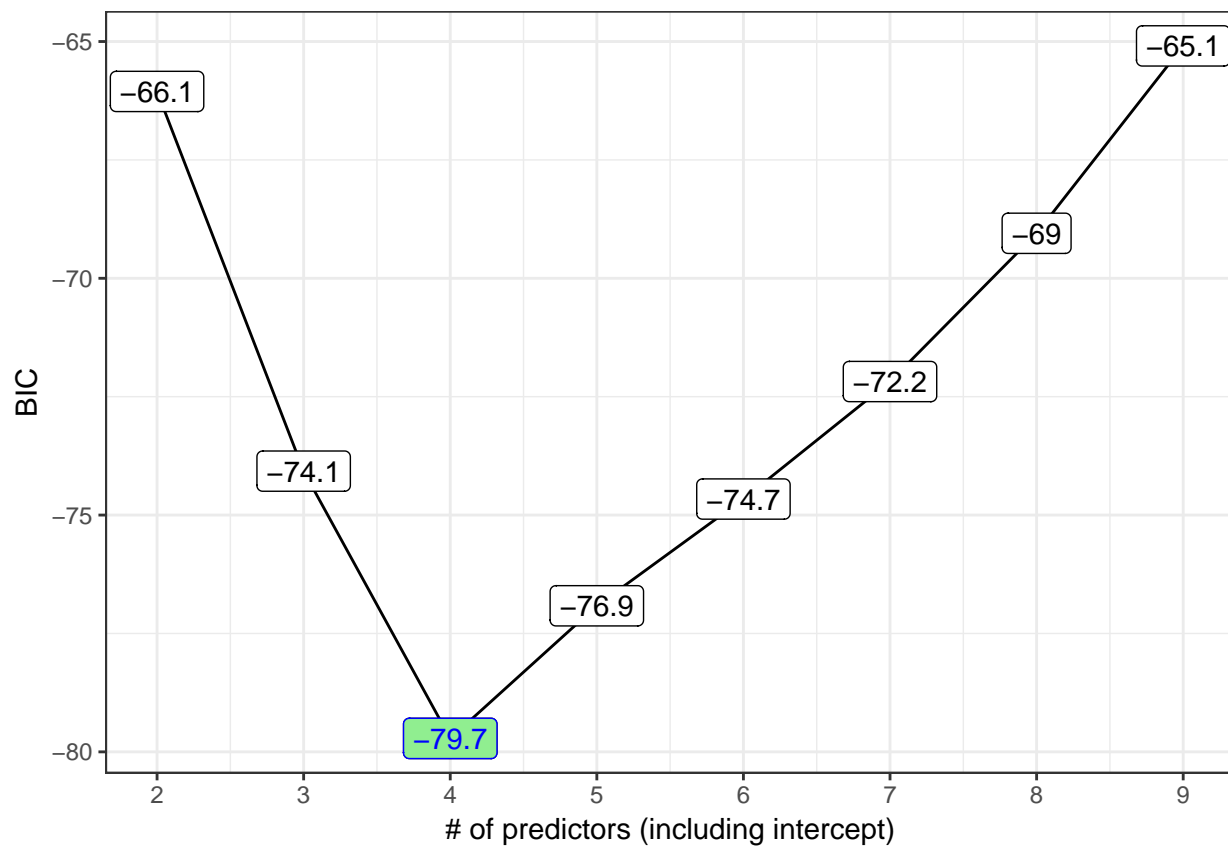


The smallest AIC_c values occur in models 4 and later, especially model 4 itself.

8.5 The BIC plot

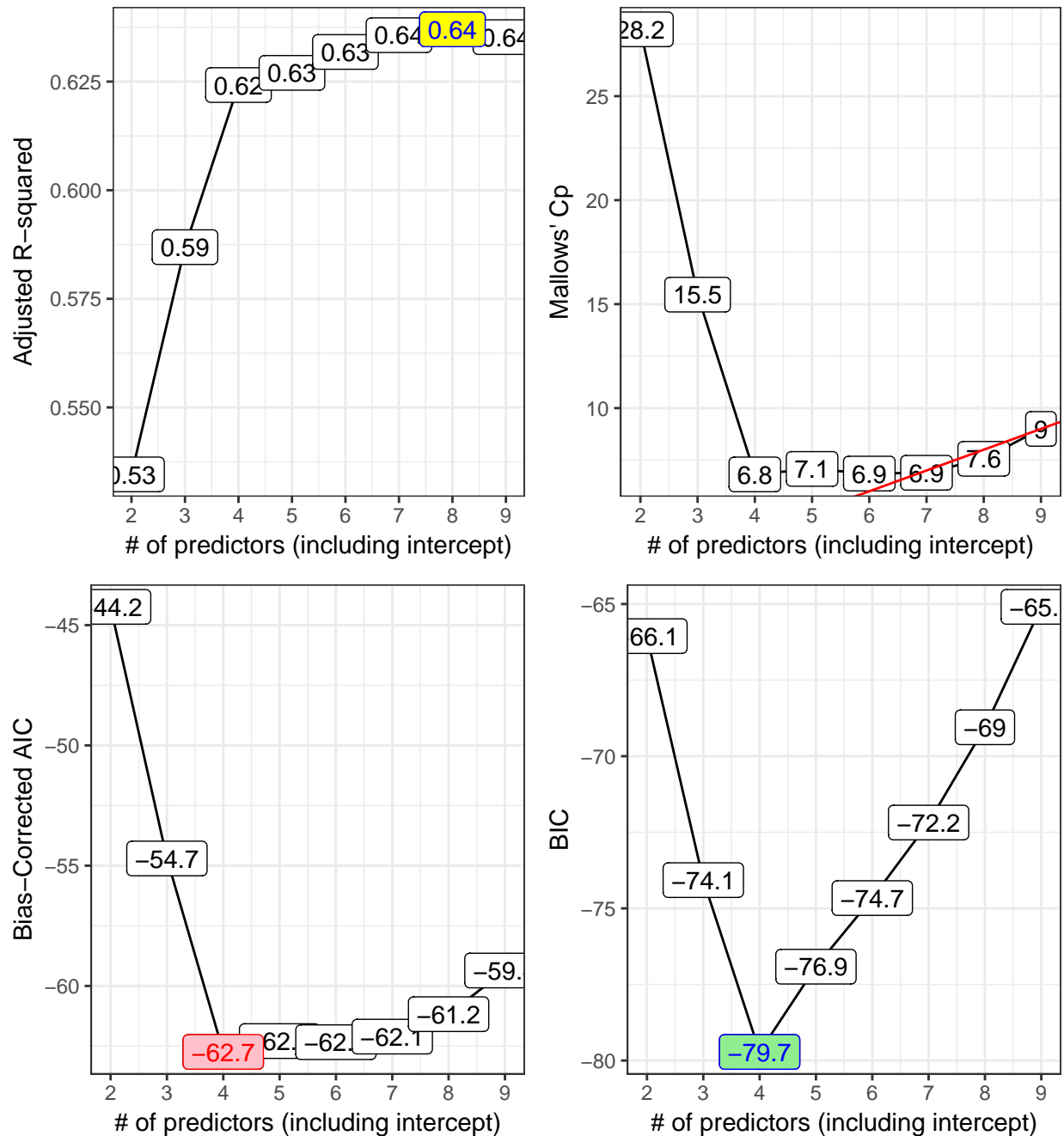
```
p4 <- ggplot(best_mods, aes(x = k, y = bic,
                           label = round(bic,1))) +
  geom_line() +
  geom_label() +
  geom_label(data = subset(best_mods, bic == min(bic)),
            aes(x = k, y = bic),
            fill = "lightgreen", col = "blue") +
  theme_bw() +
  scale_x_continuous(breaks = 2:9) +
  labs(x = "# of predictors (including intercept)",
       y = "BIC")
```

p4



8.5.1 All Four Plots in One Figure (via ggplot2)

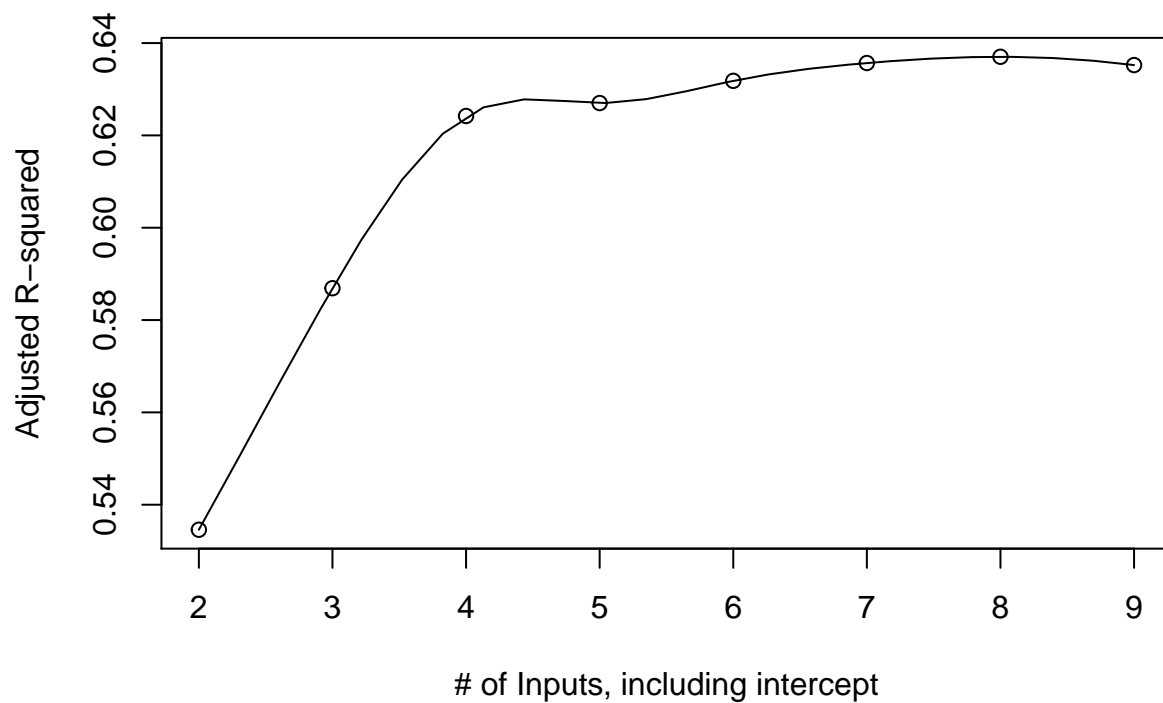
```
gridExtra::grid.arrange(p1, p2, p3, p4, nrow = 2)
```



8.6 Plotting the Best Subsets Results using base R plots

8.6.1 The Adjusted R^2 Plot

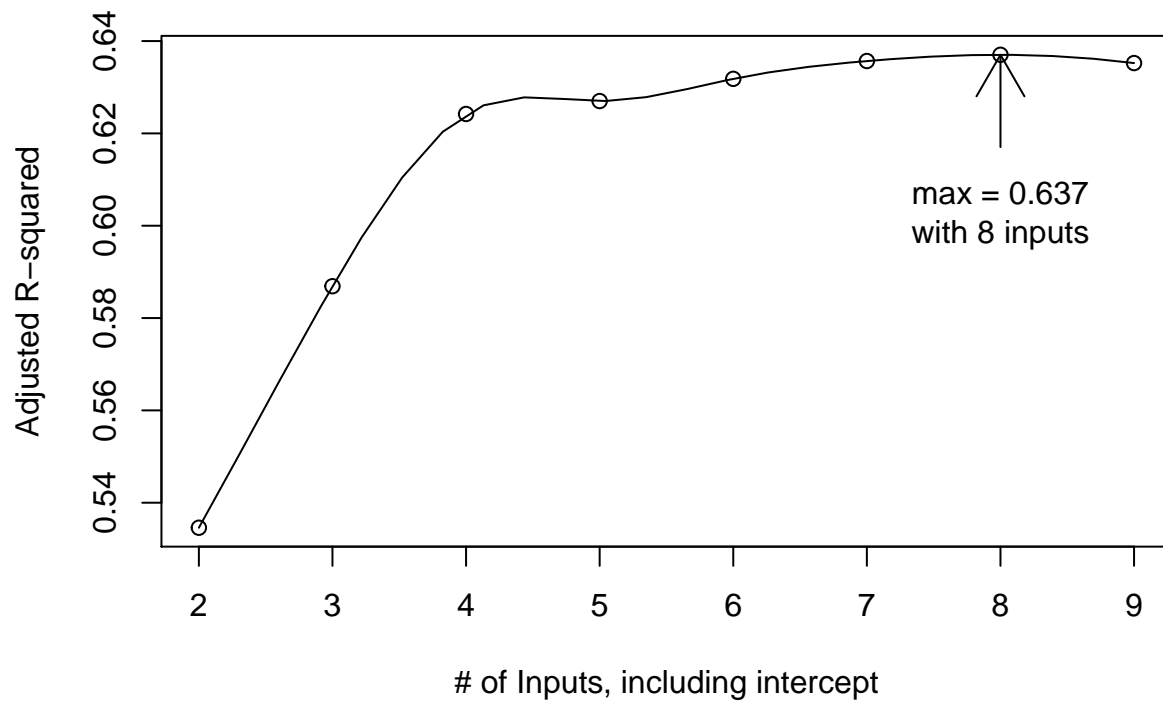
```
plot(rs$adjr2 ~ I(2:9), ylab="Adjusted R-squared",
     xlab="# of Inputs, including intercept")
lines(spline(rs$adjr2 ~ I(2:9)))
```



Again, models 4-9 all look like reasonable choices here.

8.6.2 A Fancier Version (identifying the largest adjusted R^2)

```
m2 <- max(rs$adjr2)
m1 <- which.max(rs$adjr2) + 1
plot(rs$adjr2 ~ I(2:9), ylab="Adjusted R-squared",
     xlab="# of Inputs, including intercept")
lines(spline(rs$adjr2 ~ I(2:9)))
arrows(m1, m2-0.02, m1, m2)
text(m1, m2-0.03, paste("max =", format(m2, digits=3)))
text(m1, m2-0.045, paste("with", format(m1, digits=1),
                          "inputs"), pos=3)
```

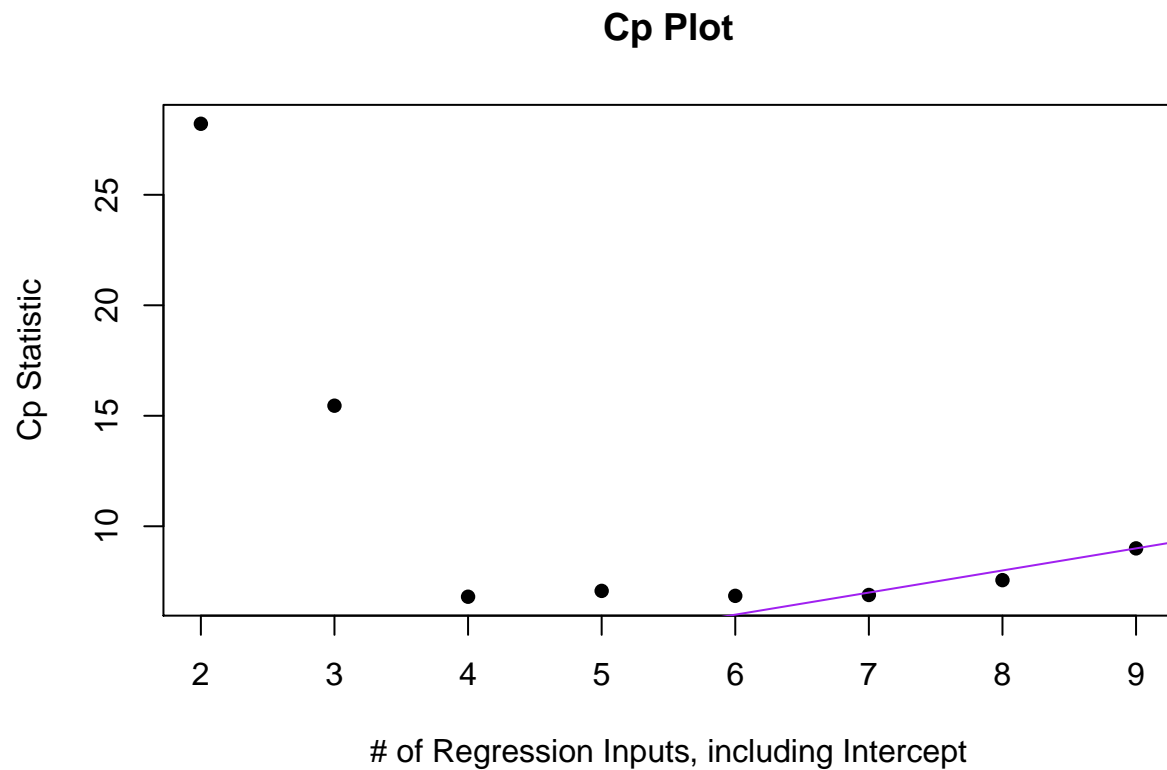


8.6.3 The C_p Plot

Again, the C_p plot is just a scatterplot of C_p on the Y-axis, and p on the X-axis.

Each of the various predictor subsets we will study is represented in a single point. A model without bias should have C_p roughly equal to p , so we'll frequently draw a line at $C_p = p$ to make that clear. We then select our model from among all models with small C_p statistics.

```
plot(rs$cp ~ 1(2:9),
     ylab="Cp Statistic",
     xlab="# of Regression Inputs, including Intercept",
     pch=16, main="Cp Plot")
abline(0,1, col = "purple")
```

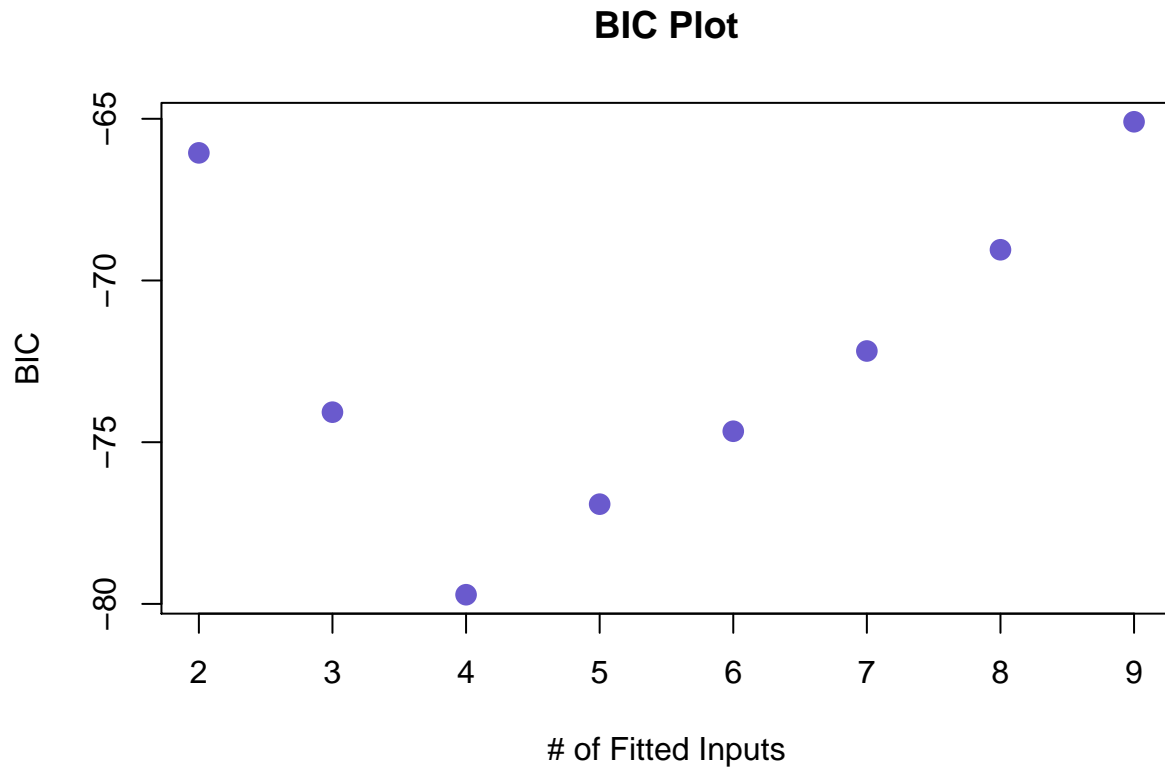


Model 4 has the smallest value of C_p (and is the leftmost of the largely comparable models 4-9) while 6 is close to and 7 is right on the $C_p = p$ line, so those are the likeliest candidates.

8.6.4 The BIC Plot

R provides the BIC directly as part of the result of running `regsubsets`, as we've seen.

```
plot(rs$bic ~ I(2:9), ylab="BIC", xlab="# of Fitted Inputs",  
     pch=16, cex=1.5, col="slateblue", main="BIC Plot")
```



We want to minimize BIC, which argues strongly for the model with 4 inputs, including the intercept.

8.6.5 The Bias-Corrected AIC (Hurwitz & Tsai)

The bias-corrected AIC formula due to Hurwitz and Tsai is, as we’ve seen:

$$AIC_c = n \log\left(\frac{RSS}{n}\right) + 2k + \frac{2k(k+1)}{n-k-1}$$

```
rs$aic.c <- 97*log(rs$rss / 97) + 2*(2:9) +
           (2 * (2:9) * ((2:9)+1) / (97 - (2:9) - 1))
```

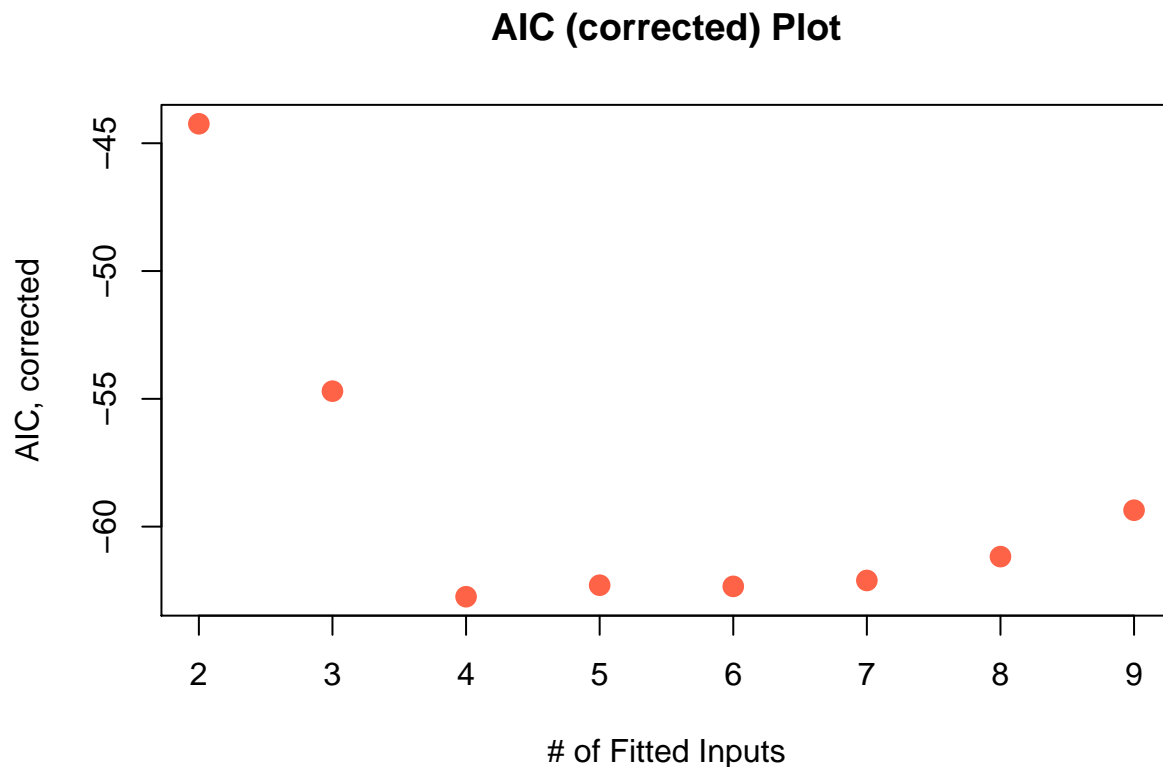
```
round(rs$aic,2) # uncorrected
```

```
[1] -44.24 -54.70 -62.74 -62.29 -62.34 -62.11 -61.17 -59.36
```

```
round(rs$aic.c,2) # bias-corrected
```

```
[1] -44.24 -54.70 -62.74 -62.29 -62.34 -62.11 -61.17 -59.36
```

```
plot(rs$aic.c ~ I(2:9), ylab="AIC, corrected", xlab="# of Fitted Inputs",
     pch=16, cex=1.5, col="tomato", main="AIC (corrected) Plot")
```

The smallest AIC_c values occur in models 4 and later, especially model 4 itself.

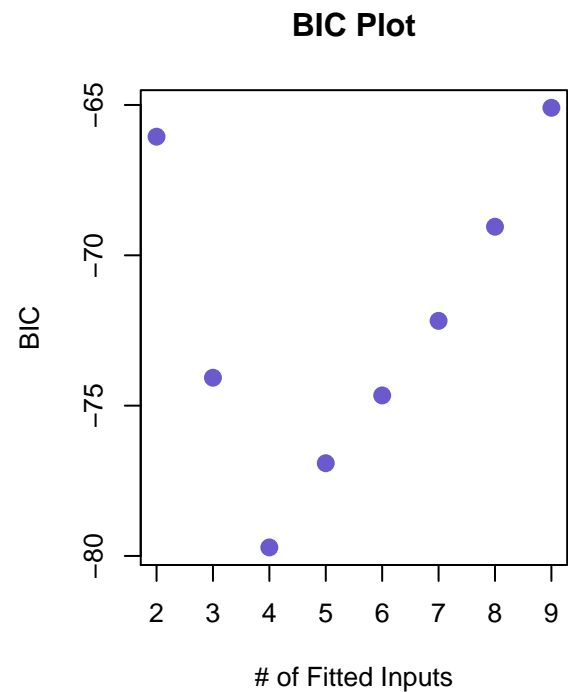
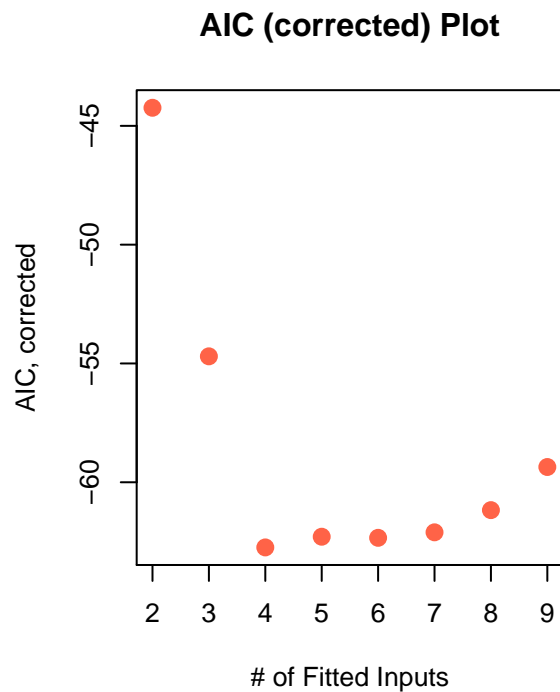
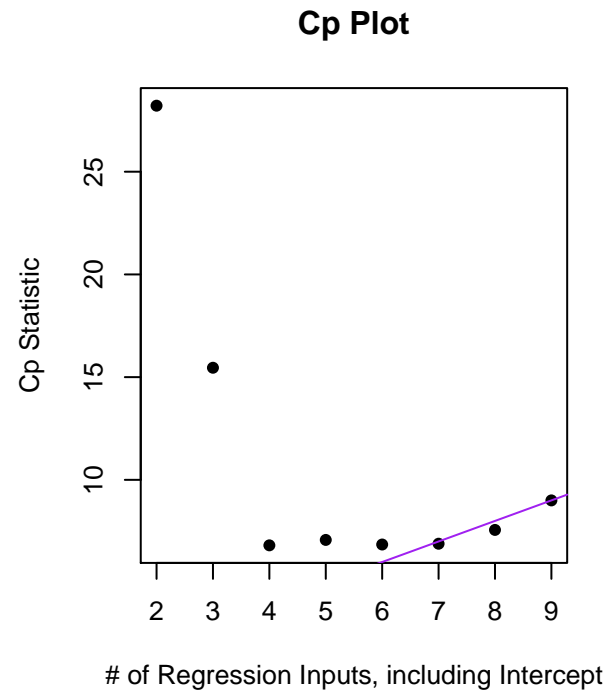
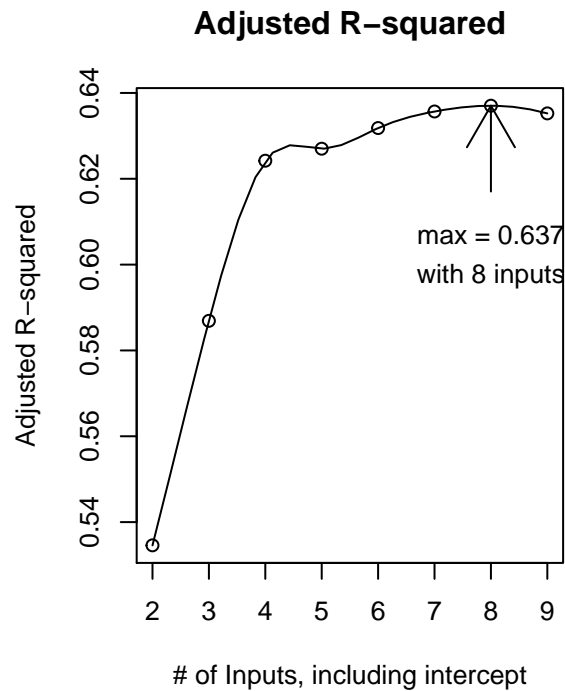
8.6.6 All Four Plots, Together (from Base R)

```
par(mfrow = c(2,2))
m2 <- max(rs$adjr2)
m1 <- which.max(rs$adjr2) + 1
plot(rs$adjr2 ~ I(2:9), ylab="Adjusted R-squared",
     xlab="# of Inputs, including intercept",
     main = "Adjusted R-squared")
lines(spline(rs$adjr2 ~ I(2:9)))
arrows(m1, m2-0.02, m1, m2)
text(m1, m2-0.03, paste("max =", format(m2, digits=3)))
text(m1, m2-0.045, paste("with", format(m1, digits=1),
                        "inputs"), pos=3)

plot(rs$cp ~ I(2:9),
     ylab="Cp Statistic",
     xlab="# of Regression Inputs, including Intercept",
     pch=16, main="Cp Plot")
abline(0,1, col = "purple")

rs$aic.c <- 97*log(rs$rss / 97) + 2*(2:9) +
           (2 * (2:9) * ((2:9)+1) / (97 - (2:9) - 1))
plot(rs$aic.c ~ I(2:9), ylab="AIC, corrected", xlab="# of Fitted Inputs",
```

```
pch=16, cex=1.5, col="tomato", main="AIC (corrected) Plot")
plot(rs$bic ~ I(2:9), ylab="BIC", xlab="# of Fitted Inputs",
     pch=16, cex=1.5, col="slateblue", main="BIC Plot")
```



```
par(mfrow = c(1,1))
```

8.7 Table of Key Results

We can build a big table, like this:

```
best_mods
```

	k	r2	adjr2	cp	aic.c	bic	(Intercept)	lcavol
1	2	0.5394320	0.5345839	28.213914	-44.23838	-66.05416	TRUE	TRUE
2	3	0.5955040	0.5868977	15.456669	-54.70040	-74.07188	TRUE	TRUE
3	4	0.6359499	0.6242063	6.811986	-62.74265	-79.71614	TRUE	TRUE
4	5	0.6425479	0.6270065	7.075509	-62.29223	-76.91557	TRUE	TRUE
5	6	0.6509970	0.6318211	6.851826	-62.33858	-74.66120	TRUE	TRUE
6	7	0.6584484	0.6356783	6.890739	-62.10692	-72.17992	TRUE	TRUE
7	8	0.6634967	0.6370302	7.562119	-61.17338	-69.04961	TRUE	TRUE
8	9	0.6656326	0.6352355	9.000000	-59.35841	-65.09253	TRUE	TRUE

	lweight	age	bph_f	svi_f	lcp	gleason_f	pgg45
1	FALSE	FALSE	FALSE	FALSE	FALSE	FALSE	FALSE
2	TRUE	FALSE	FALSE	FALSE	FALSE	FALSE	FALSE
3	TRUE	FALSE	FALSE	TRUE	FALSE	FALSE	FALSE
4	TRUE	FALSE	TRUE	TRUE	FALSE	FALSE	FALSE
5	TRUE	TRUE	TRUE	TRUE	FALSE	FALSE	FALSE
6	TRUE	TRUE	TRUE	TRUE	FALSE	TRUE	FALSE
7	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	FALSE
8	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE	TRUE

8.8 Models Worth Considering?

k	Predictors	Reason
4	lcavol lweight svi_f	minimizes BIC, AIC _c
7	+ age bph_f gleason_f	C_p near p
8	+ lcp	max R^2_{adj}

8.9 Compare these candidate models in-sample?

8.9.1 Using anova to compare nested models

Let's run an ANOVA-based comparison of these nested models to each other and to the model with the intercept alone.

- The models are **nested** because m04 is a subset of the predictors in m07, which includes a subset of the predictors in m08.

```
m.int <- lm(lpsa ~ 1, data = prost)
m04 <- lm(lpsa ~ lcavol + lweight + svi_f, data = prost)
m07 <- lm(lpsa ~ lcavol + lweight + svi_f +
          age + bph_f + gleason_f, data = prost)
m08 <- lm(lpsa ~ lcavol + lweight + svi_f +
```

```

      age + bph_f + gleason_f + lcp, data = prost)
m.full1 <- lm(lpsa ~ lcavol + lweight + svi_f +
      age + bph_f + gleason_f + lcp + pgg45, data = prost)

```

Next, we'll run...

```
anova(m.full, m08, m07, m04, m.int)
```

Analysis of Variance Table

Model 1: lpsa ~ lcavol + lweight + svi_f + age + bph_f + gleason_f + lcp +
pgg45

Model 2: lpsa ~ lcavol + lweight + svi_f + age + bph_f + gleason_f + lcp

Model 3: lpsa ~ lcavol + lweight + svi_f + age + bph_f + gleason_f

Model 4: lpsa ~ lcavol + lweight + svi_f

Model 5: lpsa ~ 1

	Res.Df	RSS	Df	Sum of Sq	F	Pr(>F)
1	86	41.057				
2	87	41.498	-1	-0.441	0.9234	0.3393
3	88	42.066	-1	-0.568	1.1891	0.2786
4	93	46.568	-5	-4.503	1.8863	0.1050
5	96	127.918	-3	-81.349	56.7991	<2e-16 ***

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

What conclusions can we draw here, on the basis of these ANOVA tests?

- The first p value, of 0.3393, compares what the `anova` called Model 1, and what we call `m.full` to what the `anova` called Model 2, and what we call `m08`. So there's no significant decline in predictive value observed when we drop from the `m.full` model to the `m08` model. This suggests that the `m08` model may be a better choice.
- The second p value, of 0.2786, compares `m08` to `m07`, and suggests that we lose no significant predictive value by dropping down to `m07`.
- The third p value, of 0.1050, compares `m07` to `m04`, and suggests that we lose no significant predictive value by dropping down to `m04`.
- But the fourth p value, of $2e-16$ (or, functionally, zero), compares `m04` to `m.int` and suggests that we do gain significant predictive value by including the predictors in `m04` as compared to a model with an intercept alone.
- So, by the significance tests, the model we'd select would be `m04`, but, of course, in-sample statistical significance alone isn't a good enough reason to select a model if we want to do prediction well.

8.10 AIC and BIC comparisons, within the training sample

Next, we'll compare the three candidate models (ignoring the intercept-only and kitchen sink models) in terms of their AIC values and BIC values, again using the same sample we used to fit the models in the first place.

```
AIC(m04, m07, m08)
```

	df	AIC
m04	5	214.0966
m07	10	214.2327
m08	11	214.9148

```
BIC(m04, m07, m08)
```

```

      df      BIC
m04  5 226.9702
m07 10 239.9798
m08 11 243.2366

```

- The model with the smallest AIC value shows the best performance within the sample on that measure.
- Similarly, smaller BIC values are associated with predictor sets that perform better in sample on that criterion.
- BIC often suggests smaller models (with fewer regression inputs) than does AIC. Does that happen in this case?
- Note that AIC and BIC can be calculated in a few different ways, so we may see some variation if we don't compare apples to apples with regard to the R functions involved.

8.11 Cross-Validation of Candidate Models out of Sample

8.11.1 20-fold Cross-Validation of model m04

Model m04 uses `lcavol`, `lweight` and `svi_f` to predict the `lpsa` outcome. Let's do 20-fold cross-validation of this modeling approach, and calculate the root mean squared prediction error and the mean absolute prediction error for that modeling scheme.

```

set.seed(43201)

cv_m04 <- prost %>%
  crossv_kfold(k = 20) %>%
  mutate(model = map(train,
    ~ lm(lpsa ~ lcavol + lweight + svi_f,
      data = .)))

cv_m04_pred <- cv_m04 %>%
  unnest(map2(model, test, ~ augment(.x, newdata = .y)))

cv_m04_results <- cv_m04_pred %>%
  summarize(Model = "m04",
    RMSE = sqrt(mean((lpsa - .fitted) ^ 2)),
    MAE = mean(abs(lpsa - .fitted)))

cv_m04_results

# A tibble: 1 x 3
  Model RMSE MAE
  <chr> <dbl> <dbl>
1 m04  0.725 0.574

```

8.11.2 20-fold Cross-Validation of model m07

Model m07 uses `lcavol`, `lweight`, `svi_f`, `age`, `bph_f`, and `gleason_f` to predict the `lpsa` outcome. Let's now do 20-fold cross-validation of this modeling approach, and calculate the root mean squared prediction error and the mean absolute prediction error for that modeling scheme. Note the small changes required, as compared to our cross-validation of model m04 a moment ago.

```

set.seed(43202)

cv_m07 <- prost %>%

```

```

crossv_kfold(k = 20) %>%
mutate(model = map(train,
  ~ lm(lpsa ~ lcavol + lweight +
        svi_f + age + bph_f +
        gleason_f,
        data = .)))

cv_m07_pred <- cv_m07 %>%
  unnest(map2(model, test, ~ augment(.x, newdata = .y)))

cv_m07_results <- cv_m07_pred %>%
  summarize(Model = "m07",
    RMSE = sqrt(mean((lpsa - .fitted) ^2)),
    MAE = mean(abs(lpsa - .fitted)))

cv_m07_results

# A tibble: 1 x 3
  Model RMSE MAE
  <chr> <dbl> <dbl>
1 m07   0.730 0.556

```

8.11.3 20-fold Cross-Validation of model m08

Model m08 uses lcavol, lweight, svi_f, age, bph_f, gleason_f and lcp to predict the lpsa outcome. Let's now do 20-fold cross-validation of this modeling approach.

```

set.seed(43202)

cv_m08 <- prost %>%
  crossv_kfold(k = 20) %>%
  mutate(model = map(train,
    ~ lm(lpsa ~ lcavol + lweight +
          svi_f + age + bph_f +
          gleason_f + lcp,
          data = .)))

cv_m08_pred <- cv_m08 %>%
  unnest(map2(model, test, ~ augment(.x, newdata = .y)))

cv_m08_results <- cv_m08_pred %>%
  summarize(Model = "m08",
    RMSE = sqrt(mean((lpsa - .fitted) ^2)),
    MAE = mean(abs(lpsa - .fitted)))

cv_m08_results

# A tibble: 1 x 3
  Model RMSE MAE
  <chr> <dbl> <dbl>
1 m08   0.729 0.557

```

8.11.4 Comparing the Results of the Cross-Validations

```
bind_rows(cv_m04_results, cv_m07_results, cv_m08_results)
```

```
# A tibble: 3 x 3  
  Model  RMSE  MAE  
  <chr> <dbl> <dbl>  
1 m04   0.725 0.574  
2 m07   0.730 0.556  
3 m08   0.729 0.557
```

It appears that model `m04` has the smallest RMSE and MAE in this case. So, that's the model with the strongest cross-validated predictive accuracy, by these two standards.

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