Models

In-class questions: 2/29/2016

We're going to try something new today. If you have small technical questions during class, go to this link and ask away.

Statistical Models

"All models are wrong, but some are useful" -George E. P. Box

When we see a confidence interval or p-value, it means a probability distribution of some sort was used to quantify the null hypothesis. Many times deciding which probability distribution to use is relatively straightforward. For example, when betting on black on roulette we can use simple probability calculations to determine probability distribution of winnings.

The CLT is backed by theoretical results that guarantee that the approximation is accurate. However, we cannot always use this approximation, such as when our sample size is too small. Previously, we described how the sample average can be approximated as t-distributed when the population data is approximately normal. However, there is no theoretical backing for this assumption. We are now *modeling*. In the case of height, we know from experience that this turns out to be a very good model.

But this does not imply that every dataset we collect will follow a normal distribution. An examples are US incomes. The normal distribution is not the only parametric distribution that is available for modeling. Here we provide a very brief introduction to some of the most widely used parametric distributions and some of their uses in the life sciences. We focus on the models and concepts needed to understand the techniques currently used to perform statistical inference on high-throughput data. To do this we also need to introduce the basics of Bayesian statistics. For more in depth description of probability models and parametric distributions please consult a Statistics textbook such as this one.

Linear Models

We have implicitly been using a very simple linear models. We have been trying to predict a fixed parameter by taking samples. For example we have tried to estimate the probability of tossing a coin and observing a head, the proportion of blue beads in a jar, the average height of a population, and the difference in the proportion of votes two candidates, for example Obama and Romney , will receive. Here we will us general notation and represent the parameter we are trying to estimate with θ.

We then obtain draws from a sampling model. We will denote the observed values with Y and use indexes to denote the fact that we make, say, N observations:

$$Y_i = \theta + \varepsilon_i, i = 1, \ldots N$$

Each observation has an *error* term ε. We assume that the expected value of the error is 0 and very often assume that the standard deviation is constant σ.

Let's consider some simple examples

Assessment 1: http://goo.gl/forms/xN35fstJky This is a contrived example, but it will help us understand how we think about models and can use them in many situations.

If we are betting on black on roulette, we can let Y_i be either -1 or 1. Now what is θ and what is the distribution of our error? What is the standard deviation of the errors? Hint: the expected value of the error must be 0.

Answer: Our parameter is $\theta = -1/19$ and our errors are $1 - \theta$ with probability $9/19$ and $-1 - \theta$ with probability $10/19$.

Double check that the expected value is 0:

```
20/19 * 9/19 - 18/19*10/19
```

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

The standard deviation we know is $2\sqrt{9/19 \times 10/19}$. We can double check with a Monte Carlo

```
B <- 10^5
theta = -1/19
Y <- sample( c(-1,1), B, replace=TRUE, prob=c(10/19, 9/19))
error <- Y - theta
prop.table(table(error))
```

```
## error
## -0.947368421052632   1.05263157894737
##            0.52861            0.47139
```

```
sqrt(mean(error^2))
```

```
## [1] 0.9983721
```

```
2*sqrt(10/19*9/19)
```

```
## [1] 0.998614
```

Assessment 2: **http://goo.gl/forms/XLQQh69MUO** Let's consider the example of a demographer trying to estimate the average height of a population. We use the heights stored in R:

```
data("father.son", package="UsingR")
y <- father.son$sheight
```

If we now take a sample

```
set.seed(1)
Y <- sample(y, 25, replace = TRUE)
```

What are θ, N, and ε_1 ?

```
## N is
length(Y)
```

```
## [1] 25
```

```
## theta is
theta <- mean(y)
## the firest error is
error_1 <- Y[1] - theta
```

Assessment 3: **http://goo.gl/forms/CfamwJBctA** Note that in this example each individual in the population has an *error*. It may sound a bit strange but, if you are 1 inch taller than the average height, we call it an "error" of 1 inch. Compute all the errors for the population and explore the distribution. What is the standard deviation of this distribution?

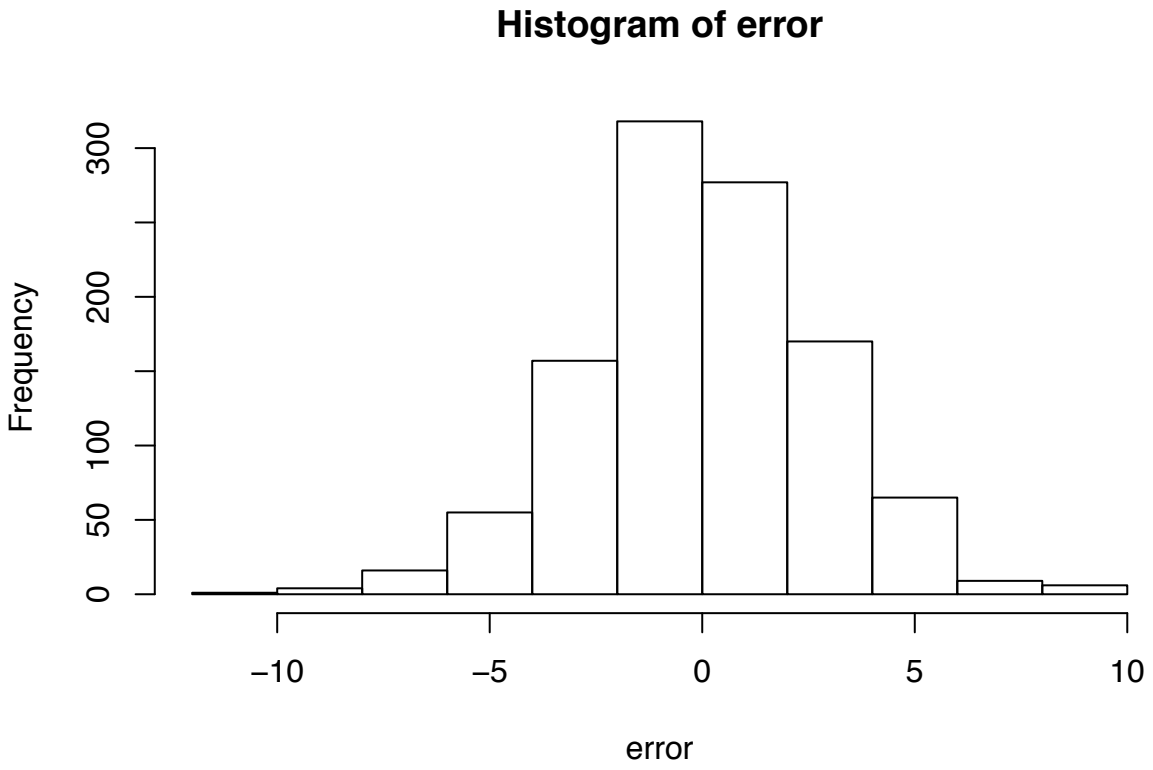
A) Exactly normal with σ of about 3 inches

B) Approximately normal with σ of about 3 inches. Tails are slightly larger.

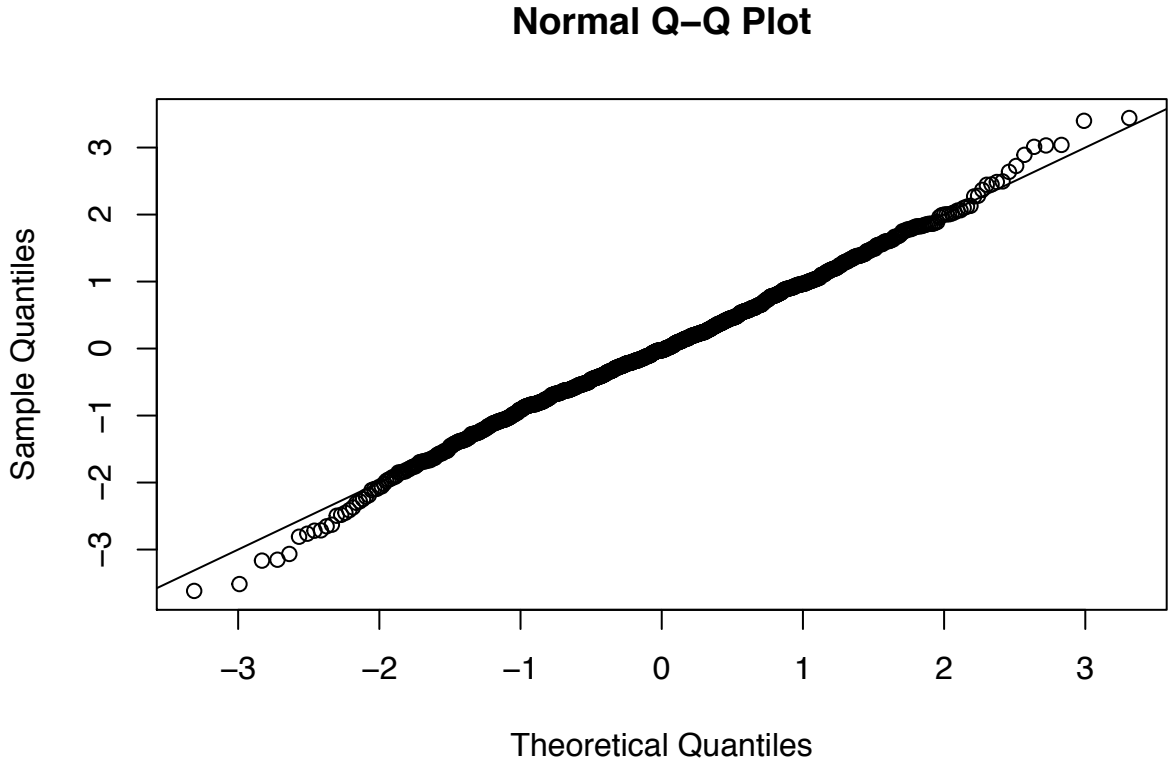
C) These are not averages or sums so it is not approximately normal.

D) Approximately normal with σ of about 9 inches. Tails are slightly larger.

```
error <- y - mean(y)
hist(error)
```




```
##the standard error is:
sigma <- sqrt( mean( (error)^2 ))
qqnorm(error/sigma)
abline(0,1)
```



Modeling Poll Results

Let's start by looking at our guess-the-percent-of-blue-beads competition data. Let's use the code from the previous section:

```
library(readr)
library(dplyr)

filename <- "https://raw.githubusercontent.com/datasciencelabs/data/master/blue-bead-com
tab <- read_csv(filename)
names(tab)<-c("timestamp", "name", "estimate","poll_sample_size","ci")
tab <- mutate(tab,estimate=ifelse(estimate<1, estimate*100, estimate)) %>%
  filter(estimate>20)
```

A total of 27 people used a sample size of about 100.

```
filter( tab, abs(poll_sample_size-100)<51) %>% nrow
```

```
## [1] 27
```

Very important: do not confuse the poll sample size with the number of observations in our model. Here each poll is an observation: $N = 27$ while the poll sizes are about 100.

Let's consider only those polls:

```
tab <- filter(tab, abs(poll_sample_size-100)<51)
```

So we can write a model:

$$Y_i = \theta + \varepsilon_i, i = 1, \ldots, N$$

with $N = 22$.

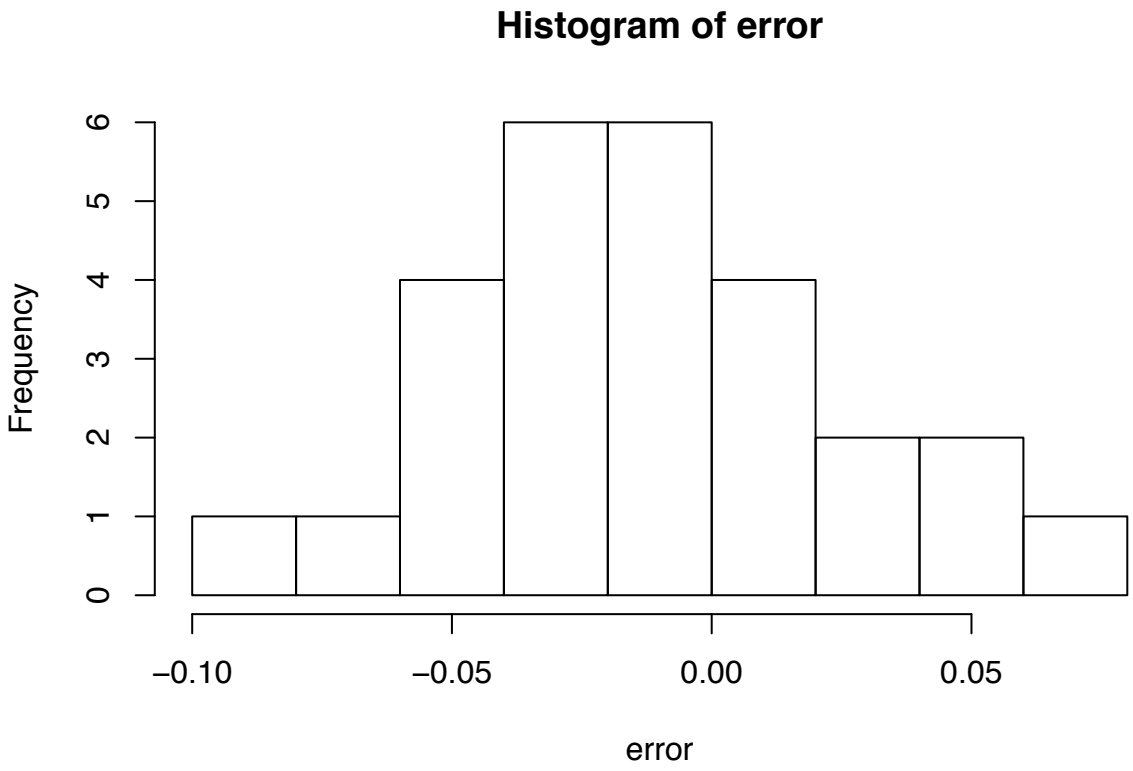
Assessment 4: **http://goo.gl/forms/iyXi76a4b0** Using the CLT theory we have learned, how do we model ε, what is the expected value and standard deviation of ε?

Answer: According to CLT

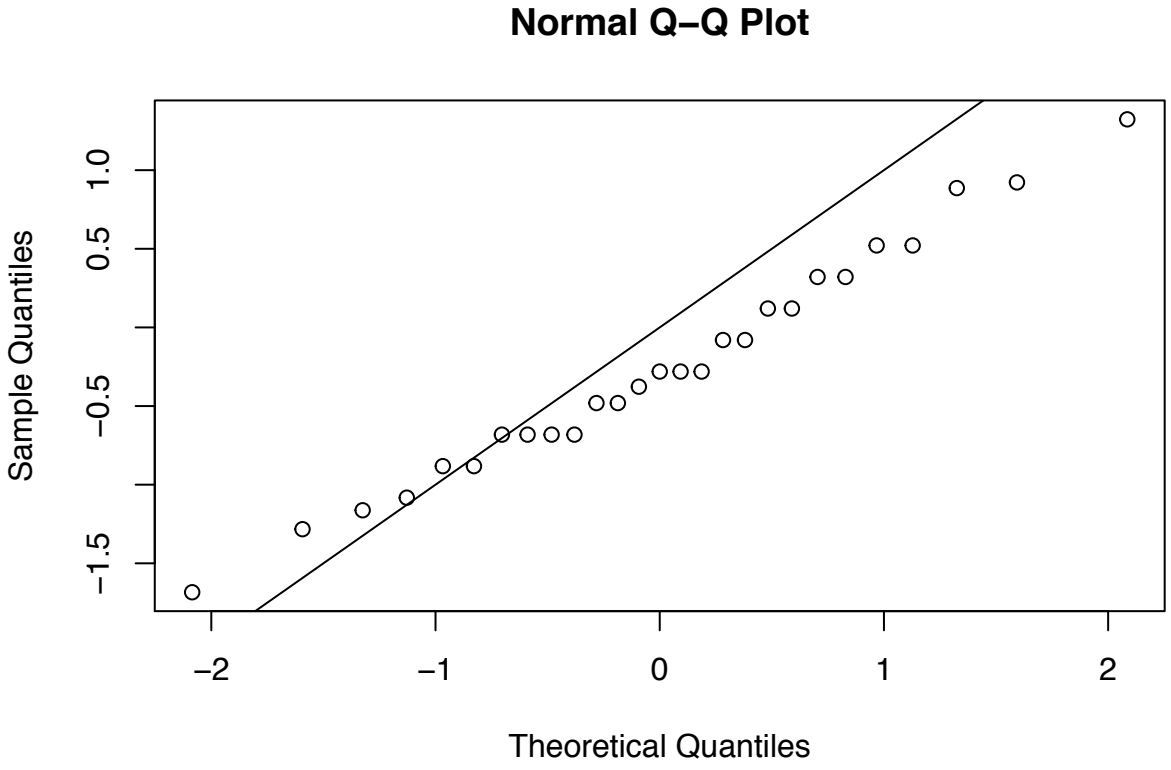
$$\varepsilon \sim \text{Normal}\left(0, \frac{\sqrt{\theta(1-\theta)}}{\sqrt{100}}\right)$$

Assessment 5: **http://goo.gl/forms/0sYp0gFnxZ** We already revealed that $\theta = 0.534$. Use this information and data exploration to check if the model assumptions make sense.

```r
theta <- 0.534
Y <- tab$estimate/100
error <- Y - theta
hist(error)
```




```r
se <- sqrt(theta*(1-theta))/sqrt(100)
qqnorm(error/se)
abline(0,1)
```



Estimating parameters

Earlier we showed how for this particular case we can aggregate results using what amounts to a weighted average. For this particular case, where we have a defensible model we can create an estimate of θ using the standard approach to fitting linear models.

The standard approach is to use the value that that minimizes the least squares equation:

$$\sum_{i=1}^{N}(Y_i - \theta)^2$$

This is called the *least squares estiamte* (LSE). In this case is easy to show, with Calculus, that it is the sample average:

$$\hat{\theta} = \frac{1}{N}\sum_{i=1}^{N} Y_i = \bar{Y}$$

Because this is a sample average from a sampling model we know its expectation is θ and it's standard error is $\sigma/\sqrt{N}$ with N the number of observations and σ the standard deviation of the distribution of ε. But what is σ?

In this particular case statistical theory tells us that σ should be:

$$\frac{\sqrt{\theta(1-\theta)}}{\sqrt{100}}$$

And this is extremely useful when we just have one poll. However, with many polls we can also use the data to estimate σ. The typical strategy is to use the the sample standard deviation:

$$s = \sqrt{\frac{1}{N-1}\sum_{i=1}^{N}(Y_i - \bar{Y})^2}$$

We can compare this empirical approach to the more theoretical approach we have been using:

```
theta <- mean(y)
sd(Y) ##compared to
```

```
## [1] 0.03611641
```

```
sqrt(theta*(1-theta))/sqrt(100) ##or to
```

```
## Warning in sqrt(theta * (1 - theta)): NaNs produced
```

```
## [1] NaN
```

```
theta_hat <- mean(Y)
sqrt(theta_hat*(1-theta_hat))/sqrt(100) ##or to
```

```
## [1] 0.04995551
```

Even if we didn't know these data came from individual polls we can still see that our model works rather well. Here is a confidence interval build with just the data, not using sampling theory for the polls:

```
theta_hat <- mean(Y)
s <- sd(Y)
## confidence interval:
theta_hat + c(-1,1)*qnorm(0.975)*s/sqrt(length(Y))
```

```
## [1] 0.5074660 0.5347118
```

Here it is slightly more appropriate to use the t-distribution approximation:

```
## or using the t-distribution
theta_hat + c(-1,1)*qt(0.975, df=length(Y)-1)*s/sqrt(length(Y))
```

```
## [1] 0.5068017 0.5353761
```

Note that this is a somewhat artificial experiment. The data were generated from a model we constructed. Let's see what happens when we try these models "in the wild".

The 2008 Presidential Elections

We are going to use the 2008 presidential election as an example. To obtain the data we are going to scrape this web site.

Scrapping data from URLs

Data often appears in tables on the web. These are typically HTML pages. From looking at the code for these pages you can see that tables follow a specific format which implies we can write computer programs to extract the data. For *markdown languages* (ML) such as HTML the `XML` package is quite useful. The function `readHTMLTable` specifically targets tables.

```
library(XML)
```

```
## Loading required package: methods
```

```
theurl <- paste0("http://www.pollster.com/08USPresGEMvO-2.html")
html_tables <- readHTMLTable(theurl,stringsAsFactors=FALSE)
```

This produces a list and the components are tables. If we look at this object we see that the first and only table is the one we are after:

```
tab <- html_tables[[1]]
```

We want to have access to the dates of the polls. Take a look at how the save dates:

```
head(tab$Dates)
```

```
## [1] "11/3/08"   "11/2-3/08" "11/1-3/08" "11/1-3/08" "11/1-3/08" "11/1-3/08"
```

We are going to need some serious wrangling here. We will learn a couple of useful functions first.

Wrangling Dates

The `tidyr`, `stringr` and `lubridate` packages include powerful tools for dealing with dates.

```
library(dplyr)
library(tidyr)
library(stringr)
library(lubridate)
```

Let's go step-by-step:

```
##use separate to split start and end dates
### we convert it to a dplyr table:
tab <- tbl_df(tab)
tab <- tab %>% separate(col=Dates, into=c("start_date","end_date"), sep="-",
                        fill="right")
select(tab, start_date, end_date)
```

```
## Source: local data frame [543 x 2]
##
##    start_date end_date
##         (chr)    (chr)
## 1     11/3/08       NA
## 2        11/2     3/08
## 3        11/1     3/08
## 4        11/1     3/08
## 5        11/1     3/08
## 6        11/1     3/08
## 7       10/31  11/3/08
## 8       10/30  11/3/08
## 9     11/2/08       NA
## 10       11/1     2/08
## ..        ...      ...
```

```
## if no end_data it means only one day was provided so use that as end as well
tab <- tab %>% mutate(end_date = ifelse(is.na(end_date), start_date, end_date))
select(tab, start_date, end_date)
```

```
## Source: local data frame [543 x 2]
##
##    start_date end_date
##         (chr)    (chr)
## 1     11/3/08  11/3/08
```

```
## 2        11/2     3/08
## 3        11/1     3/08
## 4        11/1     3/08
## 5        11/1     3/08
## 6        11/1     3/08
## 7       10/31  11/3/08
## 8       10/30  11/3/08
## 9     11/2/08  11/2/08
## 10       11/1     2/08
## ..        ...      ...
```

```
## no use seprate again to get month, day and year for start_date
tab <- tab %>% separate(start_date, c("smonth", "sday", "syear"), sep = "/",
                        convert = TRUE, fill = "right")
select(tab, smonth:syear, end_date)
```

```
## Source: local data frame [543 x 4]
##
##    smonth  sday syear end_date
##     (int) (int) (int)    (chr)
## 1      11     3     8  11/3/08
## 2      11     2    NA     3/08
## 3      11     1    NA     3/08
## 4      11     1    NA     3/08
## 5      11     1    NA     3/08
## 6      11     1    NA     3/08
## 7      10    31    NA  11/3/08
## 8      10    30    NA  11/3/08
## 9      11     2     8  11/2/08
## 10     11     1    NA     2/08
## ..    ...   ...   ...      ...
```

```
### if end data has only 1 / then it is missing month, add it
tab <- tab %>% mutate(end_date = ifelse(str_count(end_date, "/") == 1,
                                        paste(smonth, end_date, sep = "/"), end_date))
select(tab, smonth:syear, end_date)
```

```
## Source: local data frame [543 x 4]
##
##    smonth  sday syear end_date
##     (int) (int) (int)    (chr)
## 1      11     3     8  11/3/08
## 2      11     2    NA  11/3/08
```

```
## 3      11     1    NA  11/3/08
## 4      11     1    NA  11/3/08
## 5      11     1    NA  11/3/08
## 6      11     1    NA  11/3/08
## 7      10    31    NA  11/3/08
## 8      10    30    NA  11/3/08
## 9      11     2     8  11/2/08
## 10     11     1    NA  11/2/08
## ..    ...   ...   ...      ...
```

```
## now use lubridate function mdy to conver to date
tab <- tab %>% mutate(end_date = mdy(end_date))
select(tab, smonth:syear, end_date)
```

```
## Source: local data frame [543 x 4]
##
##    smonth  sday syear   end_date
##     (int) (int) (int)     (time)
## 1      11     3     8 2008-11-03
## 2      11     2    NA 2008-11-03
## 3      11     1    NA 2008-11-03
## 4      11     1    NA 2008-11-03
## 5      11     1    NA 2008-11-03
## 6      11     1    NA 2008-11-03
## 7      10    31    NA 2008-11-03
## 8      10    30    NA 2008-11-03
## 9      11     2     8 2008-11-02
## 10     11     1    NA 2008-11-02
## ..    ...   ...   ...        ...
```

```
## add 2000 to year since it is currently 7 or 8
tab <- tab %>% mutate(syear = ifelse(is.na(syear), year(end_date), syear + 2000))
select(tab, smonth:syear, end_date)
```

```
## Source: local data frame [543 x 4]
##
##    smonth  sday syear   end_date
##     (int) (int) (dbl)     (time)
## 1      11     3  2008 2008-11-03
## 2      11     2  2008 2008-11-03
## 3      11     1  2008 2008-11-03
## 4      11     1  2008 2008-11-03
## 5      11     1  2008 2008-11-03
```

```
## 6      11     1  2008 2008-11-03
## 7      10    31  2008 2008-11-03
## 8      10    30  2008 2008-11-03
## 9      11     2  2008 2008-11-02
## 10     11     1  2008 2008-11-02
## ..    ...   ...   ...        ...
```

```
## now use unite to create a m/d/y string
tab <- tab %>% unite(start_date, smonth, sday, syear)
select(tab, start_date, end_date)
```

```
## Source: local data frame [543 x 2]
##
##    start_date   end_date
##         (chr)     (time)
## 1   11_3_2008 2008-11-03
## 2   11_2_2008 2008-11-03
## 3   11_1_2008 2008-11-03
## 4   11_1_2008 2008-11-03
## 5   11_1_2008 2008-11-03
## 6   11_1_2008 2008-11-03
## 7  10_31_2008 2008-11-03
## 8  10_30_2008 2008-11-03
## 9   11_2_2008 2008-11-02
## 10  11_1_2008 2008-11-02
## ..        ...        ...
```

```
## covert it to date class
tab <- tab %>% mutate(start_date = mdy(start_date))
select(tab, start_date, end_date)
```

```
## Source: local data frame [543 x 2]
##
##    start_date   end_date
##        (time)     (time)
## 1  2008-11-03 2008-11-03
## 2  2008-11-02 2008-11-03
## 3  2008-11-01 2008-11-03
## 4  2008-11-01 2008-11-03
## 5  2008-11-01 2008-11-03
## 6  2008-11-01 2008-11-03
## 7  2008-10-31 2008-11-03
## 8  2008-10-30 2008-11-03
```

```
## 9  2008-11-02 2008-11-02
## 10 2008-11-01 2008-11-02
## ..         ...         ...
```

Note: we don't have to go step by step. Instead rewrite the above as a series of pipes.

Extracting population size and type of poll If we wanted to know the sample size of the polls we look here:

```
head(tab$`N/Pop`)
```

```
## [1] "804 LV"  "400 LV"  "1100 LV" "981 LV"  "3000 LV" "1200 LV"
```

This column combines the sample size with the type population used by the poll. For example, LV means Likely Voters. We can use split again.

```
tab <- separate(tab, `N/Pop`, into=c("N","population_type"), sep="\ ", convert=TRUE, fil
```

Adding Columns We will add a couple more columns for what we are doing: the Obama - McCAin difference, the days left before the election and the weeks left before the election:

```
tab <- mutate(tab, Obama = as.numeric(Obama)/100,
              McCain=as.numeric(McCain)/100,
              diff = Obama - McCain,
              day=as.numeric(start_date - mdy("11/04/2008")),
              week = as.numeric(floor(day/7)))
```

Modeling Poll Results (continued)

Now consider all the polls of sample size 800. There are

```
filter(tab, N==800) %>% nrow
```

```
## [1] 22
```

of these. So we can write a model:

$$Y_i = \theta + \varepsilon_i, i = 1, \ldots, N$$

with $N = 22$.

Assessment 6: **http://goo.gl/forms/BYmGozyUYX** Using the CLT theory we have learned, how do we model ε, what is the expected value and standard deviation of ε?

Assessment 7: **http://goo.gl/forms/ZAbd1crfK3** Use data exploration to check if the model assumptions make sense. Note that we have the benefit of hindsight. The election night result was $\theta = 52.9 - 45.7 = 7.2$.

A. The data are approximately normal with the expected value and standard error as predicted.

B. The expected value and standard error as predicted, but the data is not normal

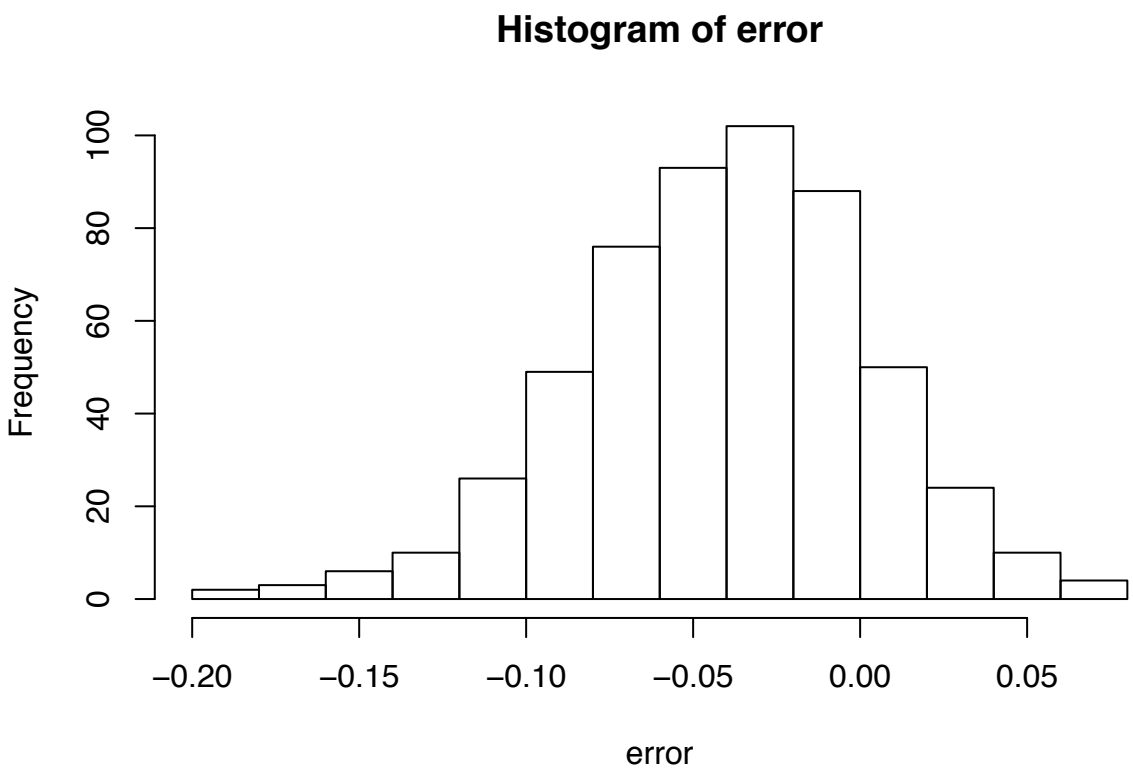
C. The data look approximately normal but the expected and standard error are not what the theory predicts

D. I have no idea what to do.

Explaining variance

In general we can see that the errors are not centered at 0 and have a much larger variability than expected:

```
error <- tab$diff - 7.2/100
hist(error)
```



What could explain this variability?

The first thing that comes to mind is that we polls are taken for over a year and the θ six months before the election might be different.

Assessment 8: **http://goo.gl/forms/GVpfbBu7V5** Use ggplot to make a plot of the estimated difference versus day. What do you observe? Just form looking at the plot what would you say is that standard deviation of θ if we let it change with time?

The SD is at least 5%

Assessment 9: **http://goo.gl/forms/9q5SSXk6iM** Take a look at polls that happened in 2008.

There seems to be clear time effect. We could amend the model to be

$$Y_{t,i} = \theta + w_t + \varepsilon_{t,i}$$

We now have two indexes t denoting week and i an index for the i-th poll during week t.

Smoothing

To estimate the model above, we could go week by week and estimating $\theta_t = \theta + w_t$ separately. Our model for week t would be

$$Y_{t,i} = \theta_t + \varepsilon_{t,i}$$

and we can use the same approach as before. We can compute the estimates using the `group_by` and `summarize` approach.

`group_by` and `summarize` A very common operation performed in data analysis is to stratify data into groups and then obtain a summary statistic, such a mean and standard deviation, from each group. Here we want to group by week. So we simply do the following

```
group_by(tab, week)
```

```
## Source: local data frame [543 x 15]
## Groups: week [72]
##
##                          Pollster start_date   end_date     N
##                             (chr)     (time)     (time) (int)
## 1                  Marist College 2008-11-03 2008-11-03   804
## 2             GWU (Lake/Tarrance) 2008-11-02 2008-11-03   400
## 3  DailyKos.com (D)/Research 2000 2008-11-01 2008-11-03  1100
## 4                        IBD/TIPP 2008-11-01 2008-11-03   981
```

```
## 5                       Rasmussen 2008-11-01 2008-11-03  3000
## 6                             ARG 2008-11-01 2008-11-03  1200
## 7          Reuters/ C-SPAN/ Zogby 2008-10-31 2008-11-03  1226
## 8              Harris Interactive 2008-10-30 2008-11-03  3946
## 9                  Marist College 2008-11-02 2008-11-02   635
## 10                        NBC/WSJ 2008-11-01 2008-11-02    NA
## ..                            ...        ...        ...   ...
## Variables not shown: population_type (chr), McCain (dbl), Obama (dbl),
##   Barr (chr), Nader (chr), Other (chr), Undecided (chr), Margin (chr),
##   diff (dbl), day (dbl), week (dbl)
```

You can see that the 543 polls have been grouped into 72. Once this is done, if you call the `summarize` function it applies a summary to each group:

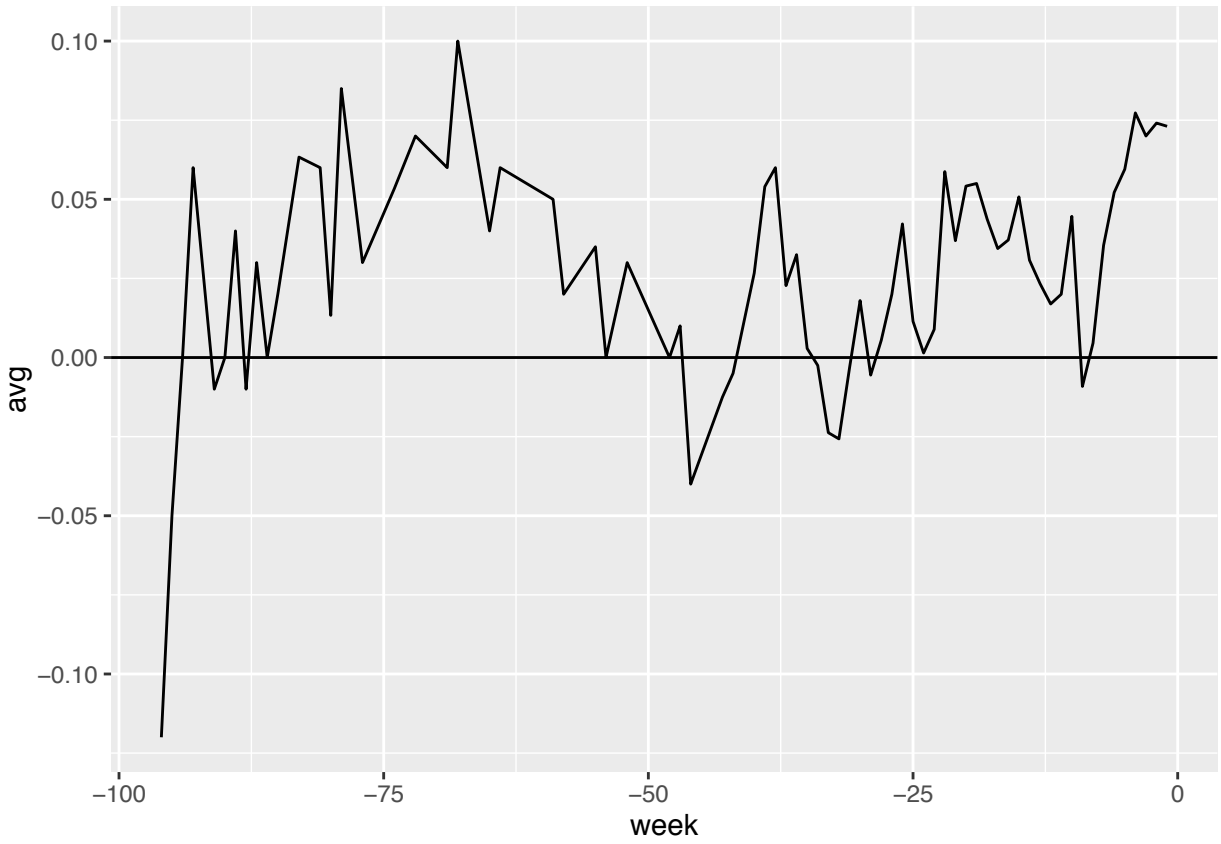
```
group_by(tab, week) %>% summarize(avg=mean(diff))
```

```
## Source: local data frame [72 x 2]
##
##     week           avg
##    (dbl)         (dbl)
## 1    -96 -1.200000e-01
## 2    -95 -5.000000e-02
## 3    -94 -1.387779e-17
## 4    -93  6.000000e-02
## 5    -91 -1.000000e-02
## 6    -90  0.000000e+00
## 7    -89  4.000000e-02
## 8    -88 -1.000000e-02
## 9    -87  3.000000e-02
## 10   -86  0.000000e+00
## ..   ...           ...
```

We can make a quick plot

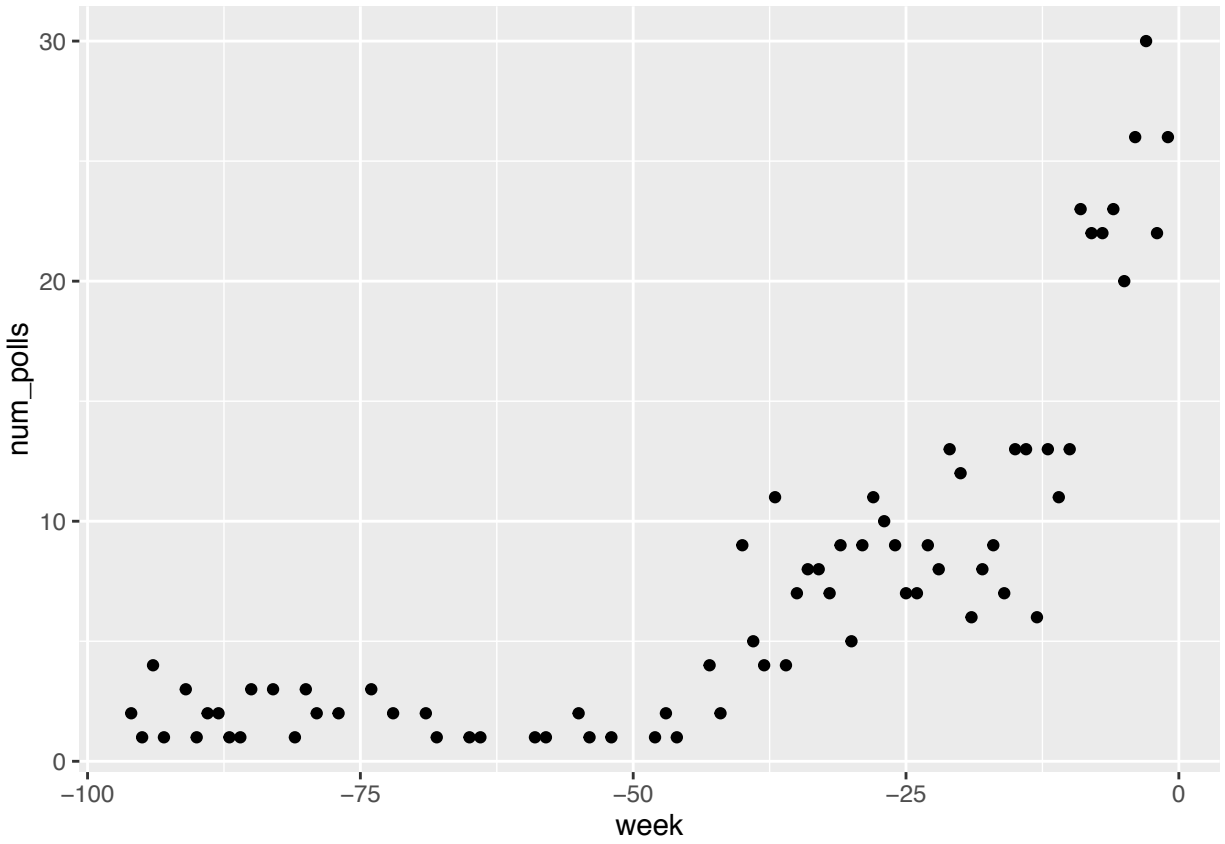
```
library(ggplot2)

group_by(tab, week) %>% summarize(avg=mean(diff)) %>%
  ggplot(aes(week, avg)) + geom_line() +
  geom_hline(aes(yintercept=0))
```



Note that the number of polls per week varies:

```
group_by(tab, week) %>% summarize(num_polls=n()) %>%
  ggplot(aes(week, num_polls)) + geom_point()
```



Supposed we only want to consider weeks in which we had 10 or more polls. We can easily group and count like this. But now the table is summarized. We don't need to summarize it. We can `ungroup` at the end.

```
group_by(tab, week) %>% mutate(num_polls=n()) %>% select(Pollster, num_polls) %>% ungrou
```

```
## Source: local data frame [543 x 3]
##
##     week                        Pollster num_polls
##    (dbl)                           (chr)     (int)
## 1     -1                 Marist College        26
## 2     -1            GWU (Lake/Tarrance)        26
## 3     -1 DailyKos.com (D)/Research 2000        26
## 4     -1                       IBD/TIPP        26
## 5     -1                      Rasmussen        26
## 6     -1                            ARG        26
## 7     -1        Reuters/ C-SPAN/ Zogby        26
## 8     -1            Harris Interactive        26
## 9     -1                Marist College        26
## 10    -1                       NBC/WSJ        26
## ..   ...                           ...       ...
```

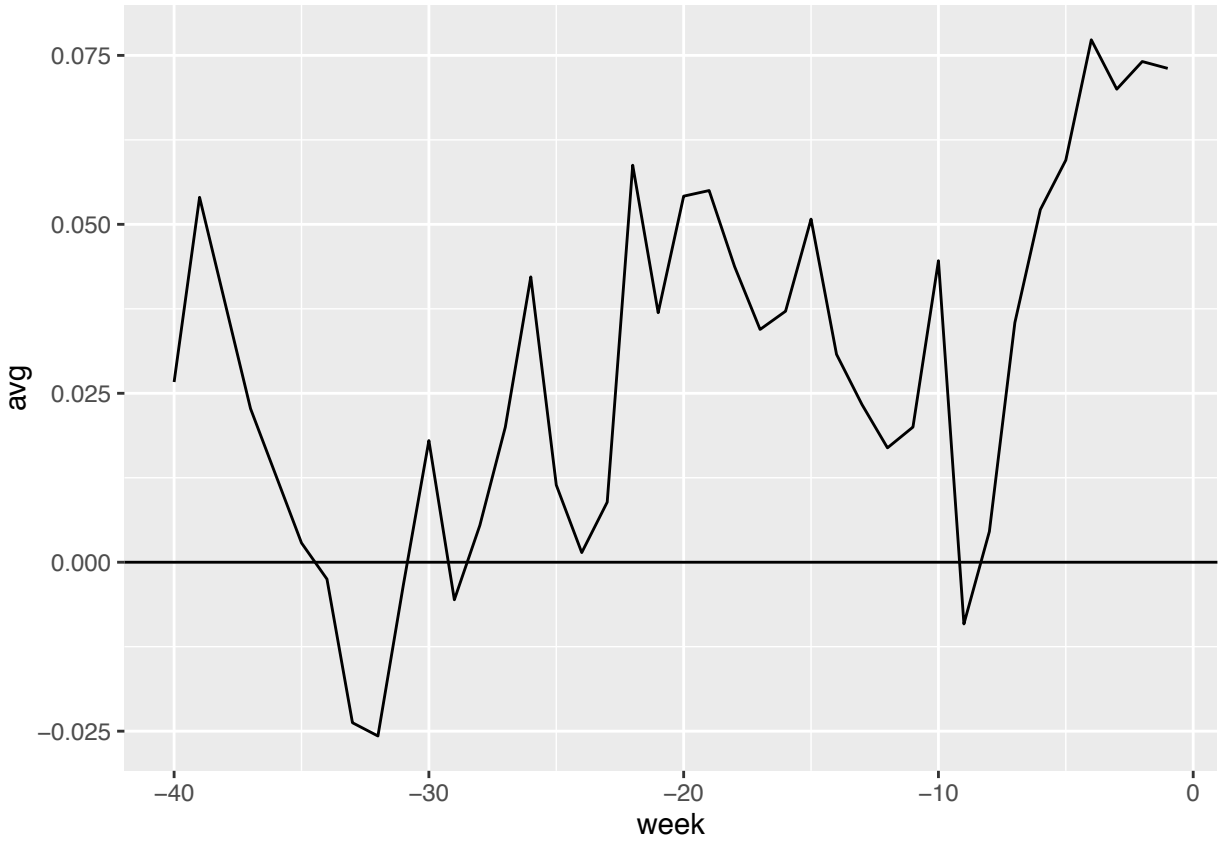
Which means we can use this to filter.

```
group_by(tab, week) %>% mutate(num_polls=n()) %>% select(Pollster, num_polls) %>% filte
```

```
## [1] 334
```

To make the plot for just these we can use:

```
group_by(tab, week) %>% mutate(num_polls=n()) %>%
  filter(num_polls>=5) %>%
  summarize(avg=mean(diff)) %>%
  ggplot(aes(week, avg)) + geom_line() +
  geom_hline(aes(yintercept=0))
```

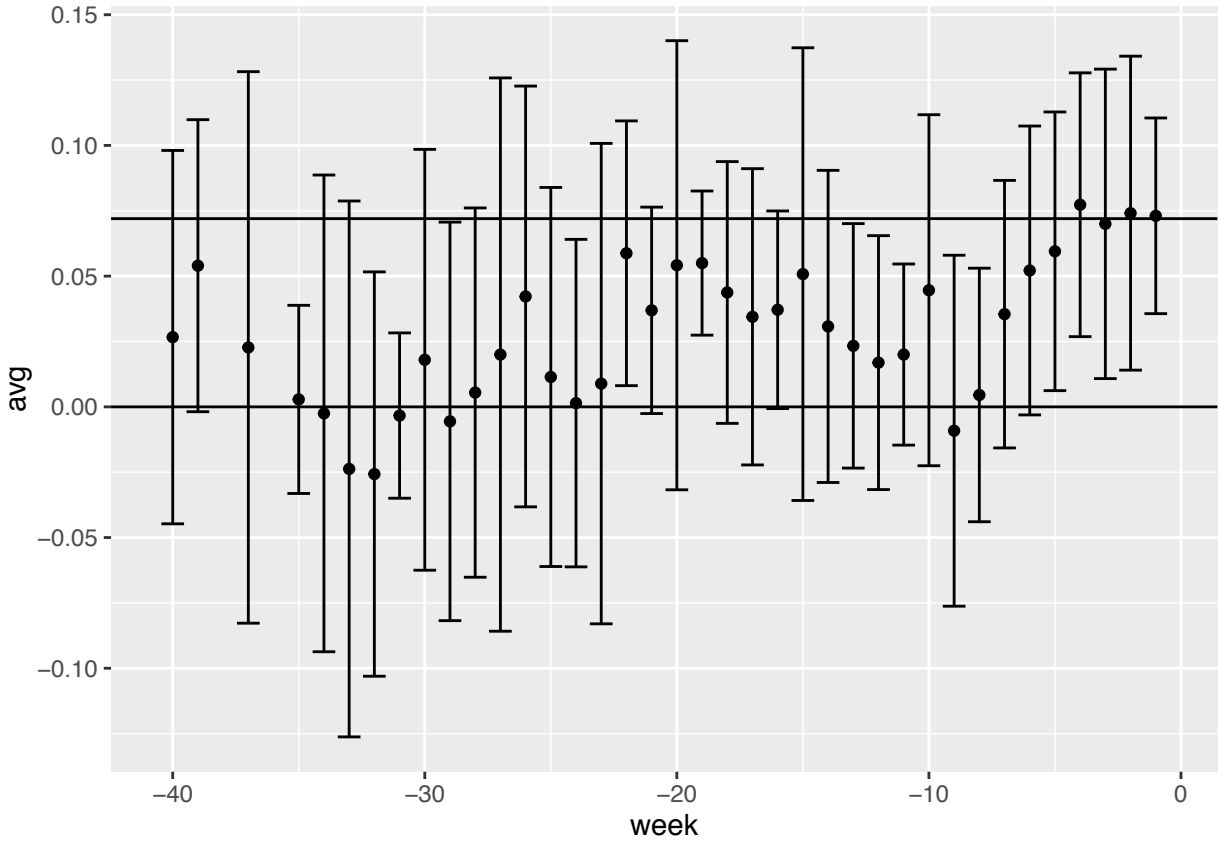


Assessment 10: http://goo.gl/forms/ntaC4r5H7m

Make the same plot to add bars that show 2 SD above and below the average. Answer the questions below.

```
group_by(tab, week) %>% mutate(num_polls=n()) %>%
  filter(num_polls>=5) %>%
  summarize(avg=mean(diff) , sd=sd(diff)) %>%
```

```
ggplot(aes(week, avg, ymin=avg-2*sd, ymax=avg+2*sd)) +
geom_point() + geom_errorbar() +
geom_hline(aes(yintercept=0))+
geom_hline(aes(yintercept=0.072))
```



We saw earlier that as the elections got closer many more plots are conducted. But the plot above does not show the standard deviations decreasing. At least not at the rate of $1/\sqrt{\text{number of polls}}$. Why is this?

A. The standard deviation is decreasing

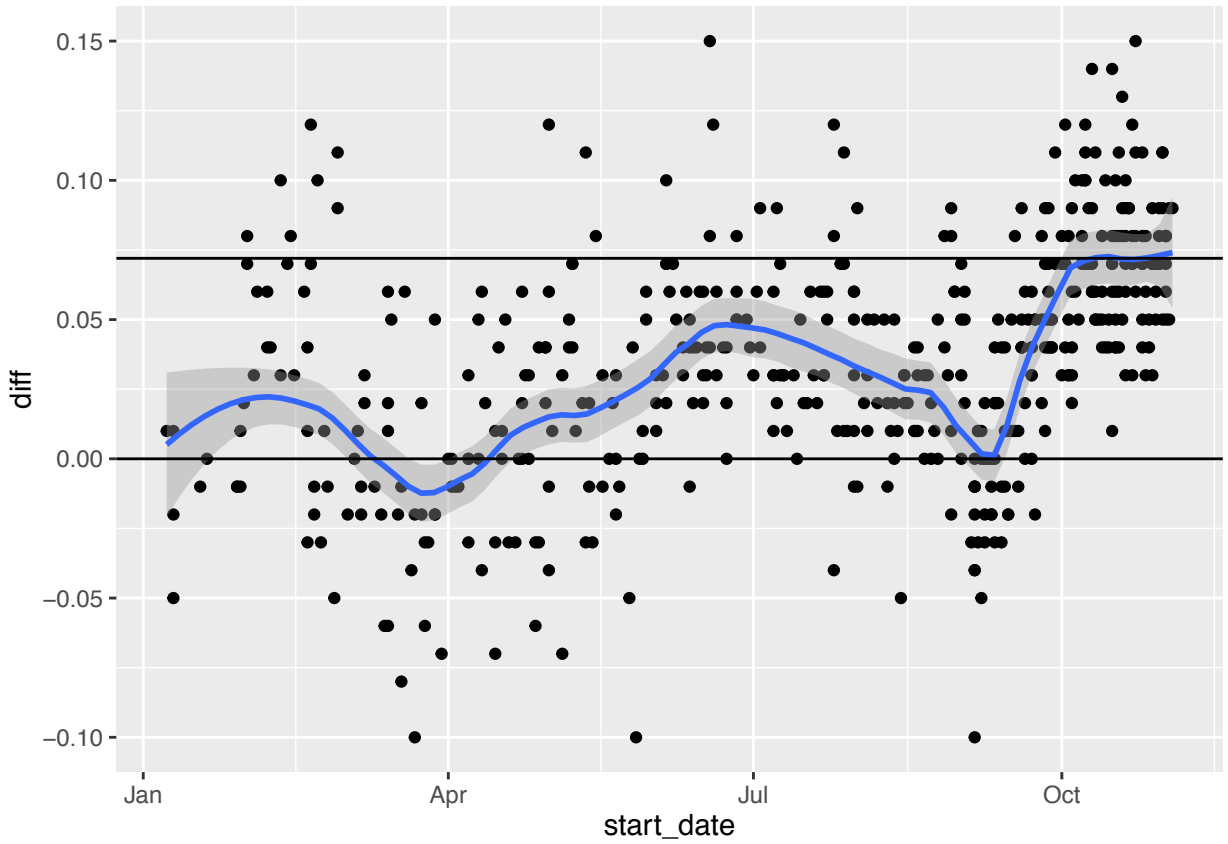
B. The standard deviation relates to the SE of each poll, which depends on poll size not number of polls

C. There is a bug in the code

D. I have no idea.

A similar plot to this can be generated with

```
filter(tab, start_date>"2008-01-01") %>% ggplot(aes(start_date, diff)) + geom_point() +
  geom_hline(aes(yintercept=0.072))
```



House Effect We have seen that there is a strong weekly effect. We saw how we could control it by, for example, stratifying the analysis. We noted that the last couple of weeks provides the original model may be "useful".

$$Y_i = \theta + \varepsilon_i$$

Now if we restrict ourselves to polls with sample sizes larger than 2,000, the the theory tells us that the standard error for the estimate of the percentage for Obama is $\hat{p}$ (notation from previous section) is

$$\sqrt{p(1-p)}/\sqrt{2000}$$

Here we are estimating the difference θ. The estimated is approximated by $\hat{p} - (1-\hat{p}) = 2\hat{p} - 1$. This implies that the standard error is $2\sqrt{p(1-p)}/\sqrt{2000}$.

Because each Y_i a separate poll then the standard deviation of ε should be about $2\sqrt{p(1-p)}/\sqrt{2000}$:

```
2* sqrt(0.5*0.5) / sqrt(2000)
```

```
## [1] 0.02236068
```

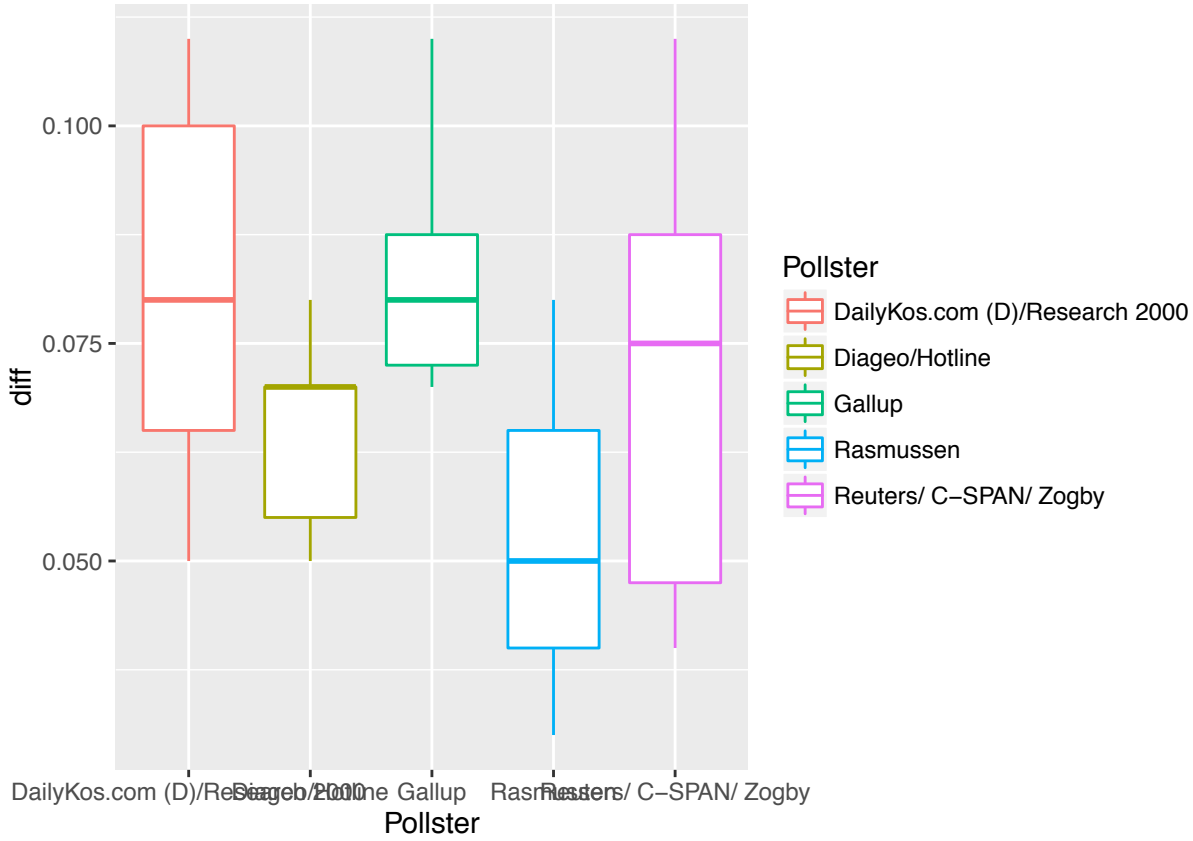
But the observed variance is slightly larger:

```
tab %>% filter( N>2000 & week > -4) %>% summarize(sd(diff))
```

```
## Source: local data frame [1 x 1]
##
##     sd(diff)
##        (dbl)
## 1 0.02624669
```

This could be due to what is referred to as the *house effect*. Note in the plot below how there appears to be a Pollster effect:

```
tab %>% filter(week > -4) %>% group_by(Pollster) %>% filter(n()>4) %>%
  ggplot(aes(Pollster, diff , col=Pollster)) + geom_boxplot()
```



An improved model will include a pollster effect

$$Y_{i,j} = \theta + p_j + \varepsilon_{i,j}$$

with p_j a pollster effect.

In more formal statistics classes you can learn about analysis of variance which does confirm strong week effect and small, but statistical significant, house effect:

```
tab2 <- filter(tab, start_date > "2008-01-01") %>% group_by(Pollster) %>% filter(n() > 1
fit <- lm(diff ~ week + Pollster, data=tab2)
summary( aov(fit) )
```

```
##              Df Sum Sq Mean Sq F value  Pr(>F)
## week          1 0.1458 0.14579 122.478 < 2e-16 ***
## Pollster     14 0.0908 0.00649   5.448 1.9e-09 ***
## Residuals   342 0.4071 0.00119
## ---
## Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Inference

Inference

We are going to have a competition. There is a prize.

You have to guess the proportion of blue beads in the jar. You can take a sample (with replacement) from the jar here:

https://dgrtwo.shinyapps.io/urn_drawing/

Each sample will cost you 10 cents ($0.10). So if you take a sample size of 100 you will have to pay me $10 to collect your prize.

Once you take your sample, please enter your guess, sample size, and an interval size. We will create an interval of this size with your guess in the middle. If the true percentage is not in your interval you are eliminated. The size of the interval will serve as a tie breaker (smaller wins).

http://goo.gl/forms/5bv4cRQWKA

The deadline to enter the competition is Monday February 22, 2016 at 9:00 AM.

Introduction

This chapter introduces the statistical concepts necessary to understand margins of errors, p-values and confidence intervals. These terms are ubiquitous in data science. Let's use polls as an example:

```
##                      pollster diff Obama Romney margin_of_error    n
## 1                      Gallup   -1    48     49            2.00 2551
## 2                   Rasmussen   -1    48     49            3.00 1500
## 3                    Monmouth    0    48     48            2.60 1417
## 4                         ARG    0    49     49            3.00 1200
## 5  Politico/GWU/Battleground    0    47     47            3.10 1000
## 6            Gravis Marketing    0    48     48            3.30  872
## 7                         CNN    0    49     49            3.50  693
## 8                     NBC/WSJ    1    48     47            2.55 1475
## 9                    IBD/TIPP    1    50     49            3.70  712
## 10     DailyKos/SEIU/PPP (D)    2    50     48            2.70 1300
## 11                        PPP    2    50     48            2.80 1200
## 12                        Pew    3    48     45            2.20 2709
## 13                  ABC/Post    3    50     47            2.50 2345
```

What does *margin of error* mean? The first step is define and understand random variables. To do this, we will generate our own imaginary election with 1 million voters of which proportion p are democrats and $1-p$ are republicans. To keep it interesting we will keep generate p at random and not peek.

```
n <- 10^6 ##number of voters
set.seed(1) ##so we all get the same answer
##pick a number between 0.45 and 0.55 (don't peek!):
p <- sample( seq(0.45,0.55,0.001),1)
x <- rep( c("D","R"), n*c( p, 1-p))
x <- sample(x) ##not necessary, but shuffle them
```

The population is now fixed. There is a true proportion p but we don't know it.

One election day we will do the following to decide who wins (don't ruin the fun by doing it now!):

```
prop.table(table(x))
```

Pollsters try to *estimate* p but asking 1 million people and actually unnecessary so instead. They take a poll. To do this they take a random sample. They pick N random voter phone numbers, call, and ask. Assuming everybody answers and every voter has a phone, we can mimic a random sample of 100 people with:

```
poll <- sample(x, 25, replace = TRUE)
```

The pollster then looks at the proportion of democrats in the sample and uses this information to predict p. In Statistics we say try to *estimate* p.

```
table(poll)
```

```
## poll
##  D  R
## 13 12
```

So our poll predicts a democrat win! Is this a good *estiamte*? We will see how powerful mathematical statistics is at informing us about exactly how good it is.

Notation: we use lower case x for the population of all voters and capital letters X for the random sample.

Random Variables

Random variable are outcomes of random process. The number of democrats out of the 25 we picked at random is an example. Let's repeat the exercise above a few times. Let's run a few other polls and see what happens:

```
X <- sample(x, 25, replace = TRUE)
sum( X=="D")
```

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

```
X <- sample(x, 25, replace = TRUE)
sum( X=="D")
```

```
## [1] 15
```

```
X <- sample(x, 25, replace = TRUE)
sum( X=="D")
```

```
## [1] 11
```

Note how the observed number varies. We refer to this as *random* or *chance* variation. How does this random variable relate to our quantity of interest p? Statistical theory has a lot to teach about this and is the main tool used by pollsters and poll aggregators.

Sampling Models

Many procedures studied and used by data scientist can be modeled quite well as a sum of draws from a jar. For example, we modeled the process of polling likely voters as drawing 0s (republicans) and 1s (democrats) from a jar. To be more specific we can turn the `x` into 0s and 1s:

```
x <- as.numeric(x=="D")
sample(x, 25, replace = TRUE)
```

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

Many other examples can be constructed. For example to model our winning after betting $1 on red (on a roulette wheel) 10 times we can use:

```
color <- rep(c("Black","Red","Green"), c(18,18,2))
X <- sample( ifelse( color=="Red", 1,-1),  10, replace = TRUE)
sum(X)
```

```
## [1] 2
```

Because we know the proportions we can do this a bit quicker by simply using:

```
X <- sample( c(-1,1), 10, replace = TRUE, prob=c(10/19, 9/19))
sum(X)
```

```
## [1] -2
```

The Expected Value and Standard Error

Now that we have described sampling models, now we can describe properties of the sum of draws. The first important concept to learn is the *expected value*. The random variable will vary around this expected value. The *standard error* gives us an idea of how the size of the variation around the expected value.

The expected value of the sum of draws is the

$$\text{number of draws} \times \text{average of the numbers in the jar}$$

Using the definition of average:

$$\mu = \frac{1}{n}\sum_{i=1}^{n} x_i$$

We can see that the average of values inside a jar with 0s and 1s is the number of 1s divided by n. This is the proportion of 1s. In general if a jar has two values a and b with proportions p and $(1-p)$ respectively, the average is $ap + b(1-p)$.

Assessment: What are the averages for the roulette examples? - Betting on black - Betting on 7

In our example with the election we know that the average of the box is p, we just don't know what p is just yet.

If our draws are independent, then the standard error of our sum is

$$\sqrt{\text{number of draws}} \times \text{ standard deviation of the numbers in the jar}$$

Using the definition of standard deviation

$$\sigma = \sqrt{\frac{1}{n}\sum_{i}^{n}(x_i - \mu)^2}$$

we can derive, with a bit of math, that if a jar has two values a and b with proportions p and $(1-p)$ respectively, the standard deviation is $\mid b - a \mid \sqrt{p(1-p)}$.

Assessment What are the expected value and standard errors of the number of democrats. Hint: The answers are functions of p, the proportion of democrats.

Let S be the number of democrats in our sample, or the sum of the 25 draws. Our expected value is

$$\mathrm{E}(S) = 25p$$

and standard error is

$$\mathrm{SE}(S) = \sqrt{25p(1-p)}$$

Two more intuitive results. If we divide S by constant, the expected value and standard error are also divided by this constant. This implies that

Now we now that the expected value of the proportion in our sample $S/25$, has expected value p.

$$\mathrm{E}(S/25) = p$$

which implies that $S/25$ will be p plus some chance error.

The SE,

$$\mathrm{SE}(S/25) = \sqrt{p(1-p)}/\sqrt{N}$$

gives us an idea of how large the error is.

We do notice that by making N larger we can make our standard error smaller. The *Law of Large Numbers* tells us that the bigger N the closer the sample average gets to the average of the jar which is the quantity we want to estimate.

Estimates

Because $S/25$ is p plus or minus some chance error we use it as our *estimate* of p. We usually put hats on top of our estimates: $\hat{p}$. We now now that when N is large

$$\hat{p} \approx p$$

.

Suppose that after we take our poll we want to give a best guess for p. One way we could do this is to report the observed value and it's standard error. Unfortunately, we need to know p to report an expected value. It turns out that plugging in the observed proportion, works out pretty well. So we can report:

```
p_hat <- mean(poll=="D")
cat("Our estimate of the percent of decomrats is",p_hat,
    "plus or minus", round( sqrt(p_hat*(1-p_hat)/25), 2))
```

```
## Our estimate of the percent of decomrats is 0.52 plus or minus 0.1
```

Which is not terribly useful. However, now we know that we can be more precise by taking a larger poll.

Assessment If $p = 0.5$, how large should the poll be to have a standard error of 2% or less ? Then take a poll and report expected value and standard error

$$\sqrt{0.25/N} = 0.02$$

implies

$$N = 0.25/0.02^2 = 625$$

.

```
N <- 625
X <- sample(x, N, replace = TRUE)
p_hat <- mean(X)
cat("Our estimate of the percent of decomrats is",p_hat,
    "plus or minus", round( sqrt(p_hat*(1-p_hat)/N), 2))
```

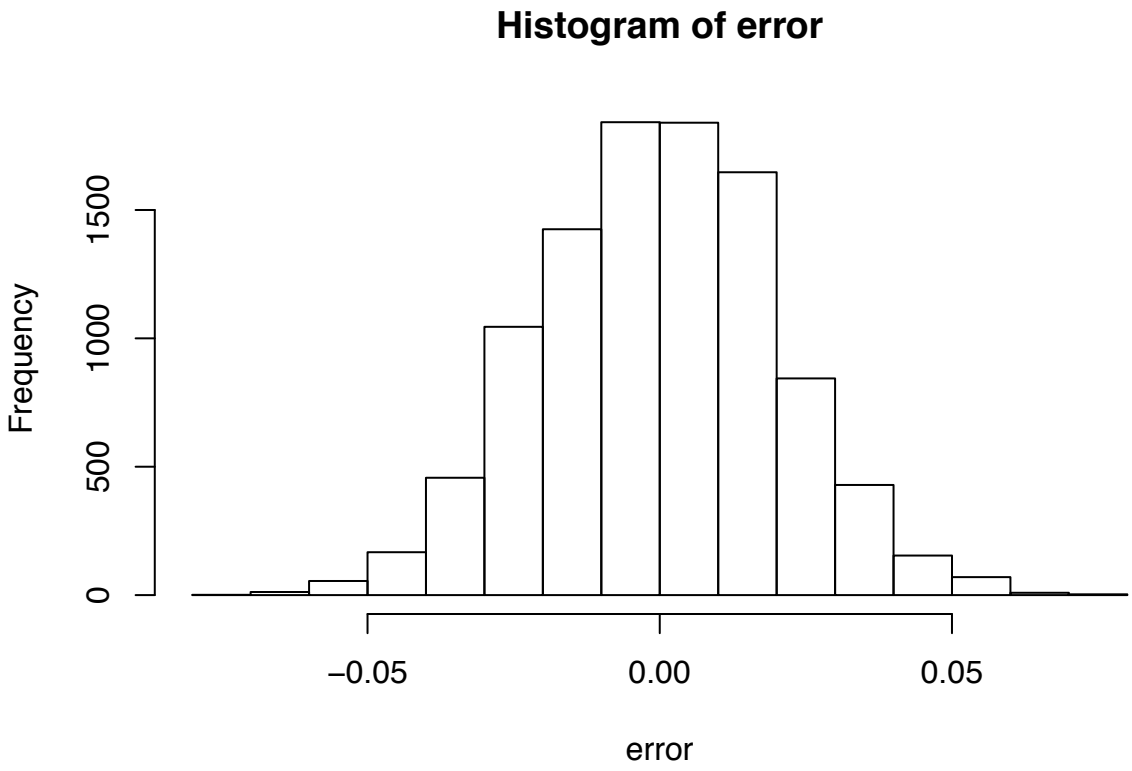
```
## Our estimate of the percent of decomrats is 0.4976 plus or minus 0.02
```

Probability Distribution for Random Variables

The plus or minus statements above are not very precise. Is it possible to say more? Can we, for example, compute the probability that $\hat{p}$ is within 1% of the actual p ? It turns out that we can. First let's start with a Monte Carlo simulation.

Assessment: Repeat the exercise of taking a poll of 625 likely voters, 10,000 times. Without peaking at p study the distribution of $\hat{p} - p$. Have we seen this distribution before? How often was our error smaller larger than 0.02?

```
N <- 625
B <- 10^4
error <- replicate(B,{
  X <- sample(x, N, replace = TRUE)
  mean(X)-p
})
hist(error)
```




```
mean(abs(error) > 0.02)
```

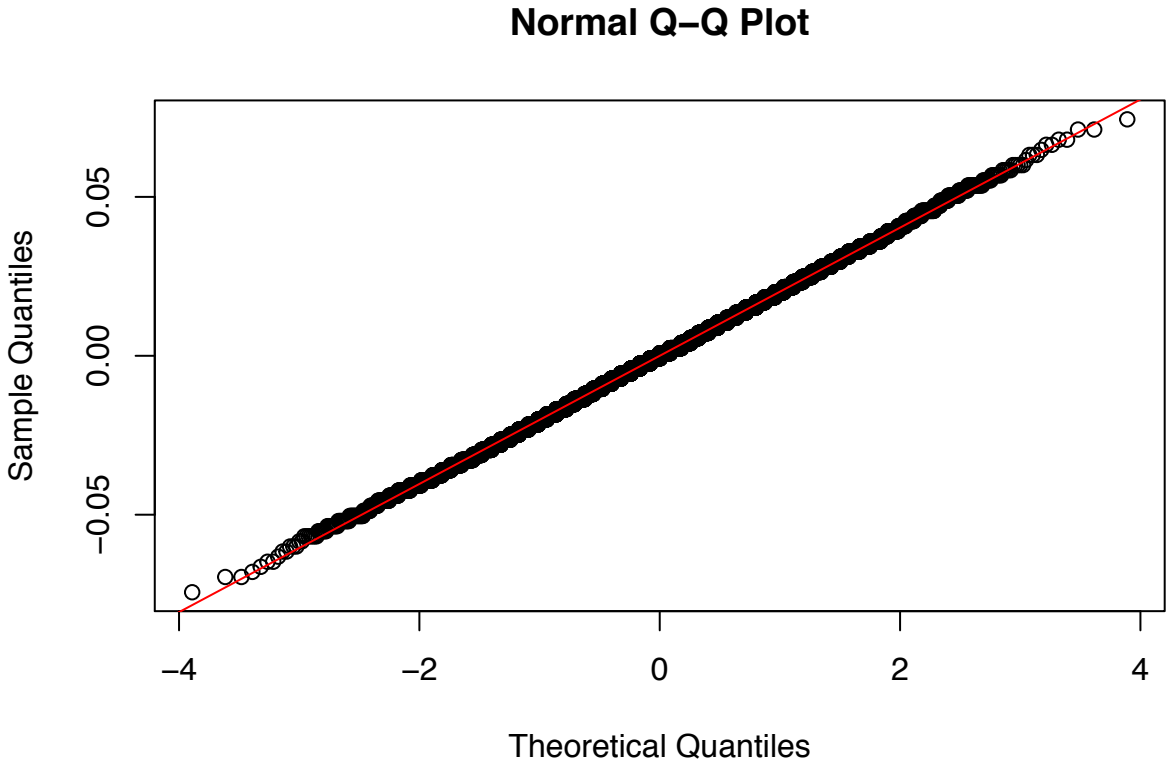
```
## [1] 0.3246
```

The distribution we see here is the *probability distribution* of our random variable. Knowing this distribution will be extremely helpful because we can, for example, report the probability that our error is smaller than a particular quantity. In the next section we describe a powerful mathematical result that helps simplify this.

Central Limit Theorem

We can see that the distribution of $\hat{p}$ is very well approximated with the normal distribution.

```
qqnorm(error)
qqline(error,col=2)
```



The fact that the distribution is centered at 0 confirms that the expected value of $\hat{p}$ is p. The fact that the standard deviation of the errors is

```
sqrt(mean( (error)^2))
```

```
## [1] 0.02024796
```

confirms that the standard error is in fact 0.02. Furthermore, we could have predicted that 32% of errors were larger than 0.02 using the normal approximation. What proportion of the normal curve is more than 1 SD away from average?

```
##compare
mean(abs(error) > 0.02)
```

```
## [1] 0.3246
```

```
##to
pnorm(-1) + (1-pnorm(1))
```

```
## [1] 0.3173105
```

Notice that the Monte Carlo simulation is like conducting 10,000 polls. This of course is practically impossible. But the mathematical theory saves us from having to do this! Without just one poll we are able to say that our estimate is $\hat{p}$ and there is 32% chance that our error is larger than 2%.

Assessment:

Suppose you are consulting for a casino. They want to know how many $1 bets a person needs to make so that the probability of negative earnings is less than 1 in 1,000.

1. We know that the average of the sampling model is -1/19 and the standard deviation is $\sigma = 2\sqrt{10/19 \times 9/19}$. Run a Monte Carlo simulation with $N = 400$ to learn about the distribution of the errors. Remember the error is the average winning minus $\mu = -1/19$.Confirm that the expected value of the error is 0 and that the standard error is $\sigma/\sqrt{N}$.

```
N <- 400
B <- 10^5
mu <- -1/19
sigma <- 2*sqrt(9/19*10/19)
error <- replicate(B,{
  X <- sample( c(-1,1), N, replace=TRUE, prob=(c(10/19,9/19)) )
  mean(X) - mu
})
mean(error)
```

```
## [1] -4.132105e-05
```

```
sqrt( mean( error^2))
```

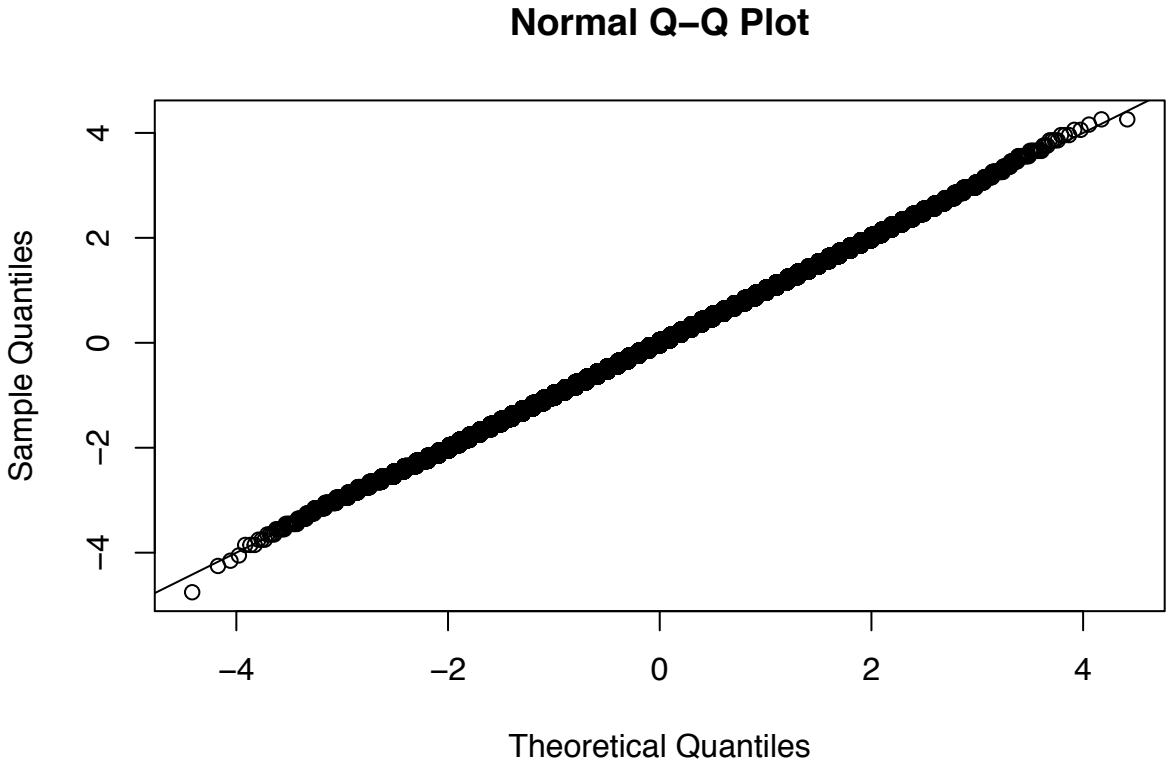
```
## [1] 0.05006588
```

```
sigma/sqrt(N)
```

```
## [1] 0.0499307
```

2. Confirm that the distribution is approximately normal with mean 0 and standard deviation σ/N

```
z <- error/ (sigma / sqrt(N)  )
qqnorm(z)
abline(0,1)
```



3. How large does the error have to be for the casino to lose money?

```
## if x is 0, the the error is:
0 - mu
```

```
## [1] 0.05263158
```

4. Use the CLT to compute the probability of a positive earnings. Confirm with the simulation results.

Let S be the sum of the draws.

$$Z = \sqrt{N}\frac{S/N - \mu}{\sigma}$$

is standard normal. We want to know

$$\Pr(\text{S/N} > 0)$$

We rewrite both sides so that Z is on the left:

$$\Pr(\sqrt{N}\frac{S/N - \mu}{\sigma} > -\sqrt{N}\frac{\mu}{\sigma})$$

which is

$$\Pr(Z > -\sqrt{N}\frac{\mu}{\sigma})$$

and we can compute

```
1 - pnorm( -sqrt(N)*mu/sigma )
```

```
## [1] 0.1459203
```

```
##and compare to
mean(error > -mu)
```

```
## [1] 0.13458
```

5. With $N = 400$ the probability of negative earnings is too high. What does N need to be for the probability of positive earnings is 0? Confirm with a simulation.

We know that if $z = \Phi^{-1}(1 - 10^{-3})$ then

$$\Pr(Z > z) = 10^{-3}$$

So we need

$$-\sqrt{N}\frac{\mu}{\sigma} = \Phi^{-1}(1 - 10^{-3})$$

or

$$N = (-\Phi^{-1}(1 - 10^{-3})\sigma/\mu)^2$$

```
N <- ceiling( -qnorm(1-10^-3)*sigma/mu )^2
```

Lets' confirm:

```
N <- ceiling( -qnorm(1-10^-3)*sigma/mu )^2
B <- 10^5
mu <- -1/19
sigma <- 2*sqrt(9/19*10/19)
profit <- replicate(B,{
  X <- sample( c(-1,1), N, replace=TRUE, prob=(c(10/19,9/19)) )
  mean(X)
})
mean(profit>0)
```

```
## [1] 0.00104
```

Assessment

In R we have access to a large population of male heights. We can access them like this

```
data(father.son, package="UsingR")
y <- father.son$sheight
```

Suppose you are demographer and want to get an estimate of the average height of this population. We can use sampling to do this as well. We will sample 25 men and measure them.

1. What is the average and standard deviation of our sampling model? What is the expected value and standard deviation.

```
mu <- mean(y)
sigma <- sqrt(mean((y-mu)^2))
```

2. Consider the random variable defined by taking a sample of size N and then computing the average. What are the expected value and standard error of this random variable:

```
N <- 25
mu
```

```
## [1] 68.68407
```

```
sigma/sqrt(N)
```

```
## [1] 0.5626792
```

3. What is the probability that our estimate is within one inch of the population average?

Let's call the sample average

$$\bar{Y} = \frac{1}{N}\sum_{i=1}^{N} Y_i$$

Then we have

$$\Pr(\mid \bar{Y} - \mu \mid \leq 1) = \Pr(\sqrt{N} \mid \bar{Y} - \mu \mid /\sigma \leq \sqrt{N}1/\sigma)$$

```
(pnorm(sqrt(N)/sigma) - pnorm(-sqrt(N)/sigma))
```

```
## [1] 0.9244666
```

Note that if we wanted to compute this last quantity in practice we need to know σ. But we don't.

A common approach is to use the sample standard deviation as a stand-in. We define the sample standard deviation as

$$s = \frac{1}{N-1}\sum_{i=1}^{N}(Y_i - \bar{Y})^2$$

The function `sd` computes this quantity

```
Y <- sample(y, N, replace=TRUE)
sd(X)
```

```
## [1] 0.5003947
```

```
1 - pnorm(sqrt(N)/sd(Y))
```

```
## [1] 0.009681883
```

```
#is an approximation of
1 - pnorm(sqrt(N)/sigma)
```

```
## [1] 0.0377667
```

```
##that is completly derived from data
```

The t-distribution (optional)

If you have heard of the t-distribution, you should know that here is where we would use it. If the original data is normal, as height data is, then there is a better approximation for

$$\sqrt{N}\frac{\bar{X}-\mu}{s}$$

than the normal distribution and it is the t-distribution. Note these are closer

```
1 - pnorm(sqrt(N)/sigma)
```

```
## [1] 0.0377667
```

```
#is an approximation of
1 - pt(sqrt(N)/sd(X), N-1)
```

```
## [1] 2.49593e-10
```

```
1 - pnorm(sqrt(N)/sd(X))
```

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

Confidence Intervals

If we create intervals that miss the target 32% of the time, we will not be considered good forecasters. We can always make less bold predictions, such as "the percent of democrats will be between 0% and 100%" but that will not help our reputation either. Can we find a better balance?

Because there is chance variation, it is impossible to hit the target 100% of time unless we state the obvious "between 0% and 100%". So let's compromise a bit. If we hit the target 95% of the time, chances are we will be considered good forecasters. Can we use the theory above to construct such interval?

What we want to do is use the result of our poll to construct an interval, say, $[A, B]$ such that

$$\Pr(A \leq p \text{ and } B \geq p) \geq 0.95$$

we want to make this interval as small as possible. How do we choose A and B?

We know $\hat{p}$ follows a normal distribution with expected value p and standard error approximately equal to $\sqrt{\hat{p}(1-\hat{p})}/\sqrt{N}$. This implies that the following random variable

$$Z = \sqrt{N}\frac{\hat{p}-p}{\sqrt{\hat{p}(1-\hat{p})}}$$

is approximately normal with expected 0 and standard deviation 1.

Assessment What value can we make z so that $\Pr(\mid Z \mid \leq z) = 0.95$?

Answer:

$$z = \Phi^{-1}(0.975)$$

Because:

```
z = qnorm(0.975)
pnorm(z) - pnorm(-z)
```

```
## [1] 0.95
```

So we have our interval. We need to actually define it in terms of $\hat{p}$, N, and z because these are the only quantity we can actually construct.

Assessment: Practice the math How do we rewrite the event

$$\mid Z \mid \leq z$$

so that it can be written as an interval of quantities we know.

$$\mid Z \mid = \sqrt{N}\frac{\mid \hat{p}-p \mid}{\sqrt{\hat{p}(1-\hat{p})}} \leq z$$

$$\mid \hat{p}-p \mid \leq z\sqrt{\hat{p}(1-\hat{p})}\sqrt{N}$$

Assuming z is positive,

$$\hat{p} - z\sqrt{\hat{p}(1-\hat{p})}/\sqrt{N} \leq p \leq \hat{p} + z\sqrt{\hat{p}(1-\hat{p})}/\sqrt{N}$$

```
p_hat + c(-1,1)*qnorm(0.975)*sqrt(p_hat*(1-p_hat))/sqrt(N)
```

```
## [1] 0.3016059 0.6935941
```

This interval has a 95% chance of *covering* the true p

Did we actually make a correct prediction? It's election night and we we will find out

```
ci <- p_hat + c(-1,1)*qnorm(0.975)*sqrt(p_hat*(1-p_hat))/sqrt(N)
p
```

```
## [1] 0.476
```

```
ci[1] <= p & ci[2] >= p
```

```
## [1] TRUE
```

Assessment Construct a 99% confidence interval. Is it more or less specific than the 95%?

```
p_hat + c(-1,1)*qnorm(0.995)*sqrt(p_hat*(1-p_hat))/sqrt(N)
```

```
## [1] 0.24002 0.75518
```

Assessment You have a coin. You want to figure out if it's fair or not. To create your coin run the following code:

```
set.seed(2016)
prob_heads <- sample(c(0.5, 0.6, 0.4),1)
```

1. Now the probability is set. The coin is either fair or not, but we don't know which. Use a Monte Carlo simulation to toss your coin 100 times. Report the proportion of heads

```
N <- 100
X <- sample(c(0,1), N, replace=TRUE,
            prob=c(1-prob_heads,prob_heads))
ph_hat <- mean(X)
ph_hat
```

```
## [1] 0.59
```

2. Is it fair? Use CLT to construct a 95% confidence based on this estimate.

```
conf_int <- ph_hat +
  c(-1,1)*qnorm(0.975)*sqrt(ph_hat*(1-ph_hat))/
  sqrt(N)
conf_int
```

```
## [1] 0.4936024 0.6863976
```

3. Does the interval cover the true value of `prob_head`?

```
prob_heads>=ci[1] & prob_heads<=ci[2]
```

```
## [1] TRUE
```

4. No use a Monte Carlo simulation to re run this experiment (keeping `prob_hear` fixed) 10000 times. Do we confirm that we cover 95% of the time?

```
B <- 10000
cover <- replicate(B,{
  X <- sample(c(0,1), N, replace=TRUE,
              prob=c(prob_heads,1-prob_heads))
  ph_hat <- mean(X)
  ci <- ph_hat +
    c(-1,1)*qnorm(0.975)*sqrt(ph_hat*(1-ph_hat))/
    sqrt(N)
  prob_heads>=ci[1] & prob_heads<=ci[2]
})
mean(cover)
```

```
## [1] 0.9463
```

Confidence Intervals: Monte Carlo Simulaion

Note that Nate Silver stated that Obama had a 90% chance of wining. Was this a confidence interval?

The description we have given up to know says nothing about the probability of winnings. In fact, the statement does not even make sense because p is fixed. It is not random. We should not make probability statements.

Later we will learn about Bayesian statistics were data-based statements such as "Obama has a 90% chance of winning" make sense. Here we clarify how we interpret margins of error and confidence intervals.

The 95% confidence interval

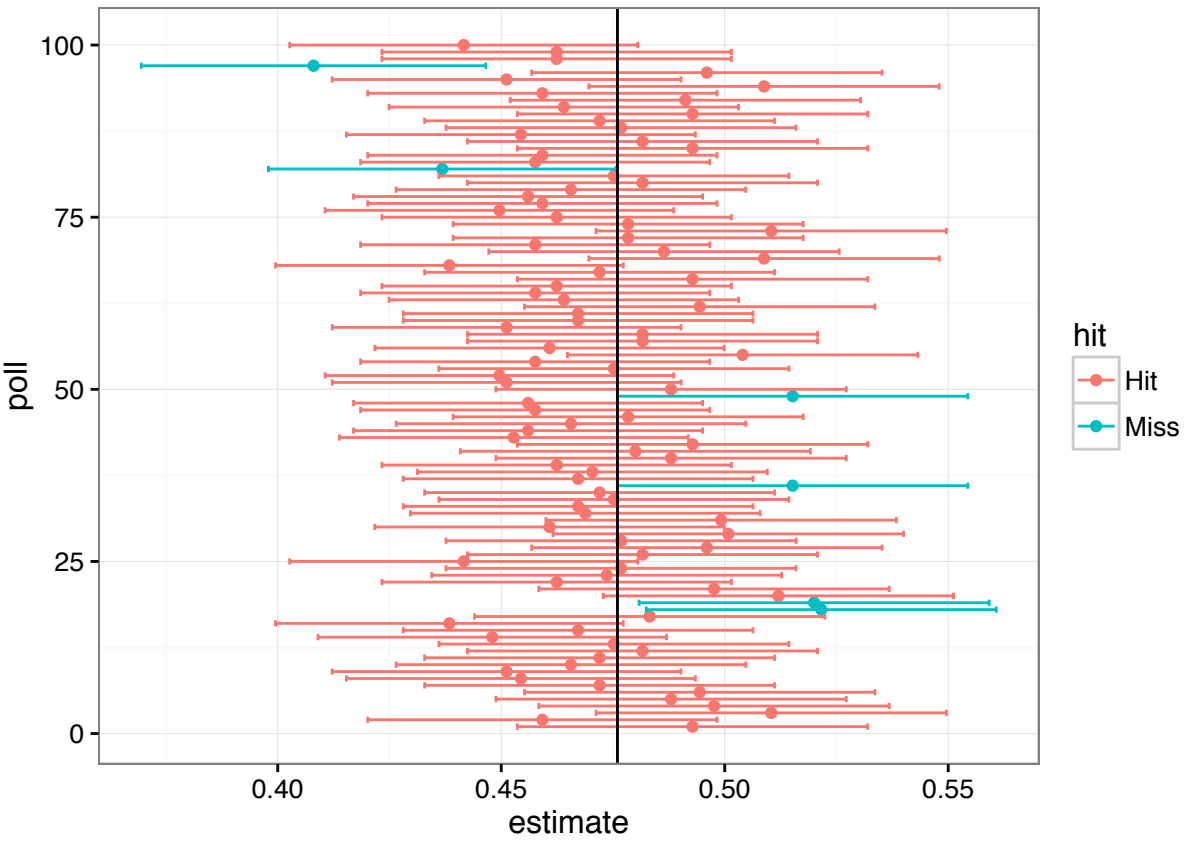
```
p_hat + c(-1,1)*qnorm(0.975)*sqrt(p_hat*(1-p_hat))/sqrt(N)
```

```
## [1] 0.3996029 0.5955971
```

is random because p_hat is random. Let's use a Monte Carlo simulation to see this:

```
library(dplyr)
library(ggplot2)
N <- 625
B <- 100
tab  <- replicate(B,{
  X <- sample(x, N, replace = TRUE)
  p_hat <- mean(X)
  ci <- p_hat + c(-1,1)*qnorm(0.975)*sqrt(p_hat*(1-p_hat))/sqrt(N)
  hit <- ci[1] <= p  & ci[2] >= p
  c(p_hat,ci,hit)
})

tab <- data.frame(poll=1:ncol(tab), t(tab))
names(tab)<-c("poll","estimate","low","high","hit")
tab <- mutate(tab, hit=ifelse(hit, "Hit","Miss") )
ggplot(tab, aes(poll,estimate,ymin=low,ymax=high,col=hit)) +geom_point(aes())+geom_errorbar() + coord_fl
```



Notice how the interval is different after each poll: it's random. So the 95% relates to the probability that this random interval falls on top of p, not that $p < .50$ or whatever other statements related to the probability of winning. In the figure above, that shows the interval for 100 polls, you can see that interval fall on p about 95% of the time.

Power

Pollsters are not successful for providing correct confidence intervals but rather for predicting who will win. Unfortunately, our confidence interval included 0.5 so if forced to declare a winner, we would have to say it was a "toss-up". A problem with our poll results is that, given the sample size and the value of p, we would have to sacrifice on the probability of an incorrect call to create an interval that does not include 50. In this particular case, the reported margin of error would have had to be about 3.5%

Assessment

What percent of confidence intervals with margins of error of 0.03 would correctly predict the election? Check with a Monte Carlo simulation.

Define

$$\delta = 0.035$$

We want to know

$$\Pr(-\delta < \mid p - \hat{p} \mid < \delta)$$

$$\Pr(|Z| < \sqrt{N}\delta / \sqrt{p(1-p)})$$

Because Z is approximately standard normal this probability is approximately

```
a = sqrt(N)*.035/sqrt(p_hat*(1-p_hat))
pnorm(a)-pnorm(-a)
```

```
## [1] 0.9198852
```

This a .91% confidence interval. Which is not bad, but it's not the 95% we set out for.

```
N <- 625
B <- 10^5
success  <- replicate(B,{
  X <- sample(x, N, replace = TRUE)
  p_hat <- mean(X)
  ci <- p_hat + c(-0.035,0.035)
  ci[1] <= p  & ci[2] >= p
})
mean(success)
```

```
## [1] 0.92121
```

Assessment

If we know the percent of democrats can be as close to 50% as, say, 48%, how large does the sample size have to be so that the margin of error is about 2%.

Solution we need: We add $z_{95}\sqrt{p(1-p)}\sqrt{N}$ and we want this to be 0.02. So

```
(qnorm(0.975)*sqrt(0.48*0.52)/0.02)^2
```

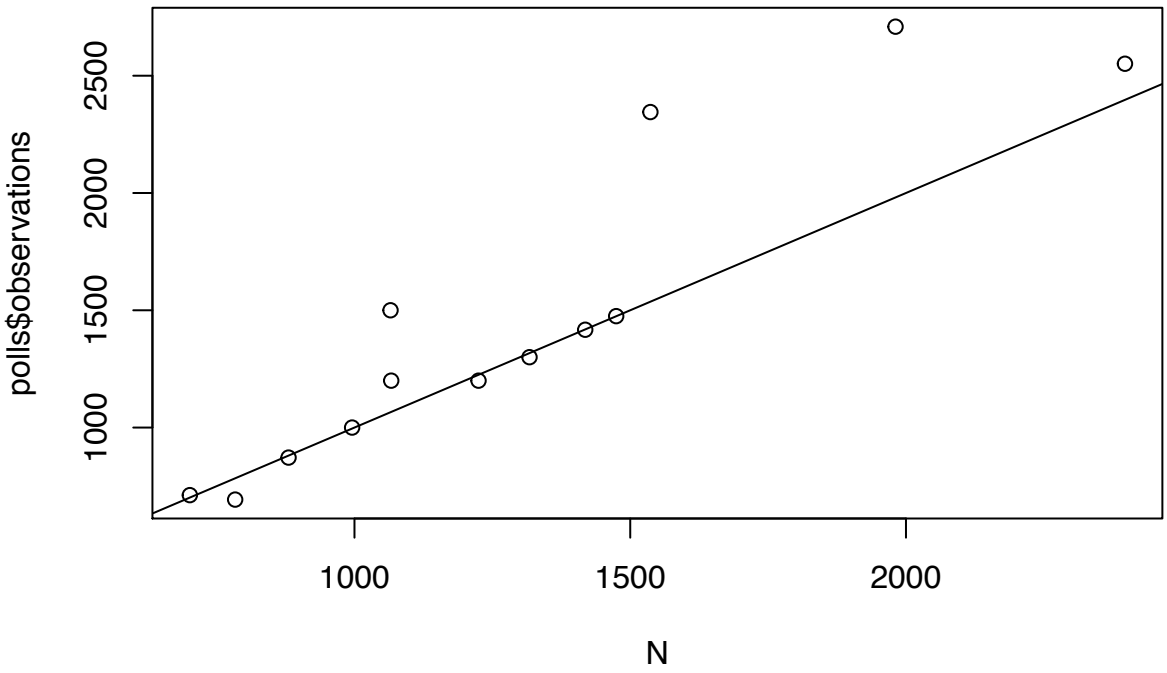
```
## [1] 2397.07
```

If you go back to the table with which we started, you notice that many polls have sample sizes between 500 and 2500.

Assessment From the `polls` object determine the sample size from the margin of error. The plot it against the reported sample size.

What do you see? A - A flat line B - Exactly a straight line C - Almost a straight line with some points off D - The function $f(x) = \sqrt{(}x)$

```
p_hat <- polls$Obama/100
N <- ( qnorm(0.975) * sqrt(p_hat*(1-p_hat)) /
         (polls$margin_of_error/100))^2
plot(N, polls$observations)
abline(0,1)
```



In-class questions: 2/29/2016

We're going to try something new today. If you have small technical questions during class, go to this link and ask away.

p-values

p-values are ubiquitous in the scientific literature. They are related to confidence interval so we introduce the concept here.

Let's consider the blue and red beads. Suppose that rather than wanting an estimate of the percent of blue beads I am more interested in the question are there more blue beads or red beads.

Suppose we take a random sample of $N = 100$ and we observe 53 blue beads. This seems to be pointing to their being more blue than red. However, as data scientists we need to be skeptical. We know there is chance involved in this process and we could get a 53 even when the proportions of red and blue are the same. We call this a *null hypothesis*. The null hypothesis is the skeptics hypothesis: the proportion of blue beads p is 0.5. We have observed a random variable $\hat{p} = 0.53$ and the p-value is the answer to the question how likely is it to see a value this large, when the null hypothesis is true. So we write

$$\Pr(\mid \hat{p} - 0.5 \mid > 0.03)$$

assuming the $p = 0.5$. Under the null we know that

$$\sqrt{N}\frac{\hat{p} - 0.5}{\sqrt{0.5(1-0.5)}}$$

is standard normal. So we can compute the probability above, which is the p-value.

$$\Pr\left(\sqrt{N}\frac{\mid \hat{p} - 0.5 \mid}{\sqrt{0.5(1-0.5)}} > \sqrt{N}\frac{0.03}{\sqrt{0.5(1-0.5)}}\right)$$

```
N=100
z <- sqrt(N)*0.03/0.5
1 - (pnorm(0.6) - pnorm(-0.6))
```

```
## [1] 0.5485062
```

So we do in fact have reason to be a skeptics. By constructing a p-value we see that

Assessment: If $\hat{p} = 51$ and $N = 10000$. What is the p-value?

We can show that if a $x \times 100\%$ confidence interval does not include 0, then the p-value must be smaller than $1 - x$. So they provide related information. However, the confidence interval is always more informative as it gives information of the size of the estimate.

Assessment: Suppose you are comparing average test scores from two school districts. You have exams from a random sample of 10000. The p-value for the difference in average scores is 0.01. Should we change the curriculum of the district with highly significant statistical differences?

Setting the random seed Before we continue, we briefly explain the following important line of code:

```
set.seed(1)
```

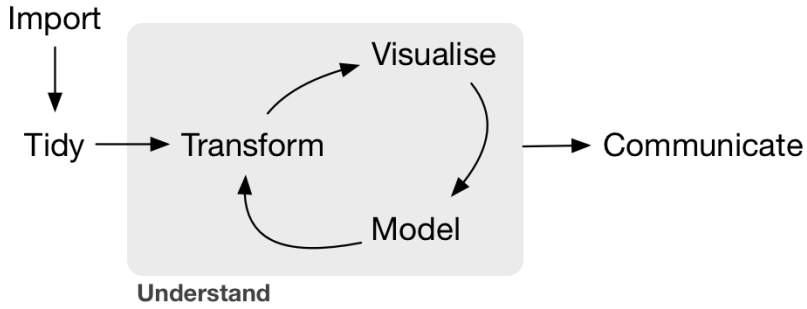
Throughout this book, we use random number generators. This implies that many of the results presented can actually change by chance, including the correct answer to problems. One way to ensure that results do not change is by setting R's random number generation seed. For more on the topic please read the help file:

```
?set.seed
```

Data Wrangling with `dplyr`

Stephanie Hicks, Rafael Irizarry

Once data has been transformed into a **tidy** tabular format, an important part of "data wrangling" or "data munging" is data transformation.



We have learned about some functions in the R package `dplyr` that can transform and summarize tabular data with rows and columns. For example, when data is a tabular format, you have seen how we can use `dplyr` to `filter()` rows, `select()` columns and add new columns using `mutate()`. Now we will explore some more advanced `dplyr` functionality.

Brief recap of dplyr

`dplyr` is a powerful R-package to transform and summarize tabular data with rows and columns.

The package contains a set of functions (or "verbs") to perform common data manipulation operations such as filtering for rows, selecting specific columns, re-ordering rows, adding new columns and summarizing data. In addition, `dplyr` contains a useful function to perform another common task which is the is the "split-apply-combine" concept. We will discuss that in a little bit.

Data

mammals sleep

The `msleep` (mammals sleep) data set contains the sleeptimes and weights for a set of mammals and is available in the `data` repository on GitHub. This data set contains 83 rows and 11 variables.

To load the `msleep` data set

```
library(readr)
library(dplyr)
library(ggplot2)

msleep <- read_csv("https://raw.githubusercontent.com/datasciencelabs/data/master/msleep_ggplot2.csv")
msleep
```

```
## Source: local data frame [83 x 11]
##
##                         name       genus  vore        order conservation
```

```
##                          (chr)       (chr) (chr)        (chr)        (chr)
## 1                      Cheetah    Acinonyx carni    Carnivora           lc
## 2                  Owl monkey       Aotus  omni     Primates           NA
## 3              Mountain beaver  Aplodontia herbi     Rodentia           nt
## 4  Greater short-tailed shrew     Blarina  omni Soricomorpha           lc
## 5                          Cow         Bos herbi Artiodactyla domesticated
## 6             Three-toed sloth    Bradypus herbi       Pilosa           NA
## 7           Northern fur seal Callorhinus carni    Carnivora           vu
## 8                Vesper mouse     Calomys    NA     Rodentia           NA
## 9                         Dog       Canis carni    Carnivora domesticated
## 10                    Roe deer   Capreolus herbi Artiodactyla           lc
## ..                         ...         ...   ...          ...          ...
## Variables not shown: sleep_total (dbl), sleep_rem (dbl), sleep_cycle
##   (dbl), awake (dbl), brainwt (dbl), bodywt (dbl)
```

The columns (in order) correspond to the following:

column name	Description
`name`	common name
`genus`	taxonomic rank
`vore`	carnivore, omnivore or herbivore?
`order`	taxonomic rank
`conservation`	the conservation status of the mammal
`sleep_total`	total amount of sleep, in hours
`sleep_rem`	rem sleep, in hours
`sleep_cycle`	length of sleep cycle, in hours
`awake`	amount of time spent awake, in hours
`brainwt`	brain weight in kilograms
`bodywt`	body weight in kilograms

Important `dplyr` verbs to remember

`dplyr` verbs	Description
`select()`	select columns
`mutate()`	create new columns
`filter()`	filter rows
`arrange()`	re-order or arrange rows
`summarise()`	summarise values
`group_by()`	allows for group operations in the "split-apply-combine" concept

`dplyr` verbs in action

`select()` and `mutate()` columns; `filter()` rows

The two most basic functions are `select()` and `filter()` which selects columns and filters rows, respectively. The function `mutate()` can be used to create new columns. We have already seen examples of all of these in class.

For example, to select a range of columns by name, use the ":" (colon) operator

```
msleep %>% select(name:order)
```

```
## Source: local data frame [83 x 4]
##
##                          name       genus  vore        order
##                         (chr)       (chr) (chr)        (chr)
## 1                     Cheetah    Acinonyx carni    Carnivora
## 2                 Owl monkey       Aotus  omni     Primates
## 3             Mountain beaver  Aplodontia herbi     Rodentia
## 4  Greater short-tailed shrew     Blarina  omni Soricomorpha
## 5                         Cow         Bos herbi Artiodactyla
## 6            Three-toed sloth    Bradypus herbi       Pilosa
## 7           Northern fur seal Callorhinus carni    Carnivora
## 8                Vesper mouse     Calomys    NA     Rodentia
## 9                         Dog       Canis carni    Carnivora
## 10                  Roe deer   Capreolus herbi Artiodactyla
## ..                       ...         ...   ...          ...
```

To select all columns that start with the character string "sl", use the function `starts_with()`

```
msleep %>% select(starts_with("sl"))
```

```
## Source: local data frame [83 x 3]
##
##    sleep_total sleep_rem sleep_cycle
##          (dbl)     (dbl)       (dbl)
## 1         12.1        NA          NA
## 2         17.0       1.8          NA
## 3         14.4       2.4          NA
## 4         14.9       2.3   0.1333333
## 5          4.0       0.7   0.6666667
## 6         14.4       2.2   0.7666667
## 7          8.7       1.4   0.3833333
## 8          7.0        NA          NA
## 9         10.1       2.9   0.3333333
## 10         3.0        NA          NA
## ..         ...       ...         ...
```

Some additional options to select columns based on a specific criteria include

1. `ends_with()` = Select columns that end with a character string
2. `contains()` = Select columns that contain a character string
3. `matches()` = Select columns that match a regular expression
4. `one_of()` = Select columns names that are from a group of names

Assessment Select all columns except those from `genus` to `conservation` and filter the rows for mammals that sleep a total of more than 16 hours and have a body weight of greater than 1 kilogram

```
## Provide your code here

msleep %>%
    select(-(genus:conservation)) %>%
    filter(sleep_total >= 16, bodywt >= 1)
```

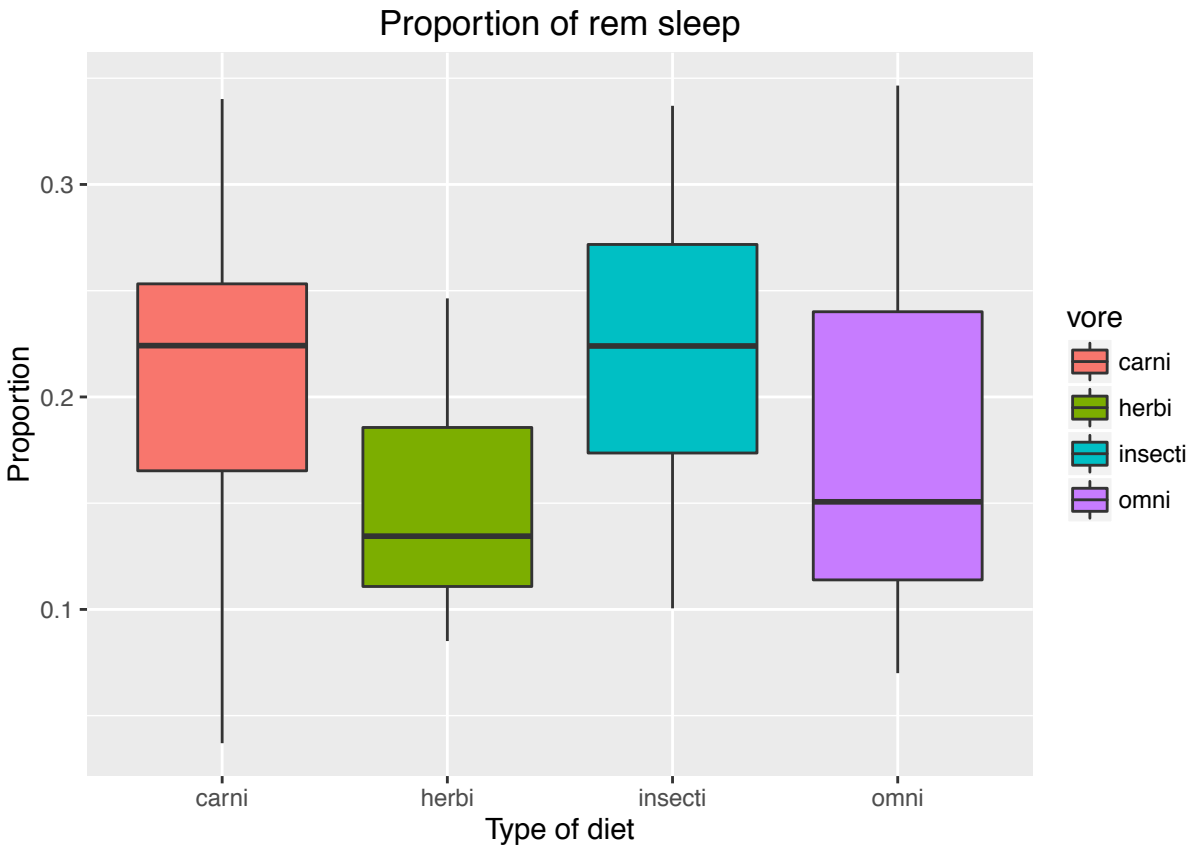
```
## Source: local data frame [3 x 7]
##
##                     name sleep_total sleep_rem sleep_cycle awake brainwt
##                    (chr)       (dbl)     (dbl)       (dbl) (dbl)   (dbl)
## 1   Long-nosed armadillo        17.4       3.1   0.3833333   6.6  0.0108
## 2 North American Opossum        18.0       4.9   0.3333333   6.0  0.0063
## 3        Giant armadillo        18.1       6.1          NA   5.9  0.0810
## Variables not shown: bodywt (dbl)
```

Assessment Create a new column called `rem_proportion` which is the ratio of rem sleep to total amount of sleep and create boxplots of the `rem_proportion` column split and colored by the `vore` column. Create labels for the `x` and `y` axis.

```
## Provide your code here

msleep %>%
    mutate(rem_proportion = sleep_rem / sleep_total) %>%
    ggplot(aes(x = vore, y = rem_proportion, fill = vore)) +
        geom_boxplot() + xlab("Type of diet") +
        ylab("Proportion") + labs(title = "Proportion of rem sleep")
```

```
## Warning: Removed 27 rows containing non-finite values (stat_boxplot).
```



Assessment (optional) Select all columns that start with the character string "sl" or ends with the character string "wt", create a new column called `rem_proportion` which is the ratio of rem sleep to total amount of sleep, create a second column `bodywt_grams` which is the bodywt column in grams and filter for the rows 20 to 30 in the msleep data set by numerical position.

Hint: Look at the `slice()` help file to filter for rows by numerical position.

```
## Provide your code here

msleep %>%
    select(starts_with("sl"), ends_with("wt")) %>%
    mutate(rem_proportion = sleep_rem / sleep_total,
           bodywt_grams = bodywt * 1000) %>%
    slice(20:30)
```

```
## Source: local data frame [11 x 7]
##
##    sleep_total sleep_rem sleep_cycle brainwt   bodywt rem_proportion
##          (dbl)     (dbl)       (dbl)   (dbl)    (dbl)          (dbl)
## 1         18.0       4.9   0.3333333  0.0063    1.700      0.2722222
## 2          3.9        NA          NA  4.6030 2547.000             NA
## 3         19.7       3.9   0.1166667  0.0003    0.023      0.1979695
## 4          2.9       0.6   1.0000000  0.6550  521.000      0.2068966
## 5          3.1       0.4          NA  0.4190  187.000      0.1290323
## 6         10.1       3.5   0.2833333  0.0035    0.770      0.3465347
## 7         10.9       1.1          NA  0.1150   10.000      0.1009174
```

```
## 8         14.9        NA          NA      NA    0.071            NA
## 9         12.5       3.2   0.4166667  0.0256    3.300     0.2560000
## 10         9.8       1.1   0.5500000  0.0050    0.200     0.1122449
## 11         1.9       0.4          NA      NA  899.995     0.2105263
## Variables not shown: bodywt_grams (dbl)
```

Arrange or re-order rows using `arrange()`

To arrange (or re-order) rows by a particular column such as the taxonomic order, list the name of the column you want to arrange the rows by

```
msleep %>%
    arrange(order)
```

```
## Source: local data frame [83 x 11]
##
##                 name       genus  vore        order conservation
##                (chr)       (chr) (chr)        (chr)        (chr)
## 1             Tenrec      Tenrec  omni Afrosoricida           NA
## 2                Cow         Bos herbi Artiodactyla domesticated
## 3          Roe deer   Capreolus herbi Artiodactyla           lc
## 4               Goat       Capri herbi Artiodactyla           lc
## 5            Giraffe     Giraffa herbi Artiodactyla           cd
## 6              Sheep        Ovis herbi Artiodactyla domesticated
## 7                Pig         Sus  omni Artiodactyla domesticated
## 8            Cheetah    Acinonyx carni    Carnivora           lc
## 9  Northern fur seal Callorhinus carni    Carnivora           vu
## 10               Dog       Canis carni    Carnivora domesticated
## ..               ...         ...   ...          ...          ...
## Variables not shown: sleep_total (dbl), sleep_rem (dbl), sleep_cycle
##   (dbl), awake (dbl), brainwt (dbl), bodywt (dbl)
```

Assessment Select all columns names with the characters "sleep" and arrange the rows for the `sleep_rem` in a decreasing order.

Hint: look at the `?arrange` help file for the `desc()` option.

```
## Provide your code here

msleep %>%
    select(matches("sleep")) %>%
    arrange(desc(sleep_rem))
```

```
## Source: local data frame [83 x 3]
##
##    sleep_total sleep_rem sleep_cycle
##          (dbl)     (dbl)       (dbl)
## 1         19.4       6.6          NA
## 2         18.1       6.1          NA
## 3         18.0       4.9   0.3333333
## 4         19.7       3.9   0.1166667
## 5         10.1       3.5   0.2833333
```

```
## 6         13.8       3.4   0.2166667
## 7         12.5       3.2   0.4166667
## 8         17.4       3.1   0.3833333
## 9         14.3       3.1   0.2000000
## 10        15.9       3.0          NA
## ..         ...       ...         ...
```

Assessment Select three columns from `msleep` (`name`, `order`, `sleep_total`), arrange the rows in the `sleep_total` column in a descending order, and filter the rows for mammals that sleep for a total of 16 or more hours.

```
## Provide your code here

msleep %>%
    select(name, order, sleep_total) %>%
    arrange(order, desc(sleep_total)) %>%
    filter(sleep_total >= 16)
```

```
## Source: local data frame [8 x 3]
##
##                     name           order sleep_total
##                    (chr)           (chr)       (dbl)
## 1       Little brown bat      Chiroptera        19.9
## 2          Big brown bat      Chiroptera        19.7
## 3        Giant armadillo       Cingulata        18.1
## 4   Long-nosed armadillo       Cingulata        17.4
## 5   Thick-tailed opposum Didelphimorphia        19.4
## 6 North American Opossum Didelphimorphia        18.0
## 7             Owl monkey        Primates        17.0
## 8 Arctic ground squirrel        Rodentia        16.6
```

Create summaries of the data frame using `summarise()`

The `summarise()` function will create summary statistics for a given column in the data frame such as finding the mean. For example, to compute the average number of hours of sleep, apply the `mean()` function to the column `sleep_total` and call the summary value `avg_sleep`.

```
msleep %>%
    summarise(avg_sleep = mean(sleep_total))
```

```
## Source: local data frame [1 x 1]
##
##   avg_sleep
##       (dbl)
## 1  10.43373
```

There are many other summary statistics you could consider such `sd()`, `min()`, `max()`, `median()`, `sum()`, `n()` (returns the length of vector), `first()` (returns first value in vector), `last()` (returns last value in vector) and `n_distinct()` (number of distinct values in vector).

Assessment Summarize `sleep_total` column in the `msleep` data set with the average sleep, the minimum and maximum amount of sleep, and the total number of mammals.

```
## Provide your code here

msleep %>%
    summarise(avg_sleep = mean(sleep_total),
              min_sleep = min(sleep_total),
              max_sleep = max(sleep_total),
              total = n())
```

```
## Source: local data frame [1 x 4]
##
##   avg_sleep min_sleep max_sleep total
##       (dbl)     (dbl)     (dbl) (int)
## 1  10.43373       1.9      19.9    83
```

Group operations using `group_by()`

The `group_by()` verb is an important function in `dplyr`. As we mentioned before it's related to concept of "split-apply-combine". We literally want to split the data frame by some variable (e.g. `vore`), apply a function to the individual data frames and then combine the output.

Say we wanted to calculate the standard deviation of the body and brain weights for each of factor in the `vore` column. First, we can look at the types of factors in the `vore` column

```
table(msleep$vore)
```

```
##
##   carni   herbi insecti    omni
##      19      32       5      20
```

Then, we could use `filter()` to filter for rows that contain "carni" in the `vore` column and summarize with the mean of the brain and body weights.

```
msleep %>%
    filter(vore == "carni") %>%
    summarize("bodywt_sd" = mean(bodywt),
              "brainwt_sd" = mean(brainwt, na.rm = TRUE))
```

```
## Source: local data frame [1 x 2]
##
##   bodywt_sd brainwt_sd
##       (dbl)      (dbl)
## 1  90.75111 0.07925556
```

We could repeat this for each factor in `vore`, which is a bit teadious. Instead, we could use this using the `group_by()` function.

Let's do that: split the `msleep` data frame by the `vore` column, then calculate the mean of body weight and brain weight for each invididual data frame. (hint: We expect a set of summary statistics for each level in `vore`.)

```
msleep %>%
    group_by(vore) %>%
    summarize("bodywt_sd" = mean(bodywt),
              "brainwt_sd" = mean(brainwt, na.rm = TRUE))
```

```
## Source: local data frame [5 x 3]
##
##      vore bodywt_sd brainwt_sd
##     (chr)     (dbl)      (dbl)
## 1   carni  90.75111 0.07925556
## 2   herbi 366.87725 0.62159750
## 3 insecti  12.92160 0.02155000
## 4    omni  12.71800 0.14573118
## 5      NA   0.85800 0.00762600
```

Assessment Split the `msleep` data frame by the taxonomic order, then for each taxonomic order summarize the `sleep_total` with the average sleep, the minimum and maximum amount of sleep, and the total number of mammals in each order.

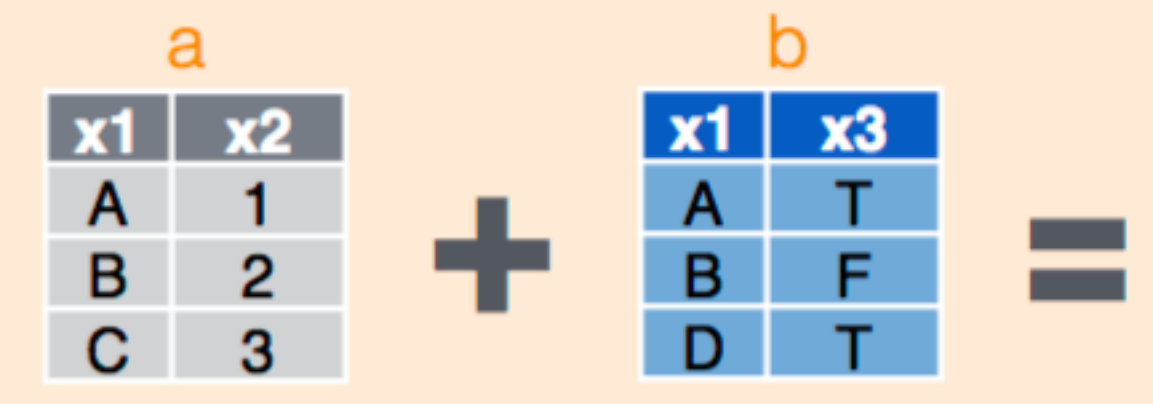
```
## Provide your code here

msleep %>%
    group_by(order) %>%
    summarise(avg_sleep = mean(sleep_total),
              min_sleep = min(sleep_total),
              max_sleep = max(sleep_total),
              total = n())
```

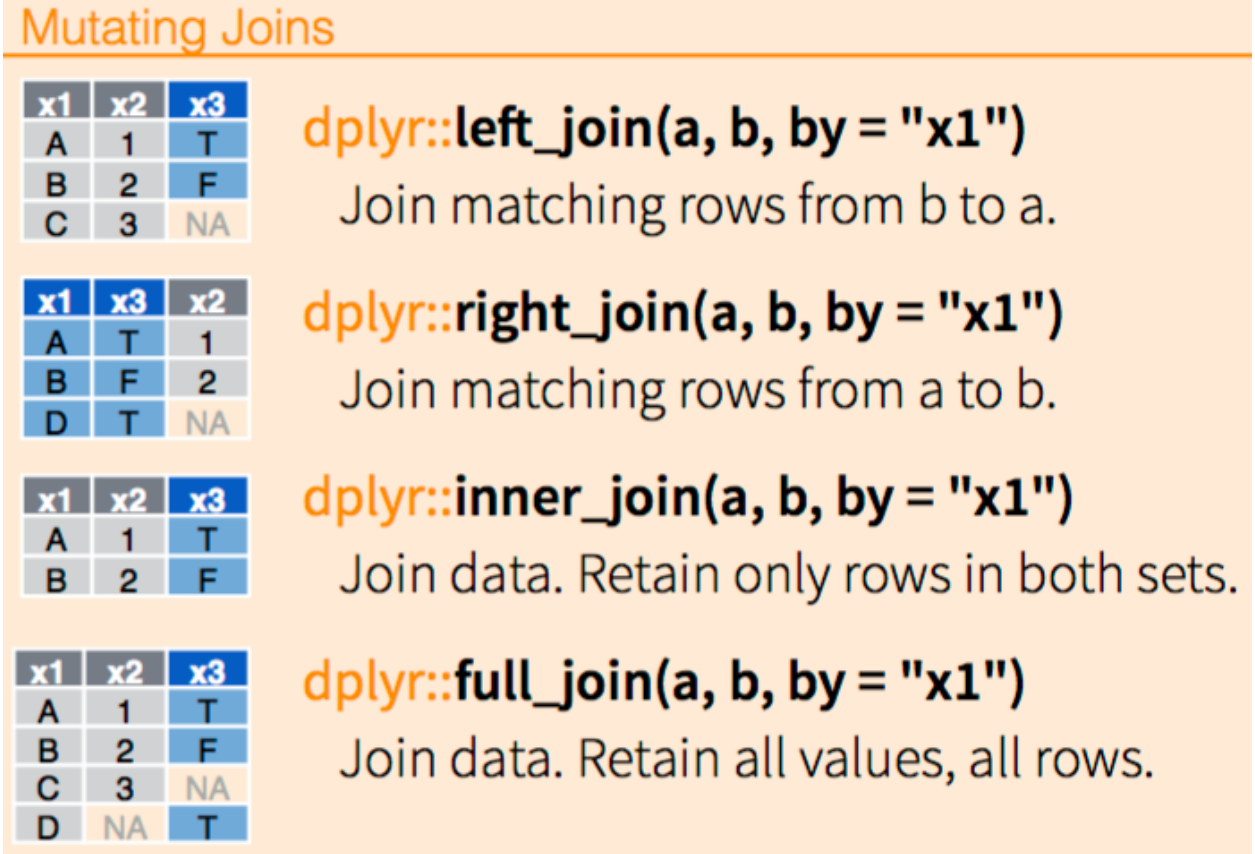
```
## Source: local data frame [19 x 5]
##
##              order avg_sleep min_sleep max_sleep total
##              (chr)     (dbl)     (dbl)     (dbl) (int)
## 1     Afrosoricida 15.600000      15.6      15.6     1
## 2     Artiodactyla  4.516667       1.9       9.1     6
## 3        Carnivora 10.116667       3.5      15.8    12
## 4          Cetacea  4.500000       2.7       5.6     3
## 5       Chiroptera 19.800000      19.7      19.9     2
## 6        Cingulata 17.750000      17.4      18.1     2
## 7  Didelphimorphia 18.700000      18.0      19.4     2
## 8    Diprotodontia 12.400000      11.1      13.7     2
## 9   Erinaceomorpha 10.200000      10.1      10.3     2
## 10      Hyracoidea  5.666667       5.3       6.3     3
## 11      Lagomorpha  8.400000       8.4       8.4     1
## 12     Monotremata  8.600000       8.6       8.6     1
## 13  Perissodactyla  3.466667       2.9       4.4     3
## 14          Pilosa 14.400000      14.4      14.4     1
## 15        Primates 10.500000       8.0      17.0    12
## 16     Proboscidea  3.600000       3.3       3.9     2
## 17        Rodentia 12.468182       7.0      16.6    22
## 18      Scandentia  8.900000       8.9       8.9     1
## 19    Soricomorpha 11.100000       8.4      14.9     5
```

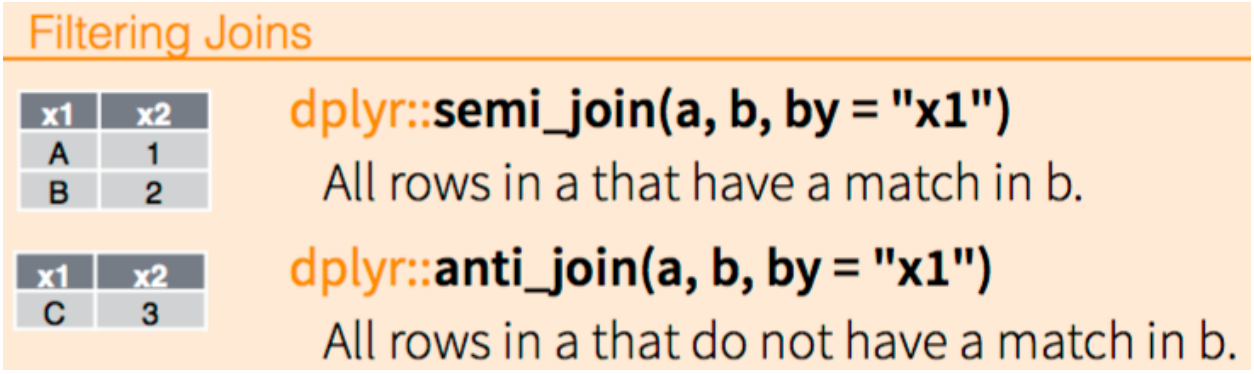
joining two data frames in `dplyr`

The last part of `dplyr` that we will discuss are a set of `dplyr` verbs that allow you to join two data sets. The following are cartoons extracted from Data Wrangling with dplyr and tidyr Cheatsheet from RStudio to illustrate the different ways to join data frames using `dplyr`.



Two types of functions to join together data frames





Data

For this section, we will work with two small data sets related to the 2016 Oscars Nominations. The two data sets are `oscars` and `movies`. The first data set contains information about the the name of the actor/actress, the name of the movie and the category for nomination. The second data set contains a list of movies and the length of the movie in minutes.

We will explore the `dplyr` verbs to join the two tables. First let's load the data.

```
library(readr)

oscars <-"
name,movie,category
Adam McKay,The Big Short,Best Director
Alejandro González Iñárritu,The Revenant,Best Director
Lenny Abrahamson,Room,Best Director
Tom McCarthy,Spotlight,Best Director
George Miller,Mad Max: Fury Road,Best Director
Bryan Cranston,Trumbo,Best Actor
Matt Damon,The Martian,Best Actor
Michael Fassbender,Steve Jobs,Best Actor
Leonardo DiCaprio,The Revenant,Best Actor
Eddie Redmayne,The Danish Girl,Best Actor
Cate Blanchett,Carol,Best Actress
Brie Larson,Room,Best Actress
Jennifer Lawrence,Joy,Best Actress
Charlotte Rampling,45 Years,Best Actress
Saoirse Ronan,Brooklyn,Best Actress
"
oscars <- read_csv(oscars, trim_ws = TRUE, skip = 1)
oscars
```

```
## Source: local data frame [15 x 3]
##
##                          name              movie      category
##                         (chr)              (chr)         (chr)
## 1                  Adam McKay      The Big Short Best Director
## 2  Alejandro González Iñárritu       The Revenant Best Director
## 3             Lenny Abrahamson               Room Best Director
## 4                 Tom McCarthy          Spotlight Best Director
## 5               George Miller Mad Max: Fury Road Best Director
```

```
## 6               Bryan Cranston             Trumbo    Best Actor
## 7                   Matt Damon        The Martian    Best Actor
## 8            Michael Fassbender         Steve Jobs    Best Actor
## 9             Leonardo DiCaprio       The Revenant    Best Actor
## 10               Eddie Redmayne    The Danish Girl    Best Actor
## 11               Cate Blanchett              Carol  Best Actress
## 12                  Brie Larson               Room  Best Actress
## 13            Jennifer Lawrence                Joy  Best Actress
## 14           Charlotte Rampling           45 Years  Best Actress
## 15                Saoirse Ronan           Brooklyn  Best Actress
```

```
movies <-"
movie,length_mins
The Big Short,130
Star Wars: The Force Awakens,135
Brooklyn,111
Mad Max: Fury Road,120
Room,118
The Martian,144
The Revenant,156
Spotlight,128
"
movies <- read_csv(movies, trim_ws = TRUE, skip = 1)
movies
```

```
## Source: local data frame [8 x 2]
##
##                          movie length_mins
##                          (chr)       (int)
## 1                The Big Short         130
## 2 Star Wars: The Force Awakens         135
## 3                      Brooklyn         111
## 4           Mad Max: Fury Road         120
## 5                          Room         118
## 6                   The Martian         144
## 7                  The Revenant         156
## 8                     Spotlight         128
```

inner_join(x,y)

This function joins all rows from x where there are matching values in y, and all columns from x and y. If there are multiple matches between x and y, all combination of the matches are returned.

```
inner_join(oscars, movies, by = "movie")
```

```
## Source: local data frame [9 x 4]
##
##                           name              movie      category length_mins
##                          (chr)              (chr)         (chr)       (int)
## 1                   Adam McKay      The Big Short Best Director         130
## 2 Alejandro González Iñárritu       The Revenant Best Director         156
## 3             Lenny Abrahamson               Room Best Director         118
```

```
## 4               Tom McCarthy          Spotlight Best Director         128
## 5             George Miller Mad Max: Fury Road Best Director         120
## 6                Matt Damon        The Martian    Best Actor         144
## 7          Leonardo DiCaprio       The Revenant    Best Actor         156
## 8               Brie Larson               Room  Best Actress         118
## 9             Saoirse Ronan           Brooklyn  Best Actress         111
```

semi_join(x,y)

This function returns all rows from x where there are matching values in y, keeping just columns from x. A semi join differs from an inner join because an inner join will return one row of x for each matching row of y, where a semi join will never duplicate rows of x.

```
semi_join(oscars, movies, by = "movie")
```

```
## Source: local data frame [9 x 3]
##
##                         name              movie      category
##                        (chr)              (chr)         (chr)
## 1                 Adam McKay      The Big Short Best Director
## 2               Saoirse Ronan           Brooklyn  Best Actress
## 3               George Miller Mad Max: Fury Road Best Director
## 4             Lenny Abrahamson               Room Best Director
## 5                  Brie Larson               Room  Best Actress
## 6                  Matt Damon        The Martian    Best Actor
## 7 Alejandro González Iñárritu       The Revenant Best Director
## 8            Leonardo DiCaprio       The Revenant    Best Actor
## 9                 Tom McCarthy          Spotlight Best Director
```

Assessment Try applying the `semi_join()` function with `x=movies` and `y=oscars`. What is the difference?

```
## Provide your code here

semi_join(movies, oscars, by = "movie")
```

```
## Source: local data frame [7 x 2]
##
##                movie length_mins
##                (chr)       (int)
## 1      The Big Short         130
## 2       The Revenant         156
## 3               Room         118
## 4          Spotlight         128
## 5 Mad Max: Fury Road         120
## 6        The Martian         144
## 7           Brooklyn         111
```

Assessment

Using the `dplyr` join functions, combine the columns from the `oscars` and `movies` data sets and return all rows from the `oscars` data set and all columns in both the `oscars` and `movies` columns.

Hint: read the help file for `left_join()` or `right_join()`.

```
## Provide your code here

left_join(oscars, movies, by = "movie")
```

```
## Source: local data frame [15 x 4]
##
##                           name              movie      category
##                          (chr)              (chr)         (chr)
## 1                   Adam McKay      The Big Short Best Director
## 2  Alejandro González Iñárritu       The Revenant Best Director
## 3             Lenny Abrahamson               Room Best Director
## 4                 Tom McCarthy          Spotlight Best Director
## 5               George Miller Mad Max: Fury Road Best Director
## 6              Bryan Cranston             Trumbo    Best Actor
## 7                  Matt Damon        The Martian    Best Actor
## 8           Michael Fassbender         Steve Jobs    Best Actor
## 9            Leonardo DiCaprio       The Revenant    Best Actor
## 10              Eddie Redmayne    The Danish Girl    Best Actor
## 11              Cate Blanchett              Carol  Best Actress
## 12                 Brie Larson               Room  Best Actress
## 13            Jennifer Lawrence                Joy  Best Actress
## 14          Charlotte Rampling           45 Years  Best Actress
## 15                Saoirse Ronan           Brooklyn  Best Actress
## Variables not shown: length_mins (int)
```

```
## or
right_join(movies, oscars, by = "movie")
```

```
## Source: local data frame [15 x 4]
##
##                 movie length_mins                        name
##                 (chr)       (int)                       (chr)
## 1       The Big Short         130                   Adam McKay
## 2        The Revenant         156 Alejandro González Iñárritu
## 3                Room         118            Lenny Abrahamson
## 4           Spotlight         128                Tom McCarthy
## 5  Mad Max: Fury Road         120              George Miller
## 6              Trumbo          NA              Bryan Cranston
## 7         The Martian         144                  Matt Damon
## 8          Steve Jobs          NA          Michael Fassbender
## 9        The Revenant         156           Leonardo DiCaprio
## 10    The Danish Girl          NA              Eddie Redmayne
## 11              Carol          NA              Cate Blanchett
## 12               Room         118                 Brie Larson
## 13                Joy          NA           Jennifer Lawrence
## 14          45 Years          NA          Charlotte Rampling
## 15          Brooklyn         111                Saoirse Ronan
## Variables not shown: category (chr)
```

Why are there NAs?

Assessment

Using the `dplyr` join functions, combine the columns from the `oscars` and `movies` data sets and return all rows from the `movies` data set and all columns in both the `oscars` and `movies` columns.

```
## Provide your code here

right_join(oscars, movies, by = "movie")
```

```
## Source: local data frame [10 x 4]
##
##                           name                        movie      category
##                          (chr)                        (chr)         (chr)
## 1                   Adam McKay                The Big Short Best Director
## 2                           NA Star Wars: The Force Awakens            NA
## 3               Saoirse Ronan                      Brooklyn  Best Actress
## 4               George Miller           Mad Max: Fury Road Best Director
## 5            Lenny Abrahamson                        Room Best Director
## 6                 Brie Larson                        Room  Best Actress
## 7                  Matt Damon                  The Martian    Best Actor
## 8  Alejandro González Iñárritu                The Revenant Best Director
## 9           Leonardo DiCaprio                The Revenant    Best Actor
## 10                Tom McCarthy                   Spotlight Best Director
## Variables not shown: length_mins (int)
```

```
## or
left_join(movies, oscars, by = "movie")
```

```
## Source: local data frame [10 x 4]
##
##                           movie length_mins                       name
##                           (chr)       (int)                      (chr)
## 1                 The Big Short         130                  Adam McKay
## 2  Star Wars: The Force Awakens         135                          NA
## 3                      Brooklyn         111               Saoirse Ronan
## 4            Mad Max: Fury Road         120               George Miller
## 5                          Room         118            Lenny Abrahamson
## 6                          Room         118                 Brie Larson
## 7                   The Martian         144                   Matt Damon
## 8                 The Revenant         156 Alejandro González Iñárritu
## 9                 The Revenant         156           Leonardo DiCaprio
## 10                   Spotlight         128                Tom McCarthy
## Variables not shown: category (chr)
```

full_join(x,y)

This function returns all rows and all columns from both x and y. When there are not matching values, it will return NA for the one missing.

```
full_join(oscars, movies, by = "movie")
```

```
## Source: local data frame [16 x 4]
##
##                          name                        movie      category
##                         (chr)                        (chr)         (chr)
## 1                   Adam McKay                The Big Short Best Director
## 2  Alejandro González Iñárritu                The Revenant Best Director
## 3              Lenny Abrahamson                        Room Best Director
## 4                  Tom McCarthy                   Spotlight Best Director
## 5                 George Miller           Mad Max: Fury Road Best Director
## 6                Bryan Cranston                      Trumbo    Best Actor
## 7                    Matt Damon                  The Martian    Best Actor
## 8            Michael Fassbender                   Steve Jobs    Best Actor
## 9             Leonardo DiCaprio                 The Revenant    Best Actor
## 10               Eddie Redmayne               The Danish Girl    Best Actor
## 11               Cate Blanchett                        Carol  Best Actress
## 12                  Brie Larson                         Room  Best Actress
## 13            Jennifer Lawrence                          Joy  Best Actress
## 14           Charlotte Rampling                    45 Years  Best Actress
## 15                Saoirse Ronan                     Brooklyn  Best Actress
## 16                           NA Star Wars: The Force Awakens            NA
## Variables not shown: length_mins (int)
```

```
full_join(movies, oscars, by = "movie")
```

```
## Source: local data frame [16 x 4]
##
##                           movie length_mins                       name
##                           (chr)       (int)                      (chr)
## 1                 The Big Short         130                  Adam McKay
## 2  Star Wars: The Force Awakens         135                          NA
## 3                       Brooklyn         111               Saoirse Ronan
## 4            Mad Max: Fury Road         120               George Miller
## 5                           Room         118             Lenny Abrahamson
## 6                           Room         118                 Brie Larson
## 7                    The Martian         144                  Matt Damon
## 8                   The Revenant         156 Alejandro González Iñárritu
## 9                   The Revenant         156           Leonardo DiCaprio
## 10                     Spotlight         128                Tom McCarthy
## 11                        Trumbo          NA              Bryan Cranston
## 12                     Steve Jobs          NA          Michael Fassbender
## 13                The Danish Girl          NA              Eddie Redmayne
## 14                          Carol          NA              Cate Blanchett
## 15                            Joy          NA           Jennifer Lawrence
## 16                      45 Years          NA          Charlotte Rampling
## Variables not shown: category (chr)
```

Assessment

Using the `dplyr` join functions, return all rows from `oscars` data set where there are not matching values in `movies`, only keeping the columns from the `oscars` data set.

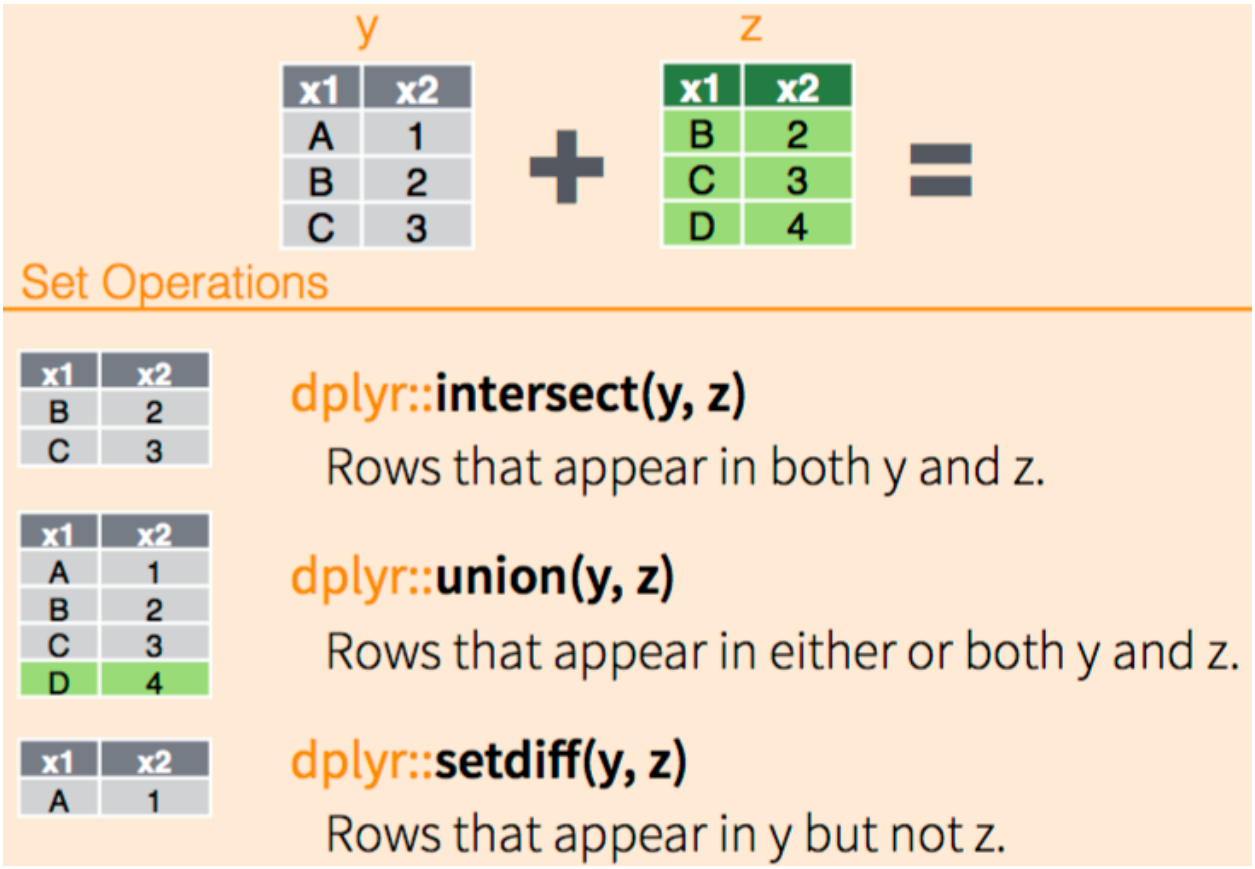
Hint: Read the help file for `anti_join()`.

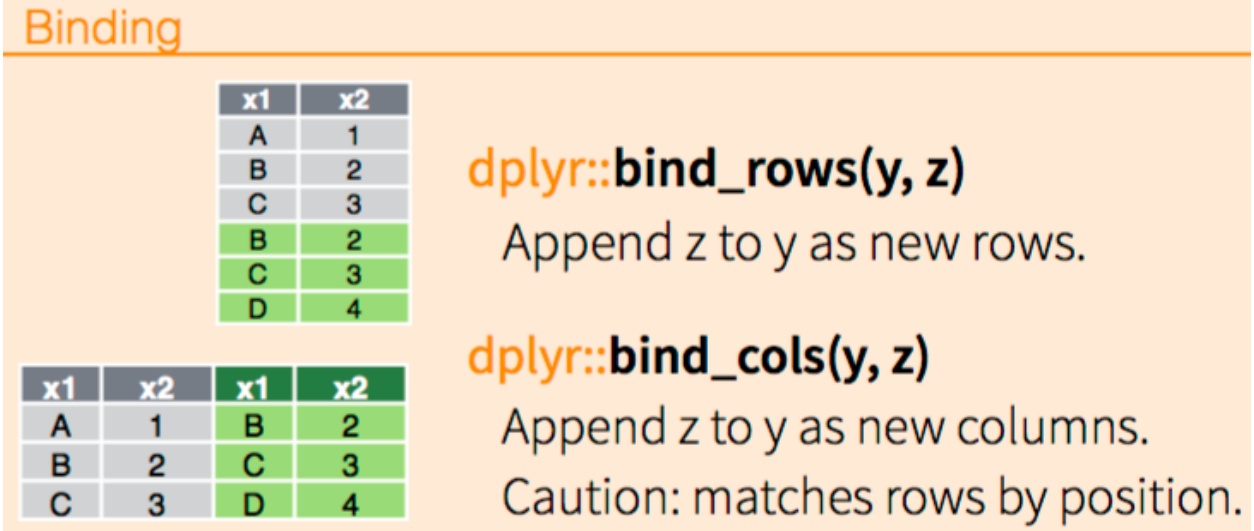
```
## Provide your code here

anti_join(oscars, movies, by = "movie")
```

```
## Source: local data frame [6 x 3]
##
##                  name           movie     category
##                 (chr)           (chr)        (chr)
## 1 Charlotte Rampling        45 Years Best Actress
## 2  Jennifer Lawrence             Joy Best Actress
## 3     Cate Blanchett           Carol Best Actress
## 4     Eddie Redmayne The Danish Girl   Best Actor
## 5 Michael Fassbender      Steve Jobs   Best Actor
## 6     Bryan Cranston          Trumbo   Best Actor
```

Other functions in `dplyr` to join together data frames





Cheatsheets

- Data Wrangling with dplyr and tidyr from RStudio

Data Wrangling

Data Wrangling

In the real world, data science projects rarely involve data that can be easily imported ready for analysis. According to Wikipedia:

> Data munging or data wrangling is loosely the process of manually converting or mapping data from one "raw" form into another format that allows for more convenient consumption of the data with the help of semi-automated tools.

Our example dataset provides an example:

```
url <- "https://raw.githubusercontent.com/datasciencelabs/data/master/bio260-heights.csv"
dat <- read.csv(url)
```

First note how we make assignments in R: we use `<-`. We can also use the equal sign `=` although here we try to stick to `<-` to make it very clear it is an assignment and not logical statement.

We also note that we have put the content of what comes out of `read.csv` into an *object*. We picked the object name `dat`.

So what is `dat` exactly? We can get a quick summary of what an object is with the function `str` (stands for structure)

```
str(dat)
```

```
## 'data.frame':    148 obs. of  3 variables:
##  $ Timestamp                      : Factor w/ 143 levels "1/25/2016 14:39:56",..: 9 10 11 12 13 13 1
##  $ What.is.your.gender.           : Factor w/ 3 levels "Female","I prefer not to disclose",..: 1 1 3
##  $ What.is.your.height..in.inches..: Factor w/ 67 levels "167","168","172",..: 38 35 53 50 58 64 52 6
```

Here we see that this object is a `data.frame`. These are one of the most widely used data types in R. They are particularly useful for storing tables.

To see more of this object we can type it

Now we want to describe the heights. We could simply report the list of numbers. But there is a problem. Take a look at the entries:

```
View(dat)
```

Notice these not all entries are numbers. Furthermore, they are not all in inches. So what to do? We need to wrangle

Extracting columns To extract columns from the data.frame we use the `$` character like this:

```
dat$Timestamp
```

This now gives us a vector. We can access elements of the vector using the `[` symbol:

```
dat$Timestamp[2]
```

```
## [1] 1/25/2016 8:15:21
## 143 Levels: 1/25/2016 14:39:56 1/25/2016 16:32:52 ... 1/27/2016 9:34:14
```

Quick Review of Vectors Vector are a sequence of data elements of the same type. Many of the operations used to analyze data are applied to vectors. In R vectors can be numeric, characters or logical.

The most basic way to creat a vector is with the function `c`

```
x <- c(1,2,3,4,5)
```

Two very common ways of generating vectors are using `:` or the `seq` function:

```
x <- 1:5
x <- seq(1,5)
```

Vecotrs can have names

```
names(x) <- letters[1:5]
x
```

```
## a b c d e
## 1 2 3 4 5
```

Coercion Vectors need to be homogenous. But when R is instructed to create a vector of different types, it does not give an error. Instead it tries to *coerce* values to be the same. Here is an example:

```
height <- c(60, 59, 55, "5'5", 70)
height
```

```
## [1] "60"  "59"  "55"  "5'5" "70"
```

Note that no warning or error was given. It simply changed everything to a character. This is important to know because sometimes we make a mistake in entering data and receive no error message.

Data Manipulation wiht `dplyr`

R provides incredibly powerful and flexible language for data manipulation. However, the syntax is somewhat hard to get used to. We will therefore introducing a package that makes the syntax much more like the English language. This package is `dplyr` which you should install if you have not done so already.

```
library(dplyr)
```

When using `dplyr` we recommend reading in data with the functions in the `readr` package:

```
library(readr)
dat <- read_csv("https://raw.githubusercontent.com/datasciencelabs/data/master/bio260-heights.csv")
```

This object is now a special type of `data.frame` called `tbl_df` that has a nicer printing method. We can now simply evaluate an expression with just the object and see a meaningful summary instead of everything.

```
dat
```

```
## Source: local data frame [148 x 3]
##
##            Timestamp What is your gender? What is your height (in inches)?
##                (chr)                (chr)                             (chr)
## 1  1/25/2016 8:15:15               Female                                63
## 2  1/25/2016 8:15:21               Female                                62
## 3  1/25/2016 8:15:25                 Male                                69
## 4  1/25/2016 8:15:29               Female                                68
## 5  1/25/2016 8:15:37                 Male                             71.65
## 6  1/25/2016 8:15:37                 Male                                75
## 7  1/25/2016 8:15:39                 Male                           68.8976
## 8  1/25/2016 8:15:40                 Male                                74
## 9  1/25/2016 8:15:41               Female                                65
## 10 1/25/2016 8:15:44               Female                              5'4
## ..               ...                  ...                               ...
```

Selecting columns Right, we are interested in looking at heights. We can select just that column using:

```
select(dat, contains("height"))
```

```
## Source: local data frame [148 x 1]
##
##    What is your height (in inches)?
##                               (chr)
## 1                                63
## 2                                62
## 3                                69
## 4                                68
## 5                             71.65
## 6                                75
## 7                           68.8976
## 8                                74
## 9                                65
## 10                             5'4
## ..                             ...
```

We have a problem: this is a `character`. We want numbers.

Renaming columns

Before we continue it will be convenient to change the names of our columns to something more convenient.

```
names(dat) <- c("time","gender","height")
```

Vectorization

```
height <- c(60, 59, 55, "5'5", 70)
height[3]
```

```
## [1] "55"
```

```
as.numeric(height[3])
```

```
## [1] 55
```

One powerful feature of R is that we can *vectorize* most operation

```
 as.numeric(height)
```

```
## Warning: NAs introduced by coercion
```

```
## [1] 60 59 55 NA 70
```

Note now we do receive an warning. This is because R has no idea how to convert "5'5" to a number.

Missing values

Note in the the `NA` value in the object above.

These are missing values. We can find out which values are missing using the function

```
?is.na
```

Adding columns

```
dat <- mutate(dat, numeric_height=as.numeric(height),
              original=height)
```

```
## Warning in eval(substitute(expr), envir, enclos): NAs introduced by
## coercion
```

Subsetting Observations

To see all the row in which we have problems:

```
filter(dat, is.na(numeric_height))
```

```
## Source: local data frame [21 x 5]
##
##                  time                    gender height numeric_height
##                 (chr)                     (chr)  (chr)          (dbl)
## 1   1/25/2016 8:15:44                    Female    5'4             NA
## 2   1/25/2016 8:15:45                    Female   5'8"             NA
## 3   1/25/2016 8:15:45                    Female    5'5             NA
## 4   1/25/2016 8:29:00                      Male    5'7             NA
## 5  1/25/2016 14:39:56                    Female    5'6             NA
## 6  1/25/2016 22:02:03                      Male  5'11"             NA
## 7   1/26/2016 8:36:33 I prefer not to disclose  5'10"             NA
## 8   1/26/2016 9:49:15                      Male   5'7"             NA
## 9   1/26/2016 9:49:19                      Male    5'7             NA
## 10  1/26/2016 9:51:19                    Female    5'8             NA
## ..                ...                       ...    ...            ...
## Variables not shown: original (chr)
```

The Pipe

```
filter(dat, is.na(numeric_height)) %>% select(height)
```

```
## Source: local data frame [21 x 1]
##
##    height
##     (chr)
## 1     5'4
## 2    5'8"
## 3     5'5
## 4     5'7
## 5     5'6
## 6   5'11"
## 7   5'10"
## 8    5'7"
## 9     5'7
## 10    5'8
## ..    ...
```

Let's see more

```
filter(dat, is.na(numeric_height)) %>% select(height) %>% print(n=21)
```

```
## Source: local data frame [21 x 1]
##
##           height
##            (chr)
## 1            5'4
## 2           5'8"
## 3            5'5
## 4            5'7
## 5            5'6
## 6          5'11"
```

```
## 7          5'10"
## 8           5'7"
## 9            5'7
## 10           5'8
## 11        5' 11"
## 12          6'1"
## 13           69"
## 14         5' 7"
## 15        5'10''
## 16          5'10
## 17          5'10
## 18  5ft 9 inches
## 19 5 ft 9 inches
## 20           5'2
## 21          5'11
```

gsub One of the most useful functions for data wranglin is `gsub`. It let's us searches for characters and substitutes it for others. More general it searches for regular expression. We will learn about those later.

Here is an example:

```
x <- dat$height[109:116]
x
```

```
## [1] "5'10"          "70"            "67.7"          "62"
## [5] "5ft 9 inches"  "5 ft 9 inches" "5'2"           "74"
```

Note that we are using both `'` and `ft` as the same thing. To simplify the problem we want to substitute one for the other. `gsub` does the trick:

```
x <- gsub("ft", "'", x)
x
```

```
## [1] "5'10"         "70"           "67.7"         "62"
## [5] "5' 9 inches"  "5 ' 9 inches" "5'2"          "74"
```

The word inches is not doing anything here so we might as well remove it.

```
x <- gsub("inches","",x)
x
```

```
## [1] "5'10"   "70"     "67.7"   "62"     "5' 9 "  "5 ' 9 " "5'2"    "74"
```

We are now ready to start fixing the height data:

```
dat <- mutate(dat, height= gsub("ft","'",height) ) %>%
  mutate(height= gsub("\"|inches|\ |''","",height) )
```

Functions

Up to now we have used prebuilt functions. However, many times we have to construct our own. We can do this in R using the `function`:

```
avg <- function(x){
  return( sum(x) / length(x) )
}
avg( 1:5 )
```

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

Assessment: Construct a function that computes the variance defined as follows for a vector $x_1, \ldots, x_n$:

$$\frac{1}{n}\sum_{i=1}^{n}(x_i - \mu)^2 \text{ with } \mu = \frac{1}{n}\sum_{i=1}^{n} x_i$$

What is the variance of `1:5` ?

Assessment: Write a function `convert` that takes two character arguments, feet and inches as characters, and returns inches

Here we construct a more complicated function that changes 5'4 to `5*12+4`

```
fixheight <- function(x){
  y <- strsplit(x, "'")
  ret <- sapply(y, function(z){
    ifelse( length(z)>1, as.numeric(z[1])*12 + as.numeric(z[2]) ,
            as.numeric(z[1]))
  })
  return(ret)
}
```

We can now test the function

```
fixheight( "70")
```

```
## [1] 70
```

```
fixheight( "5'10")
```

```
## [1] 70
```

```
fixheight( c("5'9","70","5'11"))
```

```
## [1] 69 70 71
```

Finally we can mutate our data:

```
dat <- mutate(dat, height=fixheight(height)) %>% select(-numeric_height)
```

The last call to select removes the now unecessary column `numeric_height`. Let's see the result:

```
filter(dat, is.na(height)) %>% select(height)
```

```
## Source: local data frame [0 x 1]
##
## Variables not shown: height (dbl)
```

We have removed all the NAs

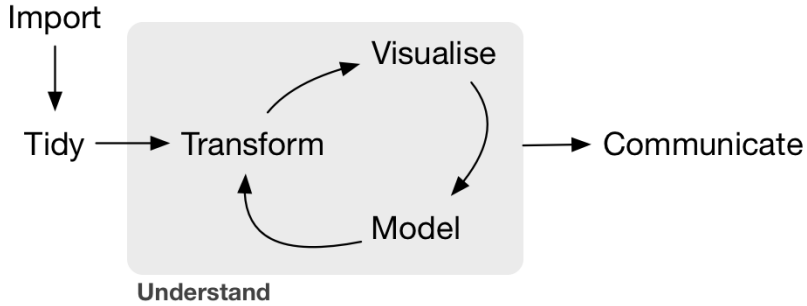
Data Wrangling with `tidyr`

Stephanie Hicks, Rafael Irizarry

The data analysis process can be thought about in four parts

1. Data cleaning
2. Data transformation
3. Data visualization
4. Modeling

where we each of these steps need their own tools and software to complete.



As we have seen in class, one of the most time-consuming aspects of the data analysis process is "data wrangling". This is also known as "data munging", which is a trendy term for *cleaning up a messy data set*. This refers to the first two steps in the data analysis process:

1. Data cleaning (or tidying data)
2. Data transformation

It can take a long time to clean and transform messy data into a format that is useful for data visualization and modeling, but there are tools that can help turn messy data into clean data.

Defining data structures

There are many ways to define the structure of a data set. Most data frames are made up of **rows** and **columns** where the columns are almost always labeled and the rows are *sometimes* labeled.

For example, a data set could be structured in the following way:

- each row represents one company (row names are companies)
- each column represent one time point
- the stock prices are defined for each row/column pair

```
> stocks
         2016-01-01 2016-01-02 2016-01-03 2016-01-04 2016-01-05
Google     99.43952   99.76982  101.55871  100.07051  100.12929
Facebook  103.43013  100.92183   97.46988   98.62629   99.10868
Twitter   104.89633  101.43926  101.60309  100.44273   97.77664
```

Alternatively, a data set can be structured in the following way:

- each row represents one time point (but no row names)
- the first column defines the time variable and the last three columns contain the stock prices for three companies

```
> stocks
        time    Google  Facebook   Twitter
1 2016-01-01  99.43952 103.43013 104.89633
2 2016-01-02  99.76982 100.92183 101.43926
3 2016-01-03 101.55871  97.46988 101.60309
4 2016-01-04 100.07051  98.62629 100.44273
5 2016-01-05 100.12929  99.10868  97.77664
```

In both cases, the data is the same, but the structure is different. This can be *frustrating* to deal with because the meaning of the values (rows and columns) in the two data sets are different. Providing a standardized way of organizing values within a data set would alleviate a major portion of this frustration.

Defining tidy data

Now, we will introduce the concept of **tidy** data. Tidy data is a standard way of mapping the meaning of a dataset to its structure. The properties of a tidy data set are based on:

- Each column is a variable
- Each rows is an observation

Working with tidy data is useful because it creates a structured way of organizing data values within a data set. This makes the data analysis process more efficient and simplifies the development of data analysis tools that work together. In this way, you can focus on the problem you are investigating, rather than the uninteresting logistics of data.

What is `tidyr`?

`tidyr` is an R package that transforms data sets to a tidy format.

There are two main functions in `tidyr`:

- `gather()` = takes multiple columns, and gathers them into key-value pairs (it makes "wide" data longer)
- `separate()` = turns a single character column into multiple columns (it makes "long" data wider)

We'll explore what it means to go between a "wide" and "long" data format using `gather()` and `separate()` next.

How do I get tidyr?

To install `tidyr`

```
install.packages("tidyr")
```

To load `tidyr` and we'll need `dplyr`

```
library(tidyr)
library(dplyr)
```

For motivation, a tidy version of the stock data we looked at above looks like this: (we'll learn how the functions work in just a moment)

```
> stocks %>%
+     gather(company, price, Google:Twitter)
         time  company     price
1  2016-01-01   Google  99.43952
2  2016-01-02   Google  99.76982
3  2016-01-03   Google 101.55871
4  2016-01-04   Google 100.07051
5  2016-01-05   Google 100.12929
6  2016-01-01 Facebook 103.43013
7  2016-01-02 Facebook 100.92183
8  2016-01-03 Facebook  97.46988
9  2016-01-04 Facebook  98.62629
10 2016-01-05 Facebook  99.10868
11 2016-01-01  Twitter 104.89633
12 2016-01-02  Twitter 101.43926
13 2016-01-03  Twitter 101.60309
14 2016-01-04  Twitter 100.44273
15 2016-01-05  Twitter  97.77664
```

In this "tidy" data set, we have three columns representing three variables (time, company name and stock price). Every row represents contains one stock price from a particular time and for a specific company.

Pipe operator: %>%

We have introduced the operator: `%>%`. dplyr imports this operator from another package (`magrittr` see help file here). This operator allows you to pipe the output from one function to the input of another function. Instead of nesting functions (reading from the inside to the outside), the idea of of piping is to read the functions from left to right.

Now in this case, we pipe the `stocks` data frame to the function that will gather multiple columns into key-value pairs.

Data

2016 Iowa Presidential Caucus

We will explore public poll data from HuffPost Pollster from the 2016 Iowa Democratic and Republican Presidential Caucus.

First we will read in the data:

```
library(readr)
dem_polls = read_csv("http://elections.huffingtonpost.com/pollster/2016-iowa-presidential-democratic-cau
rep_polls = read_csv("http://elections.huffingtonpost.com/pollster/2016-iowa-presidential-republican-cau
```

Let's take a look at data

```
View(dem_polls)
View(rep_polls)

glimpse(dem_polls)
glimpse(rep_polls)
```

We see there is a lot of information in each data frame. First let's use `dplyr` to select a subset of the columns.

```
dem_polls <- dem_polls %>%
                select(Pollster, `End Date`, Clinton:Undecided)

rep_polls <- rep_polls %>%
                select(Pollster, `End Date`, Trump:Walker)
```

In the democratic and republican polling data sets, there is one column representing the polling percentages for each candidate, similar to the stock price data set with multiple columns representing different companies. To **tidy** it, we need to *gather* these columns into a two-column *key-value* pair. This is often described as transforming a *wide* data set into a *long* data set.

gather()

This function gathers multiple columns and collapses them into new *key-value* pairs. This transform data from *wide* format into a *long* format.

- The `key` is the name of the *new* column that you are creating which contains the values of the column headings that you are gathering
- The `value` is the name of the *new* column that will contain the values themselves
- The third argument defines the columns to gather

```
dem_polls %>%
    gather(key = candidate, value = percentage, Clinton:Undecided)
```

```
## Source: local data frame [648 x 4]
##
##                                Pollster   End Date candidate percentage
```

```
##                                  (chr)     (date)     (chr)      (int)
## 1       Emerson College Polling Society 2016-01-31   Clinton         51
## 2                           Quinnipiac 2016-01-31   Clinton         46
## 3  Des Moines Register/Bloomberg/Selzer 2016-01-29   Clinton         45
## 4     Gravis Marketing/One America News 2016-01-27   Clinton         53
## 5                 PPP (D-Progress Iowa) 2016-01-27   Clinton         48
## 6                       NBC/WSJ/Marist 2016-01-26   Clinton         48
## 7                   Monmouth University 2016-01-26   Clinton         47
## 8                                   ARG 2016-01-24   Clinton         45
## 9                           Quinnipiac 2016-01-24   Clinton         45
## 10                    Iowa State/WHO-HD 2016-01-22   Clinton         47
## ..                                  ...        ...       ...        ...
```

To select a range of columns by name, use the ":" (colon) operator

Assessment Using the democratic poll data, apply the `gather()` function to tidy the poll data by *excluding* the Pollster and End Date columns, rather than directly providing the column names to gather.

Hint: Look at the `gather()` help file on how to exclude column names.

```
## Provide your code here

dem_polls %>%
    gather(key = candidate, value = percentage, -c(Pollster, `End Date`))
```

```
## Source: local data frame [648 x 4]
##
##                                Pollster   End Date candidate percentage
##                                   (chr)     (date)     (chr)      (int)
## 1       Emerson College Polling Society 2016-01-31   Clinton         51
## 2                           Quinnipiac 2016-01-31   Clinton         46
## 3  Des Moines Register/Bloomberg/Selzer 2016-01-29   Clinton         45
## 4     Gravis Marketing/One America News 2016-01-27   Clinton         53
## 5                 PPP (D-Progress Iowa) 2016-01-27   Clinton         48
## 6                       NBC/WSJ/Marist 2016-01-26   Clinton         48
## 7                   Monmouth University 2016-01-26   Clinton         47
## 8                                   ARG 2016-01-24   Clinton         45
## 9                           Quinnipiac 2016-01-24   Clinton         45
## 10                    Iowa State/WHO-HD 2016-01-22   Clinton         47
## ..                                  ...        ...       ...        ...
```

```
## To select all the columns *except* a specific column,
## use the "-" (subtraction) operator (also known as negative indexing)
```

Assessment Using the "tidy" democratic poll data, use dplyr to filter for only the following candidates (Clinton, Sanders, O'Malley) and for polls only ending after May 1, 2015.

```
## Provide your code here

dem_polls %>%
    gather(key = candidate, value = percentage, Clinton:Undecided) %>%
    filter(candidate %in% c("Clinton", "Sanders", "O'Malley") &
           `End Date` >= "2015-05-01")
```

```
## Source: local data frame [195 x 4]
##
##                                Pollster   End Date candidate percentage
##                                   (chr)     (date)     (chr)      (int)
## 1       Emerson College Polling Society 2016-01-31   Clinton         51
## 2                           Quinnipiac 2016-01-31   Clinton         46
## 3  Des Moines Register/Bloomberg/Selzer 2016-01-29   Clinton         45
## 4     Gravis Marketing/One America News 2016-01-27   Clinton         53
## 5                  PPP (D-Progress Iowa) 2016-01-27   Clinton         48
## 6                        NBC/WSJ/Marist 2016-01-26   Clinton         48
## 7                    Monmouth University 2016-01-26   Clinton         47
## 8                                   ARG 2016-01-24   Clinton         45
## 9                           Quinnipiac 2016-01-24   Clinton         45
## 10                    Iowa State/WHO-HD 2016-01-22   Clinton         47
## ..                                  ...        ...       ...        ...
```

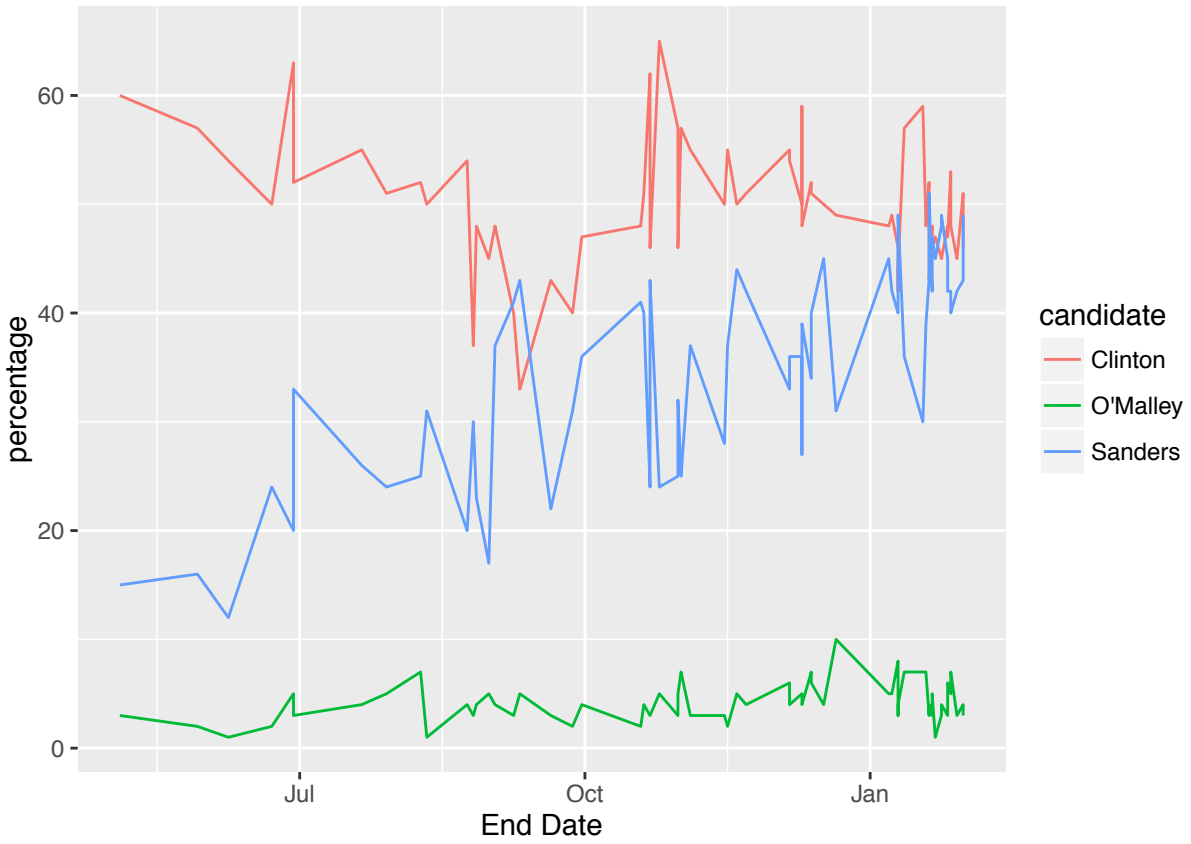
Assessment (optional) Using the tidy and filtered democratic poll data set, use `ggplot2` to plot the results from each poll (percentage) for each of the candiates. Color the lines by the candidate.

```
## Provide your code here

library(ggplot2)
```

```
## Warning: package 'ggplot2' was built under R version 3.2.4
```

```
dem_polls %>%
    gather(key = candidate, value = percentage, Clinton:Undecided) %>%
    filter(candidate %in% c("Clinton", "Sanders", "O'Malley") &
           `End Date` >= "2015-05-01") %>%
    ggplot(aes(x=`End Date`, y = percentage, color = candidate)) +
    geom_line()
```

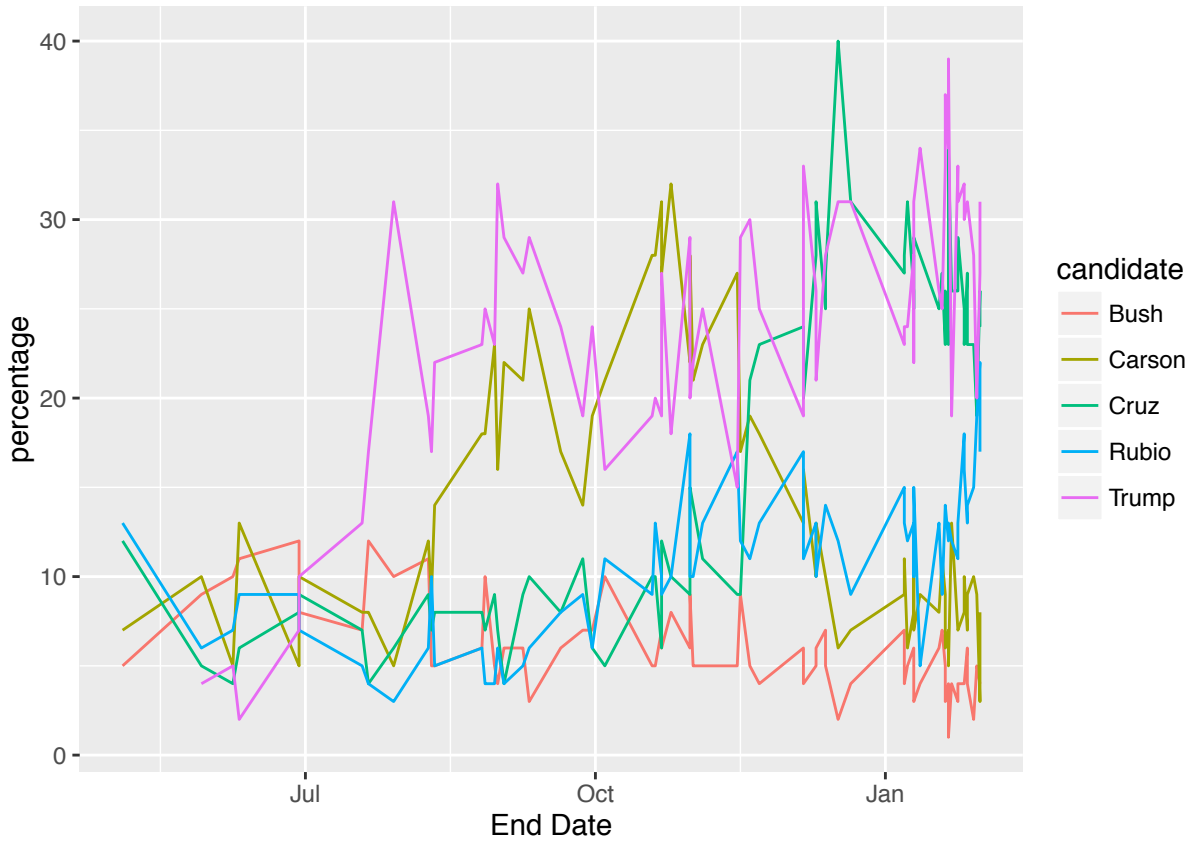


Assessment (optional) Repeat this analysis using the republican poll data. Filter for candidates (Trump, Cruz, Rubio, Carson, Bush) and for polls only after May 1, 2015. Color the lines by candidates.

```
## Provide your code here

rep_polls %>%
    gather(key = candidate, value = percentage, Trump:Walker) %>%
    filter(candidate %in% c("Trump", "Cruz", "Rubio", "Carson", "Bush") &
           `End Date` >= "2015-05-01") %>%
    ggplot(aes(x=`End Date`, y = percentage, color = candidate)) +
    geom_line()
```

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



spread()

In contrast to *gathering* multiple columns into key-value pairs, we can *spread* a key-value pair across multiple columns.

The function `spread()` does just that. It transforms data from a *long* format into a *wide* format.

- The `key` is the name of the column in your data set that contains the values of the column headings that you are spreading across multiple columns
- The `value` is the name of the column that contains the values for the multiple columns

```
dem_polls_gathered <- dem_polls %>%
                        gather(key = candidate, value = percentage,
                               Clinton:Undecided)
dem_polls_gathered
```

```
## Source: local data frame [648 x 4]
##
##                               Pollster   End Date candidate percentage
##                                  (chr)     (date)     (chr)      (int)
## 1       Emerson College Polling Society 2016-01-31   Clinton         51
## 2                             Quinnipiac 2016-01-31   Clinton         46
## 3  Des Moines Register/Bloomberg/Selzer 2016-01-29   Clinton         45
## 4     Gravis Marketing/One America News 2016-01-27   Clinton         53
```

```
## 5                 PPP (D-Progress Iowa) 2016-01-27   Clinton         48
## 6                        NBC/WSJ/Marist 2016-01-26   Clinton         48
## 7                  Monmouth University 2016-01-26   Clinton         47
## 8                                  ARG 2016-01-24   Clinton         45
## 9                           Quinnipiac 2016-01-24   Clinton         45
## 10                Iowa State/WHO-HD 2016-01-22   Clinton         47
## ..                                ...        ...       ...        ...
```

```
dem_polls_gathered %>%
    spread(key = candidate, value = percentage)
```

```
## Source: local data frame [81 x 10]
##
##      Pollster   End Date Biden Chafee Clinton Lessig O'Malley Sanders
##         (chr)     (date) (int)  (int)   (int)  (int)    (int)   (int)
## 1         ARG 2016-01-10    NA     NA      44     NA        3      47
## 2         ARG 2016-01-24    NA     NA      45     NA        3      48
## 3  CBS/YouGov 2015-09-10    10      1      33     NA        5      43
## 4  CBS/YouGov 2015-10-22    NA      1      46      0        3      43
## 5  CBS/YouGov 2015-11-19    NA     NA      50     NA        5      44
## 6  CBS/YouGov 2015-12-17    NA     NA      50     NA        4      45
## 7  CBS/YouGov 2016-01-21    NA     NA      46     NA        5      47
## 8         CNN 2014-09-10    15     NA      53     NA        2       5
## 9         CNN 2015-08-11    12      0      50     NA        1      31
## 10        CNN 2015-11-04    NA     NA      55     NA        3      37
## ..        ...        ...   ...    ...     ...    ...      ...     ...
## Variables not shown: Undecided (int), Webb (int)
```

Other supporting functions in tidyr

- `separate()` = separate one column into multiple columns
- `unite()` = unite multiple columns into one

```
dem_polls_separate <- dem_polls %>%
                        separate(col = `End Date`, into = c("y", "m", "d"))
dem_polls_separate
```

```
## Source: local data frame [81 x 12]
##
##                               Pollster     y     m     d Clinton Sanders
##                                  (chr) (chr) (chr) (chr)   (int)   (int)
## 1       Emerson College Polling Society  2016    01    31      51      43
## 2                           Quinnipiac  2016    01    31      46      49
## 3  Des Moines Register/Bloomberg/Selzer  2016    01    29      45      42
## 4     Gravis Marketing/One America News  2016    01    27      53      42
## 5                 PPP (D-Progress Iowa)  2016    01    27      48      40
## 6                        NBC/WSJ/Marist  2016    01    26      48      45
## 7                  Monmouth University  2016    01    26      47      42
## 8                                  ARG  2016    01    24      45      48
## 9                           Quinnipiac  2016    01    24      45      49
## 10                Iowa State/WHO-HD  2016    01    22      47      45
## ..                                ...   ...   ...   ...     ...     ...
```

```
## Variables not shown: O'Malley (int), Biden (int), Chafee (int), Lessig
##   (int), Webb (int), Undecided (int)
```

Assessment Use the `unite()` function to create a new column titled "end_date" that combines the columns `y`, `m` and `d` together into a single column separated by the "/" character.

```
## Provide your code here

dem_polls_separate %>%
    unite(col = end_date, y, m, d, sep = "/")
```

```
## Source: local data frame [81 x 10]
##
##                                Pollster   end_date Clinton Sanders
##                                   (chr)      (chr)   (int)   (int)
## 1       Emerson College Polling Society 2016/01/31      51      43
## 2                             Quinnipiac 2016/01/31      46      49
## 3  Des Moines Register/Bloomberg/Selzer 2016/01/29      45      42
## 4     Gravis Marketing/One America News 2016/01/27      53      42
## 5                  PPP (D-Progress Iowa) 2016/01/27      48      40
## 6                        NBC/WSJ/Marist 2016/01/26      48      45
## 7                    Monmouth University 2016/01/26      47      42
## 8                                   ARG 2016/01/24      45      48
## 9                             Quinnipiac 2016/01/24      45      49
## 10                    Iowa State/WHO-HD 2016/01/22      47      45
## ..                                   ...        ...     ...     ...
## Variables not shown: O'Malley (int), Biden (int), Chafee (int), Lessig
##   (int), Webb (int), Undecided (int)
```

Cheatsheets

- Data Wrangling with dplyr and tidyr from RStudio