The University of Texas at Austin
School of Information

Stats: Numerical Inference

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Week EIGHT

Homework

```r
x<-c(0,2,NA,2,2,1.9,1.9,1.9,1.9,0,2)
stem(x)
```

```
  The decimal point is at the |

  0 | 00
  0 |
  1 |
  1 | 9999
  2 | 0000
```

Numerical data

Recap Week 07

- Inference for Categorical Data
  - Inference for a single proportion
  - Difference of two proportions
  - Testing goodness of fit using χ^2
  - Testing independence of contingency tables

Inference for numerical data

- Textbook section 7.1 One-sample means with the t-distribution
- Textbook section 7.2 Paired data
- Textbook section 7.3 Difference of two means
- Textbook section 7.4 Power calculations for a difference of means
- Textbook section 7.5 Comparing many means with ANOVA

Textbook Section 7.1 One-sample means with the t-distribution

Modeling $\bar{x}$, the mean of a random sample from a normally distributed population, requires that the sample elements are

- independent—a random sample or a sample from a random process
- normally distributed—sample drawn from a normally distributed population

Rule of thumb for normality

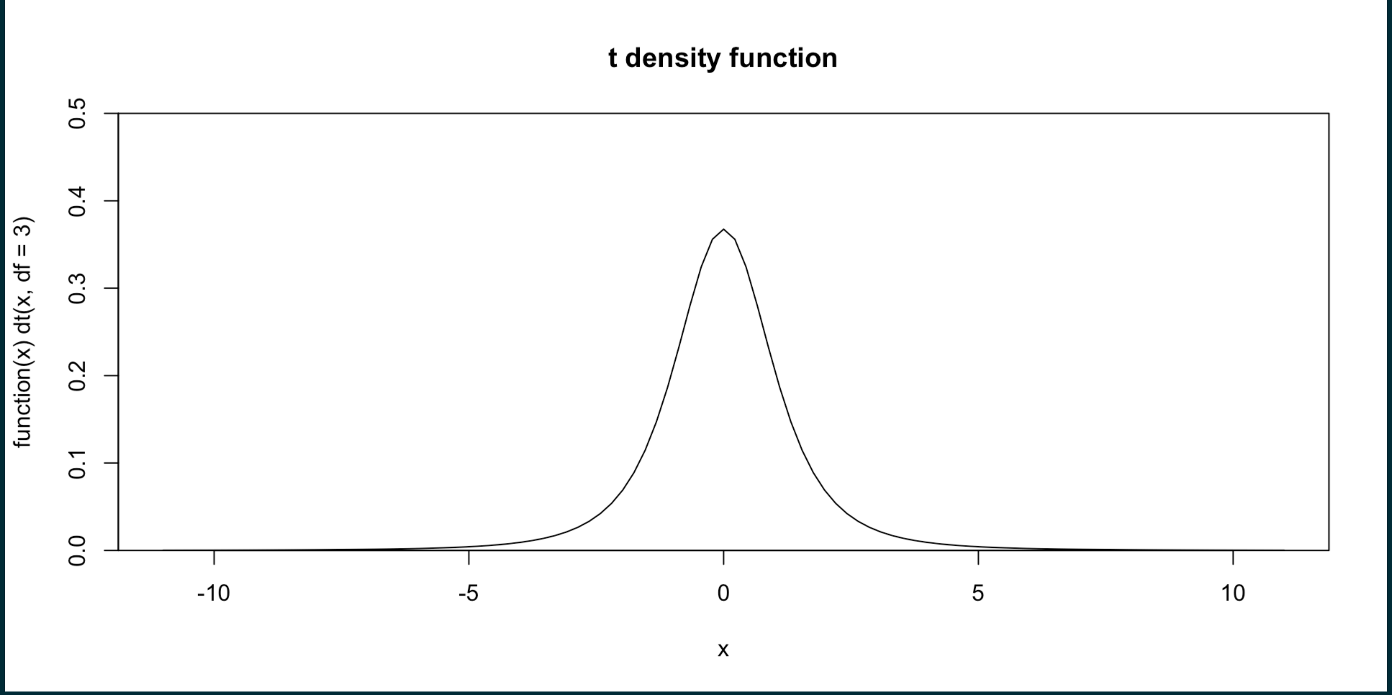
- $n < 30$ and no outliers, assume data come from a normally distributed population
- $n \geqslant 30$ and no extreme outliers, assume $\bar{x} \sim N(\mu, \sigma)$ even if data come from a not normally distributed population

t-distribution

The t-distribution is useful for small samples ($n < 30$). It was discovered when a man named Gossett was trying to figure out how few samples of beer he could get away with in tests for the Guinness brewery about 120 years ago. He preferred to remain anonymous at the time because he didn’t want his employers to question his *outside* activities, otherwise this would probably be called the Gossett’s t-distribution. Instead, he referred to himself as “A Student” so it came to be known as the Student’s t-distribution.

For sample sizes over thirty, it converges to looking like the normal distribution, but for smaller samples, it gets more and more peaked and the tails get thicker and thicker. For example, here is the density function for a sample size of 4.

```r
plot(function(x) dt(x, df = 3), -11, 11, ylim = c(0, 0.50), main = "t densi
```



Caution

Bear in mind that the `t()` function in R has nothing to do with the *t*-distribution (it's for transposing matrices and data frames). Instead, the functions for handling the *t*-distribution are the letter t prefaced by d, q, p, or r. You may have noticed that we saw functions like `pnorm()` and `dnorm()` when working with the normal distribution. These functions are analogous.

Parameter of the *t*-distribution

The t-distribution has $n - 1$ degrees of freedom, so you can tell that the above example has $n = 4$ since $\text{df} = 3$.

Also keep in mind that the mean is always zero for the t-distribution, so it just has one parameter, df. So in the above example, you could say $\bar{x} \sim t(3)$.

Calculations

Analogous to the `pnorm()` function, you can calculate regions of the t-distribution using the `pt()` function. For example, if you conduct a test that returns a t-statistic of -2.10 and $n = 19$, you can use the following to find out that the area to the left of the statistic is 0.025. (This example and the two following are illustrated in textbook Figure 7.4.)

```r
pt(-2.1,18)
```

```
[1] 0.0250452
```

Example of probability calculation

Suppose you obtain a *t*-statistic of 1.65 on 20 degrees of freedom. How much of the probability is in the upper tail? There are two obvious ways to do this.

```r
pt(1.65,20,lower.tail=FALSE)
```

```
[1] 0.05728041
```

```r
1-pt(1.65,20)
```

```
[1] 0.05728041
```

Find the probability in both tails for a *t*-statistic of ± 3 and two degrees of freedom.

```r
pt(-3,2)+pt(3,2,lower.tail=FALSE)
```

```
[1] 0.09546597
```

Calculating the *t*-statistic

Textbook example 7.8 asks you to calculate the *t*-statistic when you know the proportion. In this case, $df = 18$ and you want to know the *t*-statistic corresponding to 0.025 in the upper tail. You can use the `qt()` function where q stands for quantile. The region 0.025 in the upper tail corresponds to a 95 percent confidence interval because there will be 0.025 in each of the two tails for a total of five percent. The *t*-statistic for the lower tail would simply be the negative of the *t*-statistic for the upper tail.

```r
qt(0.025,18,lower.tail=FALSE)
```

```
[1] 2.100922
```

Confidence Intervals

To construct a confidence interval, you'll generally choose 90 or 95 percent, depending on the sensitivity of the real world problem. Then you'll plug that into the following formula.

$$\bar{x} \pm t^{*}_{df} \frac{s}{\sqrt{n}}$$

This assumes you have already checked the normality and independence constraints.

Calculating a confidence interval

For the textbook examples, you are given components of the formula. It is quite a bit simpler if you are given the raw data. For example, calculate a 95 percent confidence interval for the body mass in grams of the penguins in the Palmer penguins data frame.

```r
pacman::p_load(palmerpenguins)
model <- lm(body_mass_g ~ 1,penguins)
confint(model,level=0.95)
```

```
               2.5 %  97.5 %
(Intercept) 4116.458 4287.05
```

The preceding incantation may seem a little mysterious but you'll explore it in excruciating detail when you learn linear regression.

One sample *t*-tests

The textbook gives a lengthy example of the runner times of the Cherry Blossom race. I assume that the data are the `run10samp` and `run17samp` data frames from the textbook website, so I downloaded the RData versions of them and loaded them as follows.

```r
load(paste0(Sys.getenv("STATS_DATA_DIR"),"/run10samp.rda"))
load(paste0(Sys.getenv("STATS_DATA_DIR"),"/run17samp.rda"))
t.test(run17samp$clock_sec/60,mu=93.29,alternative="t")
```

```

    One Sample t-test

data:  run17samp$clock_sec/60
t = 1.9776, df = 99, p-value = 0.05075
alternative hypothesis: true mean is not equal to 93.29
95 percent confidence interval:
  93.26973 105.46227
sample estimates:
mean of x 
   99.366 
```

Textbook Section 7.2 Paired data

Suppose you want to know if two data frames were drawn from the same distribution or if they differ.

The textbook example is of the mean prices of textbooks on Amazon and in the UCLA campus bookstore. The data appear to be the textbooks data frame on the textbook website, although the statistics are different and the textbook says that there were two such samples (only one is on the website that I could find). Because they have precomputed the difference as the `diff` column, you can do this the same way as for a one sample test.

```r
load(paste0(Sys.getenv("STATS_DATA_DIR"),"/textbooks.rda"))
with(textbooks,t.test(diff))
```

```
    One Sample t-test

data:  diff
t = 7.6488, df = 72, p-value = 6.928e-11
alternative hypothesis: true mean is not equal to 0
95 percent confidence interval:
  9.435636 16.087652
sample estimates:
mean of x
 12.76164
```

Note that the default is that the difference is 0 and the 95 percent confidence interval is quite far from including 0. Also, the *p*-value is infinitesimal. We definitely reject the null hypothesis that the stores have similar prices.

If you didn’t have the `diff` column, you could get the same result by saying the following.

```r
with(textbooks,t.test(ucla_new,amaz_new,paired=TRUE))
```

```

	Paired t-test

data:  ucla_new and amaz_new
t = 7.6488, df = 72, p-value = 6.928e-11
alternative hypothesis: true mean difference is not equal to 0
95 percent confidence interval:
  9.435636 16.087652
sample estimates:
mean difference 
       12.76164 
```

Textbook Section 7.3 Difference of two means

In the previous section, you considered the means of the differences but in this section you consider the differences of the means. In the Amazon and UCLA example, the items were paired and we subtracted the price of a particular title sold by one seller from the price of the *same* title sold by the other seller. But what if we have data that is not paired like this? The textbook gives an example of a radical stem cell treatment given to sheep. One of two treatments is given to each sheep, but there is no correspondence between individual pairs of sheep.

In this case, there may be different variance between the two groups, as well as different means. So the standard error is calculated as

$$\mathrm{SE} = \sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}$$

Notice that this formula implies that the samples could differ in size as well as variance.

For the sheep example, heart pumping capacity was measured, where more is better. The `stem_cell` data frame on the textbook website seems to be the appropriate data frame here. Conducting the test in R follows.

```r
load(paste0(Sys.getenv("STATS_DATA_DIR"),"/stem_cell.rda"))
with(stem_cell,t.test(after-before~trmt,var.equal=FALSE))
```

```
    Welch Two Sample t-test

data:  after - before by trmt
t = -4.0073, df = 12.225, p-value = 0.001678
alternative hypothesis: true difference in means between group ctrl and group
esc is not equal to 0
95 percent confidence interval:
 -12.083750  -3.582916
sample estimates:
mean in group ctrl  mean in group esc
         -4.333333           3.500000
```

The result is a statistically significant difference between the sheep in the control group and the sheep treated with stem cells. The sheep in the stem cell group enjoyed a 3.5 unit increase in heart pumping capacity, while the poor sheep in the control group lost four and a third units. Of course, the practical question you have to ask yourself is whether these numbers have a practical significance. You would need domain knowledge to tell whether 3.5 units is a lot of heart pumping capacity!

Textbook Section 7.4 Power calculations for a difference of means

The pictures in section 7.4, particularly the two on page 280 of the textbook, are essential for understanding power calculation, so let's use the textbook exclusively for this section. To do the calculations in R, you can use the `pwr` package. However, for the weekly exercises, please use the method described in the Diez, Çetinkaya-Rundel, and Barr (2019) book instead of using the `pwr` package. This is simply so you understand the meaning of the calculations. After you've done it once, I'll describe the `pwr` approach.

All I want to say to preface our look at the textbook is to define the terms *power* and α. The statistical term *power* refers to the probability of rejecting the null hypothesis when it is false. The greek letter α, pronounced alpha, refers to the probability of rejecting the null hypothesis when it is true. It is typical in practice to use $\alpha = 0.05$ except in life or death cases (where it is set to 0.01) and to use *power*$= 0.8$.

Textbook Section 7.5 Comparing many means with ANOVA

The textbook makes three important observations about the diagnostics for ANOVA:

- Independence is always important
- The normality condition is especially important in the face of small sample sizes
- The constant variance assumption is especially important in the face sample sizes differing between groups

Textbook exercise 7.54 compares eight methods for loosening rusty bolts. Four samples were collected for each method and the results are in the `penetrating_oil` data frame on the textbook website. You can conduct an ANOVA test on the results using R as follows.

```r
load(paste0(Sys.getenv("STATS_DATA_DIR"),"/penetrating_oil.rda"))
with(penetrating_oil,anova(lm(torque~treatment)))
```

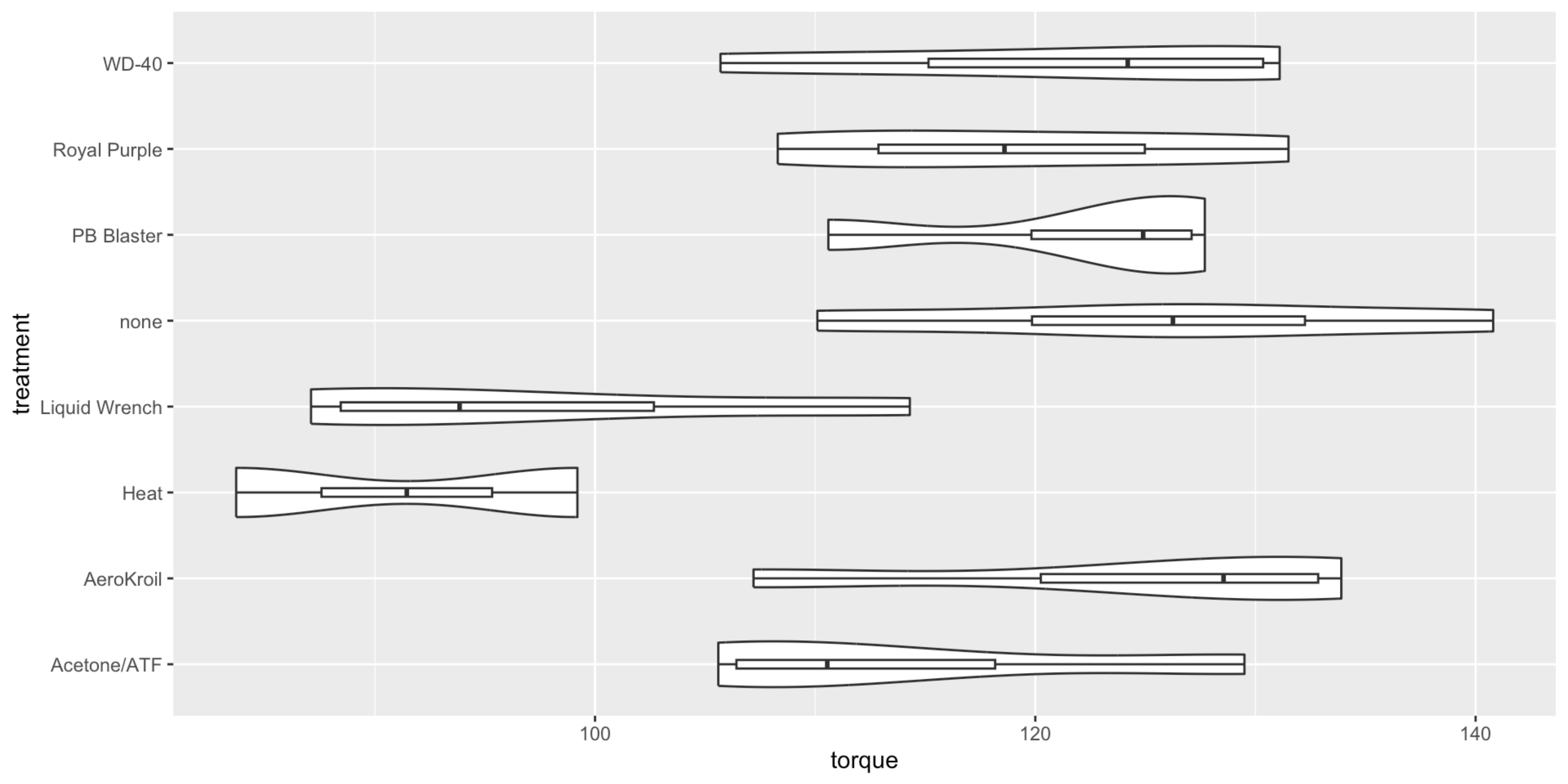
```
Analysis of Variance Table

Response: torque
          Df Sum Sq Mean Sq F value   Pr(>F)   
treatment  7 3603.4  514.78  4.0263 0.005569 **
Residuals 22 2812.8  127.85                    
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

The table shows that the numerator degrees of freedom are $k - 1 = 7$. Keep in mind that k is the number of groups, which must therefore be eight. The denominator degrees of freedom are $n - k = 22$, so there must be a total of 30 samples. Yet there are eight groups, suggesting four samples per group. Examining the data closely, you will find that there are only two samples for `heat` and four for each of the others.

Here you are comparing whether any of the eight means of torque differ. They certainly seem to, with a large F-statistic and a small p-value. It might be helpful to visualize the differences with a combination violin plot and boxplot. There are really too few samples for each treatment.

```r
pacman::p_load(tidyverse)
penetrating_oil |>
  ggplot(aes(torque,treatment)) +
  geom_violin() +
  geom_boxplot(width=0.1)
```



END

References

Diez, David, Mine Çetinkaya-Rundel, and Cristopher D Barr. 2019. *OpenIntro Statistics, Fourth Edition*. self-published. https://openintro.org/os.

Colophon

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