431 Class 13

thomaselove.github.io/431

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Today's Agenda

- Confidence Intervals for a Mean
  - with indicator variable regression or with a t distribution
  - with the bootstrap
  - with the Wilcoxon signed-rank procedure
  - Interpreting the Results
- *p* values and statistical significance
- The `dm431` data and the `dm431_2020` data files

Today's R Packages and Data

```
library(broom)
library(janitor)
library(knitr)
library(magrittr)
library(patchwork)
library(tidyverse)

theme_set(theme_bw())

dm431 <- readRDS("data/dm431_2020.Rds")
```

Fundamentals of Statistical Inference

Something Happened! Is this Signal or Noise?

Very often, sample data indicate that something has happened. . .

- the proportion of people who respond to this treatment has changed
- the mean value of this measure appears to have changed

Before we get too excited, it's worth checking whether the apparent result might possibly be the result of random sampling error.

Statistics provides a number of tools for reaching an informed choice (informed by sample information, of course) including confidence intervals and hypothesis tests (p values), in particular.

Key Questions: Making Inferences From A Sample

1. What is the population about which we aim to make an inference?
2. What is the sample available to us to make that inference?
    - Who are the individuals fueling our inference?
    - What data are available to make an inference?
3. Why might this study population not represent the target population?

For more, see Spiegelhalter, Chapter 3.

Systolic Blood Pressure in the dm431 data

Here, I will look at systolic blood pressure values from a sample of 431 adult patients living in Northeast Ohio between the ages of 31 and 70, who have a diagnosis of diabetes, as gathered in the dm431 data.

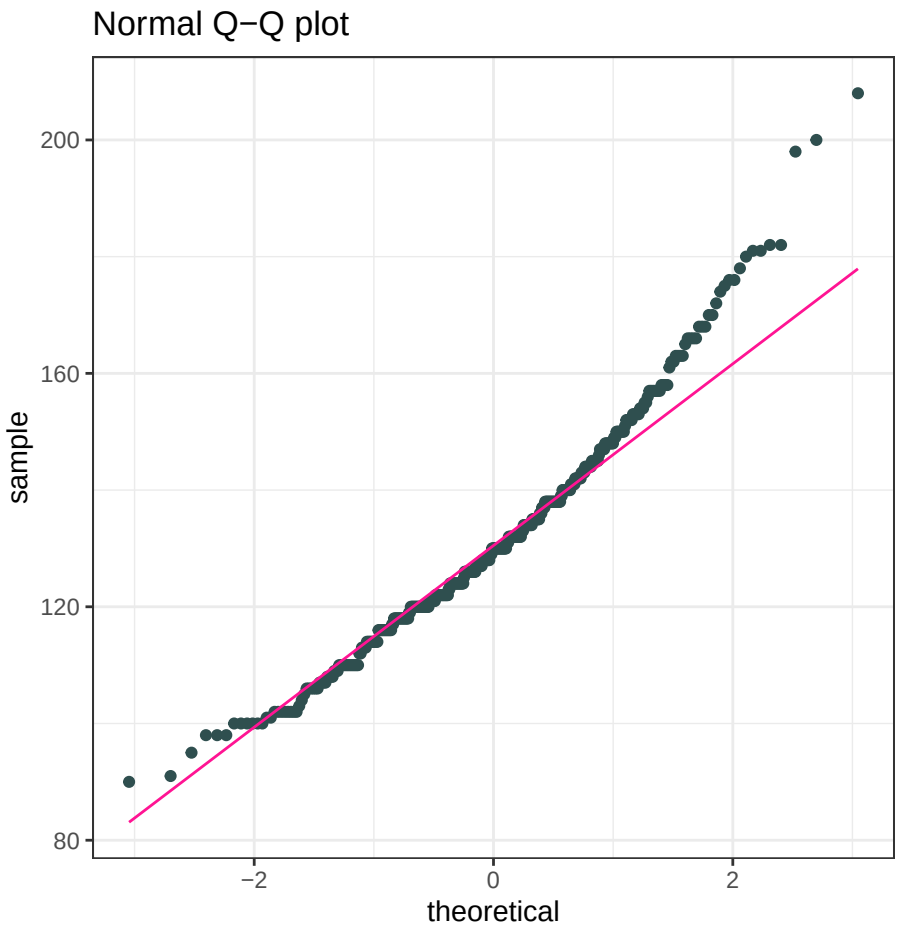
- These data are simulated to mirror some details from real data gathered by *Better Health Partnership*.
- The dm431 data contains multitudes, but for now, we're just looking at the 431 systolic blood pressure values, gathered in the sbp variable.

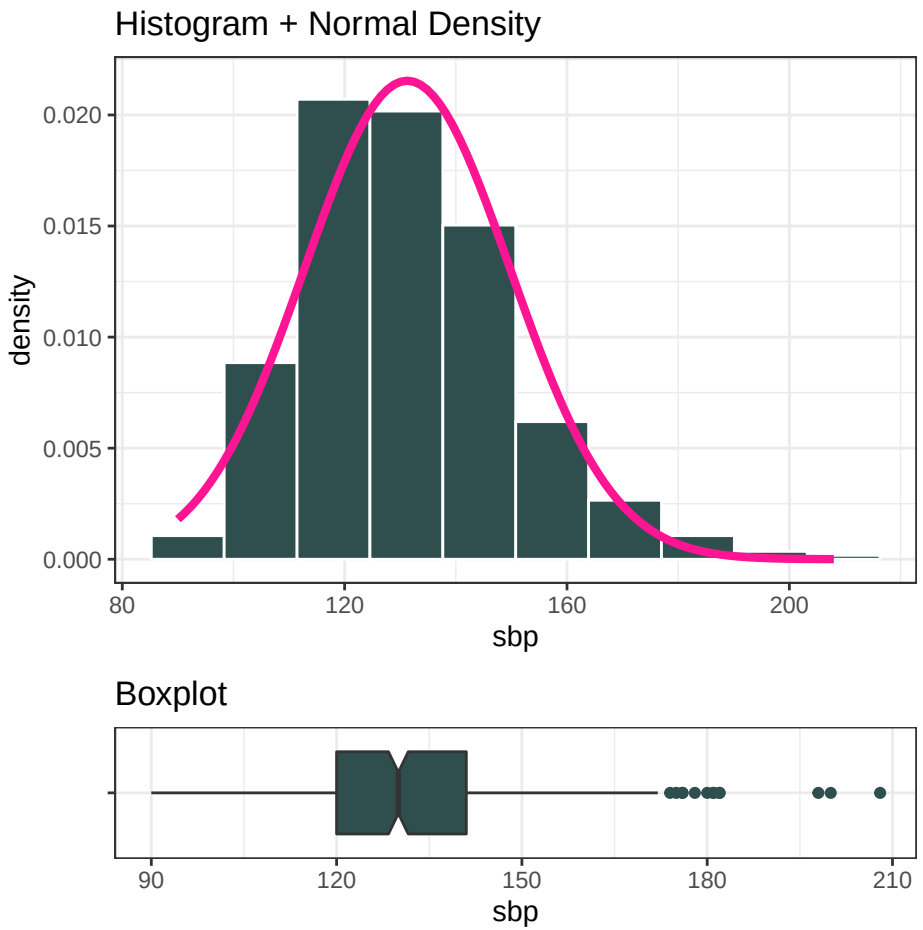
```
mosaic::favstats(~ sbp, data = dm431)
```

```
 min  Q1 median  Q3 max     mean       sd   n missing
  90 120    130 141 208 131.2645 18.52038 431       0
```

- See next slide. How reasonable is a Normal model for sbp?

Graphical Summaries: `sbp` in `dm431`





Does a Normal model seem *very*, *somewhat* or *not* reasonable?

Point Estimation and Confidence Intervals

The basic theory of estimation can be used to indicate the probable accuracy and potential for bias in estimating based on limited samples.

- A **point estimate** provides a single best guess as to the value of a population or process parameter.
- A **confidence interval** can convey how much error one must allow for in a given estimate.

A confidence interval consists of:

1. An interval estimate describing the population parameter of interest (here the population mean), and
2. A probability statement, expressed in terms of a confidence level.

The key tradeoffs are

- cost vs. precision (larger samples produce narrower intervals), and
- precision vs. confidence in the correctness of the statement.

Our Assumptions

Suppose that

- systolic BPs across the population of NE Ohio adults ages 31-70 living with diabetes follows a Normal distribution (with mean μ and standard deviation σ.)
- the 431 adults in our `dm431` tibble are a random sample from that population.

We know the sample mean (131.26 of our 431 adults, but we don't know μ, the mean across **all** NE Ohio adults ages 31-70 living with diabetes.

So we need to estimate it, by producing a **confidence interval for the true (population) mean** μ of all adults with diabetes ages 31-70 living in NE Ohio based on this sample.

Available Methods

To build a point estimate and confidence interval for the population mean, we could use

1. A **t-based** estimate and confidence interval, available from an intercept-only linear model, or (equivalently) from a t test.
    - This approach will require an assumption that the population comes from a Normal distribution.
2. A **bootstrap** confidence interval, which uses resampling to estimate the population mean.
    - This approach won't require the Normality assumption, but has some other constraints.
3. A **Wilcoxon signed rank** approach, but that won't describe the mean, only a pseudo-median.
    - This also doesn't require the Normality assumption, but no longer describes the population mean (or median) unless the population can be assumed symmetric. Instead it describes the *pseudo-median*.

Starting with A Good Answer

Use indicator variable regression to produce a t-based interval.

```
model1 <- lm(sbp ~ 1, data = dm431)

tidy(model1, conf.int = TRUE, conf.level = 0.90) %>%
  select(term, estimate, std.error,
         conf.low, conf.high, p.value) %>%
  knitr::kable(digits = 2)
```

term	estimate	std.error	conf.low	conf.high	p.value
(Intercept)	131.26	0.89	129.79	132.74	0

- Our point estimate for the population mean SBP (μ) is 131.26 mm Hg.
- Our 90% confidence interval is (129.79, 132.74) mm Hg for μ.

Interpreting A 90% Confidence Interval for μ

- Our 90% confidence interval estimate for μ turns out to be (129.79, 132.74) mm Hg. How do we interpret this result?
- Some people think this means that there is a 90% chance that the true mean of the population, μ, falls between 129.79 and 132.74 mm Hg.

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- That's not correct. Why not?
- The population mean μ is a constant **parameter** of the population of interest. That constant is not a random variable, and does not change. So the actual probability of the population mean falling inside that range is either 0 or 1.

So what do we have confidence in?

Our confidence is in our process.

- It's in the sampling method (random sampling) used to generate the data, and in the assumption that the population follows a Normal distribution.
- It's captured in our accounting for one particular type of error (called *sampling error*) in developing our interval estimate, while assuming all other potential sources of error are negligible.

So what is a more appropriate interpretation of our 90% confidence interval for μ?

A somewhat better interpretation

- Our 90% confidence interval for μ is (129.79, 132.74) mm Hg.

If we used this same method to sample data from the true population of adults ages 31-70 with diabetes in NE Ohio and built 100 such 90% confidence intervals, then 90 of them would contain the true population mean. We don't know whether this one interval we built contains μ, though.

- We call 100(1 - α)%, here, 90%, or 0.90, the *confidence* level, and
- $\alpha = 10\%$, or 0.10 is called the *significance* level.

The indicator variable approach we've used is identical to a t test.

Using t test to find the CI for μ

```
t1 <- dm431 %$%
  t.test(sbp, conf.level = 0.90, alt = "two.sided")

t1
```

```
    One Sample t-test

data:  sbp
t = 147.14, df = 430, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 0
90 percent confidence interval:
 129.794 132.735
sample estimates:
mean of x
 131.2645
```

Tidying the t test results

```
tidy(t1) %>% select(estimate, conf.low, conf.high) %>%
  kable(digits = 2)
```

estimate	conf.low	conf.high
131.26	129.79	132.74

```
tidy(t1) %>% select(method, alternative, statistic,
                    parameter, p.value) %>%
  kable()
```

method	alternative	statistic	parameter	p.value
One Sample t-test	two.sided	147.1418	430	0

- The `statistic` is the t statistic (`estimate` / standard error)
- The `parameter` describes the degrees of freedom (here, $n - 1$)

One-sided vs. Two-sided Confidence Intervals

In some situations, we are concerned with either an upper limit for the population mean μ or a lower limit for μ, but not both.

- The 90% two-sided interval is placed so as to cut off the top 5% of the distribution with its upper bound, and the bottom 5% of the distribution with its lower bound.
- The 95% "less than" one-sided interval is placed so as to have its upper bound cut off the top 5% of the distribution.

Confidence Level	α	Type of Interval	Interval Estimate for Population Mean SBP, μ
90% or 0.90	0.10	Two-Sided	(129.79, 132.74)
95% or 0.95	0.05	One Sided ($<$)	$\mu < 132.74$
95% or 0.95	0.05	One Sided ($>$)	$\mu > 129.79$

Want to calculate the t-based CI by hand?

What is the formula for the t-based CI?

Many confidence intervals follow a general strategy using a point estimate $\pm$ a margin for error.

We build a 100(1-α)% confidence interval using the t distribution, using the sample mean $\bar{x}$, the sample size n, and the sample standard deviation s_x. The two-sided 100(1-α)% confidence interval is:

$$\bar{x} \pm t_{\alpha/2,n-1}(\frac{s_x}{\sqrt{n}})$$

- $SE(\bar{x}) = \frac{s_x}{\sqrt{n}}$ is the standard error of the sample mean
- The margin of error for this CI is $t_{\alpha/2,n-1}(\frac{s_x}{\sqrt{n}})$.
- $t_{\alpha/2,n-1}$ is the value that cuts off the top $\alpha/2$ percent of the t distribution, with $n-1$ degrees of freedom. Obtain in R with:

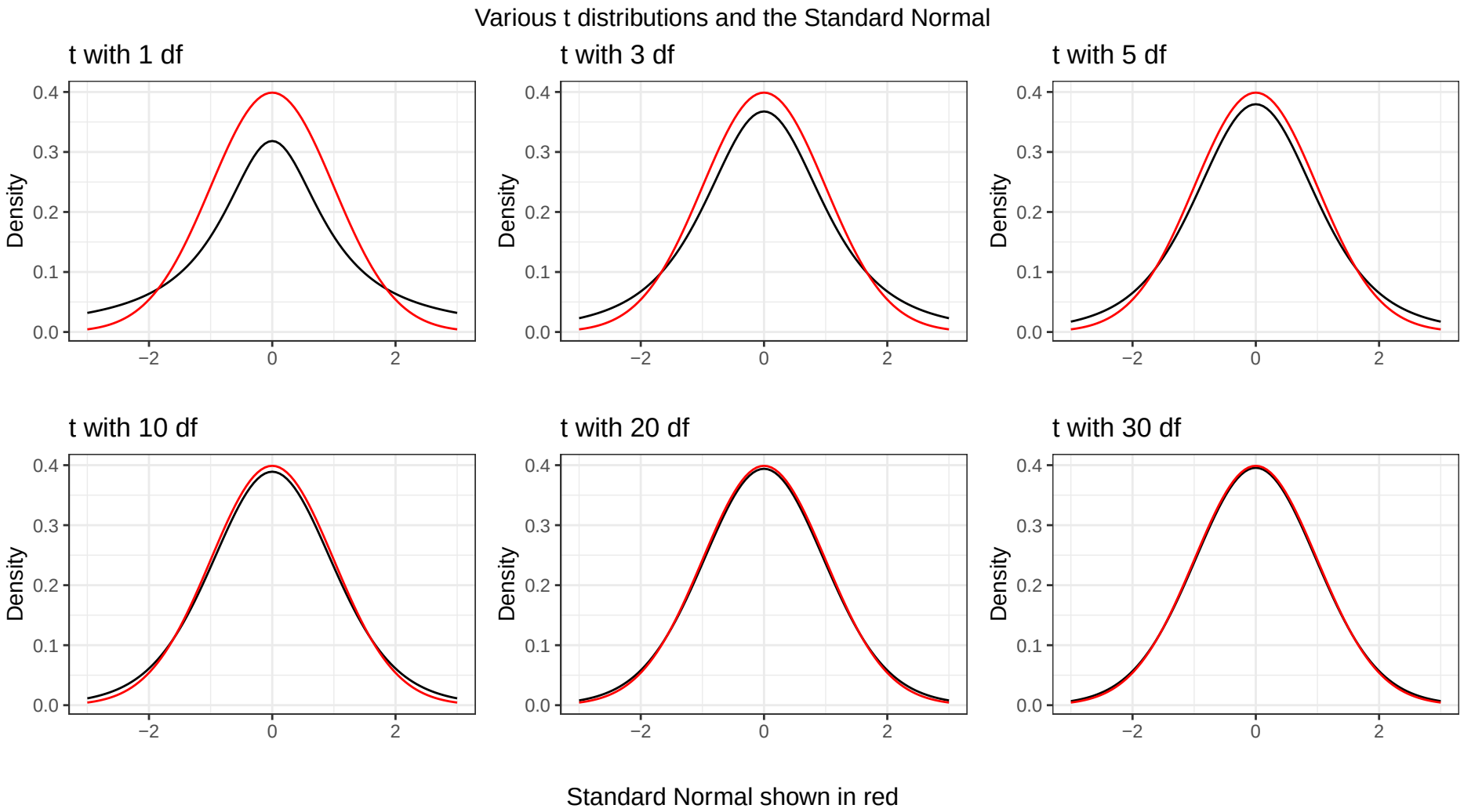
```
qt(alphaover2, df = n-1, lower.tail=FALSE)
```

Student's t distribution

Student's t distribution looks a lot like a Normal distribution, when the sample size is large. Unlike the normal distribution, which is specified by two parameters, the mean and the standard deviation, the t distribution is specified by one parameter, the degrees of freedom.

- t distributions with large numbers of degrees of freedom are more or less indistinguishable from the standard Normal distribution.
- t distributions with smaller degrees of freedom (say, with df < 30, in particular) are still symmetric, but are more outlier-prone than a Normal distribution.

Six t Distributions and a Standard Normal



"Hand-Crafting" the 90% confidence interval for μ

Let's build a 90% confidence interval for the true mean SBP across the entire population of NE Ohio adults ages 31-70 with diabetes.

α	n	$\bar{x}$	s	$\text{SE}(\bar{x}) = s/\sqrt{n}$
0.10	431	131.26	18.52	0.89

The two-sided 100(1-α)% confidence interval (based on a t test) is: $\bar{x} \pm t_{\alpha/2,n-1}(s/\sqrt{n})$, or

- The 90% CI for μ is 131.26 $\pm$ $t_{0.10/2,431-1}$ (0.89)
  - To calculate the t cutoff value for $\alpha = 0.10$ and $n = 431$, we use

`qt(0.10/2, df = 431-1, lower.tail=FALSE)` = 1.648405

- So the 90% CI for μ is 131.26 $\pm$ 1.6484 x 0.89, or
- 131.26 $\pm$ 1.47, or (129.79, 132.73)

A Few Thoughts on Hypothesis Testing about a Population Mean

Four Steps to Complete a Hypothesis Test

1. Specify the null hypothesis, H_0
2. Specify the research or alternative hypothesis, H_1, sometimes called H_A
3. Specify the approach to be used to make inferences to the population based on sample data.
    - We must specify α, the probability of incorrectly rejecting H_0 that we are willing to accept. Often, we use $\alpha = 0.05$
4. Obtain the data, and summarize it to obtain an appropriate point estimate and confidence interval (and maybe a p value.)

In our Setting

1. Null Hypothesis: $H_0 : \mu = 0$
2. Alternative Hypothesis: $H_A : \mu \neq 0$
3. Test statistic: t = estimate / standard error with $\alpha = 0.10$ since we're using a 90% confidence interval
4. Our 90% confidence interval for μ is (129.79, 132.74) mm Hg.

- Does $H_0 : \mu = 0$ seem consistent with the data, or do we find a detectable difference between our data's estimates of μ and the assumption that $\mu = 0$?
- Be careful. Data lie all the time.

Defining a p Value (but not very well)

The p value estimates the probability that we would obtain a result as much in favor or more in favor of the alternative hypothesis H_A as we did, assuming that H_0 is true.

- The p value is a conditional probability of seeing evidence as strong or stronger in favor of H_A calculated **assuming** that H_0 is true.

How people use the p Value

- If the p value is less than α, this suggests we might reject H_0 in favor of H_A, and declare the result statistically significant.

But we won't be comfortable with doing that, at least in time.

What the p Value isn't

The p value is not a lot of things. It's **NOT**

- The probability that the alternative hypothesis is true
- The probability that the null hypothesis is false
- Or anything like that.

The p value **is closer to** a statement about the amount of statistical evidence contained in the data that favors the alternative hypothesis H_A. It's a measure of the evidence's credibility.

From FiveThirtyEight

P-values have taken quite a beating lately. These widely used and commonly misapplied statistics have been blamed for giving a veneer of legitimacy to dodgy study results, encouraging bad research practices and promoting false-positive study results.

Last week, I attended the inaugural METRICS conference at Stanford, which brought together some of the world's leading experts on meta-science, or the study of studies. I figured that if anyone could explain p-values in plain English, these folks could.

(Christie Aschwanden, FiveThirtyEight, 2015-11-24)

Let's Go To The Videotape

FiveThirtyEight

Politics Sports **Science** Podcasts Video

NOV. 24, 2015, AT 12:12 PM

Not Even Scientists Can Easily Explain P-values

By Christie Aschwanden

Filed under Scientific Method

Link: https://fivethirtyeight.com/features/not-even-scientists-can-easily-explain-p-values/

This is where we stopped. The other slides originally posted here are now posted to Class 14.