2-sample t-test

Day 11: Inference for difference in means from two independent samples and Power (Sections 5.3, 5.4)

BSTA 511/611

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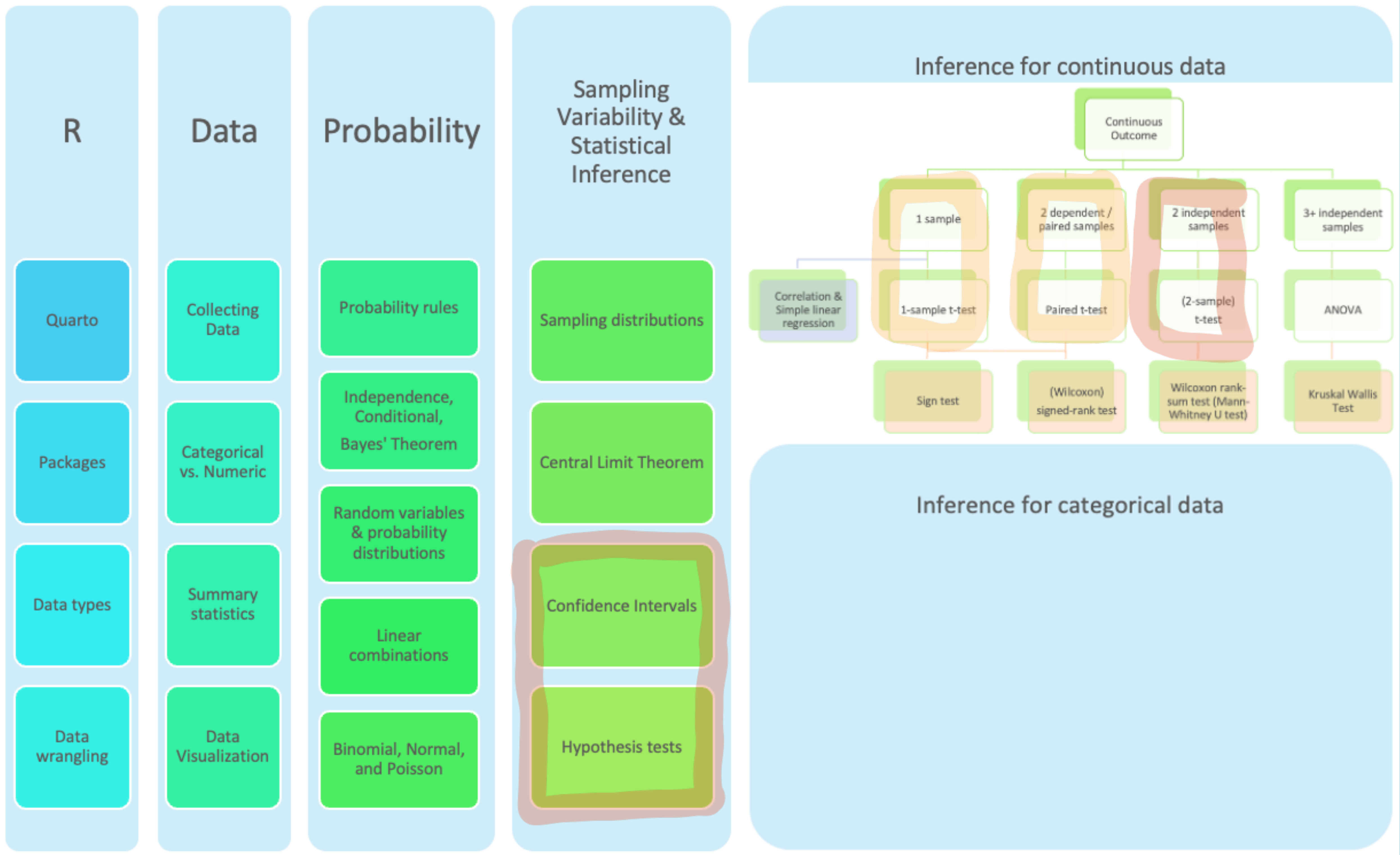
MoRitz's tip of the day

Add tabbed sections to your html file using `tabset`.

First tab Second tab Read up on tabsets

- You can make subsections appear as different tabs in your html file.
- This is the first tab.
- It was created by adding `::: panel-tabset` right above the subsection `### First tab` (see the code file).
- Look up to the right of where it says "First tab," and you will see a second tab with the creative name "Second tab."
- If you are viewing the html output of this file, you can click on the different tabs to see what's in them.
- To stop new tabs from being created, close off the original `::: panel-tabset` command with `:::` at the end.
    - In the source code file, you will see the `:::` at the end of the `### Read up on tabsets` tab.

Where are we?



R
- Quarto
- Packages
- Data types
- Data wrangling

Data
- Collecting Data
- Categorical vs. Numeric
- Summary statistics
- Data Visualization

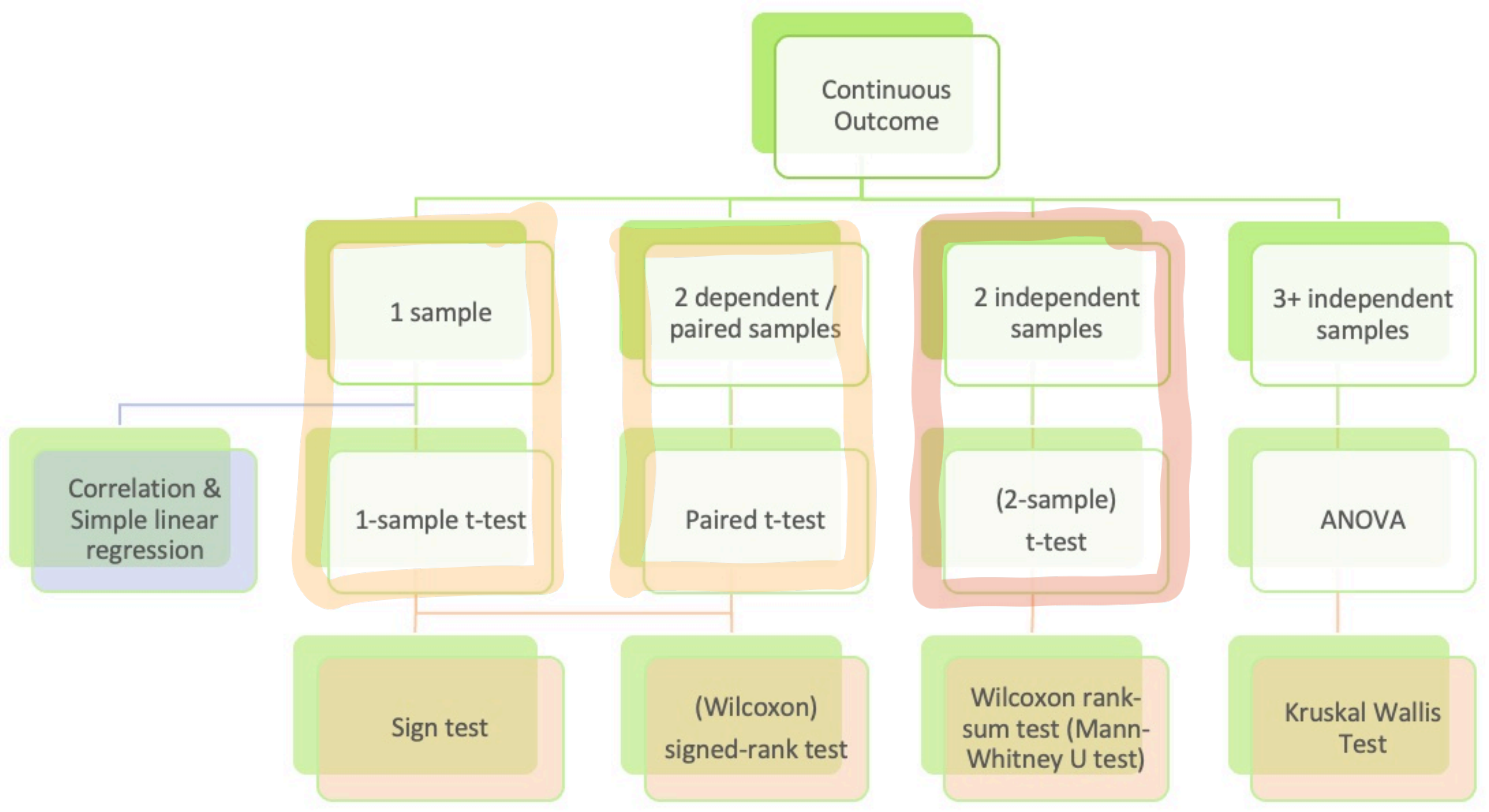
Probability
- Probability rules
- Independence, Conditional, Bayes' Theorem
- Random variables & probability distributions
- Linear combinations
- Binomial, Normal, and Poisson

Sampling Variability & Statistical Inference
- Sampling distributions
- Central Limit Theorem
- Confidence Intervals
- Hypothesis tests

Inference for continuous data

Inference for categorical data

Where are we? Continuous outcome zoomed in



Where are we?

CI's and hypothesis tests for different scenarios:

$$\text{point estimate} \pm z^*(or\ t^*) \cdot SE, \quad \text{test stat} = \frac{\text{point estimate} - \text{null value}}{SE}$$

Day	Book	Population parameter	Symbol	Point estimate	Symbol	SE
10	5.1	Pop mean	μ	Sample mean	$\bar{x}$	$\frac{s}{\sqrt{n}}$
10	5.2	Pop mean of paired diff	μ_d or δ	Sample mean of paired diff	$\bar{x}_d$	$\frac{s_d}{\sqrt{n}}$
11	5.3	Diff in pop means	$\mu_1 - \mu_2$	Diff in sample means	$\bar{x}_1 - \bar{x}_2$	???
12	8.1	Pop proportion	p	Sample prop	$\widehat{p}$	
12	8.2	Diff in pop proportions	$p_1 - p_2$	Diff in sample proportions	$\widehat{p}_1 - \widehat{p}_2$	

Goals for today

2-sample t-test (Section 5.3)

- Statistical inference for difference in means from 2 independent samples
  1. What are H_0 and H_a?
  2. What is the SE for $\bar{x}_1 - \bar{x}_2$?
  3. Hypothesis test
  4. Confidence Interval
  5. Run test in R - using long vs. wide data
  6. Satterthwaite's df
  7. Pooled SD

Power and sample size (4.3.4, 5.4, plus notes)

- Critical values & rejection region
- Type I & II errors
- Power
- How to calculate sample size needed for a study?

Examples of designs with two independent samples

- Any study where participants are randomized to a control and treatment group
- Study where create two groups based on whether they were exposed or not to some condition (can be observational)
- Book: “Does treatment using embryonic stem cells (ESCs) help improve heart function following a heart attack?”
- Book: “Is there evidence that newborns from mothers who smoke have a different average birth weight than newborns from mothers who do not smoke?”
- *The key is that the data from the two groups are independent of each other.*

& have random samples

→ within a group individuals are independent as well

Steps in a Hypothesis Test

1. Set the **level of significance α**
2. Specify the **null** (H_0) and **alternative** (H_A) **hypotheses**
    1. In symbols
    2. In words
    3. Alternative: one- or two-sided?
3. Calculate the **test statistic**.
4. Calculate the **p-value** based on the observed test statistic and its sampling distribution
5. Write a **conclusion** to the hypothesis test
    1. Do we reject or fail to reject H_0?
    2. Write a conclusion in the context of the problem

Does caffeine increase finger taps/min (on average)?

Study Design:

- 20 male college students students were trained to tap their fingers at a rapid rate.
- Each then drank 2 cups of coffee (double-blind)
    - **Control** group: decaf
    - **Caffeine** group: ~ 200 mg caffeine
- After 2 hours, students were tested.
- **Taps/minute** recorded

Hand, David J.; Daly, Fergus; McConway, K.; Lunn, D. and Ostrowski, E. (1993). A handbook of small data sets. London, U.K.: Chapman and Hall.

- Load the data from the csv file `CaffeineTaps.csv`
- The code below is for when the data file is in a folder called `data` that is in your R project folder (your working directory)

```
CaffTaps <- read_csv(here::here("data", "CaffeineTaps.csv"))

glimpse(CaffTaps)
```

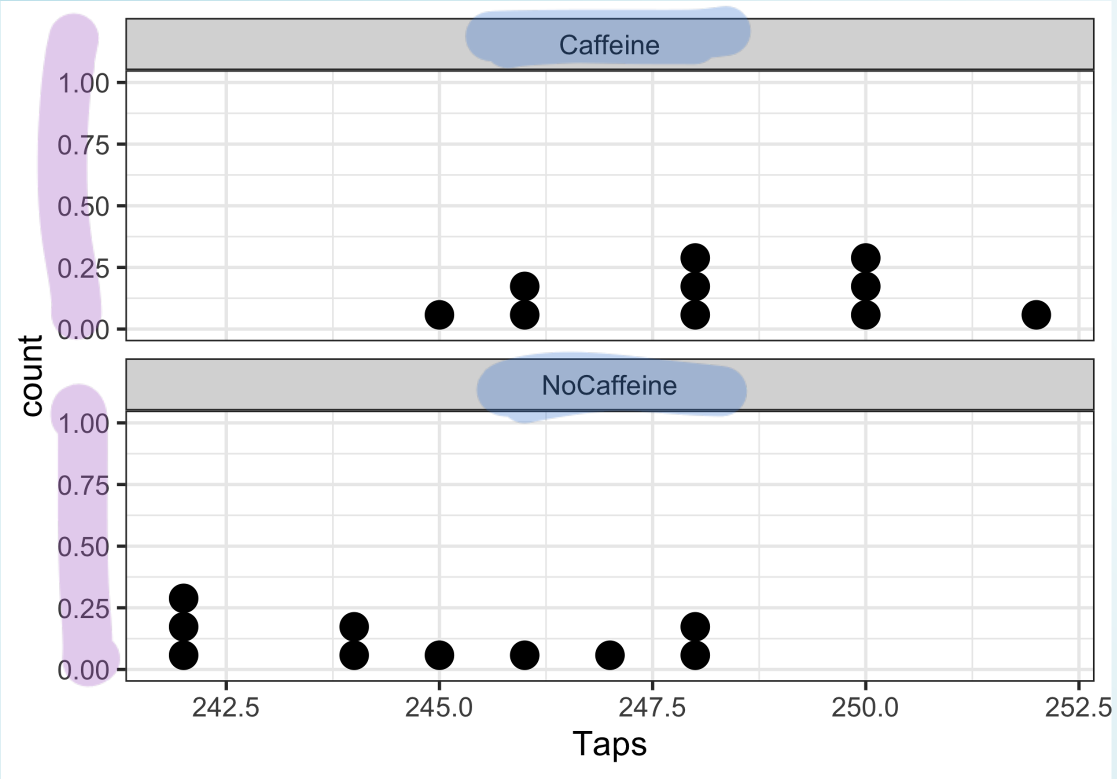
Long data

```
Rows: 20
Columns: 2
$ Taps  <dbl> 246, 248, 250, 252, 248, 250, 246, 248, 245, 250, 242, 245, 244,…
$ Group <chr> "Caffeine", "Caffeine", "Caffeine", "Caffeine", "Caffeine", "Caf…
```

EDA: Explore the finger taps data

Dotplot of taps/minute stratified by group

```r
ggplot(CaffTaps, aes(x=Taps)) +
  geom_dotplot() +
  facet_wrap(vars(Group), ncol=1)
```



Summary statistics stratified by group

```r
# get_summary_stats() from rstatix packa
sumstats <- CaffTaps %>%
  group_by(Group) %>%
  get_summary_stats(type = "mean_sd")
sumstats %>% gt()
```

Group	variable	n	mean	sd
Caffeine	Taps	10	248.3	2.214
NoCaffeine	Taps	10	244.8	2.394

```r
diff(sumstats$mean)
```

```
[1] -3.5
```

Step 2: Null & Alternative Hypotheses

- **Question**: Is there evidence to support that drinking caffeine increases the number of finger taps/min?

Null and alternative hypotheses in **words**

Include as much context as possible

- H_0: The population difference in mean finger taps/min between the caffeine and control groups is ... 0 (no change)
- H_A: The population difference in mean finger taps/min between the caffeine and control groups is ... greater than zero

Null and alternative hypotheses in **symbols**

null

$$H_0: \mu_{caff} - \mu_{ctrl} = 0$$

$$H_A: \mu_{caff} - \mu_{ctrl} > 0$$

$$H_0: \mu_{caff} = \mu_{ctrl}$$

$$H_A: \mu_{caff} > \mu_{ctrl}$$

Step 3: Test statistic (part 1)

Recall that in general the test statistic has the form:

$$\text{test stat} = \frac{\text{point estimate} - \text{null value}}{SE}$$

Thus, for a two sample independent means test, we have:

$$\text{test statistic} = \frac{\bar{x}_1 - \bar{x}_2 - 0}{SE_{\bar{x}_1 - \bar{x}_2}}$$

- What is the formula for $SE_{\bar{x}_1 - \bar{x}_2}$?
- What is the probability distribution of the test statistic?
- What assumptions need to be satisfied?

What distribution does $\bar{X}_1 - \bar{X}_2$ have?

Let $\bar{X}_1$ and $\bar{X}_2$ be the means of random samples from two independent groups, with parameters shown in table:

	Group 1	**Group 2**
sample size	n_1	n_2
pop mean	μ_1	μ_2
pop sd	σ_1	σ_2

Some theoretical statistics:

- If $\bar{X}_1$ and $\bar{X}_2$ are independent normal r.v.'s, then $\bar{X}_1 - \bar{X}_2$ is also normal
- What is the mean of $\bar{X}_1 - \bar{X}_2$?

$$\bar{X}_1 - \bar{X}_2 \sim \mathcal{N}\left(\mu_1 - \mu_2, \sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}\right)$$

$$E[\bar{X}_1 - \bar{X}_2] = E[\bar{X}_1] - E[\bar{X}_2] = \mu_1 - \mu_2$$

- What is the standard deviation of $\bar{X}_1 - \bar{X}_2$?

$$Var(\bar{X}_1 - \bar{X}_2) = Var(\bar{X}_1) + Var(\bar{X}_2) = \frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}$$

$$SD(\bar{X}_1 - \bar{X}_2) = \sqrt{\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}}$$

Step 3: Test statistic (part 2)

$$t_{\bar{x}_1-\bar{x}_2} = \frac{\bar{x}_1 - \bar{x}_2 - 0}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}}$$

- $\bar{x}_1, \bar{x}_2$ are the sample means
- $\mu_0 = 0$ is the mean value specified in H_0
- s_1, s_2 are the sample SD's
- n_1, n_2 are the sample sizes

- Statistical theory tells us that $t_{\bar{x}_1-\bar{x}_2}$ follows a **student's t-distribution** with
  - $df \approx$ smaller of $n_1 - 1$ and $n_2 - 1$
  - this is a conservative estimate (smaller than actual df)

Assumptions:

- **Independent observations & samples**
  - The observations were collected independently.
  - In particular, the observations from the two groups were not paired in any meaningful way.
- **Approximately normal samples or big n's**
  - The distributions of the samples should be approximately normal
  - *or both* their sample sizes should be at least 30.

Step 3: Test statistic (part 3)

	Group	variable	n	mean	sd
1	Caffeine	Taps	10	248.3	2.214
2	NoCaffeine	Taps	10	244.8	2.394

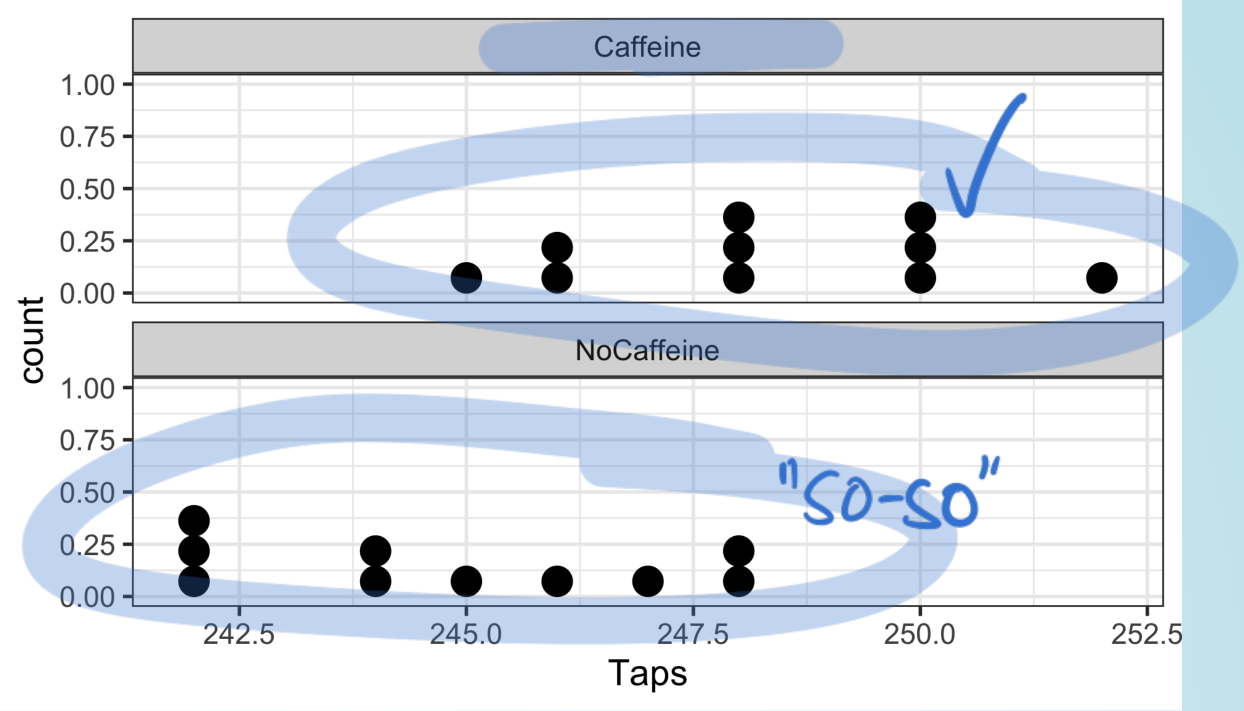
$$\text{test statistic} = t_{\bar{x}_1 - \bar{x}_2} = \frac{\bar{x}_1 - \bar{x}_2 - 0}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}} = \frac{248.3 - 244.8 - 0}{\underbrace{\sqrt{\frac{2.214^2}{10} + \frac{2.394^2}{10}}}_{SE \approx 1.03}} = 3.394216$$

Based on the value of the test statistic, do you think we are going to reject or fail to reject H_0?

Step "3b": Assumptions satisfied?

Assumptions:

- **Independent observations & samples**
  - The observations were collected independently. Yes?
  - In particular, the observations from the two groups were not paired in any meaningful way. ✓ (randomized)
- **Approximately normal samples or big n's**
  - The distributions of the samples should be approximately normal
  - *or both* their sample sizes should be at least 30.



$n_1 = n_2 = 10 < 30$

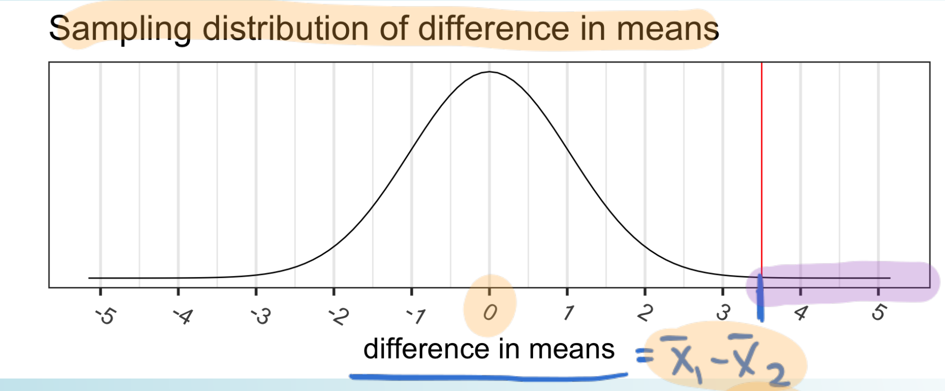
Step 4: p-value

The **p-value** is the **probability** of obtaining a test statistic *just as extreme or more extreme* than the observed test statistic assuming the null hypothesis H_0 is true.

$H_a: \mu_{caff} - \mu_{ctrl} > 0$

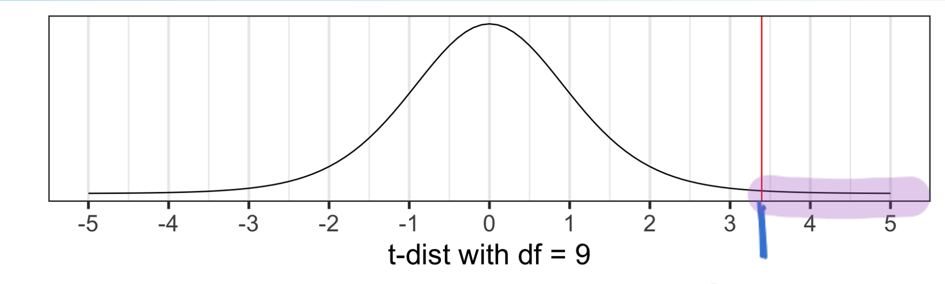
Calculate the *p*-value:

$$
\begin{aligned}
\text{p-value} &= \mathbb{P}(T > 3.394) \\
&= 1 - \mathbb{P}(T \leq 3.394) \\
&= 1 - \text{pt}(3.394, \text{df} = 10 - 1) \\
&= 0.00397
\end{aligned}
$$


Sampling distribution of difference in means

$= \bar{x}_1 - \bar{x}_2$

$= 3.5$



3.394

Step 5: Conclusion to hypothesis test

$$H_0 : \mu_{caff} - \mu_{ctrl} = 0$$
$$H_A : \mu_{caff} - \mu_{ctrl} > 0$$

- Recall the p-value = 0.00397
- Use α = 0.05.
- Do we reject or fail to reject H_0?

Conclusion statement:

- Stats class conclusion
  - There is sufficient evidence that the (population) difference in mean finger taps/min with vs. without caffeine is greater than 0 (p-value = 0.004).
- More realistic manuscript conclusion:
  - The mean finger taps/min were 244.8 (SD = 2.4) and 248.3 (SD = 2.2) for the control and caffeine groups, and the increase of 3.5 taps/min was statistically discrenible (p-value = 0.004).

95% CI for the mean difference in cholesterol levels

Group	variable	n	mean	sd
Caffeine	Taps	10	248.3	2.214
NoCaffeine	Taps	10	244.8	2.394

CI for $\mu_{caff} - \mu_{ctrl}$:

$$\bar{x}_{caff} - \bar{x}_{ctrl} \pm t^* \cdot \sqrt{\frac{s^2_{caff}}{n_{caff}} + \frac{s^2_{ctrl}}{n_{ctrl}}}$$

$$(248.3 - 244.8) \pm 2.262 \sqrt{\frac{2.214^2}{10} + \frac{2.394^2}{10}} = (1.167, 5.833)$$

$t^* = qt(0.975, df=9)$

Interpretation:
We are 95% confident that the (population) difference in mean finger taps/min between the caffeine and control groups is between 1.167 mg/dL and 5.833 mg/dL.

- *Based on the CI, is there evidence that drinking caffeine made a difference in finger taps/min? Why or why not?* 0 is not in CI ⇒ Reject H_0 if 2-sided test

R: 2-sample t-test (with long data)

- The `CaffTaps` data are in a *long* format, meaning that
  - all of the outcome values are in one column and
  - another column indicates which group the values are from
- This is a common format for data from multiple samples, especially if the sample sizes are different.

```r
(Taps_2ttest <- t.test(formula = Taps ~ Group,
                       alternative = "greater",
                       data = CaffTaps))
```

y ~ x

```
	Welch Two Sample t-test

data:  Taps by Group
t = 3.3942, df = 17.89, p-value = 0.001628
alternative hypothesis: true difference in means between group Caffeine and group NoCaffeine is greater than 0
95 percent confidence interval:
 1.711272      Inf
sample estimates:
  mean in group Caffeine mean in group NoCaffeine 
                   248.3                    244.8 
```

tidy the t.test output

```r
# use tidy command from broom package for briefer output that's a tibble
tidy(Taps_2ttest) %>% gt()
```

estimate	estimate1	estimate2	statistic	p.value	parameter	conf.low	conf.high	method	alternative
3.5	248.3	244.8	3.394168	0.001627703	17.89012	1.711272	Inf	Welch Two Sample t-test	greater

- Pull the p-value:

```r
tidy(Taps_2ttest)$p.value  # we can pull specific values from the tidy output
```

```
[1] 0.001627703
```

R: 2-sample t-test (with wide data)

```r
# make CaffTaps data wide: pivot_wider needs an ID column so that it
# knows how to "match" values from the Caffeine and NoCaffeine groups
CaffTaps_wide <- CaffTaps %>%
  mutate(id = rep(1:10, 2)) %>% #  "fake" IDs for pivot_wider step
  pivot_wider(names_from = "Group",
              values_from = "Taps")

glimpse(CaffTaps_wide)
```

1, 2, ..., 10, 1, 2, ..., 10

```
Rows: 10
Columns: 3
$ id         <int> 1, 2, 3, 4, 5, 6, 7, 8, 9, 10
$ Caffeine   <dbl> 246, 248, 250, 252, 248, 250, 246, 248, 245, 250
$ NoCaffeine <dbl> 242, 245, 244, 248, 247, 248, 242, 244, 246, 242
```

```r
t.test(x = CaffTaps_wide$Caffeine, y = CaffTaps_wide$NoCaffeine, alternative = "g
  tidy() %>% gt()
```

estimate	estimate1	estimate2	statistic	p.value	parameter	conf.low	conf.high	method	alternative
3.5	248.3	244.8	3.394168	0.001627703	17.89012	1.711272	Inf	Welch Two Sample t-test	greater

$\bar{x}_1-\bar{x}_2$ $\bar{x}_1$ $\bar{x}_2$ t

$\uparrow$ df

Why are the df's in the R output different?

From many slides ago:

- Statistical theory tells us that $t_{\bar{x}_1 - \bar{x}_2}$ follows a **student's t-distribution** with
  - $df \approx$ smaller of $n_1 - 1$ and $n_2 - 1$
  - this is a **conservative** estimate (smaller than actual df)

The actual degrees of freedom are calculated using Satterthwaite's method:

$$\nu = \frac{[(s_1^2/n_1) + (s_2^2/n_2)]^2}{(s_1^2/n_1)^2/(n_1 - 1) + (s_2^2/n_2)^2/(n_2 - 1)} = \frac{[SE_1^2 + SE_2^2]^2}{SE_1^4/df_1 + SE_2^4/df_2}$$

Verify the *p*-value in the R output using ν = 17.89012:

```r
pt(3.3942, df = 17.89012, lower.tail = FALSE)
```

```
[1] 0.001627588
```

Pooled standard deviation estimate

- Sometimes we have reasons to believe that the population SD's from the two groups are equal, such as when randomizing participants to two groups

Rule of thumb: $\frac{s_{max}}{s_{min}} < 2$

- In this case we can use a **pooled** ~~**SD**~~: variance

$$s^2_{pooled} = \frac{s^2_1(n_1 - 1) + s^2_2(n_2 - 1)}{n_1 + n_2 - 2}$$

- n_1, n_2 are the sample sizes, and
- s_1, s_2 are the sample standard deviations
- of the two groups

- We use the pooled ~~SD~~ variance instead of s^2_1 and s^2_2 when calculating the standard error

$$SE = \sqrt{\frac{s^2_{pooled}}{n_1} + \frac{s^2_{pooled}}{n_2}} = s_{pooled}\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}$$

Test statistic with pooled SD:

$$t_{\bar{x}_1 - \bar{x}_2} = \frac{\bar{x}_1 - \bar{x}_2 - 0}{s_{pooled}\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

CI with pooled SD:

$$(\bar{x}_1 - \bar{x}_2) \pm t^\star \cdot s_{pooled}\sqrt{\frac{1}{n_1} + \frac{1}{n_2}}$$

- The t distribution degrees of freedom are now:

$$df = (n_1 - 1) + (n_2 - 1) = n_1 + n_2 - 2.$$

R: 2-sample t-test with pooled SD

```r
# t-test with pooled SD
t.test(formula = Taps ~ Group,
       alternative = "greater",
       var.equal = TRUE,   # pooled SD
       data = CaffTaps) %>%
  tidy() %>%
  gt()
```

n_1+n_2-2

estimate	estimate1	estimate2	statistic	p.value	parameter	conf.low	conf.high	method	alternative
3.5	248.3	244.8	3.394168	0.001616497	18	1.711867	Inf	Two Sample t-test	greater

```r
# t-test without pooled SD
t.test(formula = Taps ~ Group,
       alternative = "greater",
       var.equal = FALSE,  # default, NOT pooled SD
       data = CaffTaps) %>%
  tidy() %>%
  gt()
```

estimate	estimate1	estimate2	statistic	p.value	parameter	conf.low	conf.high	method	alternative
3.5	248.3	244.8	3.394168	0.001627703	17.89012	1.711272	Inf	Welch Two Sample t-test	greater

Similar output in this case - why??

What's next?

CI's and hypothesis tests for different scenarios:

$$\text{point estimate} \pm z^*(or\ t^*) \cdot SE, \quad \text{test stat} = \frac{\text{point estimate} - \text{null value}}{SE}$$

Day	**Book**	**Population parameter**	**Symbol**	**Point estimate**	**Symbol**	**SE**
10	5.1	Pop mean	μ	Sample mean	$\bar{x}$	$\frac{s}{\sqrt{n}}$
10	5.2	Pop mean of paired diff	μ_d or δ	Sample mean of paired diff	$\bar{x}_d$	$\frac{s_d}{\sqrt{n}}$
11	5.3	Diff in pop means	$\mu_1 - \mu_2$	Diff in sample means	$\bar{x}_1 - \bar{x}_2$	$\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$ **or pooled**
12	8.1	Pop proportion	p	Sample prop	$\hat{p}$	???
12	8.2	Diff in pop proportions	$p_1 - p_2$	Diff in sample proportions	$\hat{p}_1 - \hat{p}_2$	???

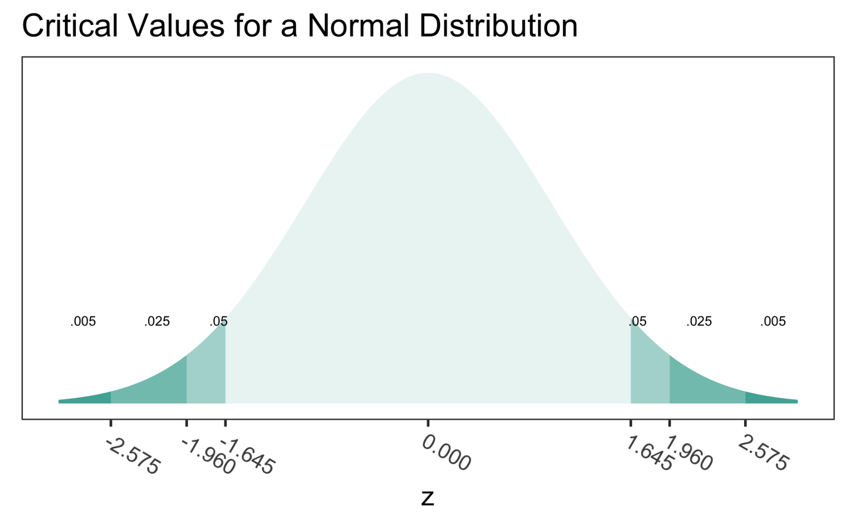
Power and sample size calculations

- Critical values & rejection region
- Type I & II errors
- Power
- How to calculate sample size needed for a study?

- Materials are from
  - **Section 4.3.4** Decision errors
  - **Section 5.4** Power calculations for a difference of means
  - plus notes

Critical values

- **Critical values** are the cutoff values that determine whether a test statistic is statistically significant or not.
- If a test statistic is greater in absolute value than the critical value, we reject H_0

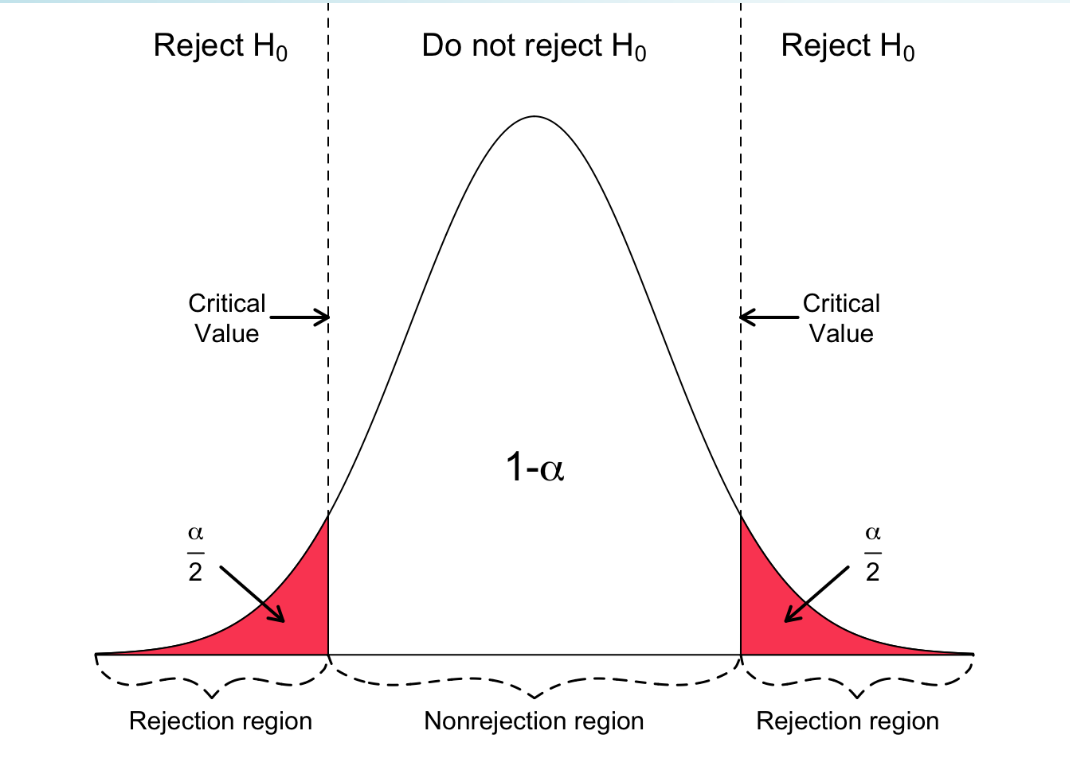


- Critical values are determined by
  - the significance level α,
  - whether a test is 1- or 2-sided, &
  - the probability distribution being used to calculate the p-value (such as normal or t-distribution).
- The critical values in the figure should look very familiar!
  - Where have we used these before?

- How can we calculate the critical values using R?

Rejection region

- If the absolute value of the test statistic is greater than the critical value, we reject H_0
  - In this case the test statistic is in the **rejection region**.
  - Otherwise it’s in the nonrejection region.

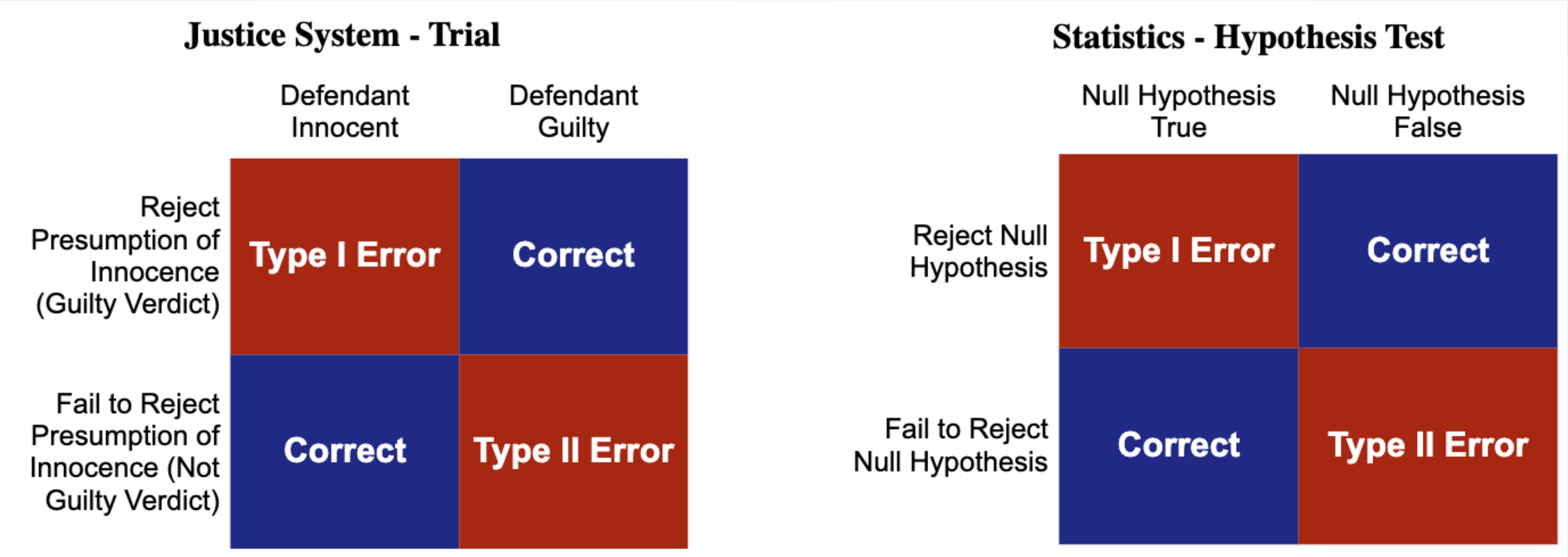


- What do rejection regions look like for 1-sided tests?

Hypothesis Testing “Errors”

StatisticsSolutions

Justice system analogy



Justice System - Trial

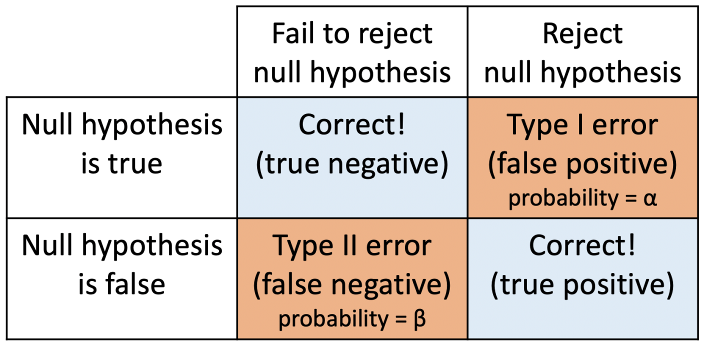
	Defendant Innocent	Defendant Guilty
Reject Presumption of Innocence (Guilty Verdict)	Type I Error	Correct
Fail to Reject Presumption of Innocence (Not Guilty Verdict)	Correct	Type II Error

Statistics - Hypothesis Test

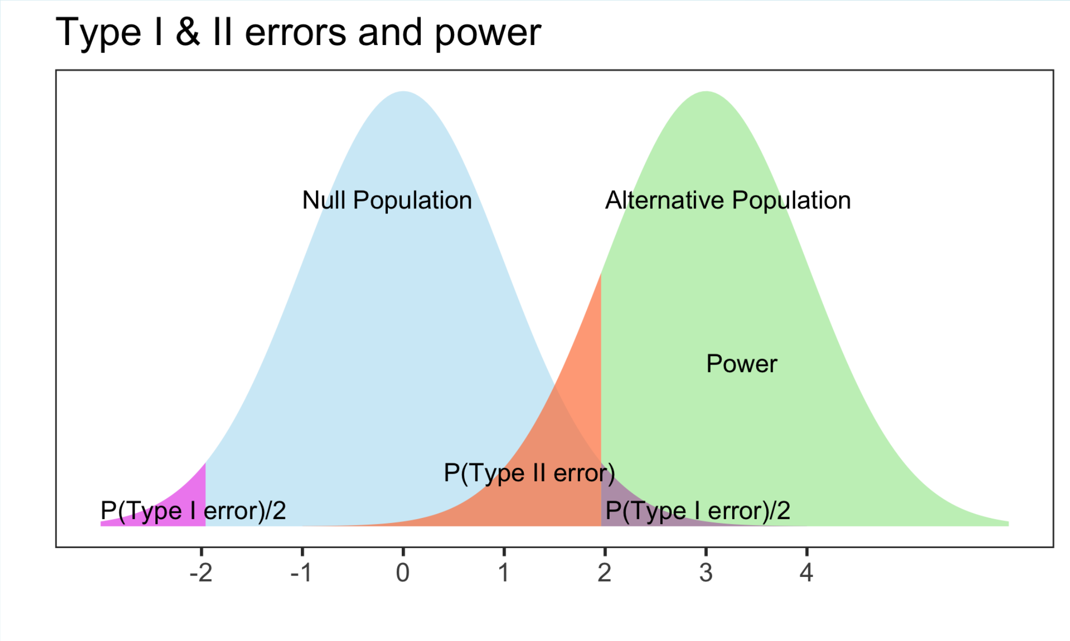
	Null Hypothesis True	Null Hypothesis False
Reject Null Hypothesis	Type I Error	Correct
Fail to Reject Null Hypothesis	Correct	Type II Error

Type I and Type II Errors - Making Mistakes in the Justice System

Type I & II Errors



	Fail to reject null hypothesis	Reject null hypothesis
Null hypothesis is true	Correct! (true negative)	Type I error (false positive) probability = α
Null hypothesis is false	Type II error (false negative) probability = β	Correct! (true positive)



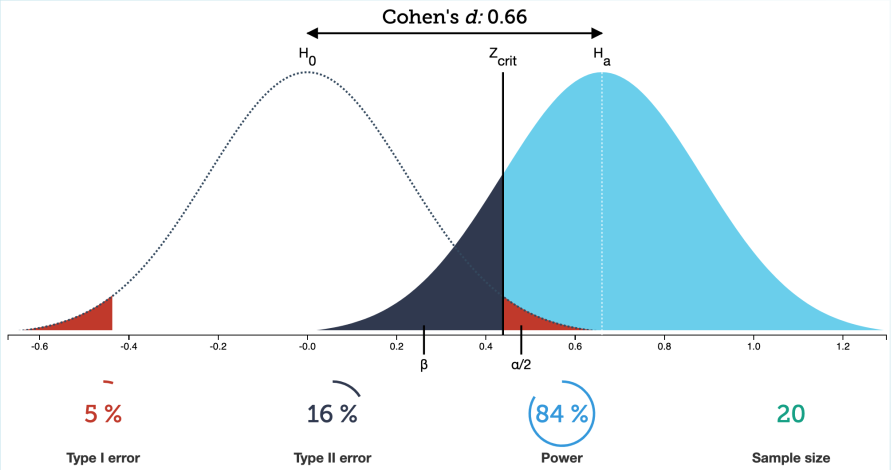
- α = probability of making a **Type I error**
  - This is the significance level (usually 0.05)
  - Set before study starts
- β = probability of making a **Type II error**
- Ideally we want
  - small Type I & II errors and
  - big power

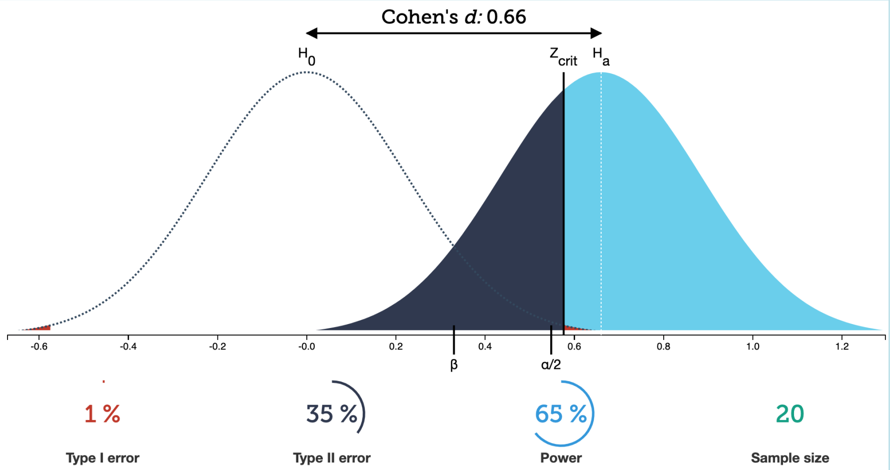
Applet for visualizing Type I & II errors and power: https://rpsychologist.com/d3/NHST/

Relationship between Type I & II errors

- **Type I vs. Type II error**
  - Decreasing P(Type I error) leads to
    - increasing P(Type II error)
  - We typically keep P(Type I error) = α set to 0.05

From the applet at https://rpsychologist.com/d3/NHST/

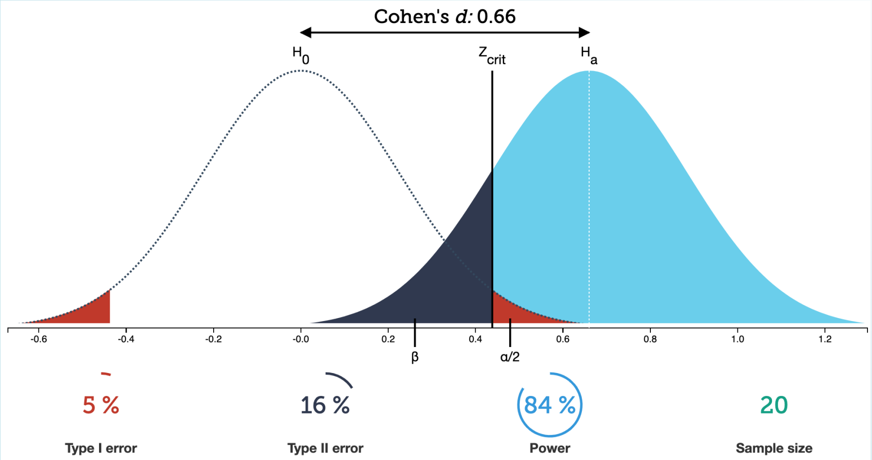




Relationship between Type II errors and power

Power = P(correctly rejecting the null hypothesis)

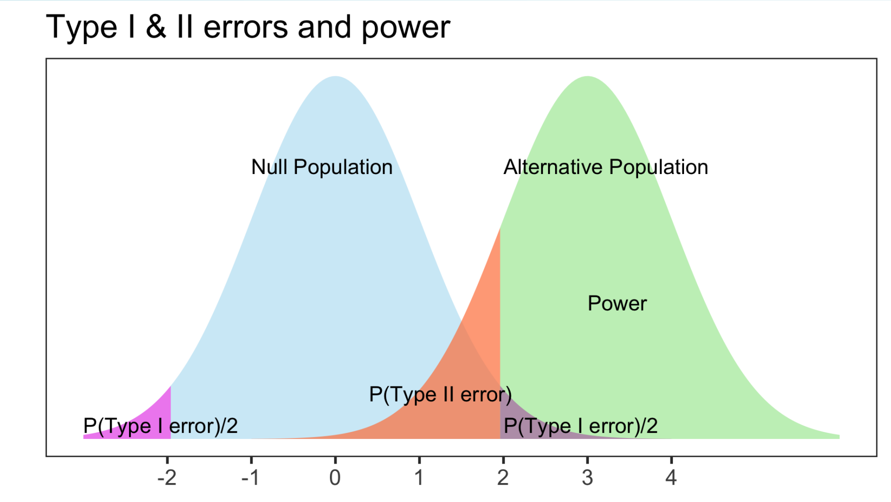
- Power is also called the
  - true positive rate,
  - probability of detection, or
  - the *sensitivity* of a test



- **Power vs. Type II error**
  - Power = 1 - P(Type II error) = 1 - β
  - Thus as β = P(Type II error) decreases, the power increases
  - P(Type II error) decreases as the mean of the alternative population shits further away from the mean of the null population (effect size gets bigger).
  - Typically want at least 80% power; 90% power is good

Example calculating power

- Suppose the mean of the null population is 0 ($H_0 : \mu = 0$) with standard error 1
- Find the power of a 2-sided test if the actual $\mu = 3$, assuming the SE doesn't change.



- Power = $P($Reject H_0 when alternative pop is $N(3,1))$
- When α = 0.05, we reject H_0 when the test statistic z is at least 1.96
- Thus for $X \sim N(3,1)$ we need to calculate $P(X \leq -1.96) + P(X \geq 1.96)$:

```r
# left tail + right tail:
pnorm(-1.96, mean=3, sd=1, lower.tail=TRUE) + pnorm(1.96, mean=3, sd=1, lower.tail=FALSE)
```

```
[1] 0.8508304
```

The left tail probability `pnorm(-1.96, mean=3, sd=1, lower.tail=TRUE)` is essentially 0 in this case.

- Note that this power calculation specified the value of the SE instead of the standard deviation and sample size n individually.

Sample size calculation for testing one mean

- Recall in our body temperature example that $\mu_0 = 98.6$ °F and $\bar{x} = 98.25$ °F.
  - The *p*-value from the hypothesis test was highly significant (very small).
  - What would the sample size n need to be for 80% power?
- **Calculate** n,
  - given α, power ($1-\beta$), “true” alternative mean μ, and null μ_0,
  - *assuming* the test statistic is normal (instead of t-distribution):

$$n = \left(s\frac{z_{1-\alpha/2}+z_{1-\beta}}{\mu-\mu_0}\right)^2$$

```r
mu <- 98.25
mu0 <- 98.6
sd <- 0.73
alpha <- 0.05
beta <- 0.20
n <- (sd*(qnorm(1-alpha/2) + qnorm(1-beta)) / (mu-mu0))^2
n
```

```
[1] 34.14423
```

```r
ceiling(n)  # always round UP to the next highest integer
```

```
[1] 35
```

We would only need a sample size of 35 for 80% power!
However, this is an under-estimate since we used the normal instead of t-distribution.

See http://powerandsamplesize.com/Calculators/Test-1-Mean/1-Sample-Equality.

Power calculation for testing one mean

Conversely, we can calculate how much power we had in our body temperature one-sample test, given the sample size of 130.

- **Calculate power**,
  - given α, n, "true" alternative mean μ, and null μ_0,
  - *assuming* the test statistic is normal (instead of t-distribution)

$$1-\beta = \Phi\left(z - z_{1-\alpha/2}\right) + \Phi\left(-z - z_{1-\alpha/2}\right) \quad , \quad \text{where } z = \frac{\mu-\mu_0}{s/\sqrt{n}}$$

Φ is the probability for a standard normal distribution

```r
mu <- 98.25; mu0 <- 98.6; sd <- 0.73; alpha <- 0.05; n <- 130
(z <- (mu-mu0) / (sd/sqrt(n)) )
```

```
[1] -5.466595
```

```r
Power <- pnorm(z-qnorm(1-alpha/2)) + pnorm(-z-qnorm(1-alpha/2))
Power
```

```
[1] 0.9997731
```

If the population mean is 98.2 instead of 98.6, we have a 99.98% chance of correctly rejecting H_0 when the sample size is 130.

R package pwr for power analyses

- Use `pwr.t.test` for both one- and two-sample t-tests.
- Specify all parameters *except for* the one being solved for.

```
pwr.t.test(n = NULL, d = NULL, sig.level = 0.05, power = NULL,
type = c("two.sample", "one.sample", "paired"),
alternative = c("two.sided", "less", "greater"))
```

`d` is **Cohen's d** effect size: small = 0.2, medium = 0.5, large = 0.8

One-sample test (or paired t-test):

$$d = \frac{\mu - \mu_0}{s}$$

Two-sample test (independent):

$$d = \frac{\bar{x}_1 - \bar{x}_2}{s_{pooled}}$$

- $\bar{x}_1 - \bar{x}_2$ is the difference in means between the two groups that one would want to be able to detect as being significant,
- s_{pooled} is the pooled SD between the two groups - often assume have same sd in each group
- R package `pwr` for basic statistical tests
  - https://cran.r-project.org/web/packages/pwr/vignettes/pwr-vignette.html

pwr: **sample size** for one mean test

`pwr.t.test(n = NULL, d = NULL, sig.level = 0.05, power = NULL, type = c("two.sample", "one.sample", "paired"), alternative = c("two.sided", "less", "greater"))`

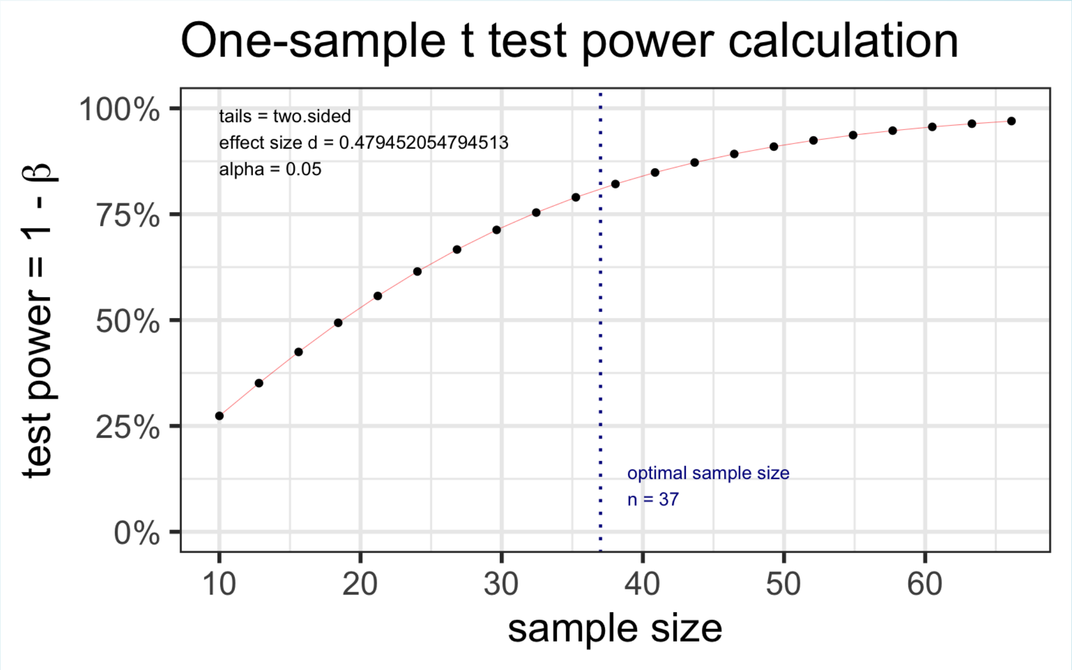
- d is **Cohen's d** effect size: $d = \frac{\mu - \mu_0}{s}$

Specify all parameters *except for* the sample size:

```r
library(pwr)
t.n <- pwr.t.test(
  d = (98.6-98.25)/0.73,
  sig.level = 0.05,
  power = 0.80,
  type = "one.sample")

t.n
```

```

     One-sample t test power calculation 

              n = 36.11196
              d = 0.4794521
      sig.level = 0.05
          power = 0.8
    alternative = two.sided
```

```r
plot(t.n)
```



pwr: **power** for one mean test

`pwr.t.test(n = NULL, d = NULL, sig.level = 0.05, power = NULL, type = c("two.sample", "one.sample", "paired"), alternative = c("two.sided", "less", "greater"))`

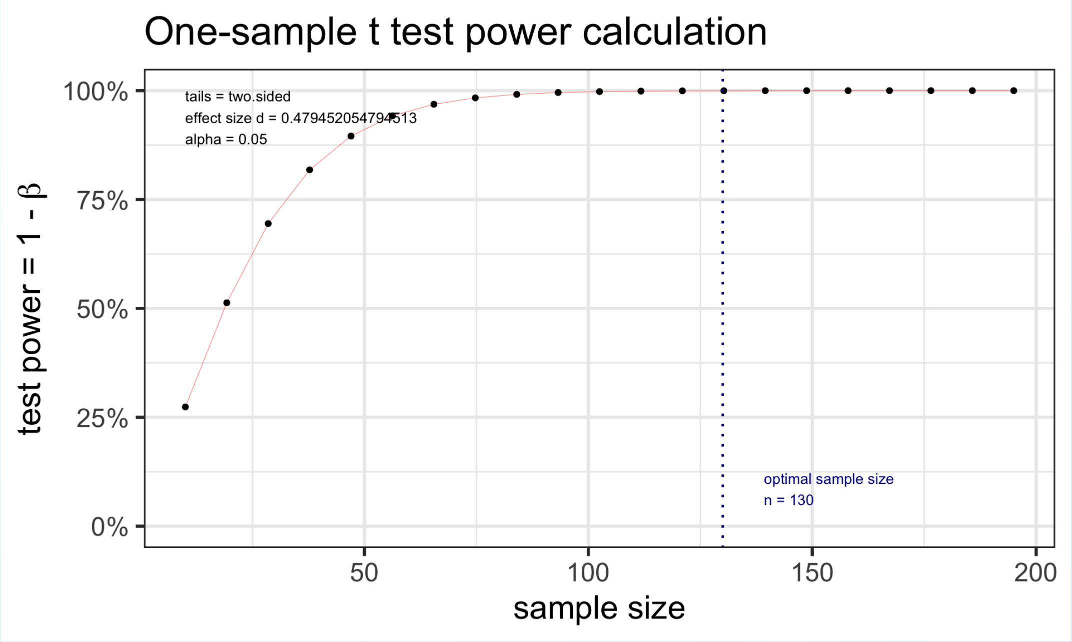
- d is **Cohen's d** effect size: $d = \frac{\mu - \mu_0}{s}$

Specify all parameters *except for* the power:

```r
t.power <- pwr.t.test(
  d = (98.6-98.25)/0.73,
  sig.level = 0.05,
  # power = 0.80,
  n = 130,
  type = "one.sample")

t.power
```

```
     One-sample t test power calculation 

              n = 130
              d = 0.4794521
      sig.level = 0.05
          power = 0.9997354
    alternative = two.sided
```

```r
plot(t.power)
```



pwr: Two-sample t-test: **sample size**

```
pwr.t.test(n = NULL, d = NULL, sig.level = 0.05, power = NULL,
type = c("two.sample", "one.sample", "paired"), alternative = c("two.sided", "less",
"greater"))
```

- d is **Cohen's d** effect size: $d = \frac{\bar{x}_1 - \bar{x}_2}{s_{pooled}}$

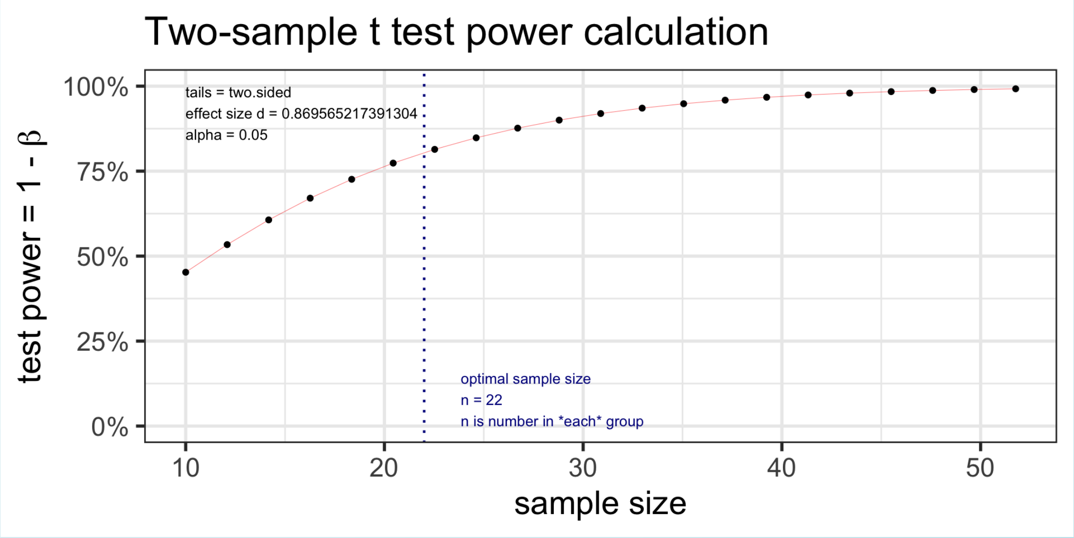
Example: Suppose the data collected for the caffeine taps study were pilot day for a larger study. Investigators want to know what sample size they would need to detect a 2 point difference between the two groups. Assume the SD in both groups is 2.3.

Specify all parameters *except for* the sample size:

```r
t2.n <- pwr.t.test(
  d = 2/2.3,
  sig.level = 0.05,
  power = 0.80,
  type = "two.sample")

t2.n
```

```

     Two-sample t test power calculation 

              n = 21.76365
              d = 0.8695652
      sig.level = 0.05
          power = 0.8
    alternative = two.sided

NOTE: n is number in *each* group
```

```r
plot(t2.n)
```



pwr: Two-sample t-test: **power**

```
pwr.t.test(n = NULL, d = NULL, sig.level = 0.05, power = NULL,
type = c("two.sample", "one.sample", "paired"), alternative = c("two.sided", "less",
"greater"))
```

- d is **Cohen's d** effect size: $d = \frac{\bar{x}_1 - \bar{x}_2}{s_{pooled}}$

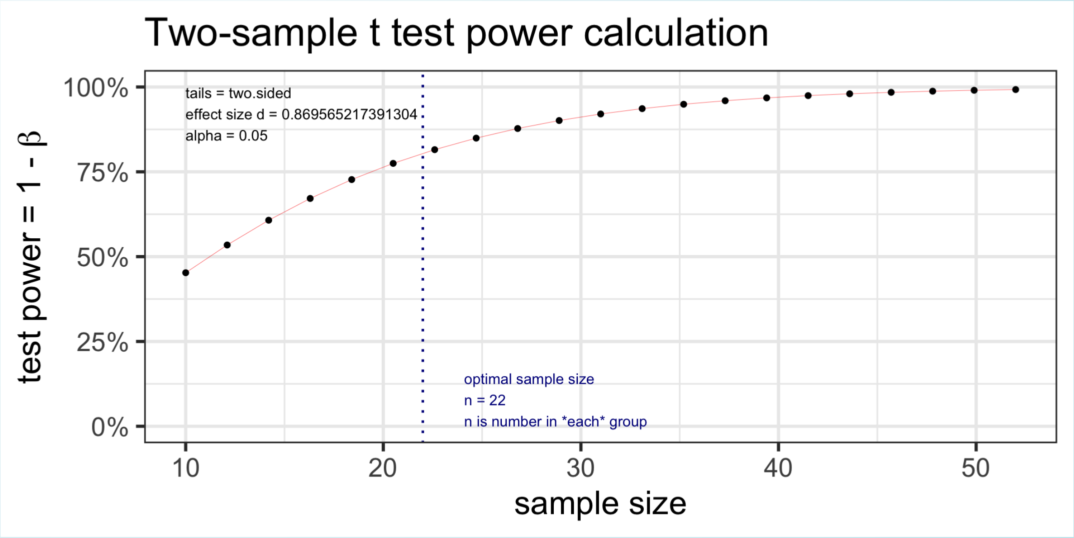
Example: Suppose the data collected for the caffeine taps study were pilot day for a larger study. Investigators want to know what sample size they would need to detect a 2 point difference between the two groups. Assume the SD in both groups is 2.3.

Specify all parameters *except for* the power:

```r
t2.power <- pwr.t.test(
  d = 2/2.3,
  sig.level = 0.05,
  # power = 0.80,
  n = 22,
  type = "two.sample")

t2.power
```

```

     Two-sample t test power calculation 

              n = 22
              d = 0.8695652
      sig.level = 0.05
          power = 0.8044288
    alternative = two.sided

NOTE: n is number in *each* group
```

```r
plot(t2.power)
```



What information do we need for a power (or sample size) calculation?

There are 4 pieces of information:

1. Level of significance α
    - Usually fixed to 0.05
2. Power
    - Ideally at least 0.80
3. Sample size
4. Effect size (expected change)

Given any 3 pieces of information, we can solve for the 4th.

```r
pwr.t.test(
  d = (98.6-98.25)/0.73,
  sig.level = 0.05,
  # power = 0.80,
  n=130,
  type = "one.sample")
```

```

     One-sample t test power calculation 

              n = 130
              d = 0.4794521
      sig.level = 0.05
          power = 0.9997354
    alternative = two.sided
```

More software for power and sample size calculations: PASS

- PASS is a very powerful (& expensive) software that does power and sample size calculations for many advanced statistical modeling techniques.
  - Even if you don’t have access to PASS, their documentation is very good and free online.
  - Documentation includes formulas and references.
  - PASS documentation for powering means
    - One mean, paired means, two independent means
- One-sample t-test documentation: https://www.ncss.com/wp-content/themes/ncss/pdf/Procedures/PASS/One-Sample_T-Tests.pdf

OCTRI-BERD power & sample size presentations

- **Power and Sample Size 101**
  - Presented by Meike Niederhausen; April 13, 2023
  - Slides: http://bit.ly/PSS101-BERD-April2023
  - Recording
- **Power and Sample Size for Clinical Trials: An Introduction**
  - Presented by Yiyi Chen; Feb 18, 2021
  - Slides: http://bit.ly/PSS-ClinicalTrials
  - Recording
- **Planning a Study with Power and Sample Size Considerations in Mind**
  - Presented by David Yanez; May 29, 2019
  - Slides
  - Recording
- **Power and Sample Size Simulations in R**
  - Presented by Robin Baudier; Sept 21, 2023
  - Slides
  - Recording