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

BSTA 511/611

Meike Niederhausen, PhD
OHSU-PSU School of Public Health

2023-11-06

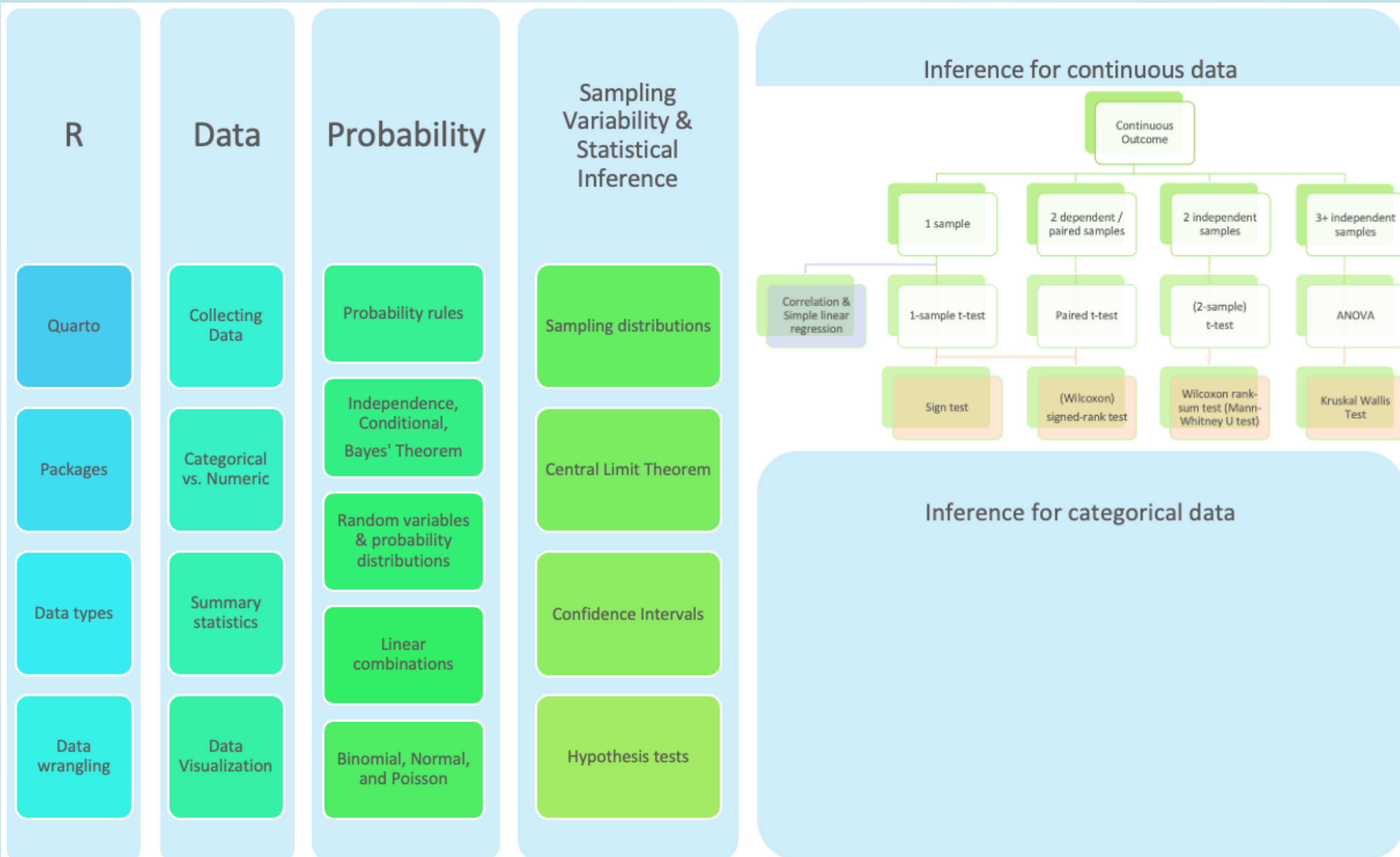
# MoRitz's tip of the day

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

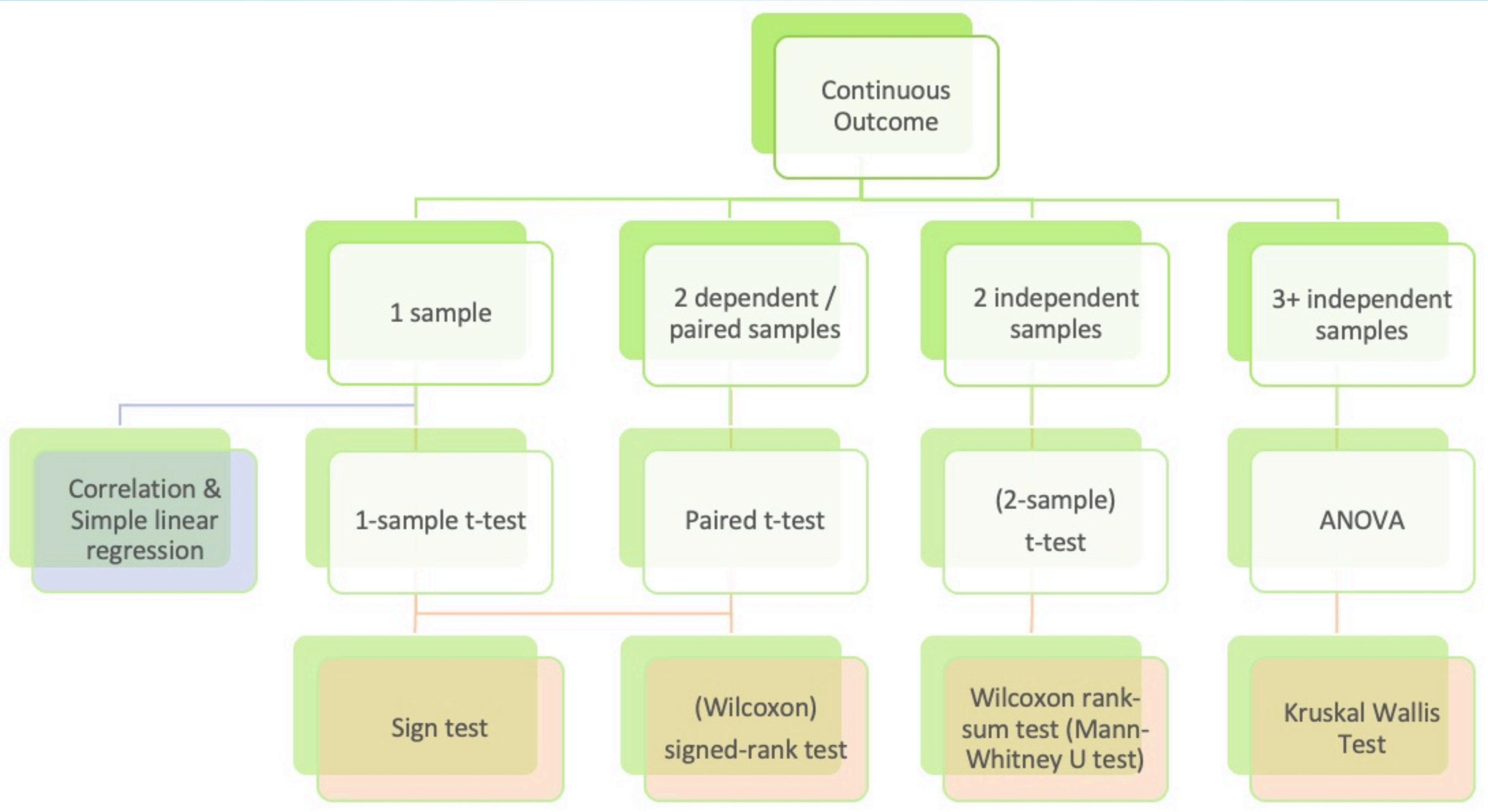
First tab | Second tab | Read up on tabsets

- 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
Continuous Outcome
1 sample
2 dependent / paired samples
2 independent samples
3+ independent samples
Correlation & Simple linear regression
1-sample t-test
Paired t-test
(2-sample) t-test
ANOVA
Sign test
(Wilcoxon) signed-rank test
Wilcoxon rank-sum test (Mann-Whitney U test)
Kruskal Wallis Test
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 | $\mu$ | Sample mean | $\bar{x}$ | $\frac{s}{\sqrt{n}}$ |
| 10 | 5.2 | Pop mean of paired diff | $\mu_d$ or $\delta$ | 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.*

# Steps in a Hypothesis Test

1. Set the **level of significance** $\alpha$
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)

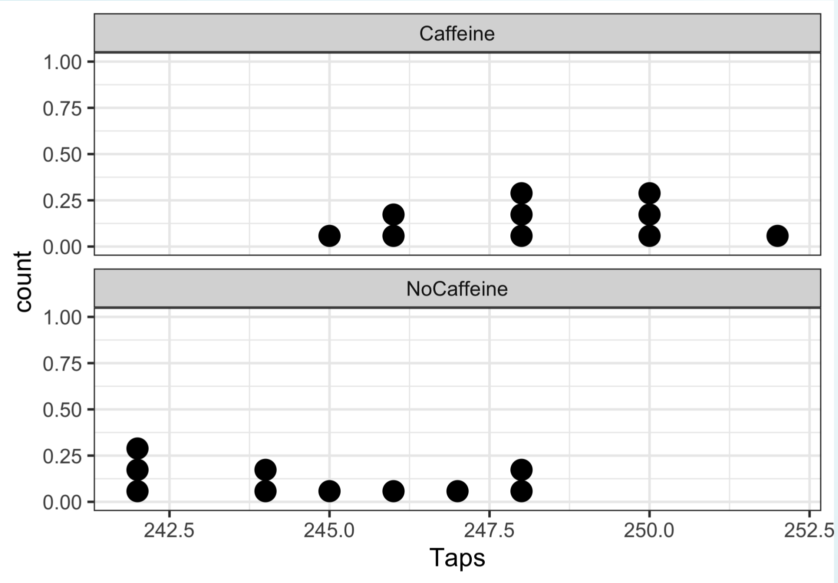
```
CaffTaps <- read_csv(here::here("data", "CaffeineTaps.csv"))

glimpse(CaffTaps)
```

```
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

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




## Summary statistics stratified by group

```
# 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 |

```
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 …
- $H_A$: The population difference in mean finger taps/min between the caffeine and control groups is …

Null and alternative hypotheses in **symbols**

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

# 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 | $\mu_1$ | $\mu_2$ |
| pop sd | $\sigma_1$ | $\sigma_2$ |

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 $\bar{X}_1 - \bar{X}_2$?

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

- 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 |
|---|---|---|---|---|
| Caffeine | Taps | 10 | 248.3 | 2.214 |
| NoCaffeine | Taps | 10 | 244.8 | 2.394 |

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

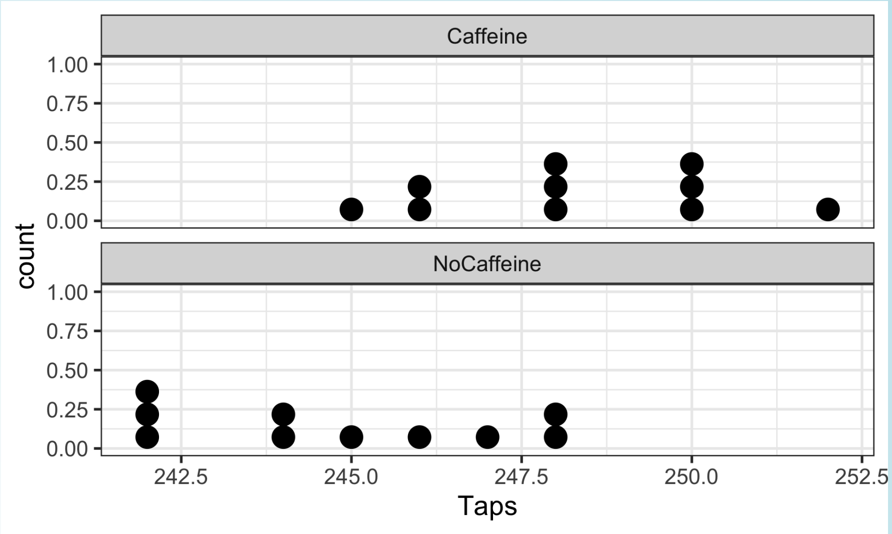
---

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?

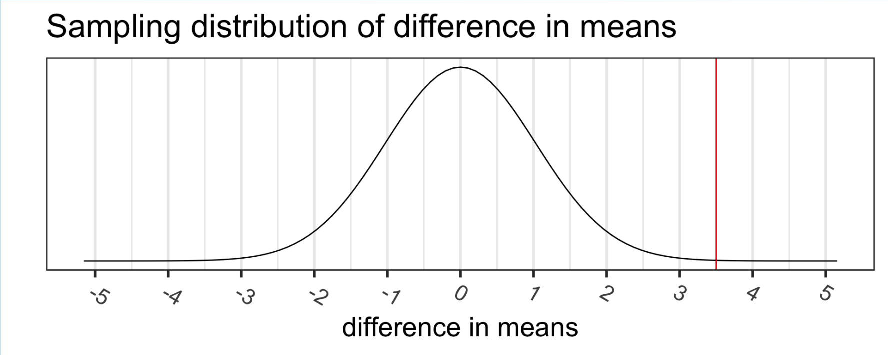
**Assumptions**:

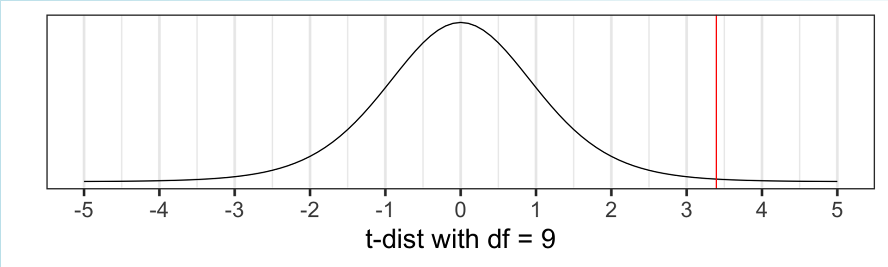
- **Independent observations & samples**
  - The observations were collected independently.
  - In particular, the observations from the two groups were not paired in any meaningful way.
- **Approximately normal samples or big n's**
  - The distributions of the samples should be approximately normal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



# Step 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.




Calculate the *p*-value:

# 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 $\alpha$ = 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 $\mu_{caff} - \mu_{ctrl}$:

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

**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?*

# 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.

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

```

	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)
```

```
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 |

# 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 $\nu$ = 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

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

$$s^2_{pooled} = \frac{s_1^2(n_1 - 1) + s_2^2(n_2 - 1)}{n_1 + n_2 - 2}$$

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

- We use the pooled SD instead of $s_1^2$ 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()
```

| 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 | $\mu$ | Sample mean | $\bar{x}$ | $\frac{s}{\sqrt{n}}$ |
| 10 | 5.2 | Pop mean of paired diff | $\mu_d$ or $\delta$ | 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

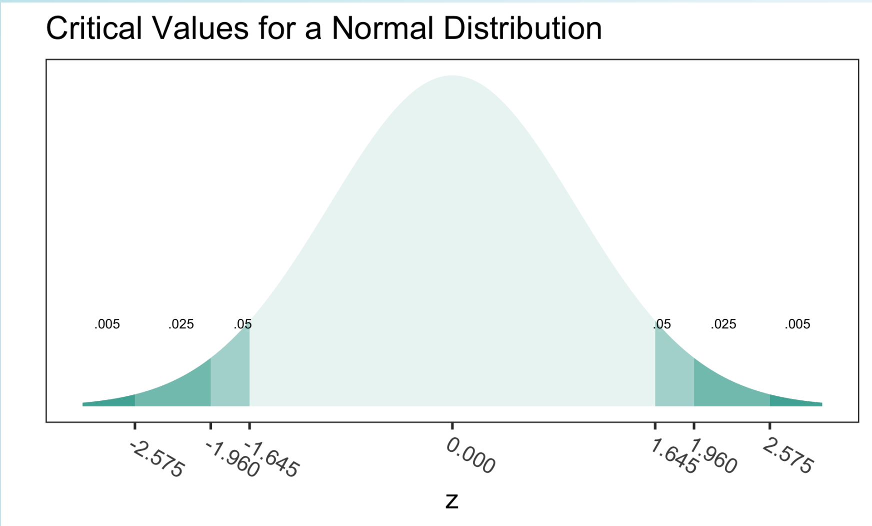
- Critical values & rejection region
- Type I & II errors
- Power
- How to calculate sample size needed for a study?

---

- 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 $H_0$

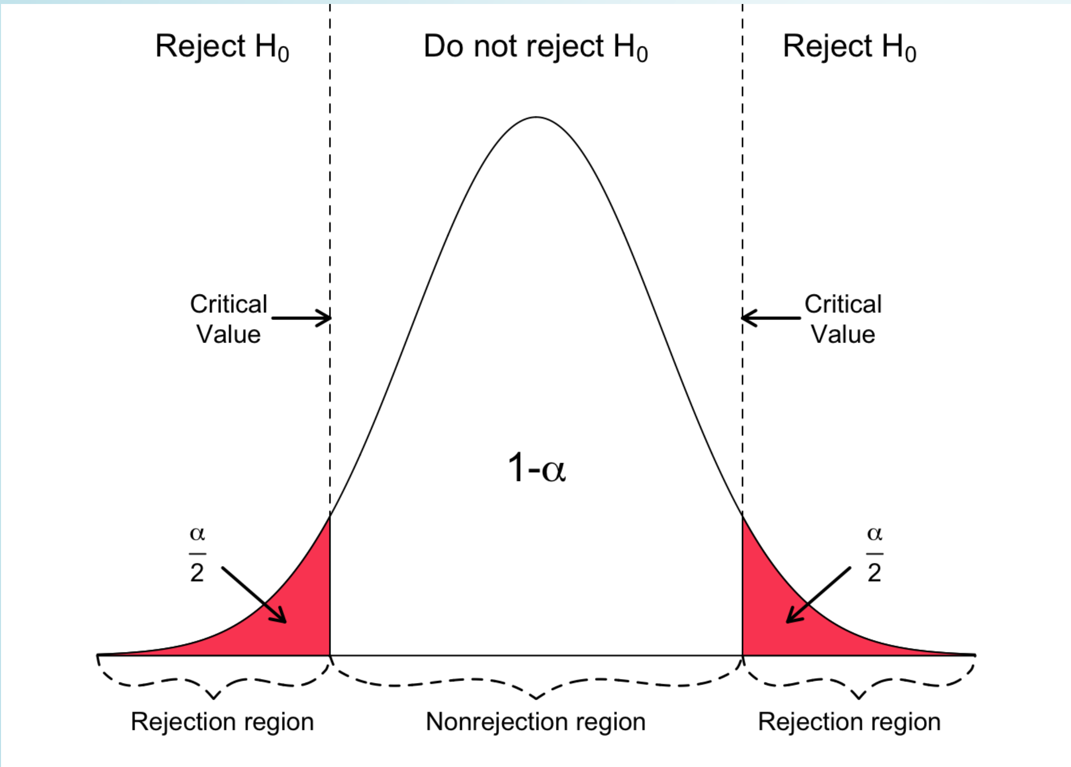



- Critical values are determined by
  - the significance level $\alpha$,
  - whether a test is 1- or 2-sided, &
  - the probability distribution being used to calculate the p-value (such as normal or t-distribution).
- The critical values in the figure should look very familiar!
  - Where have we used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

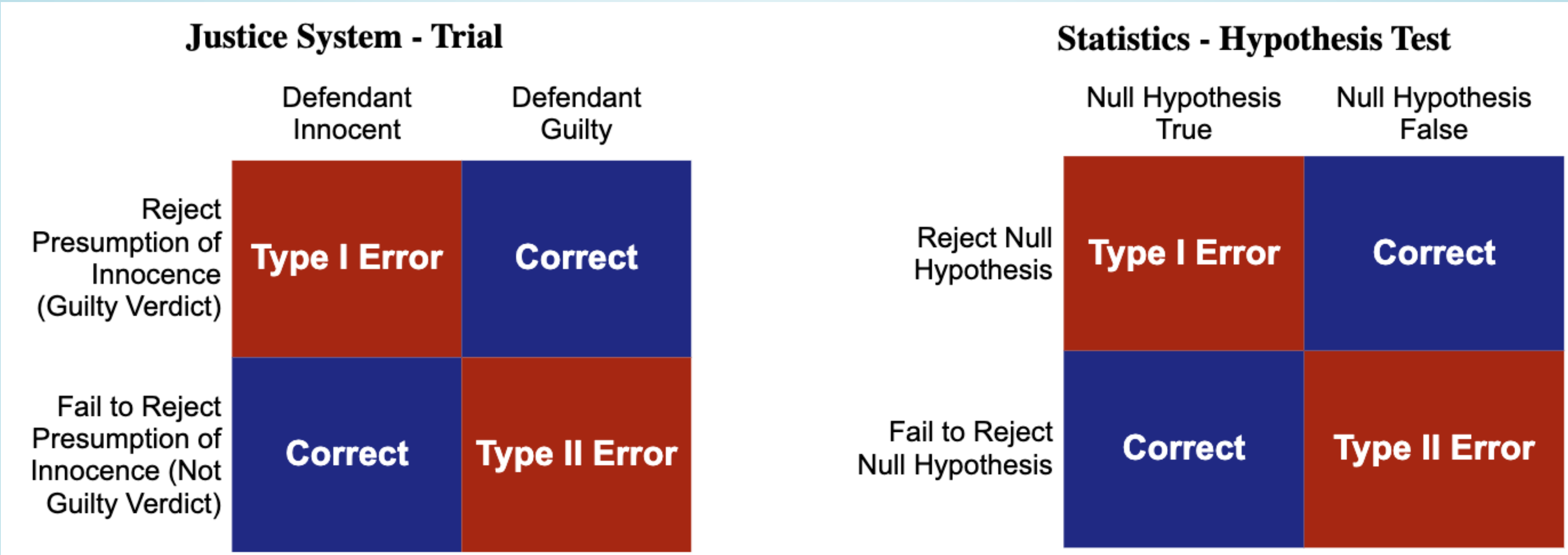



- What do rejection regions look like for 1-sided tests?

# 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**

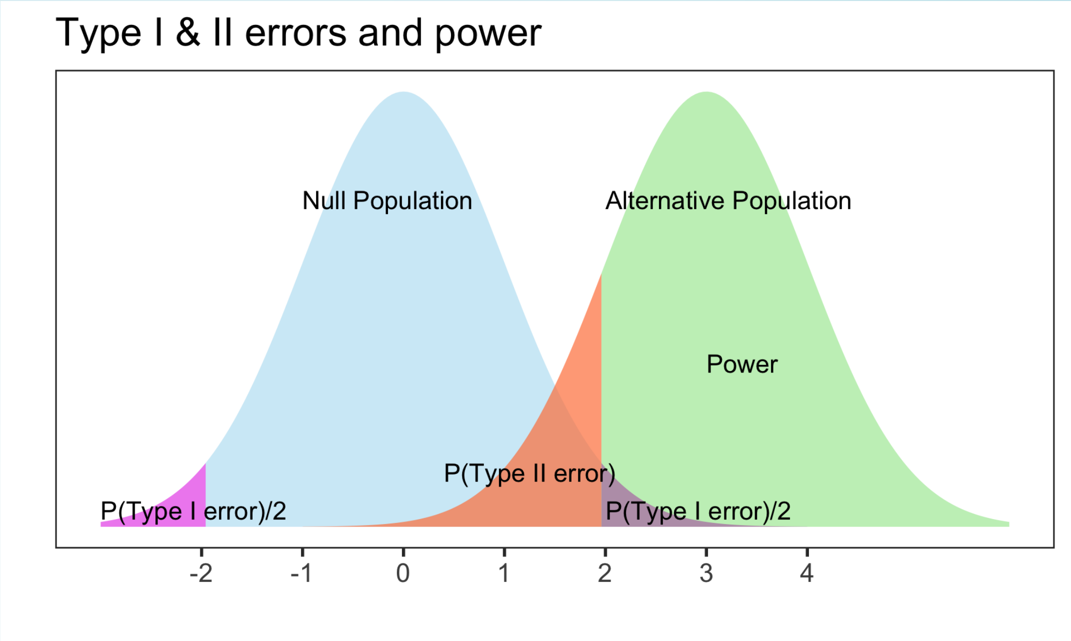
| | Null Hypothesis True | Null Hypothesis False |
|---|---|---|
| Reject Null Hypothesis | Type I Error | Correct |
| Fail to Reject Null Hypothesis | Correct | Type II Error |

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) |

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

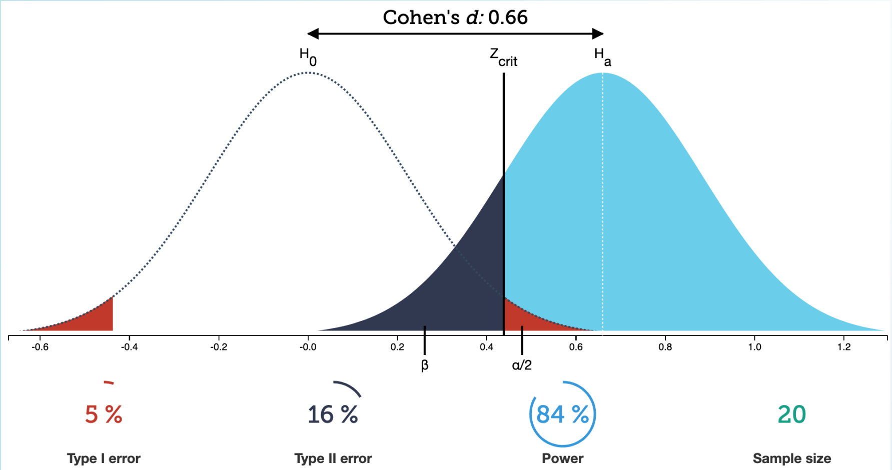


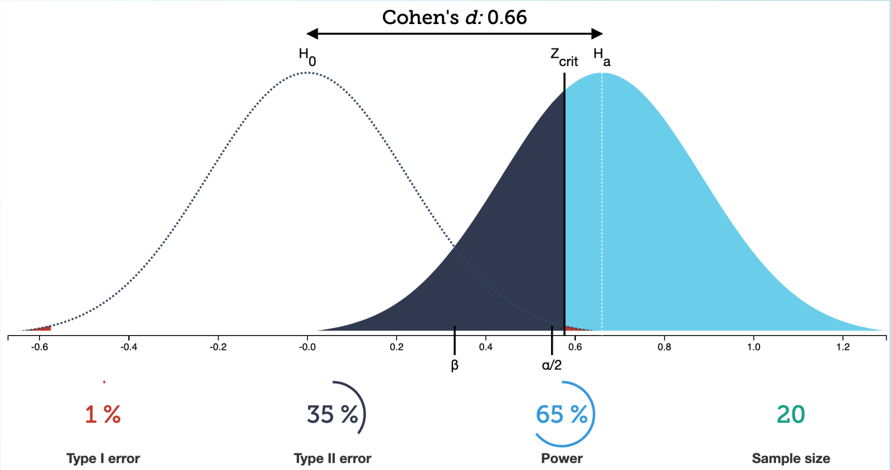

Applet for visualizing Type I & II errors and power: https://rpsychologist.com/d3/NHST/

# 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) = $\alpha$ set to 0.05

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

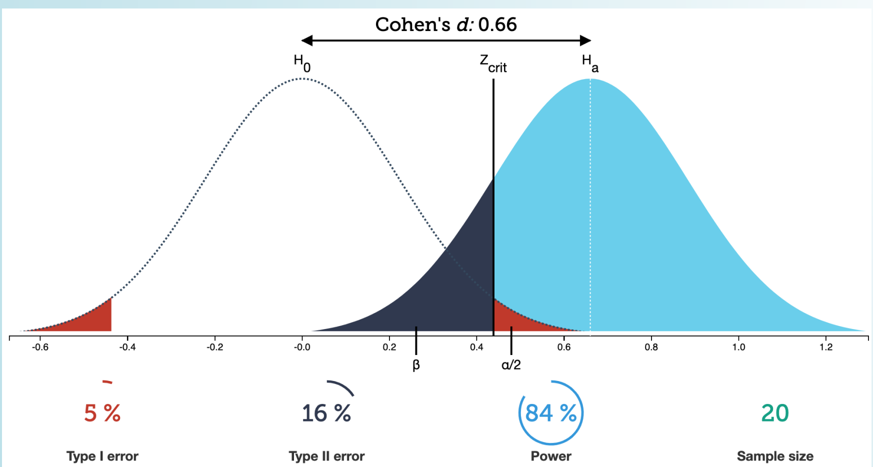


# Relationship between Type II errors and power

**Power** = P(correctly rejecting the null hypothesis)

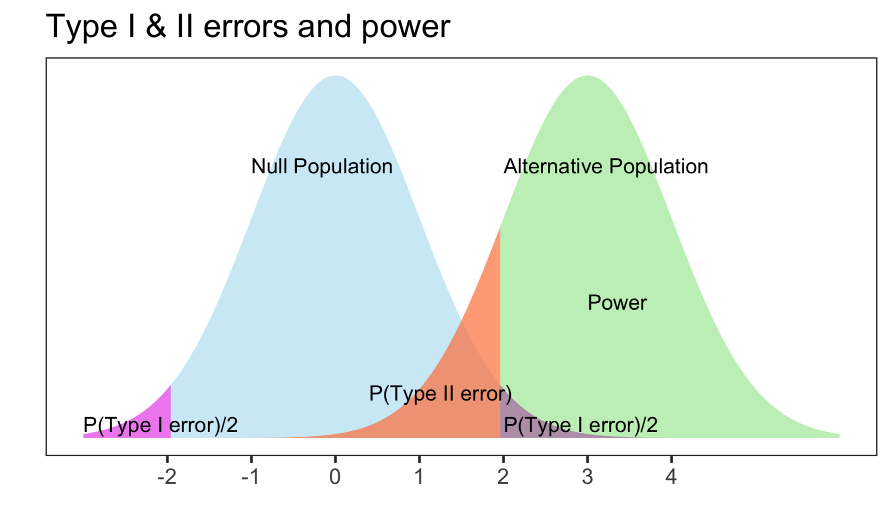
- Power is also called the
  - true positive rate,
  - probability of detection, or
  - the *sensitivity* of a test




- **Power vs. Type II error**
  - Power = 1 - P(Type II error) = 1 - $\beta$
  - Thus as $\beta$ = 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 $\alpha$ = 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 $\alpha$, power ( $1-\beta$ ), "true" alternative mean $\mu$, and null $\mu_0$,
  - *assuming* the test statistic is normal (instead of t-distribution):

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

```
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
```

```
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 $\alpha$, $n$, "true" alternative mean $\mu$, and null $\mu_0$,
  - *assuming* the test statistic is normal (instead of t-distribution)

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

$\Phi$ 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"))
```

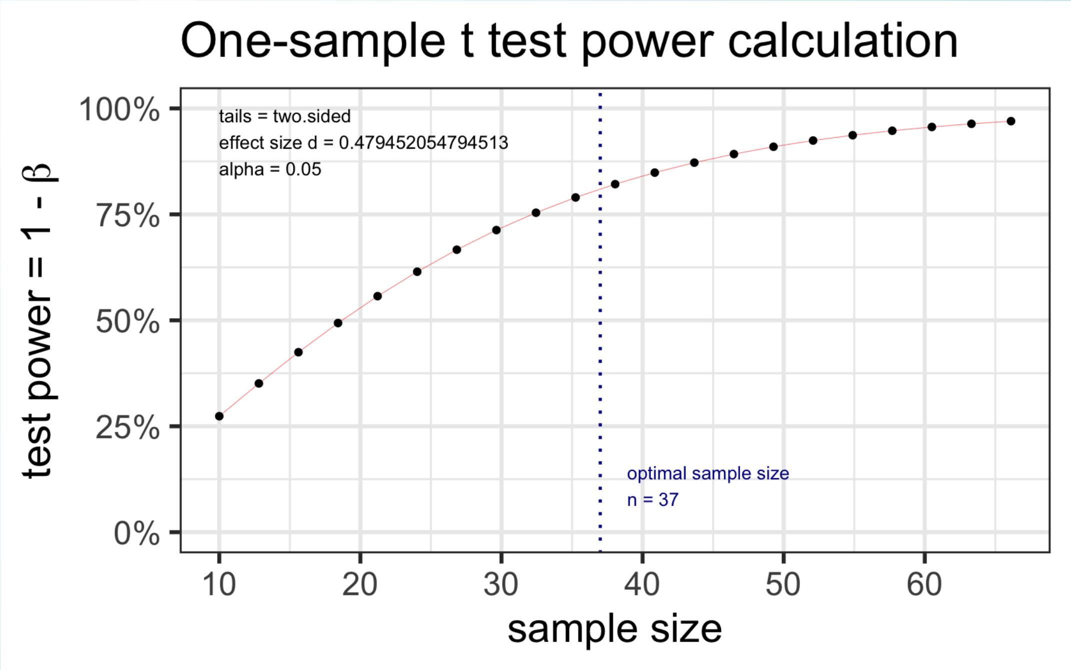
- d is **Cohen's d** effect size: $d = \frac{\mu - \mu_0}{s}$

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"))
```

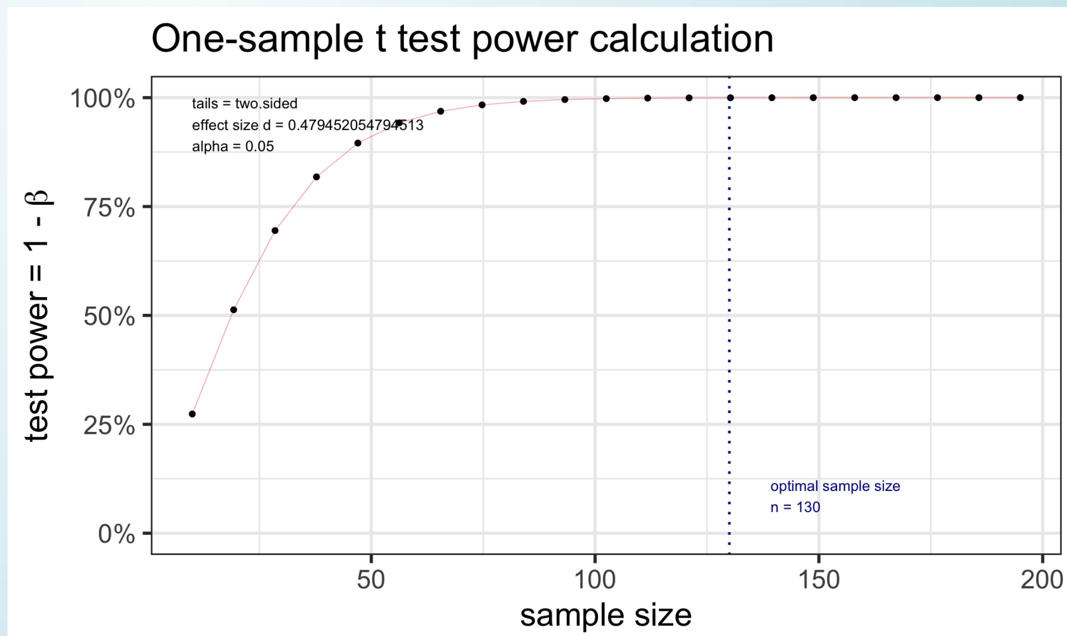
- d is **Cohen's d** effect size: $d = \frac{\mu - \mu_0}{s}$

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

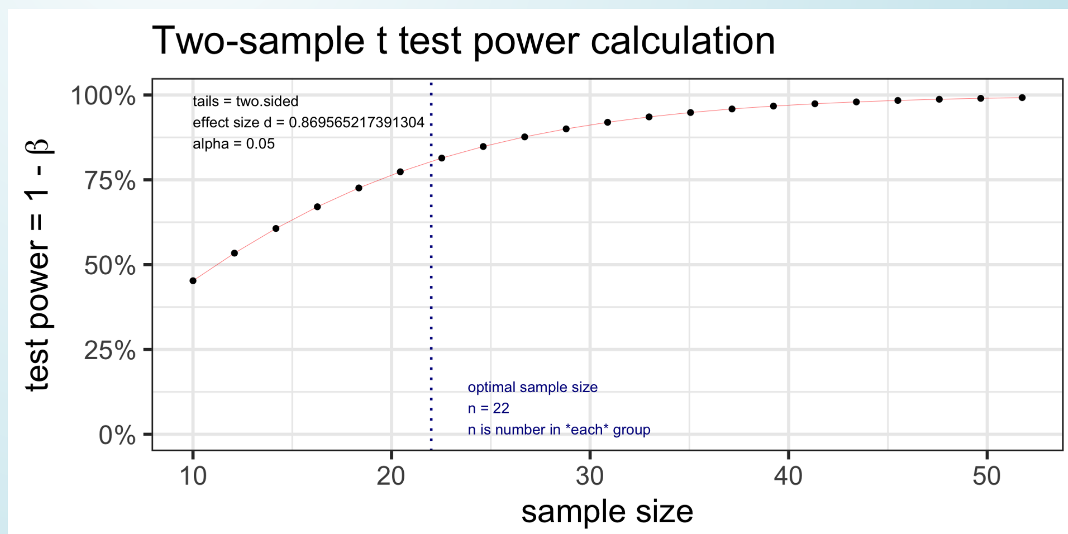
**Example**: Suppose the data collected for the caffeine taps study were pilot day for a larger study. Investigators want to know what sample size they would need to detect a 2 point difference between the two groups. Assume the SD in both groups is 2.3.

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

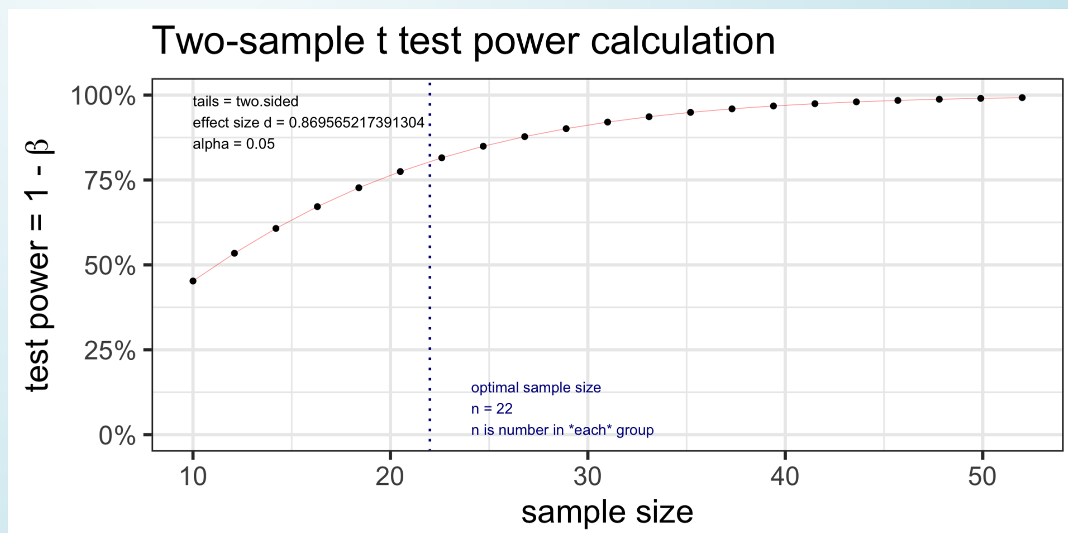
**Example**: Suppose the data collected for the caffeine taps study were pilot day for a larger study. Investigators want to know what sample size they would need to detect a 2 point difference between the two groups. Assume the SD in both groups is 2.3.

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 $\alpha$
   - 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