

# MIE237

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# Comments on confidence intervals

They're all pretty much the same. And to be honest I can't think of a good reason to select a confidence level that isn't 95%.

$$\text{Estimator} \pm "2" \sqrt{\text{Standard Error}}$$

"Standard Error" is short for "the standard deviation of the estimator".

# Comments on hypothesis testing

- You learned the basics and everything was mathematically correct, but the context tended to be artificial ("one-sample") and as such things were possibly baffling.
- There are two distinct approaches:
  - "Classical" with a rejection region and a "reject/not reject" decision-theoretic framework.
  - p-value
- But then people try to take a p-value and draw a "reject/not reject" conclusion anyway. P-values are better interpreted as "strength of evidence".
- "One-sided alternatives"...based on the hopes and dreams of the experimenter...mathematically valid but scientific nonsense.

Inference with two  
independent numerical  
samples (9.8 and 10.5)

# The population model(s)

- Populations  $N(\mu_1, \sigma_1^2)$  and  $N(\mu_2, \sigma_2^2)$
- Equivalent:  $Y_{ij} = \mu_i + \varepsilon_{ij}$  with  $\varepsilon_{ij} \sim N(0, \sigma_i^2)$  and  $i \in \{1, 2\}$
- Main interest: the difference between  $\mu_1$  and  $\mu_2$ .
- Two cases:
  - Equal variances:  $\sigma_1^2 = \sigma_2^2$  so we just call them both  $\sigma^2$  (this is the "special case".)
  - Unequal variances, which is typically the default implemented in software and is more realistic.
- Samples:  $Y_{11}, \dots, Y_{1n_1}$  and  $Y_{21}, \dots, Y_{2n_2}$
- $\bar{Y}_{1\cdot} - \bar{Y}_{2\cdot} \sim N\left(\mu_1 - \mu_2, \sigma^2 \left(\frac{1}{n_1} + \frac{1}{n_2}\right)\right)$

# "The Key Fact" - equal variance version

$$\frac{(\bar{Y}_{1\cdot} - \bar{Y}_{2\cdot}) - (\mu_1 - \mu_2)}{\sigma \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}} \sim N(0, 1)$$

We need to estimate  $\sigma$ . Let's pool the data from both samples:

$$S_p^2 = \frac{(n_1 - 1)S_1^2 + (n_2 - 1)S_2^2}{(n_1 - 1) + (n_2 - 1)}$$

Key fact:

$$\frac{(\bar{Y}_{1\cdot} - \bar{Y}_{2\cdot}) - (\mu_1 - \mu_2)}{S_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}} \sim t_{(n_1-1)+(n_2-1)}$$

# "The Key Fact" eq. var. model assumptions

- The Key Fact is approximately true as long as sample sizes are "big enough" (also checking normal plots of both samples), and the true population variances are equal (check boxplots and sample SDs, allow for plenty of difference, say 3:1 even.)
- There is reliable method to formally test the difference in variance between two independent populations.

## Example (9.40 from text)

In a study conducted at Virginia Tech on the development of ectomycorrhizal, a symbiotic relationship between the roots of trees and a fungus, in which minerals are transferred from the fungus to the trees and sugars from the trees to the fungus, 20 northern red oak seedlings exposed to the fungus *Pisolithus tinctorius* were grown in a greenhouse. All seedlings were planted in the same type of soil and received the same amount of sunshine and water. Half received no nitrogen at planting time, to serve as a control, and the other half received 368 ppm of nitrogen in the form  $\text{NaNO}_3$ . The stem weights, in grams, at the end of 140 days were recorded...



## 9.40 continues

```
library(rio)
nitro <- import("Ex09.40.txt")
t.test(nitro$NoNitrogen, nitro$Nitrogen, var.equal = TRUE)
```

```
##
## Two Sample t-test
##
## data:  nitro$NoNitrogen and nitro$Nitrogen
## t = -2.6191, df = 18, p-value = 0.01739
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -0.29915788 -0.03284212
## sample estimates:
## mean of x mean of y
##      0.399      0.565
```

## 9.40 with data in "real" form

```
library(tidyr)
nitro_tidy <- gather(nitro, treatment, weight)
t.test(weight ~ treatment, data=nitro_tidy, var.equal = TRUE)
```

```
##
## Two Sample t-test
##
## data: weight by treatment
## t = -2.6191, df = 18, p-value = 0.01739
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
## -0.29915788 -0.03284212
## sample estimates:
## mean in group NoNitrogen    mean in group Nitrogen
##                0.399                0.565
```