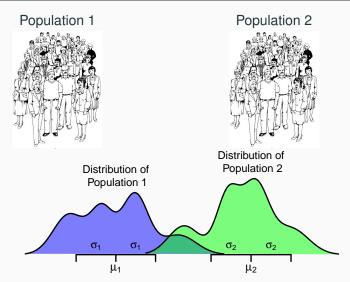
STAT 22000 Lecture Slides Analysis of Two-Sample Data

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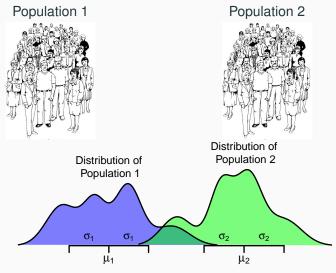
Coverage

This set of slides covers Section 5.3 in the 3rd edition of *OpenIntro Statistics* (or Section 7.3 in the 4th edition).

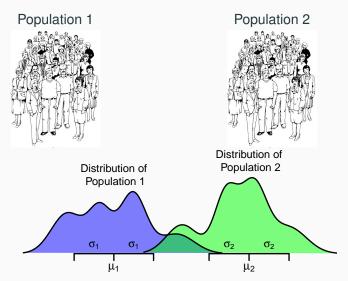
- E.g., is the air more polluted in Chicago than in LA?
- E.g., are smokers suffering less from depression than non-smokers?
- E.g., are the response in the treatment group different from that in the control group?



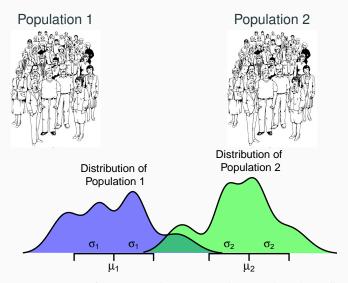
Population distributions may NOT be normal or of the same shape for large samples.



Population SDs σ_1 and σ_2 may not be equal.



Goal: inference about difference of population means $\mu_1 - \mu_2$.



Data may come from experiments or observational studies.

Two Sample Data

For an Observational Study:

Population 1
$$\longrightarrow$$
 random sample $X_{1,1}, X_{1,2}, \dots, X_{1,n_1}$
Population 2 \longrightarrow random sample $X_{2,1}, X_{2,2}, \dots, X_{2,n_2}$

For a Randomized Experiment:

Treatment 1
$$\longrightarrow$$
 observations $X_{1,1}, X_{1,2}, \dots, X_{1,n_1}$
Treatment 2 (Control) \longrightarrow observations $X_{2,1}, X_{2,2}, \dots, X_{2,n_2}$

 The responses in each group are independent of those in the other group

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A natural estimate of $\mu_1 - \mu_2$ is the difference of the two sample means $\overline{X}_1 - \overline{X}_2$.

How close is $\overline{X}_1 - \overline{X}_2$ to $\mu_1 - \mu_2$?

Recall that

$$E(\overline{X}_1) = \mu_1, \quad V(\overline{X}_1) = \sigma_1^2/n_1$$

 $E(\overline{X}_2) = \mu_2, \quad V(\overline{X}_2) = \sigma_2^2/n_2.$

Observe $\overline{X}_1 - \overline{X}_2$ is an **unbiased estimate** of $\mu_1 - \mu_2$ because

$$E(\overline{X}_1 - \overline{X}_2) = E(\overline{X}_1) - E(\overline{X}_2) = \mu_1 - \mu_2.$$

Furthermore, since the two samples are *independent*, \overline{X}_1 and \overline{X}_2 are independent, we have

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

Thus the **standard error** of $\overline{X}_1 - \overline{X}_2$ is

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

Two-Sample *t*-Statistic When σ_1 , σ_2 Are Unknown

Of course, σ_1^2 and σ_2^2 are often unknown. Thus we substitute them by the sample variances s_1^2 and s_2^2 .

$$t = \frac{(\overline{X}_1 - \overline{X}_2) - (\mu_1 - \mu_2)}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}} \quad \text{where} \quad s_1^2 = \frac{\sum_{i=1}^{n_1} (X_{1,i} - \overline{X}_1)^2}{n_1 - 1} \\ s_2^2 = \frac{\sum_{i=1}^{n_2} (X_{2,i} - \overline{X}_2)^2}{n_2 - 1}$$

- Unfortunately, the two-sample t-statistic does NOT have a t-distribution
- Fortunately, it can be approximated by a *t*-distribution with a certain degrees of freedom.

See the next slide for the approximation

Approximate Distribution of the Two-Sample *t*-Statistic

The two-sample t-statistic has an **approximate** t_k **distribution**. For the degrees of freedom k we have two formulas:

1. software formula:

$$k = \frac{(w_1 + w_2)^2}{w_1^2/(n_1 - 1) + w_2^2/(n_2 - 1)}, \quad \text{where} \quad \begin{aligned} w_1 &= s_1^2/n_1, \\ w_2 &= s_2^2/n_2. \end{aligned}$$

2. simple formula: $k = \min(n_1 - 1, n_2 - 1)$

Comparison of the two formulas:

- The software formula is more accurate. It gives larger d.f. and yields shorter CIs and smaller p-value
- The simple formula is conservative. I.e., it yields wider CIs and larger p-values than the actual p-value
- In STAT 220, it is fine to just use the simple formula.

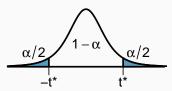
Confidence Intervals for $\mu_1 - \mu_2$

A $(1-\alpha)100\%$ CI for $\mu_1 - \mu_2$ is given by

$$(\overline{X}_1 - \overline{X}_2) \pm t^* \sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$$

where t^* is the value of the t distribution with k degrees of freedom such that

density curve of t_k



which can be found in R using the qt() command.

Example: Nitrogen Effect on Tree Growth

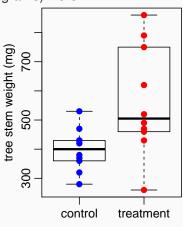
20 northern red oak seedlings

half received nitrogen, and half didn't.

All grown in same type of soil in same greenhouse

After 140 days, stem weights (in milligrams) were:

Control no nitrogen		Treatment nitrogen	
320	430	260	750
530	360	430	790
280	420	470	860
370	380	490	620
470	430	520	460
mean = 399		mean = 565	
SD = 72.79		SD = 186.74	
$n_{C} = 10$		$n_T = 10$	



Example: CI for the Nitrogen Effect on Tree Growth

The df is min(10 - 1, 10 - 1) = 9. The critical value $t^* \approx 2.26$ for 95% CI can be found in R as follows

So the 95% CI for $\mu_T - \mu_C$ (treatment mean - control mean) is

$$\overline{X}_T - \overline{X}_C \pm t^* \sqrt{\frac{s_T^2}{n_1} + \frac{s_C^2}{n_2}} = 565 - 399 \pm 2.26 \sqrt{\frac{(186.74)^2}{10} + \frac{(72.79)^2}{10}}$$

$$\approx 166 \pm 143.4 = (22.6, 309.4)$$

Since 0 (zero) is NOT inside the CI, it appears that there **is** a difference in the population mean stem weights of the treatment and control groups.

We conclude that Nitrogen has an effect on stem weight.

Hypothesis Tests for $\mu_1 - \mu_2$

To test H_0 : $\mu_1 - \mu_2 = \delta_0$, the two-sample *t*-statistic is

$$t = rac{(\overline{X}_1 - \overline{X}_2) - \delta_0}{\sqrt{s_1^2/n_1 + s_2^2/n_2}} \sim ext{approx. } t_k$$

where the df is $k = \min(n_1 - 1, n_2 - 1)$, or the one given by the software formula, and the *p*-value is computed as follows depending on H_a .

H _a	$\mu_1 - \mu_2 \neq \delta_0$	$\mu_1 - \mu_2 < \delta_0$	$\mu_1 - \mu_2 > \delta_0$
p-value			
	—lti lti	t	t

The bell curve above is the t-curve with k degrees of freedom.

Example: Test for the Nitrogen Effect on Tree Growth

For testing $H_0: \mu_T - \mu_C = 0$ v.s. $H_a: \mu_T - \mu_C \neq 0$, the *t*-statistic is

$$t = \frac{\overline{X}_T - \overline{X}_C}{\sqrt{s_T^2/n_T + s_C^2/n_C}} = \frac{565 - 399}{\sqrt{\frac{(186.74)^2}{10} + \frac{(72.79)^2}{10}}} = \frac{166}{63.38} \approx 2.62.$$

The degrees of freedom is 10 - 1 = 9. The two-sided *P*-value can be found in R to be ≈ 0.0278 .

The difference is significant at 5% level.

We conclude that Nitrogen has an effect on stem weight.

Two-Sample Tests/Cls in R

```
> ctrl = c(320,430,530,360,280,420,370,380,470,430)
> trt = c(260,750,430,790,470,860,490,620,520,460)
By default, the R command t.test does NOT assume \sigma_1 = \sigma_2.
> t.test(ctrl, trt)
Welch Two Sample t-test
data: ctrl and trt
t = -2.6191, df = 11.673, p-value = 0.02286
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -304.52438 -27.47562
sample estimates:
mean of x mean of y
                565
      399
```

Note the df = 11.673 given above is based on the software formula, which is more accurate than the simple formula.

Robustness of Two-Sample *t*-Procedures (1)

Even when the populations are not normal, the two-sample statistics

$$t = \frac{(\overline{X}_1 - \overline{X}_2) - (\mu_1 - \mu_2)}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}}$$

can be well-approximated by *t*-distributions, as long as *the sample* sizes are not too small.

This is the so-called **robustness** of the two-sample *t*-procedures.

Robustness of Two-Sample *t*-Procedures (2)

- The t-approximation is generally good if n₁ + n₂ is not too small (both ≥ 15), the data are not strongly skewed, and there are no outliers.
 - Check histograms or side-by-side boxplots of the data
- With n₁ + n₂ sufficiently large (say both ≥ 30), the approximation is good even when the data are clearly skewed.
- Given a fixed sum of the sample sizes $n = n_1 + n_2$ the t-approximation works the best when the sample sizes are equal $n_1 = n_2$
 - In planning a two-sample study, choose equal sample sizes if you can

Analysis of Two Sample Data When $\sigma_1 = \sigma_2$ (Optional Topic)

What if $\sigma_1 = \sigma_2$?

So far we have assumed that $\sigma_1 \neq \sigma_2$. What if we have reason to believe $\sigma_1 = \sigma_2 = \sigma$ albeit σ is unknown?

When $\sigma_1^2=\sigma_2^2=\sigma^2$, both s_1^2 and s_2^2 are unbiased estimates of σ^2 . We can combine s_1^2 and s_2^2 to get a better estimate for σ^2 , which is the so-called **pooled sample variances**

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

Observe that s_p^2 is a weighted average of s_1^2 and s_2^2 , and it gives more weights to the sample with larger size.

Moreover, as $s^2 = \frac{1}{n-1} \sum_i (X_i - \overline{X})^2$, we can see that

$$s_p^2 = \frac{\sum_i (X_{1,i} - \overline{X}_1)^2 + \sum_i (X_{2,i} - \overline{X}_2)^2}{n_1 + n_2 - 2}$$

is simply an "average" of the squared deviations from the corresponding means, though we divide by $n_1 + n_2 - 2$ but not $n_1 + n_2$.

The Pooled Two-Sample *t*-Statistic (When $\sigma_1 = \sigma_2$)

The two-sample *t*-statistic then becomes

$$T = \frac{(\overline{X}_1 - \overline{X}_2) - (\mu_1 - \mu_2)}{\sqrt{\frac{s_p^2}{n_1} + \frac{s_p^2}{n_2}}} = \frac{(\overline{X}_1 - \overline{X}_2) - (\mu_1 - \mu_2)}{s_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}}$$

which is specifically called **the pooled two-sample** *t***-statistic**.

- It has an exact t-distribution with n₁ + n₂ 2 degrees of freedom when the two populations are normal.
- It is approximately $t_{(n_1+n_2-2)}$ as long as the sample size n_1 , n_2 is not too small.
- The degrees of freedom, $n_1 + n_2 2$ is greater the degrees of freedom given by the software formula or the simple formula when $\sigma_1 \neq \sigma_2$

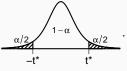
Two Sample Problems w/ Equal but Unknown σ s

A $(1 - \alpha)100\%$ CI for $\mu_1 - \mu_2$ is

$$(\overline{X}_1 - \overline{X}_2) \pm t^* s_p \sqrt{\frac{1}{n_1} + \frac{1}{n_2}}$$

where where t^* is the value of the t distribution with $n_1 + n_2 - 2$

degrees of freedom such that



To test the hypothesis $H_0: \mu_1 - \mu_2 = \delta_0$, we use

$$t=rac{\overline{X}_1-\overline{X}_2-\delta_0}{s_p\,\sqrt{rac{1}{n_1}+rac{1}{n_2}}}\sim t_{n_1+n_2-2} \quad ext{ under } H_0$$

Tree Growth Example Revisit: Assuming $\sigma_1=\sigma_2$

If assuming $\sigma_1 = \sigma_2$, the pooled SD is

$$s_p = \sqrt{\frac{(10-1)(186.74)^2 + (10-1)(72.79)^2}{10+10-2}} \approx 141.72$$

The degrees of freedom is $n_T + n_C - 2 = 10 + 10 - 2 = 18$. The critical value $t^* \approx 2.101$ for 95% CI can be found in R as follows

So the 95% CI for $\mu_T - \mu_C$ (treatment mean - control mean) is

$$\overline{X}_T - \overline{X}_C \pm t^* s_p \sqrt{\frac{1}{n_T} + \frac{1}{n_C}} = 565 - 399 \pm 2.101 \times 141.72 \times \sqrt{\frac{1}{10} + \frac{1}{10}}$$

$$\approx 166 \pm 133.2 = (32.8, 299.2)$$

Observe the CI become shorter. As the degrees of freedom k increases, the critical value t^* decreases.

Tree Growth Example Revisit: Assuming $\sigma_1=\sigma_2$

For testing H₀ : $\mu_T - \mu_C = 0$ v.s. H_a : $\mu_T - \mu_C \neq 0$, assuming $\sigma_1 = \sigma_2$ the pooled *t*-statistic is

$$t = \frac{\overline{X}_T - \overline{X}_C}{s_p \sqrt{1/n_T + 1/n_C}} = \frac{565 - 399}{141.72 \sqrt{1/10 + 1/10}} = \frac{166}{63.38} \approx 2.619.$$

The df is $n_T + n_C - 2 = 10 + 10 - 2 = 18$.

The two-sided P-value can be found in R to be

The pooled *t*-test gives smaller *p*-value and the result appears more significant.

Two-Sample Tests/Cls in R

One can force σ_1, σ_2 to be equal by the argument var.equal = T.

```
> t.test(ctrl, trt, var.equal = T)
Two Sample t-test
data: ctrl and trt
t = -2.6191, df = 18, p-value = 0.01739
alternative hypothesis: true difference in means is not equal to 0
95 percent confidence interval:
 -299.15788 -32.84212
sample estimates:
mean of x mean of y
                565
      399
```

Which Two-Sample Tests/Cls to Use?

We have introduced two different two-sample tests/CIs:

- the one assuming $\sigma_1 = \sigma_2$ used the **pooled SD**.
- the one w/o assuming $\sigma_1 = \sigma_2$ is called **Welch's method**.

Though in many cases, the two methods agree in the conclusion, but they can provide different answers when:

- the sample SDs are very different, and
- the sizes of the groups are also very different

So which method should I use?

- When σ_1 and σ_2 are indeed equal, the method based on pooled SD is more powerful
- However, it is usually hard to check whether $\sigma_1 = \sigma_2$. So it's safer to use Welch's method.