STAT 3011 Discussion 015

Week 11: Two-Sample Comparisons

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Two-Sample Comparison Framework

| Independent Samples | Matched Pairs |
|--|--|
| Compare μ_1 vs μ_2 $ar{x}_1 - ar{x}_2$ | Compare μ_D (pair differences) $ar{x}_D$ (mean of differences) |
| Example : Test scores from two different classrooms | Example : Twins assigned to different treatments |

Key Distinction

- Independent: Two completely separate groups with no pairing
- Paired: Individuals paired by characteristics (age, weight, etc.)

Note

Matched pairs could be the same subject measured twice

Assumptions

| Independent Samples | Matched Pairs |
|---|--|
| 1. Two independent random samples 2. Both populations normal OR $n_1, n_2 \ge 30$ | Random sample of pairs Differences normally distributed OR large enough sample size |

Confidence Intervals for Two-Sample Comparisons

| Independent Samples | Matched Pairs |
|---|---|
| $egin{aligned} (ar{x}_1 - ar{x}_2) \pm t_{lpha/2} \sqrt{rac{s_1^2}{n_1} + rac{s_2^2}{n_2}} \ 	ext{df} &= \min(n_1 - 1, n_2 - 1) \end{aligned}$ | $ar{x}_D \pm t_{lpha/2} rac{s_D}{\sqrt{n_D}} \ 	ext{df} = n_D - 1$ |

Intuitive Interpretation

- **CI excludes 0**: The true difference is unlikely to be zero ("statistically significant")
 - Example: If 95% CI (1.2, 3.4) kg for weight loss \implies Effective treatment
- Cl includes 0: No evidence of difference ("null plausible")
 - Example: If 95% CI (-0.5, 1.5) kg \implies Might just be random variation

Hypothesis Testing for Two Samples

Independent Samples

Hypotheses:

- $H_0: \mu_1 = \mu_2$
- $H_a: \mu_1 \neq \mu_2$ (two-tailed)
- $H_a: \mu_1 < \mu_2$ (left-tailed)
- $H_a: \mu_1 > \mu_2$ (right-tailed)

Test Statistic:

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

Matched Pairs

Hypotheses:

- $H_0: \mu_D = 0$
- $H_a: \mu_D \neq 0$ (two-tailed)
- H_a : μ_D < 0 (left-tailed)
- $H_a: \mu_D > 0$ (right-tailed)

Test Statistic:

$$t^* = rac{ar{x}_D}{s_D/\sqrt{n_D}}$$

p-values and Conclusions

Calculating p-values

- Left-tailed: pt(t*, df, lower.tail=TRUE)
- Right-tailed: pt(t*, df, lower.tail=FALSE)
- Two-tailed: 2*pt(abs(t*), df, lower.tail=FALSE)

Conclusion

- if p-value $\leq \alpha \implies$ Reject H_0 and Accept H_a
- if p-value $> \alpha \implies$ Fail to reject H_0

Crucial Nuance

• We never **accept** H_0 - we only fail to reject it

R Commands

Independent Samples

t.test(group1, group2, var.equal=FALSE)

Paired Samples

t.test(group1, group2, paired=TRUE)

Output Includes

- Confidence interval
- Test statistic
- p-value

Questions?

Scenario:

A researcher randomly samples four patients with high blood pressure and measures their blood pressure initially. The researcher then assigned the patients to walk briskly for half an hour a day. A month later, those patients' blood pressure was measured again.

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Answer: Matched Pairs

Explanation:

Each patient's blood pressure is measured before and after treatment. Same subjects measured twice = matched pairs design.

Scenario:

A STAT 3011 student compares textbook prices at Amazon vs. Barnes Noble. She randomly selects 10 textbooks used that term and records the price of each book at both sites.

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Answer: Matched Pairs

Explanation:

Each book has two prices — one from each site — so prices can be directly matched by textbook. If she had sampled different books from each site, it would be independent.

Scenario:

A researcher is studying smoking and lung capacity. Participants are paired — one smoker and one non-smoker — matched on age, gender, and BMI. Each participant's lung capacity is measured.

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Answer: Matched Pairs

Explanation:

Participants are deliberately paired based on similar characteristics. This creates matched pairs suitable for paired analysis.

Scenario:

In an experiment, researchers either stared or didn't stare at drivers at a stop sign, then timed how long it took the drivers to cross. They want to test whether staring affects crossing time.

Data:

No-stare group: 14 observations

Stare group: 13 observations

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Data:

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Answer: Independent Samples

Explanation:

There's no way to meaningfully match drivers between the two groups. Also, sample sizes differ. This is a classic two-sample independent design.