Statistics 305/605: Introduction to Biostatistical Methods for Health Sciences

Chapter 11 : Inference for Two Means

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Comparison of Two Means (Chapter 11)

Context

- We have measurements sampled from two populations.
- Want to make inference about the difference between the populations.
- In particular, interested in the difference between the two population means, denoted μ_1 and μ_2.

Notation

- Let $x_{11}, \ldots, x_{1n_1}$ denote a sample from the first population and $x_{21}, \ldots, x_{2n_2}$ denote a sample from the second.
- The sample averages $\bar{x}_1$ and $\bar{x}_2$ estimate the population means μ_1 and μ_2, respectively; so $\bar{x}_1 - \bar{x}_2$ estimates $\mu_1 - \mu_2$.
- We're interested in confidence intervals for $\mu_1 - \mu_2$ and tests of $H_0 : \mu_1 - \mu_2 = 0$ vs. $H_a : \mu_1 - \mu_2 \neq 0$.

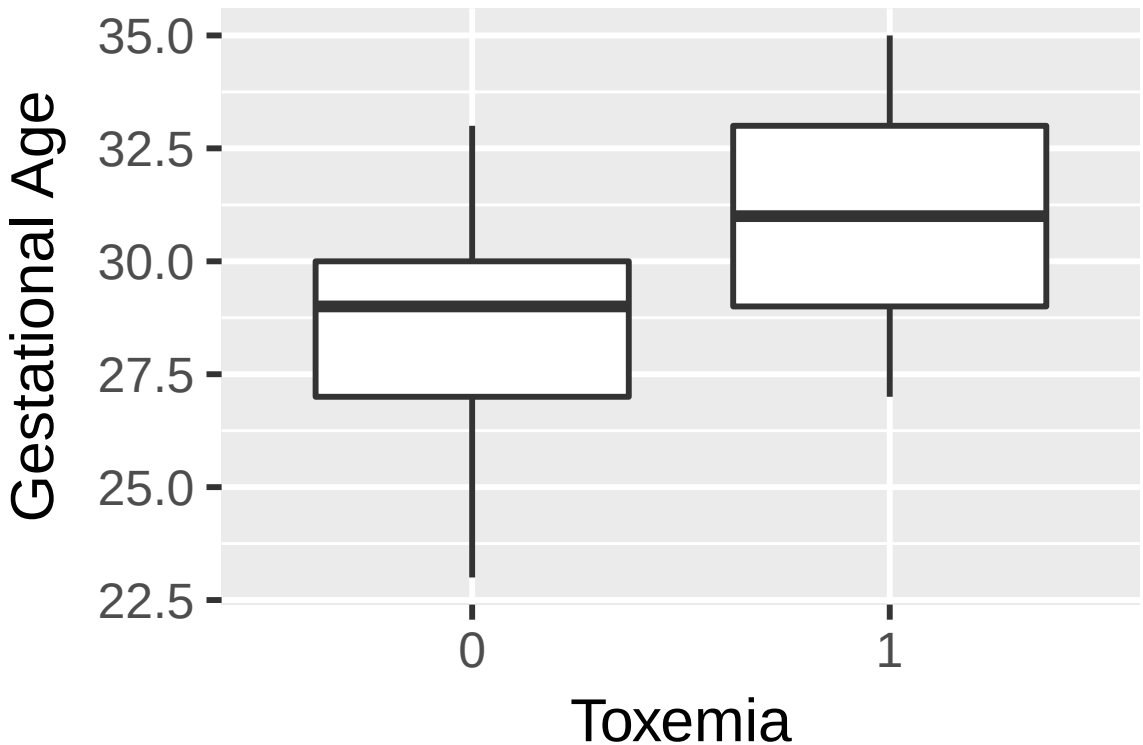
Example: Low Birthweight Infants

- Data on 100 infants with birth weight less than 1500g.
  - Variables are: head circumference (cm), birth length (cm), gestational age (wks), birth weight (g), mother's age (yrs), and mother's status for toxemia (1=high blood pressure during pregnancy, 0=not)
- Compare the distribution of variables such as age and birth weight in moms with to mom's without toxemia
- The first few rows of the data set are as follows:

```
##   headcirc length gestage birthwt momage toxemia
## 1       27     41      29    1360     37       0
## 2       29     40      31    1490     34       0
## 3       30     38      33    1490     32       0
## 4       28     38      31    1180     37       0
## 5       29     38      30    1200     29       1
## 6       23     32      25     680     19       0
```

Gestational Age by Toxemia

- Question: Does the distribution of gestational age differ in moms with toxemia vs. moms without toxemia?
- Explore differences by toxemia status graphically, using boxplots (below) and histograms (next slide) in the sample.



Gestational Age by Toxemia: Histograms

Gestational Age by Toxemia: Summary Statistics

- The sample means and SDs of gestational age for each toxemia category are summarized below.

```
## # A tibble: 2 x 3
##   toxCateg  mean    sd
##   <fct>    <dbl> <dbl>
## 1 0         28.4  2.32
## 2 1         30.9  2.32
```

- The sample means of the gestational ages differ between the toxemia groups, but the sample SDs look the same.
- Could the difference in the sample means be due to chance?

Outline of Inference Approach

- Same basic approach to inference as in the one-sample problem:
  - Inference is based on the sampling distribution of the statistic $\bar{X}_1 - \bar{X}_2$
- Transform $\bar{X}_1 - \bar{X}_2$ to a *pivotal quantity*, Z, if population SDs σ_1 and σ_2 are known.
- When σ's are unknown, as is typically the case, we substitute estimates to obtain a *pivotal quantity* T.
- Confidence intervals and hypothesis tests follow from the sampling distribution of T.
- Note: We omit the following topics in this course:
  - Paired-samples t-test (Section 11.1 of text)
  - Two-sample t-test assuming equal SDs (Section 11.2.1)

Sampling Distribution of $\bar{X}_1 - \bar{X}_2$

- We have simple random samples (SRSs) of size n_1 for group 1 and n_2 for group 2.
- These samples are independent.
- Then the distribution of $\bar{X}_1 - \bar{X}_2$ has
  - mean $\mu_1 - \mu_2$ and
  - SD $\sqrt{\sigma_1^2/n_1 + \sigma_2^2/n_2}$, where σ_1 and σ_2 are the population SDs for group 1 and group 2, respectively.
- If the sample sizes are large enough, the CLT tells us that the shape of this distribution is approximately normal.

Z Transformation

- "Standardizing" a random variable by subtracting its population mean and dividing by its population SD gives a random variable with mean 0 & SD 1.
- For normal random variables, the transformation does not change the distribution; the standardized random variable is still normally distributed.
- Conclude that if $\bar{X}_1 - \bar{X}_2$ is approximately normal with mean $\mu_1 - \mu_2$ and SD $\sqrt{\sigma_1^2/n_1 + \sigma_2^2/n_2}$, then

$$Z = \frac{(\bar{X}_1 - \bar{X}_2) - (\mu_1 - \mu_2)}{\sqrt{\sigma_1^2/n_1 + \sigma_2^2/n_2}} \sim N(0, 1),$$

where $\sim$ means "is distributed as".

T Transformation

- Inserting sample SDs s_1 and s_2 for the parameters σ_1 and σ_2 in Z gives

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

- What is the distribution of T?
  - Turns out we can approximate it by a t-distribution with ν df.
  - We won't ever use the formula for ν but if you're curious it is given on page 270 of the text.
- Instead, computer software such as R automatically calculates ν for us, as shown next.

Illustration with Gestational Age and Toxemia

- The following is the output of the `t.test()` function for these data (see the R demo for details):

```
##
##  Welch Two Sample t-test
##
## data:  gestage by toxCateg
## t = -4.4745, df = 31.465, p-value = 9.365e-05
## alternative hypothesis: true difference in means is not equal to 0
## 95 percent confidence interval:
##  -3.712089 -1.388574
## sample estimates:
## mean in group 0 mean in group 1
##        28.35443        30.90476
```

- The df is $\nu = 31.465$.
- We can also see that the software computed a 95% confidence interval and p-value. More on these in a few slides.

Confidence Intervals for $\mu_1 - \mu_2$

- The level-C CI for $\mu_1 - \mu_2$ is of the form

$$\text{estimate} \pm \text{margin of error}$$

- The estimate is $\bar{x}_1 - \bar{x}_2$
- The margin of error is $t^* \times SE$ where
  - t^* is the upper $(1 - C)/2$ critical value of the t-distribution with ν df, and
  - SE is the **estimated SD** of $\bar{x}_1 - \bar{x}_2$: $\sqrt{s_1^2/n_1 + s_2^2/n_2}$

Application to Gestational Age and Toxemia

- Calculate a 90% CI for the difference between mean gestational age in the toxemia and non-toxemia groups.
- The relevant sample statistics to four digits are as follows:

group	sample mean ($\bar{x}$)	sample SD (s)	sample size (n)
1: non-toxemia	28.35	2.321	79
2: toxemia	30.90	2.322	21

- Estimate is $\bar{x}_1 - \bar{x}_2 = 28.35 - 30.90 = -2.55$
- Margin of error is $t^* \times SE$ where
  - computer software calculates a critical value of $t^* = 1.695$ (see the R demo).
  - the SE is $\sqrt{s_1^2/n_1 + s_2^2/n_2} = \sqrt{2.321^2/79 + 2.322^2/21} = 0.570$.
  - Hence the margin of error is $1.696 \times 0.570 = 0.966$.
- CI is $(-2.55 - 0.966, -2.55 + 0.966) = (-3.516, -1.584)$.

Interpretation

- The 90% CI is approximately $(-3.5, -1.6)$.
- The text suggests an interpretation such as:
  - "90% of intervals constructed in this way cover the true difference between mean gestational age in the **non-toxemia** and **toxemia** groups."
- Another common style of interpretation is:
  - "We are 90% confident that the true difference between mean gestational age in the **non-toxemia** and **toxemia** groups is between -3.5 and -1.6."
- Or, we might find it more natural to switch the order of the groups, which would switch the sign of the difference:
  - "We are 90% confident that the true difference between mean gestational age in the **toxemia** and **non-toxemia** groups is between 1.6 and 3.5"

Hypothesis Test

- For the null hypothesis $H_0 : \mu_1 - \mu_2 = 0$ of no difference between the groups, the formula for the observed t-statistic is

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

- Observed values of t that are extreme in the sense of being more compatible with H_a are taken as evidence against $H_0 : \mu_1 - \mu_2 = 0$.
- The p-value is the chance of a value that is as or more extreme than what we observed, under H_0.
- Taking T to have a t distribution on ν df, we get a p-value of $p = 2P(T \geq |t|)$ when $H_a : \mu_1 - \mu_2 \neq 0$.

Application to Gestational Age and Toxemia

- We can re-use the calculations from the CI example (page 13), for the difference in sample means ($\bar{x}_1 - \bar{x}_2 = -2.55$) and the SE of the difference ($\sqrt{s_1^2/n_1 + s_2^2/n_2} = 0.570$):

$$t = \frac{(\bar{x}_1 - \bar{x}_2) - 0}{\sqrt{s_1^2/n_1 + s_2^2/n_2}} = \frac{-2.55}{0.570} = -4.474.$$

- Computer software (R demo) returns a p-value of 9.4×10^{-5}, or 0.000094, for a 2-sided alternative hypothesis.

Interpretation

- Small p-values (e.g. $< .05$) are taken as evidence against the null hypothesis.
- Our p-value of 9.4×10^{-5} is very small.
- If we had set a level of $\alpha = 10\%$ for the test, we'd declare that:

  "We reject the null hypothesis that the mean gestational age is the same in the toxemia and non-toxemia groups at the 10% level."

- If we hadn't set a level of the test in advance, we might report our results as:

  "There is strong evidence that the mean gestational age is different in the toxemia and non-toxemia groups ($p < 0.001$)."

Cause and Effect

- Our two-sample t test has revealed that toxemia and gestational age are **associated**.
  - The distribution of gestational age is different in the two toxemia groups (different means, lower in toxemia group).
- But, an association does **not** mean that toxemia has a causal effect on gestational age.
  - It could be that gestational age affects toxemia.
  - Or, there could be a hidden *confounding variable* that affects both toxemia and gestational age, that accounts for their association.

(More on confounding later, when we study multiple regression.)

Relationship Between Confidence Intervals and Tests

- In the low birth weight example, the 90% CI does not cover zero, and the hypothesis test of $H_0 : \mu_1 - \mu_2 = 0$ *vs* $H_a : \mu_1 - \mu_2 \neq 0$ rejects the null hypothesis at the 10% level.
- Conversely, when a 90% CI **does** cover zero, the corresponding test against a two-sided alternative will **retain** the null hypothesis at the 10% level.
- This is a general property of tests of a population parameter θ.
  - A level-α test of $H_0 : \theta = \theta_0$ *versus* $H_a : \theta \neq \theta_0$ retains the null hypothesis if and only if the level $(1 - \alpha) \times 100\%$ CI covers θ_0.

Assumptions

- We assume that:
  - The data are two random samples from the 2 parent populations (e.g. moms with toxemia and moms without toxemia).
  - Also, either
    1. the data measurements in the parent populations are normally distributed with mean μ_i and sd σ_i, written $N(\mu_i, \sigma_i)$, or
    2. the sample size $n = n_1 + n_2$ is large enough to rely on the CLT for the sample means $\bar{X}_1$ and $\bar{X}_2$ being approximately normally distributed.
- Guidelines for n (*Basic Practice of Statistics* by D. Moore) when population sd's unknown:
  - For $n < 15$, use the t-based CI and hypothesis test if the data look approximately normally distributed.
  - For $15 \leq n < 40$, use the t-based CI and hypothesis test, *except* in the presence of outliers or strong skewness in the data distribution.
  - For large samples ($n \geq 40$), can use the t-based CI and hypothesis test, even for clearly skewed distributions (because of the CLT).

Checking the assumptions for the low-birth-weight example

- There were $n = 100$ babies in this data set.
- According to the rules-of-thumb on the previous slide, we can use the t-based CI and hypothesis test even if the population distributions are skewed.

Summary

- Inference for the difference between two population means is based on either Z (SDs known) or T (SDs unknown).
- Confidence intervals are of the form estimate $\pm$ margin of error
  - the margin of error is a critical value times SE
- To test the null hypothesis $H_0 : \mu_1 - \mu_2 = 0$ against an alternative H_a we compute a test statistic t (or z if SDs known) and p-value
  - can compare p-value to a significance level α to obtain a test
- Inference is considered reliable when the parent populations are normal, or when rules of thumb for sample sizes are satisfied.