

Section 8.1 Paired Samples

Paired design: The data we are analyzing are *differences* between pairs of values.

Section 8.2 The Paired-Sample t Test and Confidence Interval

See **Table 8.1.1**, **Figure 8.1.1**, **Table 8.1.2**, then **Book Example 8.2.1/2**.

Summary, using $H_A: \mu_D \neq 0$, 95% confidence (so $\alpha = .05$), $df = 9 - 1 = 8$:

	Drug	Placebo	Difference
Mean	55.3	84.9	-29.6
SD	31.5	34.1	32.8

$$-29.6 \pm 2.306 \left(\frac{32.8}{\sqrt{9}} \right) = (-54.8, -4.4) \quad t_s = \frac{-29.6}{32.8/\sqrt{9}} \approx -2.71 \Rightarrow 0.02 < P < 0.04$$

The **formulas are summarized** on page 316. H_A is $\mu \neq 0$, so it is a two-tailed test. In **Book Example 8.2.3**, they find the test statistic t_s and again conclude that $\mu_D \neq 0$. To be clear: we are interested in the *one set of differences*, not the *two different samples*.

Question: what if the order of the data were reversed (that is, swap column 1 with column 2 in Table 8.1.1)? Answer: all signs would simply be reversed:

Confidence interval (4.4, 54.8) and test statistic $t_s = +2.71$.

Confidence interval $(-54.8, -4.4)$ is plotted on a number line below.

For comparison, let's look at this same example but changing the second value in the Drug column from 48 to 68. That is, change Subject 2 to

Drug	Placebo	Difference
68	54	14

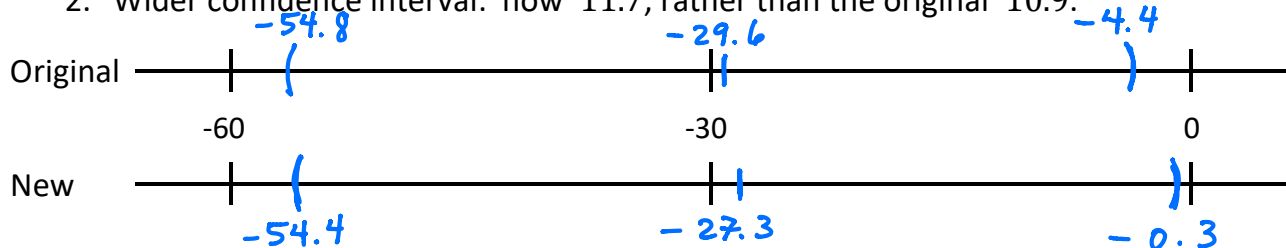
With this change we have

	Drug	Placebo	Difference
Mean	57.6	84.9	-27.3
SD	31.7	34.1	35.2

$$-27.3 \pm 2.306 \left(\frac{35.2}{\sqrt{9}} \right) = (-54.4, -0.3) \quad t_s = \frac{-27.3}{35.2/\sqrt{9}} \approx -2.33 \Rightarrow 0.04 < P < 0.05$$

In this second case, there are two reasons the confidence interval $(-54.4, -0.3)$ is “closer” to including $\mu_D = 0$ (in which case we would *not* conclude $\mu_D \neq 0$):

- \bar{y}_D is closer to 0: \bar{y}_D is now -27.3 rather than -29.6 .
- Wider confidence interval: now 11.7, rather than the original 10.9.



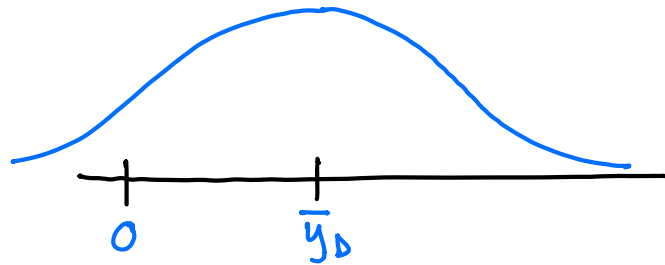
Warning: **ignore pairing** \Rightarrow **loss of information** \Rightarrow **change the results**. In particular, pairing makes our analysis *more powerful*, that is, we are more likely to conclude that $\mu_D \neq 0$ if that is indeed the case. Ignoring pairing results in *loss of power*. Let's look at this for the above example (using the data with the original values).

	(Correctly) Paired	(Incorrectly) Unpaired
SE	$\sqrt{\frac{32.8^2}{9}} \approx 10.9$	$\sqrt{\frac{31.5^2}{9} + \frac{34.1^2}{9}} \approx 15.5$
df	$9 - 1 = 8$	≈ 16
$t_{\alpha/2}$	2.306	2.210
95% CI	$-29.6 \pm 2.306(10.9)$ $\approx (-54.8, -4.4)$	$-29.6 \pm 2.210(15.5)$ $\approx (-62.6, 3.4)$
t_s	$-\frac{29.6 - 0}{10.9} \approx -2.71$	$\frac{(55.3 - 84.9) - 0}{15.5} \approx -1.91$
$P < \alpha?$	$.02 < P < .04$ $\Rightarrow P < \alpha = .05$	$.06 < P < .08$ $\Rightarrow P \text{ not } < \alpha = .05$
Conclusion	Reject H_0 (possible Type I Error)	Don't reject $H: \mu_D = 0$ (possible Type II Error)

If we ignore pairing, we would be treating these as two unrelated groups of people, which would be inappropriate and lead to inappropriate results. On the other hand, **worse than ignoring pairing when it does exist is assuming pairing when it does not**.

In general, there are (at least) four things that make the conclusion $\mu_D \neq 0$ more likely (i.e. if 0 is not included in the confidence interval).

In each case, compare the confidence intervals to what the original confidence interval might look like:



Change	$t_{\alpha/2} \cdot \frac{s_D}{\sqrt{n_D}}$	Diagram
Larger \bar{d}	Same	
Smaller s_D	Smaller	
Larger n	Smaller	
Smaller confidence	Smaller	

Section 8.3 Paired Design

Matched pair: if we can't actually do pairing, we get as close as we can. Given two groups (e.g. 10 smokers and 10 non-smokers), we match one person from each group with one person from the other. We want all (or as many as possible) other variables to match, e.g. age, gender, ethnicity, alcohol consumption, diet, etc. Also, interestingly, what is more useful to us is if we have

similarity within each pair (obvious) but *variation between* pairs (not so obvious)

If time, I'll comment on **Figure 8.3.1** (from the data on p. 321).