

Two sided, two sample t-tests.

I. Brief review of one sample tests:

1) We are interested in how a sample compares to some pre-conceived notion. For example:

- a) IQ = 100
- b) Average height for men = 5'10"
- c) Average number of white blood cells per cubic millimeter is 7,000.

2) We frame our question in terms of a hypothesis:

- a) H_0 : mean(IQ) = 100
- b) H_0 : mean (height for men) = 5'10"
- c) H_0 : mean (# of white blood cells) = 7,000.

(in all cases, our hypothesis is about the POPULATION mean).

3) We develop an alternative hypothesis:

- a) H_1 : mean (IQ) \neq 100

etc.

4) We decide on what level of $\alpha = \Pr\{\text{type I error}\}$ we are willing to live with (e.g., $\alpha = .05$).

5) We calculate a t value from our data:

$$t^* = \frac{\bar{y} - \mu}{s / \sqrt{n}}$$

6) We look up a t value from our t-tables or from the computer:

$$t_{\nu, \alpha}$$

where $\nu = \text{degrees of freedom}$

7) We compare our t ($= t^*$ or t_s) to the tabulated t :

if $|t^| \geq t_{\text{table}}$ we reject H_0*

if $|t^| < t_{\text{table}}$ we fail to reject H_0*

8) We then proceed with our study accordingly.

II. The two-sampled t-test.

1) Unfortunately, you'll discover that the one-sampled t -test is not terribly useful in biology. Usually we don't have a preconceived notion of what μ might be (though quite often we might be interested in putting a confidence interval around some result).

2) But what we often do:

a) Compare two groups - say males and females.

b) See if these two groups have different "responses", or differ significantly about something.

c) For example:

i) Group "A" gets a new medicine. Group "B" gets a placebo. Does the new medicine work??

ii) Are men the same average height as women?

iii) Do lions and tigers have the same average litter size? (Yes, this isn't normal, but we'll worry about that later).

d) This kind of situation develops quite often in biology.

2) So how do we proceed? Well, let's start by developing hypotheses for the above examples (in all cases these involve the *population* mean(s)):

a) H_0 : mean (group A) = mean (group B)

(we didn't say what we're measuring here)

b) H_0 : mean (height for men) = mean (height for women)

c) H_0 : mean (litter size for lions) = mean (litter size for tigers)

3) How is this different from our one-sampled test?

a) we're comparing two means. In the one sample test we compared one mean with a "preconceived idea"

b) note that again we're interested in the population means, but we're using our samples to get at the information we want.

4) So now let's set up our alternative hypotheses:

a) H_1 : mean (group A) \neq mean (group B)

Comment: yes, we could do:

H_2 : mean (group A) $<$ mean(group B)

We will look at one sided tests soon.

5) Then we decide on α .

6) We calculate our t -star. But what is our t^* now?

- we have two estimates for the standard error! One from our first sample, one from our second sample.

- we also have two sample means floating around.

- Question: are we willing to believe that the standard errors in our samples are really the same?

- Let's assume for the moment that we don't think the two standard errors are the same (we're *assuming* this - more on assumptions later).

- Like with the one-sample test, we put a difference in the numerator, and our standard error in the denominator. We just need to figure out our difference, and then our standard error.

- Instead of $(\bar{y} - \mu)$, we now use $(\bar{y}_1 - \bar{y}_2)$

(technically, it's $\bar{y}_1 - \mu_1 - (\bar{y}_2 - \mu_2)$, but since $\mu_1 = \mu_2$ (our H_0 says $\mu_1 = \mu_2$), the μ 's cancel out.

- Instead of our single standard error, we now find some way of "averaging" our two standard errors and put this in the denominator.

- Here's the formula:

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

- That, hopefully makes sense. You can see that the denominator is a kind of average between our two estimates for the standard error.

7) Now we look up our tabulated t -value.

a) Problem! How many degrees of freedom do we have?? (what is ν ?)

b) As it turns out, it's not an easy answer. It does turn out, though that:

$$\min(n_1-1, n_2-1) < df < (n_1 + n_2 - 2)$$

which unfortunately isn't very useful (if you need a quick and dirty estimate, go with the $\min(n_1-1, n_2-2)$) - that will give you a conservative estimate.

c) What is it really??

$$v = \frac{(SE_1^2 + SE_2^2)^2}{\frac{SE_1^4}{n_1-1} + \frac{SE_2^4}{n_2-1}}$$

(OUCH!)

d) Most statistical software will automatically do this for you, and so will some calculators [but you want to verify your calculator actually uses this before you start spitting out answers!].

e) so now we can look up our tabulated t with the appropriate degrees of freedom and our predetermined value of α .

8) The last step is then identical to what we did before:

if $|t^| \geq t_{\text{table}}$ we reject H_0*

if $|t^| < t_{\text{table}}$ we fail to reject H_0*

9) Note: we'll take a look at how things work if we can assume equal variances next time.

10) So here's an example, exercise 7.24 on p. 249 [7.29, p. 244] {7.2.7, p. 232}.

a) (a kind of morbid example). Amines have been suspected of being involved in spasms of the coronary arteries. So some researchers measured the levels of serotonin (an amine) in patients who died of heart disease and then compared these levels to those in patients who did not die of heart disease (died due to other causes). Let's look at the results:

	Heart disease	No heart disease
n	8	12
\bar{y}	3,840	5,310
SE	850	640

In the text, they calculate a lot of the stuff for you, but let's see how they did it:

$$t^* = \frac{\bar{y}_1 - \bar{y}_2}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}} = \frac{3,840 - 5,310}{\sqrt{SE_1^2 + SE_2^2}} = \frac{1,470}{\sqrt{850^2 + 640^2}}$$

$$= -\frac{1,470}{1,064} = -1.38$$

We can see where they got the Standard Error of $(\bar{y}_1 - \bar{y}_2)$, and also the calculated t-value (reported in the answer section in the back of the book).

Now we need to figure out our tabulated t-value. For α the book says to use .05 (in each tail), and our degrees of freedom are:

$$v = df = \frac{(SE_1^2 + SE_2^2)^2}{\frac{SE_1^4}{n_1 - 1} + \frac{SE_2^4}{n_2 - 1}} = \frac{(850^2 + 640^2)^2}{\frac{850^4}{7} + \frac{640^4}{11}}$$

$$= \frac{1.2817 \times 10^{12}}{7.4572 \times 10^{10} + 1.5252 \times 10^{10}} = 14.27$$

So we look up the tabulated t-value:

$$t_{14, .05} = 2.145$$

Note: we *always* round down our degrees of freedom. For example, 14.98 = 14 degrees of freedom. Also, we always pick the lower number for degrees of freedom from the t-table if our number (after rounding down) isn't in the table.

And since:

$$|t^*| < t_{14, .05}$$

We conclude that we don't have any evidence that serotonin levels are different in patients with heart disease compared to those with no heart disease.

Incidentally, we should have explicitly stated:

H₀: mean serotonin level (heart disease) =
mean serotonin level (no heart disease)

H₁: mean 1 ≠ mean 2 (you can fill in the exact wording)

Sometimes we get lazy and simply say H₀: $\mu_1 = \mu_2$ and H₁: $\mu_1 \neq \mu_2$, but on problems and exams you should always write out the exact H₀ and H₁ you're using.

11) Let's do another example: [Exercise 7.37 p. 247] {7.2.16, p. 233}:

Researchers wanted to know if soap affects the number of bacterial colonies in petri dishes. They found the following results:

	Control	Soap
	30	76
	36	27
	66	16
	21	30
	63	26
	38	46
	35	6
	45	
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n	8	7
\bar{y}	41.8	32.4
s	15.6	22.8
SE	5.5	8.6

Note:

$$SE_{control} = \frac{15.6}{\sqrt{8}} = 5.5$$

$$SE_{soap} = \frac{22.8}{\sqrt{7}} = 8.6$$

(Get input for the following:)

What hypothesis do we want to test?

H_0 : mean number of colonies for control dishes is the same as for soap dishes

in symbols:

$$H_0: \mu_1 = \mu_2$$

What alternative hypothesis do we want to use?

H_1 : mean number of colonies for control dishes is not the same as for soap dishes

in symbols:

$$H_1: \mu_1 \neq \mu_2 \quad (\text{does this really make sense? Why or why not?})$$

What level of α do we want?

$$\alpha = ??$$

Now let's calculate t^* :

$$t^* = \frac{\bar{y}_1 - \bar{y}_2}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}} = \frac{\bar{y}_1 - \bar{y}_2}{\sqrt{SE_1^2 + SE_2^2}} = \frac{41.8 - 32.4}{\sqrt{\frac{15.6^2}{8} + \frac{22.8^2}{7}}} = \frac{41.8 - 32.4}{\sqrt{5.5^2 + 8.6^2}} = 0.9187$$

Figuring out our degrees of freedom ($= \nu$):

$$d.f. = \nu = \frac{(SE_1^2 + SE_2^2)^2}{\frac{SE_1^4}{n_1 - 1} + \frac{SE_2^4}{n_2 - 1}} = \frac{(5.5^2 + 8.6^2)^2}{\frac{5.5^4}{7} + \frac{8.6^4}{6}} = 10.42$$

Finally, we need to look up $t_{\alpha,10}$:

Look up value in table for level of α picked above.

Conclusion:

Pretty much for any sensible of α we fail to reject H_0 .

We conclude that soap doesn't appear to make much of a difference in the number of bacterial colonies in petri dishes.

12) Also look at examples 7.10 through 7.14 *{7.2.2 through 7.2.5}*. Note: **[7.14]** *{7.2.5}* are different in the 2nd vs. 3rd or 4th editions, but they cover the same material.

If you're not sure what's going on, go through these examples carefully!