Lecture 23 (Ch 7–8)

Last time we discussed the concept of paired data, and the corresponding C.I (often called "paired CI")

$$\bar{d} \pm z^* \, s_d/\sqrt{n} \,,$$

Then, we came-up with "new" CI. formulas for the situation when we don't know σ_x (or if n = small). We found that the only change is $z^* \to t^*$, where t^* are multipliers designed to make sure the CI has correct coverage. They are determined like the z^* (from Table I), but from table VI.

E.g. 1-sample CI for μ_x : $\bar{x} \pm t^* \frac{s}{\sqrt{n}}$ with $df = n-1$.

The one (major) difference between z and t CIs is that the latter assume the pop. is normal. If it's not; there are no simple expressions for the CIs. Try bootstrap (see labs)

What about 2-sample CIs? $d = x_2 - x_1$

"paired CI" for $\mu_2 - \mu_1$: $\bar{d} \pm t^* \frac{s_d}{\sqrt{n}}$, $df = n-1$

CI for (independent, unpaired data) $\mu_2 - \mu_1$: $(\bar{x}_2 - \bar{x}_1) \pm t^* \sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$

Welch's formula.

$$df \simeq \frac{\left(\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}\right)^2}{\frac{1}{n_1-1}\left(\frac{s_1^2}{n_1}\right)^2 + \frac{1}{n_2-1}\left(\frac{s_2^2}{n_2}\right)^2}$$

Try $1 \leftrightarrow 2$

And for proportions? Not known! (Try bootstrap; see labs)

Summary of CIs.

So far, we have

z-based CIs for μ, π, $\mu_1 - \mu_2$, $\pi_1 - \pi_2$ z-interval

$\bar{x} \pm z^* \frac{s}{\sqrt{n}}$ $\quad p \pm z^* \sqrt{\frac{p(1-p)}{n}}$ $\quad (\bar{x}_1 - \bar{x}_2) \pm z^* \sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$ $\quad$ 7.25

t-based CIs for μ, $\cancel{\pi}$, $\mu_1 - \mu_2$, $\cancel{\pi_1 - \pi_2}$ t-interval
from Normal pop.

$z^* \longrightarrow t^*$ $\quad$ df = n-1 $\quad$ df = welch

These come in the 2-sided and 1-sided variety,
as well as paired and unpaired (ie. independent samples)

df = n-1 $\quad$ df = welch

This completes the list of "easy" CIs.
But you can also compute a CI for σ, $\frac{\pi_1}{\pi_2}$, ... (in hw, in book)
and more, later.

Read last lect (last page) to see why the t-intervals, which are derived by acknowledging that we don't know σ_x, are usually associated with n = small.

Transition to Ch. 8

We have built lots of CI's. They are good for 2 things:

1) Convey uncertainty [Reliability]
2) aid in making Yes/No decisions.

→ Suppose a 2-sided 99% CI for μ_x is $[1.1, 2.3]$

Someone claims $\mu_x = 0$, $\mu_x = 1.5$, $\mu = 3$

Reject or [Not Reject / $\neq$ Accept]? Reject cannot reject Reject.

→ Suppose a 2-sided 99% CI for $\mu_1 - \mu_2$ is $[1.1, 2.3]$

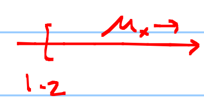
Someone claims $\mu_1 = \mu_2$. Reject

→ Suppose a 2-sided 99% CI for $\mu_1 - \mu_2$ is $[-1.1, 2.3]$

Someone claims $\mu_1 = \mu_2$. Cannot

$\neq$ Accept.

Suppose a 99%, 1 (1-sided) Lower conf. bound is 1.2



Someone claims $\mu_x < 1.5$

Someone claims $\mu_x < 1.1$ Etc. Tricky!

" $\mu_x > 1.5$

" $\mu_x > 1.1$

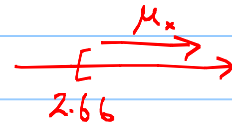
If Decision-Making (ie. Reject / not-reject) is the final goal of your study, then the machinery of computing C.I. can be massaged to form a more direct response. The revised methodology is called hypothesis testing.

The logic of the methodology is very tricky!
It requires assuming a statement/claim about a pop. parameter, so that we can compute some probabilities.
Then the question one asks is
"Does data provide sufficient evidence contrary to the assumption?"
If yes, then reject the assumption/claim.
If No, then cannot reject the assumption/claim.
i.e., we just don't know!
Notice: cannot reject claim $\neq$ Accept claim!

One can also ask
"Does the data provide sufficient evidence in support of some claim (ie. the opposite of the assumption)?"

Suppose a sample of size 25 yields $\bar{x}_{obs} = 3$ $s = 1$.
And suppose we want to know how small μ_x can be?

95% lower conf. bound: $3 - 1.711 \frac{1}{\sqrt{25}} = 2.66$



So, a claim $\mu_x < 1$ can be rejected (with some confidence).

Now, here is a different way of arriving at The last conclusion:

Suppose $\mu_x < 1$: Assumption / Null hypothesis.
Now, let's find evidence to The contrary. Q: what's contrary?
A: Really large $\bar{x}$'s justify rejecting $\mu_x < 1$. So, let's find

$$pr(\bar{x} > \bar{x}_{obs} \mid \text{if } \mu_x < 1).$$

But That prob. already assumes $\mu_x < 1$; so if That prob is small, Then That's evidence against $\mu_x < 1$, ie. reject $\mu_x < 1$.

Let's start by computing That prob, if $\mu_x = 1$:

$$\underbrace{prob(\bar{x} > \bar{x}_{obs} \mid \mu_x = 1)}_{\text{one type of "p-value"}} = prob\left(\underbrace{\frac{\bar{x} - \mu_x}{s/\sqrt{n}}}_{t} > \underbrace{\frac{\bar{x}_{obs} - \mu_x}{s/\sqrt{n}}}_{t_{obs}} \;\middle|\; \mu_x = 1 \right)$$

$$= prob(t > 10 \mid \mu_x = 1) \simeq 0 \qquad t_{obs} = \frac{\bar{x}_{obs} - \mu_x}{s/\sqrt{n}} = \frac{3 - 1}{1/\sqrt{25}} = 10$$

So, let's Think! If we assume μ_x is as big as it can get according to The claim, ie. $\mu_x = 1$, Then The prob. of getting $\bar{x}$ larger Than $\bar{x}_{obs}$ is nearly zero.

df = 24, Table VI
(Note: right areas)

If μ_x is even smaller (Than 1), The prob of $\bar{x} > \bar{x}_{obs}$ will be

A) even smaller B) same C) larger

with a smaller μ_x, t_{obs} is bigger. Then $pr(t > t_{obs})$ is smaller.

$\boxed{\text{IMPORTANT}}$:

Blue note

In fact, because prob$(\bar{x} > \bar{x}_{obs} | \mu_x = 1)$ = small,
we can reject $\mu_x < 1$, not just $\mu_x = 1$.
This is because, if $\mu_x < 1$, then t_{obs} is even larger (than 10), which means that the p-value is even smaller.
In short, it's sufficient to test $\mu_x = 1$

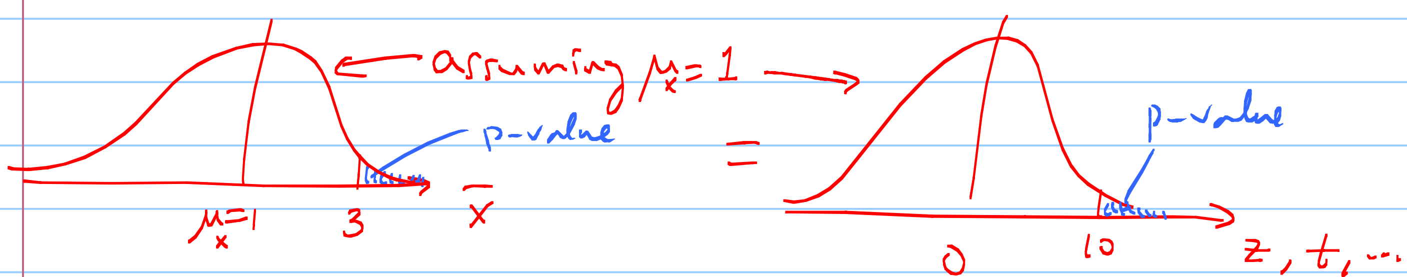
FYI

<u>For the skeptical students</u>: One may think that one should compute the prob of $(\bar{x} > \bar{x}_{obs})$ for <u>all</u> possible values of $\mu_x < 1$, not just $\mu_x = 1$. It turns out (not too obviously) that when we compute the above prob., if $\mu_x = 1$, we are already accounting for <u>all</u> possible $\mu_x < 1$! See last page below.

Prob$(\bar{x} > \bar{x}_{obs} | \mu_x = 1)$ is an example of a $\boxed{\text{p-value}}$.

Technically, this makes no sense; it's just a reminder that $\mu_x = 1$.

Pictorially, a p-value is an area:



One element of this process that has not been explicitly addressed is the alternative <u>in whose favor</u> $\mu_x < 1$ is rejected. That <u>alternative hypothesis</u> is, in fact, an important part of the hypothesis testing machinery.
So, let's do things a bit more generally & systematically.

general procedure for hypothesis testing for μ:

Dropping subscript.

In our example

1) Decide the pop. parameter being tested — μ

See Blue Note

sufficient to test $=$

2) Set-up H_0 : $\mu > \mu_0$, $\mu < \mu_0$, $\mu = \mu_0$ — $\mu < 1$ $(\mu_0 = 1)$

null hypothesis. Based on prior (to data) belief.

3) " " H_1 : $\mu < \mu_0$, $\mu > \mu_0$, $\mu \neq \mu_0$ — $\mu > 1$

Alternative hypothesis.

4) Choose appropriate statistic : z, t, ... — t

5) Assume $H_0 = $ TRUE (ie. set $\mu = \mu_0$) Null param. — $\mu = 1$

6) Compute test statistic for $\underbrace{\text{observed data}}_{\text{Sample}}$ $t_{obs} = \dfrac{\bar{x}_{obs} - \mu_0}{s/\sqrt{n}}$ — 10

7) Find prob of getting a random test statistic $\boxed{\text{more extreme}}$ than the observed one,] p-value

e.g. $\text{prob}(\bar{x} > \bar{x}_{obs}) = \text{prob}(t > t_{obs})$ — $\text{prob}(t > 10) \approx 0$

8) Decide if p-value is $\boxed{\text{sufficiently small}}$ to reject H_0 in favor of H_1. — ? See below.

2 questions : $\left\{ \begin{array}{l} \text{more extreme ?} \\ \text{sufficently small ?} \end{array} \right.$

!! Typo on p.352 in book : $H_0 \to H_a$ in 2 places !!
See Typo.pdf on web site.

Q: More extreme?

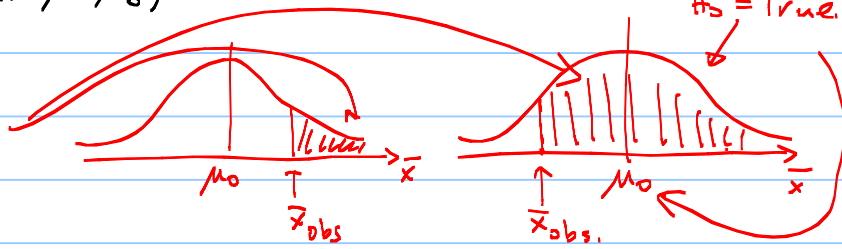
A: Depends on (H_0, H_1):

Because of the blue note, above, it is sufficient to test $\mu=\mu_0$

1-sided

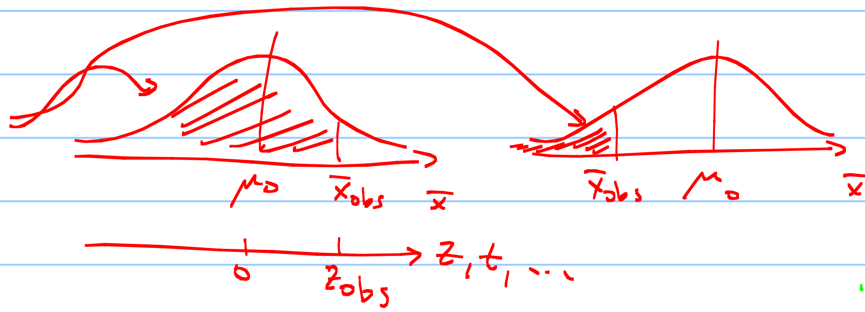
If $H_0: \mu \leq \mu_0$ (or $\mu=\mu_0$)
$H_1: \mu > \mu_0$

then p-value =



If $H_0: \mu \geq \mu_0$ (or $\mu=\mu_0$)
$H_1: \mu < \mu_0$

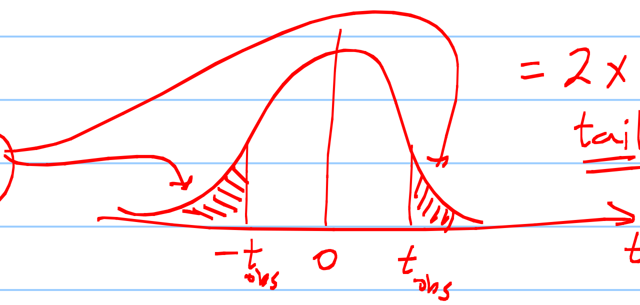
then p-value =



2-sided

If $H_0: \mu = \mu_0$
$H_1: \mu \neq \mu_0$

Then p-value = Sum



= 2 × 1-sided tail area.

In short: $H_1: \mu > \mu_0$: p-value = right-area
$H_1: \mu < \mu_0$: = left-area
$H_1: \mu \neq \mu_0$: = left + right = 2 × (1 tail)

Q = Who decides what's "sufficiently small"?

A = You do! (or The book does)

This "threshold probability" is labeled α.
The same α that showed-up in C.I.

It's called significance level. (= 1 − Conf. level)
.05 sign. level = 95% Conf. level.

Some common values are .05, .01, .001, but the choice depends on the cost of making the wrong decision (ie. of rejecting H_0 when it's True).

In short, to make a decision:

1) You choose the value of α.

2) Compute p-value from the above procedure.

3) If p-value $< \alpha$, Then Reject H_0 in favor of H_1.
Else, cannot reject " " " " "

$\boxed{\text{Example}}$: Data says: $n = 64$, $\bar{x}_{obs} = 34.4$, $S = 1.1$.

Does the data provide evidence to support $\mu > 34$?

1) The param. of interest : μ (dropping subscript x).

2,3) H_0 : $\mu < 34$ (or $\mu = 34$) $\mu_0 = 34$

H_1 : $\mu > 34$

Setting up H_0, H_1 is the hardest part of these problems.

The next page offers 2 way of deciding.

4) Appropriate test statistic : z, t

z is appropriate, because n = large. But I'll use t for illustration.

5) Assume $H_0 = T$. (I.e. set $\mu = 34$)

6) Compute statistic assuming $H_0 = \text{True}$ (ie. $\mu = \mu_0$) $t_{obs} = \dfrac{34.4 - 34}{1.1/\sqrt{64}} = 2.91$

See prev. page.

7) p-value $= \text{prob}(\bar{x} > \bar{x}_{obs})$ = prob. of getting an $\bar{x}$ as large as (or larger) than the obs. $\bar{x}$.

$= \text{prob}(t > 2.91) \simeq .0025$

$df = n - 1 = 63$

$1 - pt(2.91, 63)$ in R.

Conclusion : At $\alpha = .05$, p-value $< \alpha$.

Therefore,

Data provides sufficient evidence to reject $\overset{\mu<34}{H_0}$ in favor of $\overset{\mu>34}{H_1}$.

Or

Data provides suff. evidence in favor of $\overset{\mu>34}{H_1}$.

At $\alpha = 0.001$, pvalue $> \alpha$

Therefore, we cannot reject $\overset{\mu<34}{H_0}$ in favor of $\overset{\mu>34}{H_1}$.

Note: You cannot say that $\mu < 34$.

All we can say is that we cannot reject $\mu < 34$.

Two ways I go about deciding what H_0, H_1 should be:

1) The question asks "does data provide evidence." Meanwhile, the hyp. testing procedure begins by assuming H_0 is True. So, it makes no sense to assume the statement we are trying to test.

→ Don't assume what the data is supposed to test.

2) The data provides evidence for H_1 (against H_0), because of the way the whole procedure is set-up. Recall that the procedure requires assuming H_0 = True. Then, if the evidence is weak (e.g. when there is no data at all), then the procedure leaves you with H_0. So ask yourself this: what conclusion should the procedure yield if the evidence is really really weak, e.g. no data at all? The answer is your H_0. In this example, if there is no data, then we should "conclude" $\mu < 34$. That tells us $H_0: \mu < 34$.

→ Ask yourself what statement you should be left with if there is no data at all! The answer to that question tells you what H_0 should be, which in turn determines H_1.

3) Another way of deciding on H_0, H_1 will be discussed later, when we learn the meaning of α.

The hardest part of hyp. testing is setting up H_0, H_1.
In doing so, keep the following in mind:

The whole procedure is set-up so that

→ H_0 is assumed to be true.
→ The data provide evidence for H_1 (against H_0).

So, you should not assume what you are trying to see if the data is supporting. Otherwise, you are assuming what you want to test.

→ H_0 and H_1 are statements about some/any pop. param.

→ Reject H_0 in favor of H_1, if data provide sufficient evidence against (the assumed true) H_0, in favor of H_1.

→ p-value is the quantity that represents the evidence provided by the data, in favor of H_1.

→ But note that smaller p-value means more evidence.

→ Some problems ask you to test some prior belief (ie. some claim based on something other than data). Then, that belief should be H_0.

→ If you cannot reject H_0 in favor of H_1, then we don't know anything! Not rejecting H_0 is not the same thing as accepting it. Making the mistake of interpreting the lack of evidence for H_1 as support for H_0 is the source of many contradictory findings in the literature.

→ In general, we cannot accept a claim about an unknown pop. parameter (e.g. $H_0: \mu \leq 1$). All we can do is either reject it, or not, based on evidence from data (through t_{obs}, or p-value). The mathematical way to see this is to note that the p-value is a "conditional prob", i.e. it assumes the claim H_0 is True.

Summary

We now have a method for testing hypotheses with p-values.
The method involves the prob of getting more extreme (than obs.) events, and whether that prob is sufficiently small.

Q More extreme?
Depends on (H_0, H_1):

Because of the blue note, above, it is sufficient to test $\mu = \mu_0$

1-sided
If $H_0: \mu \le \mu_0$ (or $\mu = \mu_0$)
$H_1: \mu > \mu_0$ p-value = right-area

If $H_0: \mu \ge \mu_0$ (or $\mu = \mu_0$)
$H_1: \mu < \mu_0$ p-value = left-area

2-sided
If $H_0: \mu = \mu_0$ p-value = left + right = 2 × (1 tail)
$H_1: \mu \neq \mu_0$

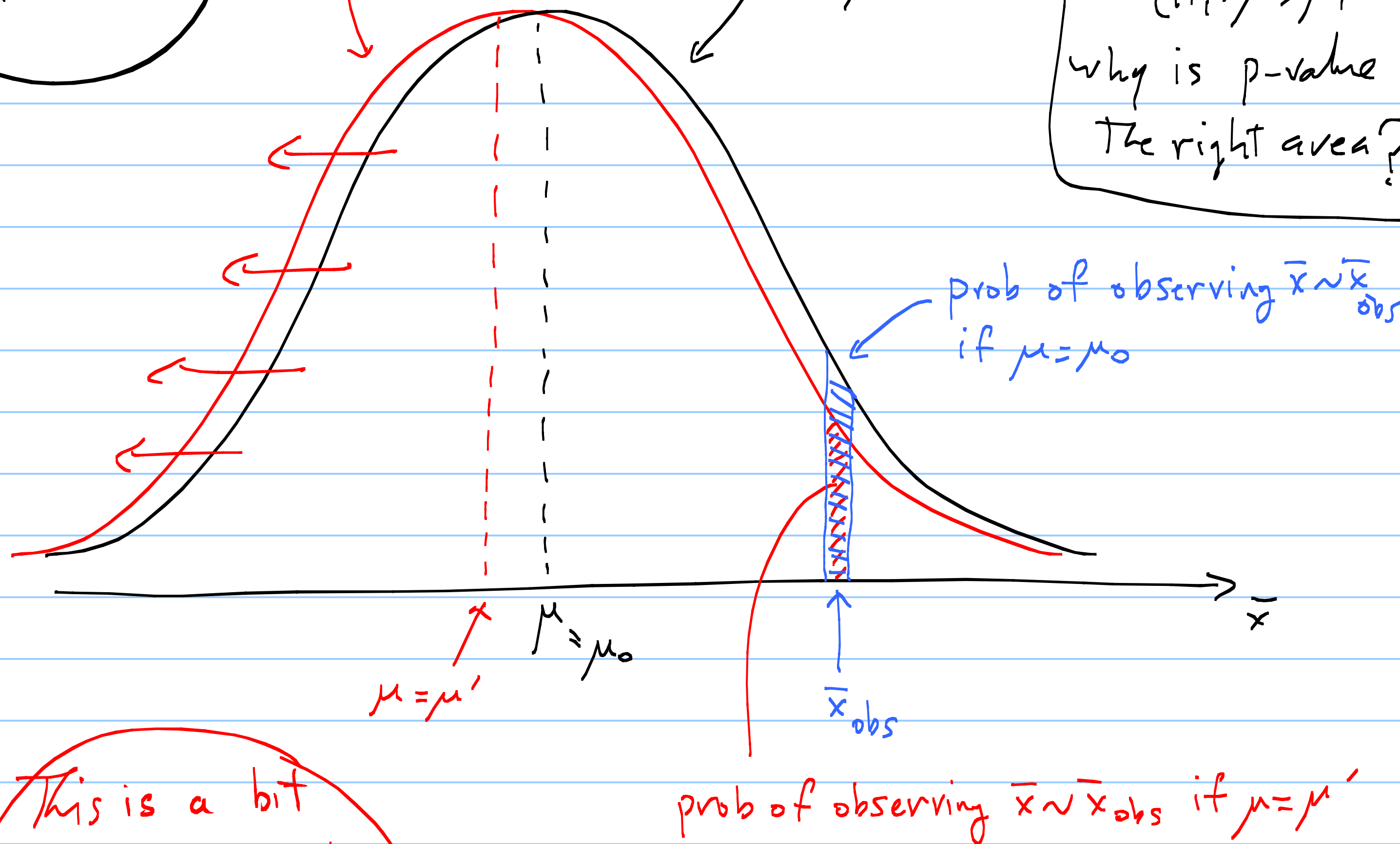
Who decides what's "sufficiently small"? You do!
That "threshold prob" is called significance level, denoted α, and it is 1 − conf. level. More, later.
Some common values are .05, .01, .001, but the choice depends on the cost of making the wrong decision (ie. of rejecting H_0 when it's True).

In Summary:

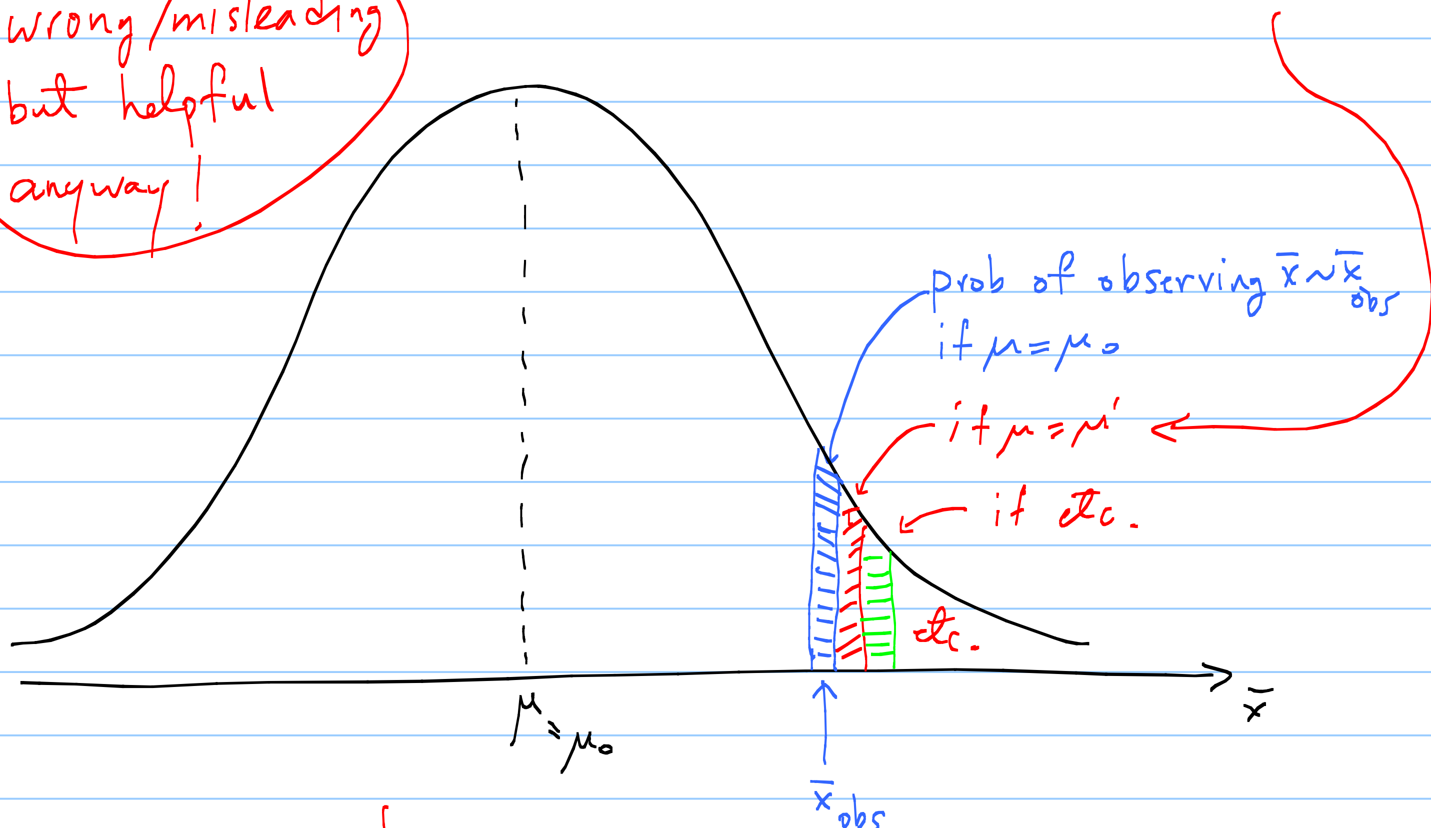
1) You choose the value of α.
2) Compute p-value from the above procedure.
3) If p-value $< \alpha$, Then Reject H_0 in favor of H_1.
Else, cannot reject " " " " "

FYI

If $\begin{cases} H_0: \mu \le \mu_0 \\ H_1: \mu > \mu_1 \end{cases}$ why is p-value the right area?



This is a bit wrong/misleading but helpful anyway!



So, if $H_0: \mu \le \mu_0$, then the p-value $= \text{prob}(\bar{x} > \bar{x}_{obs})$

I.e. $H_1: \mu > \mu_0$ mnemonic $=$ right area hw-lect23-1

8.23 revised.
Consider the following sample observations: 2781, 2900, 3013, 2856, and 2888.
Suppose we want to do a two-sided test of the pop mean, i.e.,
H0: mu = 3000
H1: mu != 3000

a) Compute the p-value, and state the conclusion "In English" (i.e., is there evidence that mu is not 3000?) using alpha = 0.05.

b) Compute the appropriate confidence interval (CI). Is the conclusion the same as in part a? Explain.

One can also arrive at the same conclusion, without the p-value and CI, by what is called the rejection method. I'll walk you through it:

c) If H0 is true, compute the values of x_bar that have an area of 0.025 to the right and 0.025 to the left.(Together these areas add-up to 0.05, i.e., alpha). These values of x_bar are called the critical values, and the regions beyond them (i.e., larger than the larger one, and smaller than the smaller one) are called the rejection region. So, in this part of the problem you are computing the rejection region.

d) Is the observed value of x_bar in the rejection region? If so, one can reject H0 in favor of H1; otherwise, one cannot say anything.