

def: Null Hypothesis $\equiv H_0 \equiv$ statement (such as $\mu = \mu_0$)
whose plausibility we examine

def: Alternative Hypothesis $\equiv H_A \equiv$ opposite of null hypothesis
($\mu \neq \mu_0$, for example)

The basic idea of hypothesis testing is to decide whether the null hypothesis is so unlikely, given observed data, that we can confidently reject the hypothesis.

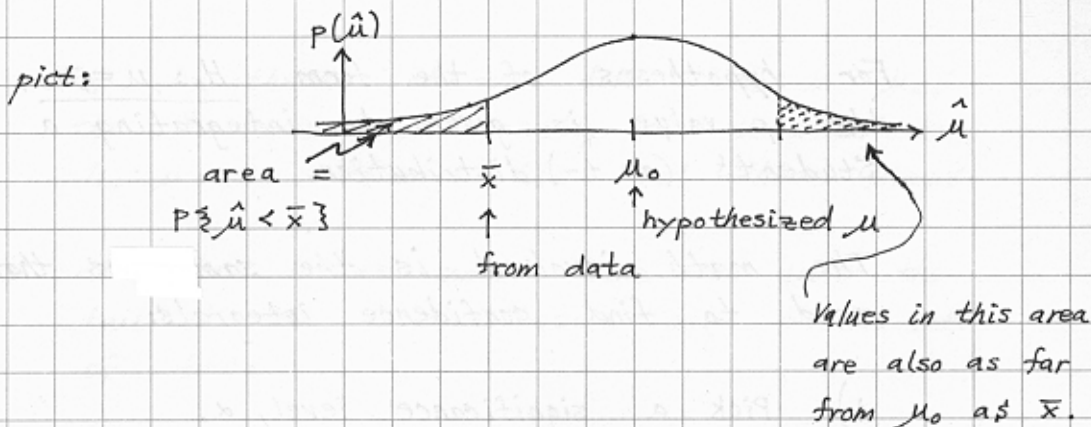
Because we are dealing with random events, we can never be certain that a null hypothesis, H_0 , is false. We can only ^{say} that the probability that it is true is less than some value α .

Say $\alpha = 0.01$ or 1%. Then our data may indicate a probability $< 1\%$ that H_0 is true, in which case we reject H_0 .

Often, the null hypothesis, H_0 , seems to be clearly false. If H_0 is the claim that $\mu = \mu_0$, for example, we might assume H_0 is false because the probability that mean μ (a real number) is exactly equal to μ_0 is zero. (The probability that the average temperature today will be exactly 50° is zero. It could be a number very close to 50° such as $50.0010305\dots$, but it won't be exactly $50.000\dots$). Curiously, though, we can't prove $\mu \neq \mu_0$, either. We never have enough data to be absolutely certain that $\mu \neq \mu_0$.

Our solution to this dilemma is to collect data, calculate $\hat{\mu} = \bar{x}$, and determine the probability of getting $\hat{\mu}$ as far away from μ_0 (or farther) as our observed $\hat{\mu} = \bar{x}$ is from μ_0 .

So we calculate $P\left\{\begin{array}{l} \hat{\mu} \text{ is as far or farther from } \mu_0 \text{ than } \bar{x} \\ \text{if } \mu = \mu_0 \end{array}\right\}$

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def: p value $\equiv P\{\text{getting actual data that is as bad or worse than what we observed}\}$

Here, "bad" means "unlikely given the hypothesis" and "worse" means "even more unlikely given the hypothesis."

p = total hatched and dotted areas in above diagram

Note: The p value intuitively corresponds to the probability that the null hypothesis, H_0 , is true.

Comment: This may seem backward at first, but the hatched and dotted areas (i.e., the p value) will get larger if $\bar{x}$ is closer to μ_0 . Thus, a larger p value means H_0 is more likely to be true.

def: significance level (or size) $\equiv \alpha \equiv$

- if $p \text{ value} < \alpha$ then we reject H_0
- if $p \text{ value} > \alpha$ then we accept H_0

Note: Accepting H_0 only means H_0 is plausible. It does not mean we are sure H_0 is true. Just as we can never be certain H_0 is false, we can never be sure H_0 is true.

For hypotheses of the form $H_0: \mu = \mu_0$, the p value is given by integrating a Student's (or t-) distribution.

The math involved is the same as that used to find confidence intervals:

1) Pick a significance level, α .

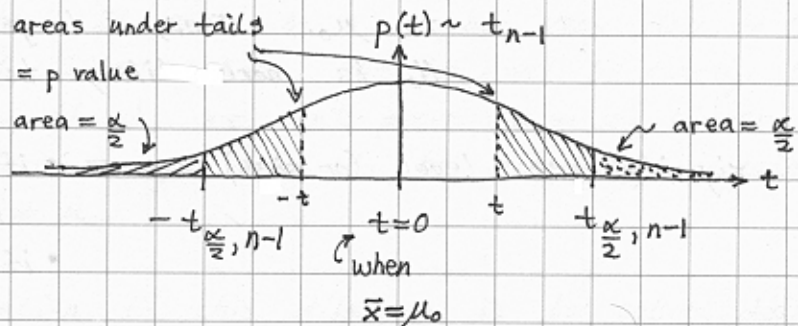
2) Define $T \equiv \frac{\bar{X} - \mu_0}{S/\sqrt{n}}$ where $\bar{X} \equiv$ est mean
 $S \equiv$ est standard deviation

$T \sim t_{n-1}$ In other words, T is distributed as a t-distribution with $n-1$ degrees of freedom.

3) Gather data and calculate

$$t = \frac{\bar{x} - \mu_0}{s/\sqrt{n}}$$

4) Use a table to find the value of t that corresponds to $p \text{ value} = \alpha$. That is, find $t_{\frac{\alpha}{2}, n-1}$:



5) Reject H_0 if t is farther from zero than $t_{\frac{\alpha}{2}, n-1}$. Otherwise, accept H_0 . That is:

$$|t| > t_{\frac{\alpha}{2}, n-1} \Rightarrow \text{reject } H_0 \quad \text{Otherwise, accept } H_0.$$

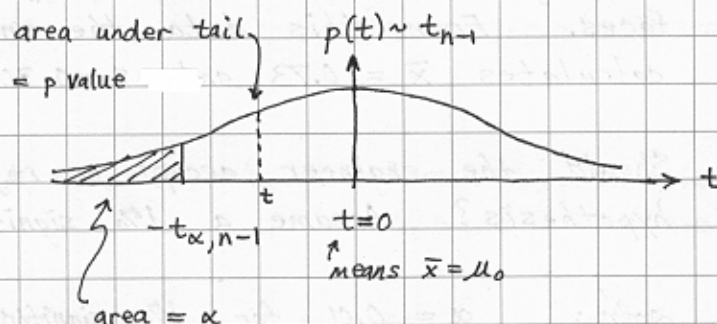
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For hypotheses of the form $H_0: \mu \geq \mu_0$, the procedure is exactly the same as for $H_0: \mu = \mu_0$ through the first three steps.

At step 4 we consider the area under the tail of the t distribution only to the left of $t=0$:

- 4) Use a table to find the value of t that corresponds to $p \text{ value} = \alpha$. That is, find $t_{\alpha, n-1}$:



Note: We use $t_{\alpha, n-1}$ instead of $t_{\frac{\alpha}{2}, n-1}$.

- 5) Reject H_0 if t is to the left of $-t_{\alpha, n-1}$. Otherwise, accept H_0 . That is:

$$t < -t_{\alpha, n-1} \Rightarrow \text{reject } H_0 \quad \text{Otherwise, accept } H_0.$$

Note: $\alpha = 0.01$ or 1% is typical as a choice for α in hypothesis testing.

ex: A company called ICU manufactures a system that recognizes faces. An engineer has modified the system. The old system has been tested very extensively, and it is known to have a recognition rate of $\mu_0 = 0.85$ or 85 %.

The engineer wishes to test the following null hypothesis: $H_0: \mu > \mu_0$ where μ is the mean of the new system.

The engineer tests the new system with 61 faces. From this data the engineer calculates $\bar{x} = 0.73$ and $s = 0.30$.

Should the engineer accept or reject the hypothesis? Assume a 1% significance level.

soln: $\alpha = 0.01$ for 1% significance level

$$t_{\alpha, n-1} = t_{0.01, 60} = 2.390 \quad \text{From table of critical points for } t \text{ distribution.}$$

$$t = \frac{\bar{x} - \mu_0}{s/\sqrt{n}} = \frac{0.73 - 0.85}{0.30/\sqrt{61}} = \frac{-0.12\sqrt{61}}{0.30}$$

$$t = -3.124$$

Thus, $t < -t_{\alpha, n-1}$ and we reject the null hypothesis.

This means there is less than a 1% chance that the new system is better than the old one.

Note: The engineer argued that the data was a result of 1 in a hundred chance of bad luck...