

Null Hypothesis Significance Testing I

Class 17, 18.05

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1 Learning Goals

1. Know the definitions of the significance testing terms: null hypothesis, alternative hypothesis, NHST, simple hypothesis, composite hypothesis, significance level, power.
2. Be able to design and run a significance test for Bernoulli or binomial data.
3. Be able to compute a p -value for a normal hypothesis and use it in a significance test.

2 Introduction

Frequentist statistics is often applied in the framework of null hypothesis significance testing (NHST). We will look at the [Neyman-Pearson](#) paradigm which focuses on one hypothesis called the [null hypothesis](#): for example, that the tested treatment has no effect on the progress of the disease. There are other paradigms for hypothesis testing, but Neyman-Pearson is the most common. Stated simply, this method [asks if the data is well outside the region where we would expect to see it under the null hypothesis](#). If so, then we [reject the null hypothesis](#). The reasoning is that [such extreme data is very unlikely in a world where the null hypothesis is true](#).

We will always use the term [alternative hypothesis](#) to mean simply the complement of the null hypothesis: in the example above, that the tested treatment *does* affect the progress of the disease. For us, the possible universes are always divided between the null hypothesis and the alternative hypothesis, so [rejecting the null hypothesis means accepting the alternative hypothesis](#). Experimental design and statistical computations will always be phrased in terms of the null hypothesis. If (as is generally the case) what you care about is the *alternative* hypothesis, then you should choose your alternative hypothesis first, and make the null hypothesis its complement.

Some users of statistics allow an “alternative hypothesis” that is smaller than the whole complement of the null hypothesis. You need to pay attention to that: with such language, rejecting the null hypothesis does **not** mean accepting the alternative hypothesis.

The computations done here all involve the likelihood function. There are two main differences between what we’ll do here and what we did in Bayesian updating.

1. The evidence of the data will be considered purely through the likelihood function: it will not be weighted by our prior beliefs.
2. We will need a notion of extreme data, e.g. 95 out of 100 heads in a coin toss or a mayfly that lives for a month.

2.1 Motivating examples

Example 1. Suppose you want to decide whether a coin is fair. If you toss it 100 times and get 85 heads, would you think the coin is likely to be unfair? What about 60 heads? Or 52 heads? Most people would guess that 85 heads is strong evidence that the coin is unfair, whereas 52 heads is no evidence at all. Sixty heads is less clear. [Null hypothesis significance testing \(NHST\)](#) is a frequentist approach to thinking quantitatively about these questions.

Example 2. Suppose you want to compare a new medical treatment to a placebo or to the current standard of care. What sort of evidence would convince you that the new treatment is better than the placebo or the current standard? Again, NHST is a quantitative framework for answering these questions.

3 Significance testing

We'll start by listing the ingredients for NHST. Formally they are pretty simple. There is an art to choosing good ingredients. We will explore the art in examples. If you have never seen NHST before just scan this list now and come back to it after reading through the examples and explanations given below.

3.1 Ingredients

- H_0 : the [null hypothesis](#). This is the default assumption for the model generating the data.
- H_A : the [alternative hypothesis](#): the complement of the null hypothesis. If we reject the null hypothesis we accept this alternative as the best explanation for the data.
- X : the [test statistic](#). We compute this from the data. It's a random variable, because we think of collecting random data (described either by H_0 or by H_A) as a repeatable trial.
- [Null distribution](#): the probability distribution of X assuming H_0 .
- [Rejection region](#): if X is in the rejection region we reject H_0 in favor of H_A .
- [Non-rejection region](#): the complement to the rejection region. If X is in this region we do not reject H_0 . Note that we say 'do not reject' rather than 'accept' because usually the best we can say is that the data does not support rejecting H_0 .

The null hypothesis H_0 and the alternative hypothesis H_A play different roles. Typically we choose H_0 to be either a simple hypothesis or the default which we'll only reject if we have enough evidence against it. The examples below will clarify this.

4 NHST Terminology

In this section we will use one extended example to introduce and explore the terminology used in null hypothesis significance testing (NHST).

Example 3. To test whether a coin is fair we flip it 10 times. If we get an unexpectedly large or small number of heads we'll suspect the coin is unfair. To make this precise in the language of NHST we set up the ingredients as follows. Let θ be the probability that the coin lands heads when flipped.

1. Null hypothesis: $H_0 =$ 'the coin is fair', i.e. $\theta = 0.5$.
2. Alternative hypothesis: $H_A =$ 'the coin is not fair', i.e. $\theta \neq .5$
3. Test statistic: $X =$ number of heads in 10 flips
4. Null distribution: This is the probability function based on the null hypothesis

$$p(x | \theta = 0.5) \sim \text{binomial}(10, 0.5).$$

Here is the probability table for the null distribution.

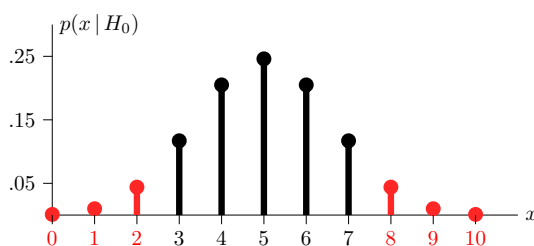
x	0	1	2	3	4	5	6	7	8	9	10
$p(x H_0)$.001	.010	.044	.117	.205	.246	.205	.117	.044	.010	.001

5. Rejection region: under the null hypothesis we expect to get about 5 heads in 10 tosses. We'll reject H_0 if the number of heads is much fewer or greater than 5. Let's set the rejection region as $\{0, 1, 2, 8, 9, 10\}$. That is, if the number of heads in 10 tosses is in this region we will reject the hypothesis that the coin is fair in favor of the hypothesis that it is not.

We can summarize all this in the graph and probability table below. The rejection region consists of those values of x in red. The probabilities corresponding to it are shaded in red. We also show the null distribution as a stem plot with the rejection values of x in red.

x	0	1	2	3	4	5	6	7	8	9	10
$p(x H_0)$.001	.010	.044	.117	.205	.246	.205	.117	.044	.010	.001

Rejection region and null probabilities as a table for Example 3.



Rejection region and null probabilities as a stem plot for Example 3.

Notes for Example 3:

1. The null hypothesis is the **cautious default**: we won't claim the coin is unfair unless we have compelling evidence.
2. The rejection region consists of data that is **extreme under the null hypothesis**. That is, it consists of the outcomes that are in the tail of the null distribution away from the high probability center. As we'll discuss soon, how far away depends on the significance level α of the test.
3. If we get 3 heads in 10 tosses, then the test statistic is in the non-rejection region. The

usual scientific language would be to say that the data ‘does not support rejecting the null hypothesis’. Even if we got 5 heads, we would **not** claim that the data proves the null hypothesis is true.

Question: If we have a fair coin what is the probability that we will decide incorrectly it is unfair?

answer: The null hypothesis is that the coin is fair. The question asks for the probability the data from a fair coin will be in the rejection region. That is, the probability that we will get 0, 1, 2, 8, 9 or 10 heads in 10 tosses. This is the sum of the probabilities in red. That is,

$$P(\text{rejecting } H_0 \mid H_0 \text{ is true}) = 0.11$$

Below we will continue with Example 3, define more terms used in NHST and see how to quantify properties of the significance test.

4.1 Simple and composite hypotheses

Definition: simple hypothesis: A **simple hypothesis** is one for which we can specify its distribution completely. A typical simple hypothesis is that a parameter of interest takes a specific value.

Definition: composite hypotheses: If its distribution cannot be fully specified, we say that the hypothesis is **composite**. A typical composite hypothesis is that a parameter of interest lies in a range of values.

In Example 3 the null hypothesis is that $\theta = 0.5$, so the null distribution is $\text{binomial}(10, 0.5)$. Since the null distribution is fully specified, H_0 is simple. The alternative hypothesis is that $\theta \neq 0.5$. This is really many hypotheses in one: θ could be 0.51, 0.7, 0.99, etc. Since the alternative distribution $\text{binomial}(10, \theta)$ is not fully specified, H_A is composite.

Example 4. Suppose we have data x_1, \dots, x_n . Suppose also that our hypotheses are

H_0 : the data is drawn from $N(0, 1)$

H_A : the data is drawn from $N(1, 1)$.

These are both **simple hypotheses** – each hypothesis completely specifies a distribution.

Example 5. (Composite hypotheses.) Now suppose that our hypotheses are

H_0 : the data is drawn from a Poisson distribution of unknown parameter.

H_A : the data is not drawn from a Poisson distribution.

These are both composite hypotheses, as they don’t fully specify the distribution.

Example 6. In an ESP experiment a subject is asked to identify the suits of 100 cards drawn (with replacement) from a deck of cards. Let T be the number of successes. The (simple) null hypothesis that the subject does not have ESP is given by

$$H_0: T \sim \text{binomial}(100, 0.25)$$

The (composite) alternative hypothesis that the subject has ESP is given by

$$H_A: T \sim \text{binomial}(100, p) \text{ with } p > 0.25$$

Another (composite) alternative hypothesis that something besides pure chance is going on, i.e. the subject has ESP or anti-ESP. This is given by

$$H_A: T \sim \text{binomial}(100, p), \text{ with } p \neq 0.25$$

Values of $p < 0.25$ represent hypotheses that the subject has a kind of anti-esp.

4.2 Types of error

There are two types of errors we can make. We can incorrectly reject the null hypothesis when it is true or we can incorrectly fail to reject it when it is false. These are unimaginatively labeled **type I** and **type II errors**. We summarize this in the following table.

		True state of nature	
		H_0	H_A
Our decision	Reject H_0	Type I error	correct decision
	'Don't reject' H_0	correct decision	Type II error

Type I: false rejection of H_0

Type II: false non-rejection ('acceptance') of H_0

4.3 Significance level and power

Significance level and power are used to quantify the quality of the significance test. Ideally a significance test would not make errors. That is, it would not reject H_0 when H_0 was true and would reject H_0 in favor of H_A when H_A was true. Altogether there are 4 important probabilities corresponding to the 2×2 table just above.

$$\begin{array}{ll} P(\text{reject } H_0 | H_0) & P(\text{reject } H_0 | H_A) \\ P(\text{do not reject } H_0 | H_0) & P(\text{do not reject } H_0 | H_A) \end{array}$$

The two probabilities we focus on are:

$$\begin{aligned} \text{Significance level} &= P(\text{reject } H_0 | H_0) \\ &= \text{probability we incorrectly reject } H_0 \\ &= P(\text{type I error}). \end{aligned}$$

$$\begin{aligned} \text{Power} &= \text{probability we correctly reject } H_0 \\ &= P(\text{reject } H_0 | H_A) \\ &= 1 - P(\text{type II error}). \end{aligned}$$

Ideally, a hypothesis test should have a small significance level (near 0) and a large power (near 1). Here are two analogies to help you remember the meanings of significance and power.

Some analogies

1. Think of H_0 as the hypothesis 'nothing noteworthy is going on', i.e. 'the coin is fair', 'the treatment is no better than placebo' etc. And think of H_A as the opposite: 'something interesting is happening'. Then power is the probability of detecting something interesting when it's present and significance level is the probability of mistakenly claiming something interesting has occurred.

2. In the U.S. criminal defendants are presumed innocent until proven guilty beyond a reasonable doubt. We can phrase this in NHST terms as

H_0 : the defendant is innocent (the default)

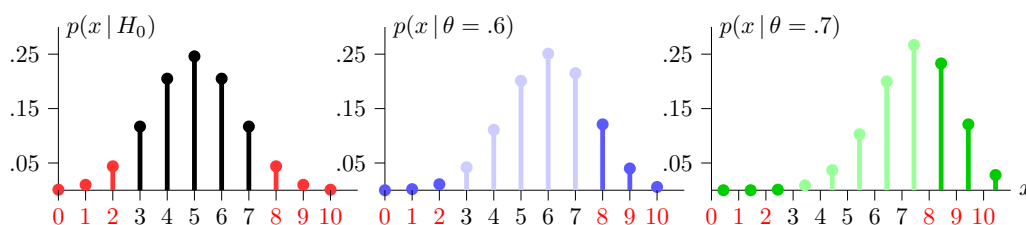
H_A : the defendant is guilty.

Significance level is the probability of finding an innocent person guilty. Power is the probability of correctly finding a guilty party guilty. ‘Beyond a reasonable doubt’ means we should demand the significance level be very small.

Composite hypotheses

H_A is composite in Example 3, so the power is different for different values of θ . We expand the previous probability table to include some alternate values of θ . We do the same with the stem plots. As always in the NHST game, we look at [likelihoods](#): the probability of the data given a hypothesis.

x	0	1	2	3	4	5	6	7	8	9	10
$H_0 : p(x \theta = 0.5)$.001	.010	.044	.117	.205	.246	.205	.117	.044	.010	.001
$H_A : p(x \theta = 0.6)$.000	.002	.011	.042	.111	.201	.251	.215	.121	.040	.006
$H_A : p(x \theta = 0.7)$.000	.0001	.001	.009	.037	.103	.200	.267	.233	.121	.028



Rejection region and null and alternative probabilities for example 3

We use the probability table to compute the significance level and power of this test.

Significance level = probability we reject H_0 when it is true
 = probability the test statistic is in the rejection region when H_0 is true
 = probability the test stat. is in the rejection region of the H_0 row of the table
 = sum of red boxes in the $\theta = 0.5$ row
 = 0.11

Power when $\theta = 0.6$ = probability we reject H_0 when $\theta = 0.6$
 = probability the test statistic is in the rejection region when $\theta = 0.6$
 = probability the test stat. is in the rejection region of the $\theta = 0.6$ row of the table
 = sum of dark blue boxes in the $\theta = 0.6$ row
 = 0.180

Power when $\theta = 0.7$ = probability we reject H_0 when $\theta = 0.7$
 = probability the test statistic is in the rejection region when $\theta = 0.7$
 = probability the test stat. is in the rejection region of the $\theta = 0.7$ row of the table
 = sum of dark green boxes in the $\theta = 0.7$ row
 = 0.384

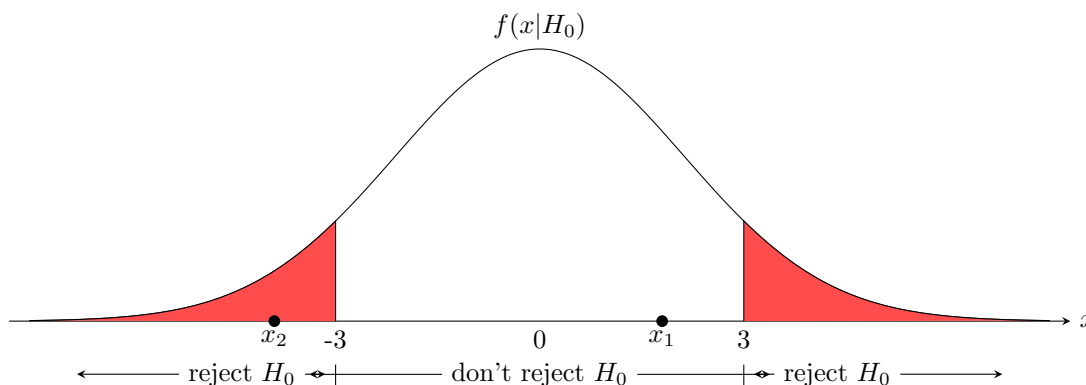
We see that the power is greater for $\theta = 0.7$ than for $\theta = 0.6$. This isn't surprising since we expect it to be easier to recognize that a 0.7 coin is unfair than it is to recognize 0.6 coin is unfair. Typically, we get higher power when the alternate hypothesis is farther from the null hypothesis. In Example 3, it would be quite hard to distinguish a fair coin from one with $\theta = 0.51$.

4.4 Conceptual sketches

We illustrate the notions of null hypothesis, rejection region and power with some sketches of the pdfs for the null and alternative hypotheses.

4.4.1 Null distribution: rejection and non-rejection regions

The first diagram below illustrates a null distribution with rejection and non-rejection regions. Also shown are two possible test statistics: x_1 and x_2 .



The test statistic x_1 is in the non-rejection region. So, if our data produced the test statistic x_1 then we would not reject the null hypothesis H_0 . On the other hand the test statistic x_2 is in the rejection region, so if our data produced x_2 then we would reject the null hypothesis in favor of the alternative hypothesis.

There are several things to note in this picture.

1. The rejection region consists of values far from the center of the null distribution.
2. The rejection region is two-sided. We will also see examples of one-sided rejection regions as well.
3. The alternative hypothesis is not mentioned. We reject or don't reject H_0 based only on the likelihood $f(x|H_0)$, i.e. the probability of the test statistic conditioned on H_0 . As we will see, the alternative hypothesis H_A should be considered when choosing a rejection region, but formally it does not play a role in rejecting or not rejecting H_0 .
4. Sometimes we rather lazily call the non-rejection region the [acceptance region](#). This is technically incorrect because we never truly accept the null hypothesis. We either reject or say the data does not support rejecting H_0 . This is often summarized by the statement: [you can never prove the null hypothesis](#).

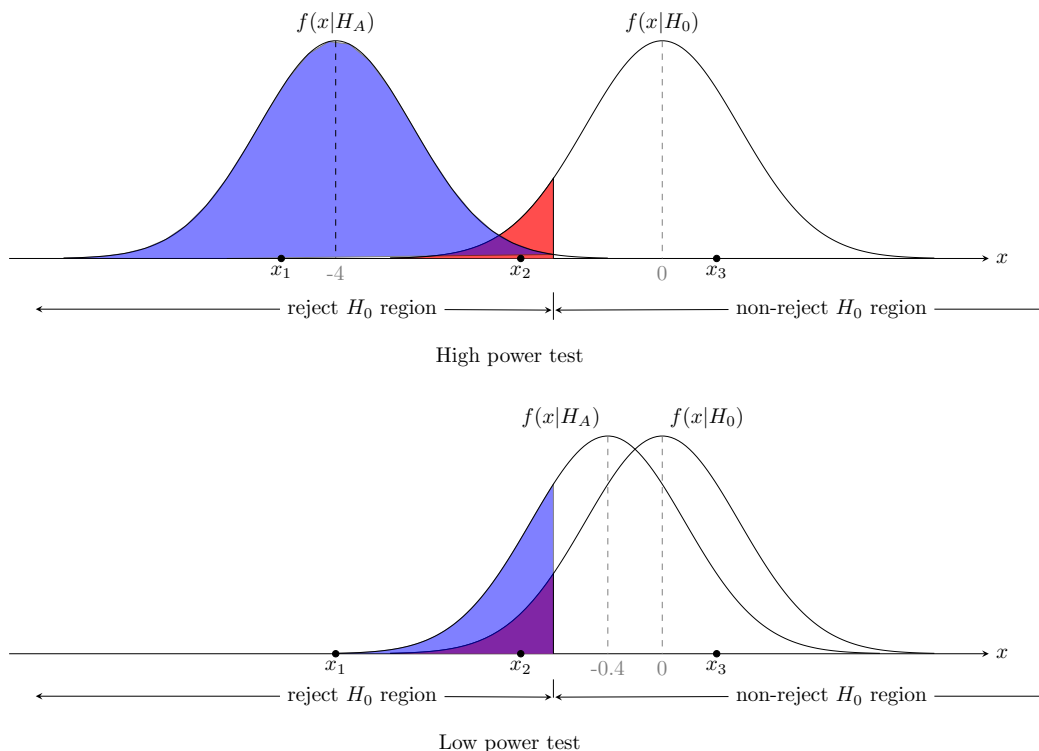
4.4.2 High and low power tests

The next two figures show high and low power tests.

The shaded area under $f(x|H_0)$ represents the significance level. Remember the significance level is

- The probability of falsely rejecting the null hypothesis when it is true.
- The probability the test statistic falls in the rejection region even though H_0 is true.

Likewise, the shaded area under $f(x|H_A)$ represents the power, i.e. the probability that the test statistic is in the rejection (of H_0) region when H_A is true. Both tests have the same significance level, but if $f(x|H_A)$ has considerable overlap with $f(x|H_0)$ the power is much lower. It is well worth your while to thoroughly understand these graphical representations of significance testing.



In both tests the distributions for $(x|H_0)$ and $(x|H_A)$ are normal with variance 1, and the null distributions are the same (having mean 0). So the rejection region and significance level are all the same. (The significance level is the red/purple area under $f(x|H_0)$ and above the rejection region.) In the top figure we see the means of the two distributions are 4 standard deviations apart. Since the areas under the densities have very little overlap the test has high power. That is, if the data x is drawn from H_A it will almost certainly be in the rejection region. For example x_3 would be a very surprising outcome for the H_A distribution.

In the bottom figure we see the means of the two distributions are just 0.4 standard deviations apart. Since the areas under the densities have a lot of overlap the test has low power. That is, if the data x is drawn from H_A it is highly likely to be in the non-rejection region. For example x_3 would not be a very surprising outcome for the H_A distribution.

Typically we can increase the power of a test by increasing the amount of data and thereby decreasing the variance of the null and alternative distributions. In experimental design it is important to determine ahead of time the number of trials or subjects needed to achieve a desired power.

Example 7. Suppose a drug for a disease is being compared to a placebo. We choose our null and alternative hypotheses as

H_0 = the drug does not work better than the placebo

H_A = the drug works better than the placebo

The power of the hypothesis test is the probability that the test will conclude that the drug is better, if it is indeed truly better. The significance level is the probability that the test will conclude that the drug works better, when in fact it does not.

5 Designing a hypothesis test

Formally all a hypothesis test requires is H_0 , H_A , a test statistic and a rejection region. In practice the design is often done using the following steps.

1. Pick the null hypothesis H_0 .

The choice of H_0 and H_A is not mathematics. It's art and custom. We often choose H_0 to be simple. Or we often choose H_0 to be the simplest or most cautious explanation, i.e. no effect of drug, no ESP, no bias in the coin.

2. Decide if H_A is one-sided or two-sided.

In the example 3 we wanted to know if the coin was unfair. An unfair coin could be biased for or against heads, so $H_A : \theta \neq 0.5$ is a two-sided hypothesis. If we only care whether or not the coin is biased for heads we could use the one-sided hypothesis $H_A : \theta > 0.5$.

3. Pick a test statistic.

For example, the sample mean, sample total, or sample variance. Often the choice is obvious. Some standard statistics that we will encounter are z , t , and χ^2 . We will learn to use these statistics as we work examples over the next few classes. One thing we will say repeatedly is that the distributions that go with these statistics are always conditioned on the null hypothesis. That is, we will compute likelihoods such as $f(z | H_0)$.

4. Pick a significance level and determine the rejection region.

We will usually use α to denote the significance level. The Neyman-Pearson paradigm is to pick α in advance. Typical values are 0.1, 0.05, 0.01. Recall that the significance level is the probability of a type I error, i.e. of incorrectly rejecting the null hypothesis when it is true. The value we choose will depend on the consequences of a type I error.

Once the significance level is chosen we can determine the rejection region in the tail(s) of the null distribution. In Example 3, H_A is two sided so the rejection region is split between the two tails of the null distribution. This distribution is given in the following table:

x	0	1	2	3	4	5	6	7	8	9	10
$p(x H_0)$.001	.010	.044	.117	.205	.246	.205	.117	.044	.010	.001

If we set $\alpha = 0.05$ then the rejection region must contain at most .05 probability. For a two-sided rejection region we get

$$\{0, 1, 9, 10\}.$$

If we set $\alpha = 0.01$ the rejection region is

$$\{0, 10\}.$$

Suppose we change H_A to ‘the coin is biased in favor of heads’. We now have a one-sided hypothesis $\theta > 0.5$. Our rejection region will now be in the right-hand tail since we don’t want to reject H_0 in favor of H_A if we get a small number of heads. Now if $\alpha = 0.05$ the rejection region is the one-sided range

$$\{9, 10\}.$$

If we set $\alpha = 0.01$ then the rejection region is

$$\{10\}.$$

5. Determine the power(s).

As we saw in Example 3, once the rejection region is set we can determine the power of the test at various values of the alternate hypothesis.

Example 8. (Consequences of significance) If $\alpha = 0.1$ then we’d expect a 10% type I error rate. That is, we expect to reject the null hypothesis in 10% of those experiments where the null hypothesis is true. Whether 0.1 is a reasonable significance level depends on the decisions that will be made using it.

For example, if you were running an experiment to determine if your chocolate is more than 72% cocoa then a 10% error type I error rate is probably okay. That is, falsely believing some 72% chocolate is greater than 72%, is probably acceptable. On the other hand, if your forensic lab is identifying fingerprints for a murder trial then a 10% type I error rate, i.e. mistakenly claiming that fingerprints found at the crime scene belonged to someone who was truly innocent, is definitely not acceptable.

Significance for a composite null hypothesis. If H_0 is composite then $P(\text{type I error})$ depends on which member of H_0 is true. In this case the significance level is defined as the maximum of these probabilities.

6 Critical values

Critical values are like quantiles except they refer to the probability to the right of the value instead of the left.

Example 9. Use R to find the 0.05 critical value for the standard normal distribution.

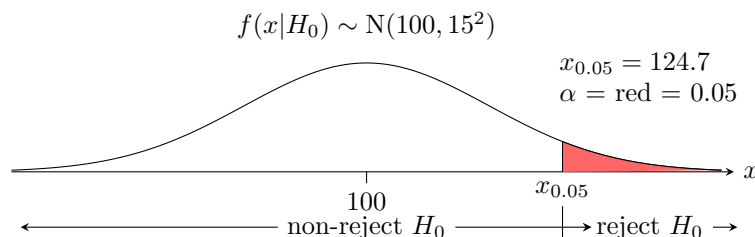
answer: We label this critical value $z_{0.05}$. The critical value $z_{0.05}$ is just the 0.95 quantile, i.e. it has 5% probability to its right and therefore 95% probability to its left. We computed it with the R function `qnorm(0.95, 0, 1)`, which returns 1.64.

In a typical significance test the rejection region consists of one or both tails of the null distribution. The value of the test significant that marks the start of the rejection region is a **critical value**. We show this and the notation used in some examples.

Example 10. Critical values and rejection regions. Suppose our test statistic x has null distribution is $N(100, 15^2)$, i.e. $f(x|H_0) \sim N(100, 15^2)$. Suppose also that our rejection region is right-sided and we have a significance level of 0.05. Find the critical value and sketch the null distribution and rejection region.

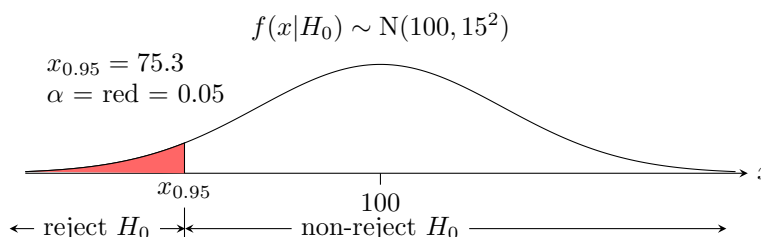
answer: The notation used for the critical value with right tail containing probability 0.05 is $x_{0.05}$. The critical value $x_{0.05}$ is just the 0.95 quantile, i.e. it has 5% probability to its

right and therefore 95% probability to its left. We computed it with the R function `qnorm(0.95, 100, 15)`, which returned 124.7. This is shown in the figure below.



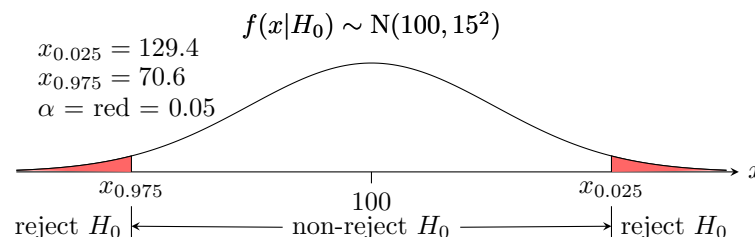
Example 11. Critical values and rejection regions. Repeat the previous example for a left-sided rejection region with significance level 0.05. In this case, the start of the rejection region is at the 0.05 quantile. Since there is 95%

answer: In this case the critical value has 0.05 probability to its left and therefore 0.95 probability to its right. So we label it $x_{0.95}$. Since it is the 0.05 quantile compute it with the R function: `qnorm(0.05, 100, 15)`, which returned 75.3.



Example 12. Critical values. Repeat the previous example for a two-sided rejection region. Put half the significance in each tail.

answer: To have a total significance of 0.05 we put 0.025 in each tail. That is, the left tail starts at $x_{0.975} = q_{0.025}$ and the right tail starts at $x_{0.025} = q_{0.975}$. We compute these values with `qnorm(0.025, 100, 15)` and `qnorm(0.975, 100, 15)`. The values are shown in the figure below.



7 p -values

In practice people often specify the significance level and do the significance test using what are called p -values. We will first define p -value and then see that

If the p -value is less than the significance level α then we reject H_0 . Otherwise we do not reject H_0 .

Definition. The p -value is the probability, assuming the null hypothesis, of seeing data [at least as extreme as the experimental data](#). What ‘at least as extreme’ means depends on the experimental design.

We illustrate the definition and use of p -values with a simple one-sided example. In later classes we will look at two-sided examples. This example also introduces the z -test. All this means is that our test statistic is standard normal (or approximately standard normal).

Example 13. The z -test for normal hypotheses

IQ is normally distributed in the population according to a $N(100, 15^2)$ distribution. We suspect that most MIT students have above average IQ so we frame the following hypotheses.

$$\begin{aligned} H_0 &= \text{MIT student IQs are distributed identically to the general population} \\ &= \text{MIT IQ's follow a } N(100, 15^2) \text{ distribution.} \\ H_A &= \text{MIT student IQs tend to be higher than those of the general population} \\ &= \text{the average MIT student IQ is greater than 100.} \end{aligned}$$

Notice that H_A is one-sided.

Suppose we test 9 students and find they have an average IQ of $\bar{x} = 112$. Can we reject H_0 at a significance level $\alpha = 0.05$?

answer: To compute p we first standardize the data: Under the null hypothesis $\bar{x} \sim N(100, 15^2/9)$ and therefore

$$z = \frac{\bar{x} - 100}{15/\sqrt{9}} = \frac{36}{15} = 2.4 \sim N(0, 1).$$

That is, the null distribution for z is standard normal. We call z a z -statistic, we will use it as our test statistic.

For a right-sided alternative hypothesis the phrase ‘data at least as extreme’ is a one-sided tail to the right of z . The p -value is then

$$p = P(Z \geq 2.4) = 1 - \text{pnorm}(2.4, 0, 1) = 0.0081975.$$

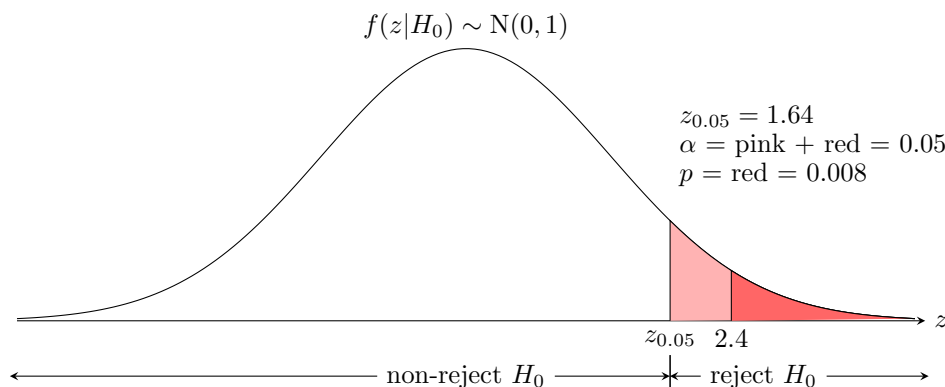
Since $p \leq \alpha$ we reject the null hypothesis. The reason this works is explained below. We phrase our conclusion as

We reject the null hypothesis in favor of the alternative hypothesis that MIT students have higher IQs on average. We have done this at significance level 0.05 with a p -value of 0.008.

Notes: **1.** The average $\bar{x} = 112$ is random: if we ran the experiment again we could get a different value for \bar{x} .

2. We could use the statistic \bar{x} directly. Standardizing is fairly standard because, with practice, we will have a good feel for the meaning of different z -values.

The justification for rejecting H_0 when $p \leq \alpha$ is given in the following figure.



In this example $\alpha = 0.05$, $z_{0.05} = 1.64$ and the rejection region is the range to the right of $z_{0.05}$. Also, $z = 2.4$ and the p -value is the probability to the right of z . The picture illustrates that

- $z = 2.64$ is in the rejection region
- is the same as z is to the right of $z_{0.05}$
- is the same as the probability to the right of z is less than 0.05
- which means $p < 0.05$.

8 More examples

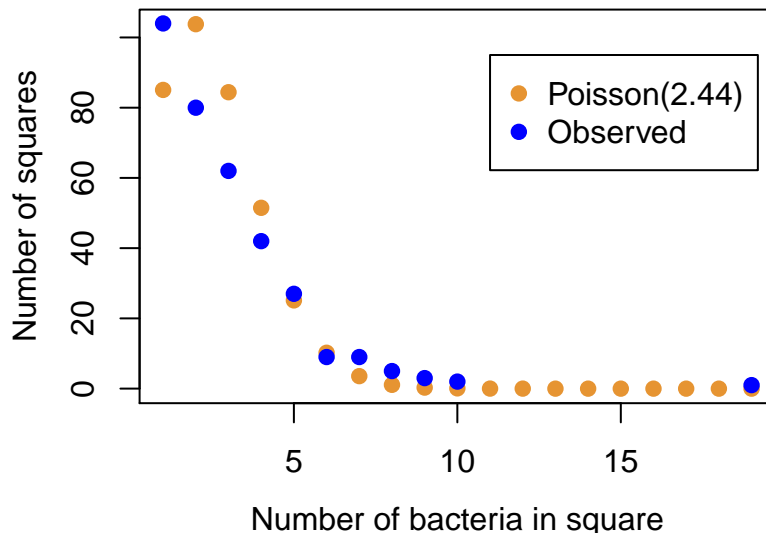
Hypothesis testing is widely used in inferential statistics. We don't expect that the following examples will make perfect sense at this time. Read them quickly just to get a sense of how hypothesis testing is used. We will explore the details of these examples in class.

Example 14. The chi-square statistic and goodness of fit. (Rice, example B, p.313)

To test the level of bacterial contamination, milk was spread over a grid with 400 squares. The amount of bacteria in each square was measured. We summarize in the table below. The bottom row of the table is the number of different squares that had a given amount of bacteria.

Amount of bacteria	0	1	2	3	4	5	6	7	8	9	10	19
Number of squares	56	104	80	62	42	27	9	9	5	3	2	1

We compute that the average amount of bacteria per square is 2.44. Since the Poisson(λ) distribution is used to model counts of relatively rare events and the parameter λ is the expected value of the distribution. we decide to see if these counts could come from a Poisson distribution. To do this we first graphically compare the observed frequencies with those expected from Poisson(2.44).



The picture is suggestive, so we do a hypothesis test with

H_0 : the samples come from a Poisson(2.44) distribution.

H_A : the samples come from a different distribution.

We use a chi-square statistic, so called because it (approximately) follows a chi-square distribution. To compute X^2 we first combine the last few cells in the table so that the minimum expected count is around 5 (a general rule-of-thumb in this game.)

The expected number of squares with a certain amount of bacteria comes from considering 400 trials from a Poisson(2.44) distribution, e.g., with $l = 2.44$ the expected number of squares with 3 bacteria is $400 \times e^{-l} \frac{l^3}{3!} = 84.4$.

The chi-square statistic is $\sum \frac{(O_i - E_i)^2}{E_i}$, where O_i is the observed number and E_i is the expected number.

Number per square	0	1	2	3	4	5	6	> 6
Observed	56	104	80	62	42	27	9	20
Expected	34.9	85.1	103.8	84.4	51.5	25.1	10.2	5.0
Component of X^2	12.8	4.2	5.5	6.0	1.7	0.14	0.15	44.5

Summing up we get $X^2 = 74.9$.

Since the mean (2.44) and the total number of trials (400) are fixed, the 8 cells only have 6 degrees of freedom. So, assuming H_0 , our chi-square statistic follows (approximately) a χ_6^2 distribution. Using this distribution, $P(X^2 > 74.59) = 0$ (to at least 6 decimal places). Thus we decisively reject the null hypothesis in favor of the alternate hypothesis that the distribution is not Poisson(2.44).

To analyze further, look at the individual components of X^2 . There are large contributions in the tail of the distribution, so that is where the fit goes awry.

Example 15. Student's t test.

Suppose we want to compare a medical treatment for increasing life expectancy with a placebo. We give n people the treatment and m people the placebo. Let X_1, \dots, X_n be the number of years people live after receiving the treatment. Likewise, let Y_1, \dots, Y_m be the number of years people live after receiving the placebo. Let \bar{X} and \bar{Y} be the sample means. We want to know if the difference between \bar{X} and \bar{Y} is statistically significant. We frame this as a hypothesis test. Let μ_X and μ_Y be the (unknown) means.

$$H_0 : \mu_X = \mu_Y, \quad H_A : \mu_X \neq \mu_Y.$$

With certain assumptions and a proper formula for the pooled standard error s_p the test statistic $t = \frac{\bar{X} - \bar{Y}}{s_p}$ follow a t distribution with $n + m - 2$ degrees of freedom. So our rejection region is determined by a threshold t_0 with $P(t > t_0) = \alpha$.