

TRGN 599: Applied Data Science and Bioinformatics

UNIT III. Supervised Statistical Tests

Week 6 - Lecture 1

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Topics

- Hypothesis Testing



Hypothesis Testing

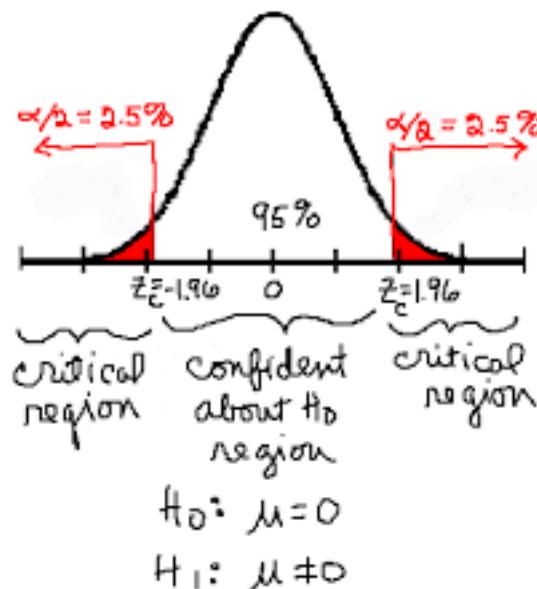
- We will review about:
 - Estimators
 - Their sampling distributions
 - Their specific values from observed data to evaluate hypotheses
- Scientific investigations start by expressing a hypothesis.
- Example:
 - Mackowiak et al. hypothesized that the average normal (i.e., for healthy people) body temperature is less than the widely accepted value of 98.6°F.
 - If we denote the population mean of normal body temperature as μ , then we can express this hypothesis as $\mu < 98.6$.



Hypothesis Testing

- From this example:

- We refer to this hypothesis as the null hypothesis and denote it as **H₀**.
- The null hypothesis usually reflects the “status quo” or “nothing of interest”.
- In contrast, we refer to our hypothesis (i.e., the hypothesis we are investigating through a scientific study) as the alternative hypothesis and denote it as **H_A**.
- In simple terms:
 - $H_A : \mu < 98.6$
 - $H_0 : \mu = 98.6$



The value of 1.96 is based on the fact that 95% of the area of a normal distribution is within 1.96 standard deviations of the mean.

Hypothesis Testing

- The procedure for evaluating a hypothesis is called hypothesis testing.
- A common approach for hypothesis testing is to focus on the null hypothesis,
 - Which is usually simpler than the alternative hypothesis, and decide whether or not to **reject it**.
- It is examined the evidence that the observed data provide against the null hypothesis H_0 .
 - If the evidence against H_0 is strong, we reject H_0 .
 - If not, we state that the evidence provided by the data is not strong enough to reject H_0 , and we fail to reject it.

		DECISION	
		Accept H_0	Accept H_A
		OK (True Negative)	TYPE I ERROR (False Positive)
TRUTH	H_0	(1- α)	(α)
	H_A	TYPE II ERROR (False Negative)	OK (True Positive)
		(β)	(1- β)

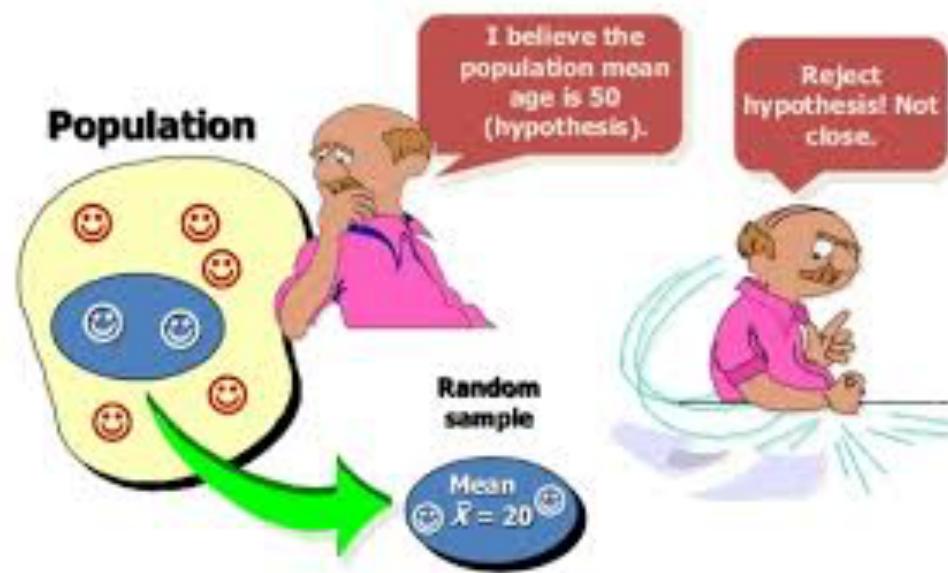
Hypothesis Testing

- With respect to our decision regarding the null hypothesis H_0 , we might make two types of errors:
 - Type I error: we reject H_0 when it is true and should not be rejected.
 - Type II error: we fail to reject H_0 when it is false and should be rejected.
- We denote the probability of making type I error as α and the probability of making type II error as β .

		Conclusion about null hypothesis from statistical test	
		Accept Null	Reject Null
Truth about null hypothesis in population	True	Correct	Type I error Observe difference when none exists
	False	Type II error Fail to observe difference when one exists	Correct

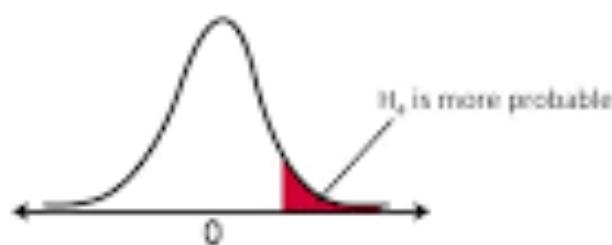
Hypothesis Testing

- Now suppose that we have a hypothesis testing procedure that fails to reject the null hypothesis when it should be rejected with probability β .
 - This means that our test correctly rejects the null hypothesis with probability $1 - \beta$. (Note that the two events are complementary.)
 - We refer to this probability (i.e., $1 - \beta$) as the **power** of the test.
 - In practice, it is common to first agree on a tolerable type I error rate α , such as 0.01, 0.05, and 0.1.
 - Then try to find a test procedure with the highest power among all reasonable testing procedures.



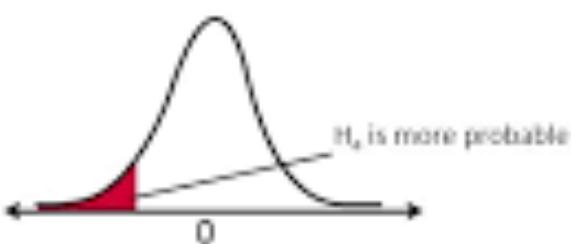
Hypothesis Testing

- We will review some commonly used testing procedures when the hypothesis is related to the population mean, μ , without explicit discussion of type I and type II errors.



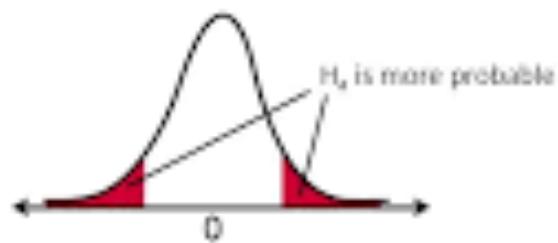
Right-tail test

$$H_a: \mu > \text{value}$$



Left-tail test

$$H_a: \mu < \text{value}$$

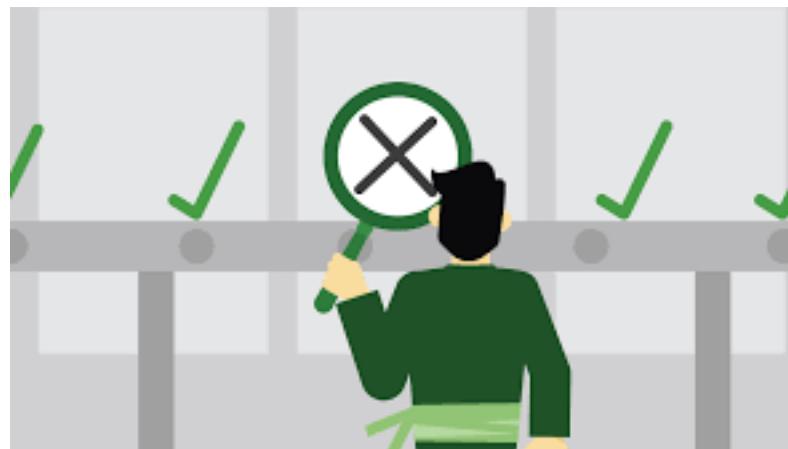


Two-tail test

$$H_a: \mu \neq \text{value}$$

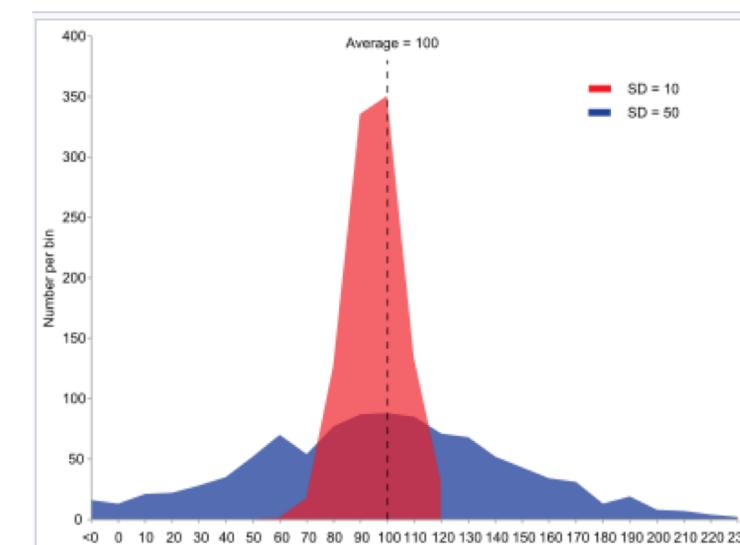
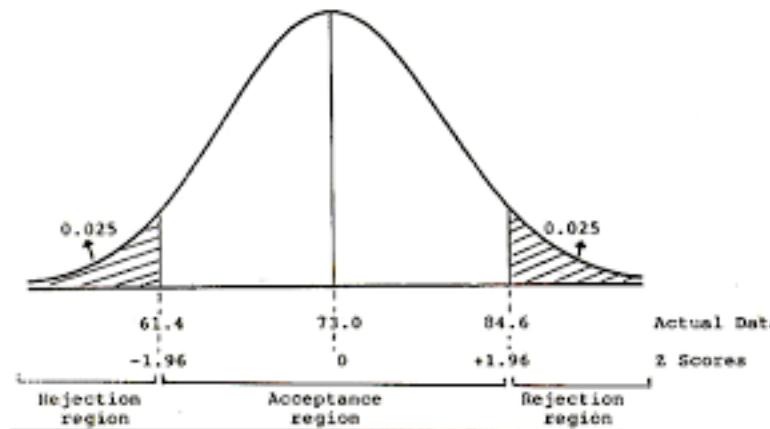
Hypothesis Testing for the Population Mean

- To decide whether we should reject the null hypothesis, we quantify the empirical support (provided by the observed data) against the null hypothesis using some statistics.
- Recall that a statistic is what we calculate based on the observed data only (i.e., it does not depend on any unknown parameter)
- Since these statistics are used to evaluate our hypotheses, we refer to them as **test statistics**.
- To evaluate hypotheses regarding the population mean, we use the sample mean \bar{X} as the test statistic.



Hypothesis Testing for the Population Mean

- For a statistic to be considered as a test statistic, its sampling distribution must be fully known (exactly or approximately) under the null hypothesis.
- That is, we should know the distribution of the test statistic if we assume that the null hypothesis is true.
- For the sample mean, the CLT states that the sampling distribution is approximately normal when the sample size is large.
 - The distribution is exactly normal if the variable itself is normal and the population variance is known.



Hypothesis Testing for the Population Mean

- Now consider the body temperature example, where we want to examine the null hypothesis $H_0 : \mu = 98.6$ against the alternative hypothesis $H_A : \mu < 98.6$.
- To start, suppose that $\sigma^2 = 1$ is known. (Later, we will discuss situations where σ^2 is unknown.)
- Further, suppose that we have randomly selected a sample of 25 healthy people from the population and measured their body temperature.
- Using the Central Limit Theorem, the sampling distribution of \bar{X} is approximately normal as follows:

$$\bar{X} \sim N(\mu, \sigma^2/n).$$

$$\bar{X} \sim N(\mu, 1/25).$$

Hypothesis Testing for the Population Mean

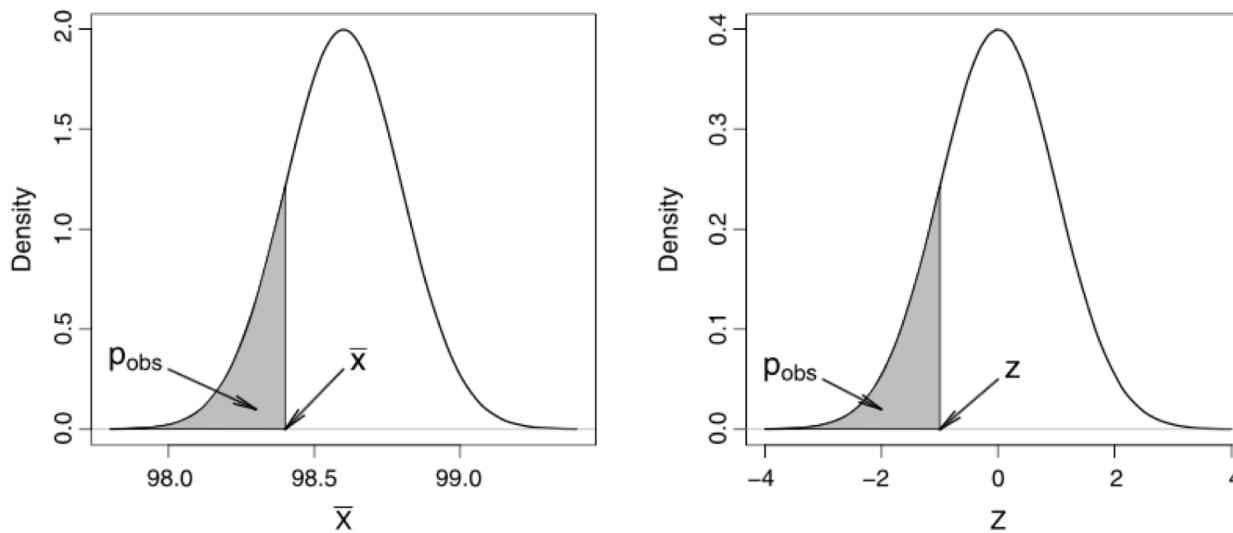
- Now, suppose that the null hypothesis is true and the population mean is $\mu = 98.6$.
- By setting μ to 98.6, the sampling distribution of \bar{X} becomes:

$$\bar{X} | H_0 \sim N(98.6, 0.04).$$

- Note that the distribution of \bar{X} is obtained conditional (hence the notation for conditional probability) on the assumption that the null hypothesis is true.
- The distribution is fully specified if we assume that H_0 is true.
- Therefore, we can use the sample mean \bar{X} as a test statistic for the population mean μ .

Hypothesis Testing for the Population Mean

- In what follows, we refer to the distribution of test statistics under the null hypothesis as the null distribution.
- For the above example, the null distributions is $N(98.6, 0.04)$.



For the normal body temperature example, we are examining the hypotheses $H_0 : \mu = 98.6$ against $H_A : \mu < 98.6$.

Left panel: The shaded area shows the lower-tail probability of the observed sample mean, $\bar{x} = 98.4$.

This is the observed significance level, p-value, which is denoted as p_{obs} .

Right panel: After standardizing, the p-value corresponds to the lower tail probability of $z = -1$ based on the standard normal distribution

z-Tests of the Population Mean

- In practice, it is more common to use the standardized version of the sample mean as our test statistic.
- For the body temperature example:
 - We standardize the test statistic
 - \bar{x} by subtracting the mean $\mu = 98.6$ (under the null) and dividing the result by the $\sqrt{0.04} = 0.2$
 - Make standard deviation $\sqrt{0.04} = 0.2$.
 - We denote the resulting random variable Z:

$$Z = \frac{\bar{X} - 98.6}{0.2}.$$

- Random variable is normally distributed (as it is the case for \bar{X}), subtracting the mean and dividing by standard deviation creates a new random variable with standard normal distribution. Therefore,

$$Z \sim N(0, 1).$$

z-Tests of the Population Mean

- The observed value of \bar{x} in the body temperature example was $\bar{x} = 98.4$.
- To find the corresponding value for the random variable Z , we standardize \bar{x} in the same way we standardized \bar{X} .
- We denote this value as z :

$$z = \frac{98.4 - 98.6}{0.2} = -1.$$

- Now, instead of finding the p-value based on the lower tail probability of $\bar{x} = 98.4$, we can find it based on the lower tail probability of $z = -1$:

$$p_{\text{obs}} = P(Z \leq -1).$$

z-Tests of the Population Mean

- The p-value obtained based on the standardized test statistic Z is exactly the same as the p-value obtained based on the original test statistic \bar{X} .
- To see this, we can start by the definition of p-value based on \bar{X} and show that it is equivalent to its definition based on Z.
- For the above example:

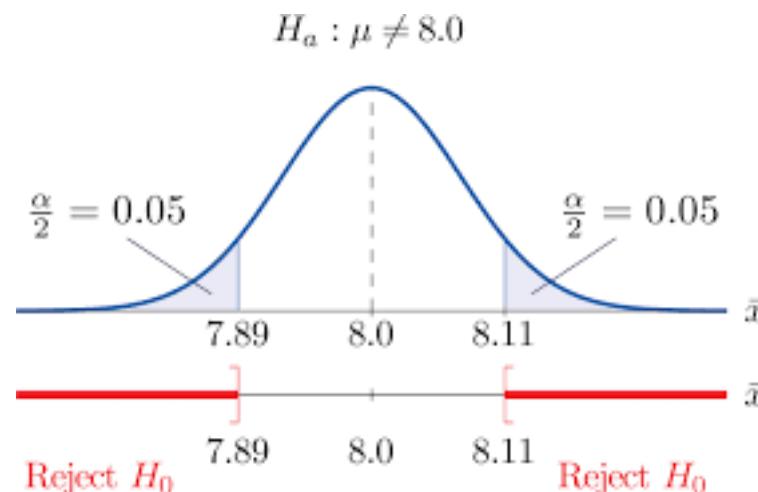
$$p_{\text{obs}} = P(\bar{X} \leq 98.4).$$

- We can subtract 98.6 from both sides of the inequality and divide the results by 0.2:

$$p_{\text{obs}} = P\left(\frac{\bar{X} - 98.6}{0.2} \leq \frac{98.4 - 98.6}{0.2}\right) = P(Z \leq -1).$$

z-Tests of the Population Mean

- We refer to the standardized value of the observed test statistic as the **z-score** and the corresponding hypothesis test of the population mean as the **z-test**, or more specifically, **single-sample z-test**.
- In a z-test, instead of comparing the observed sample mean \bar{x} to the population mean according to the null hypothesis, we compare the z-score to 0.
- Therefore, the p-value becomes the probability of seeing values as extreme or more extreme than the observed z-score under the standard normal distribution.



z-Tests of the Population Mean

- To perform the z-test in R, we can use the function *pnorm()* in order to find the p-value.
- For the body temperature example discussed before, the z-score was -1 .
- For the one-sided hypothesis of the form $H_0 : \mu < \mu_0$, we find the lower tail probability of -1 as follows:

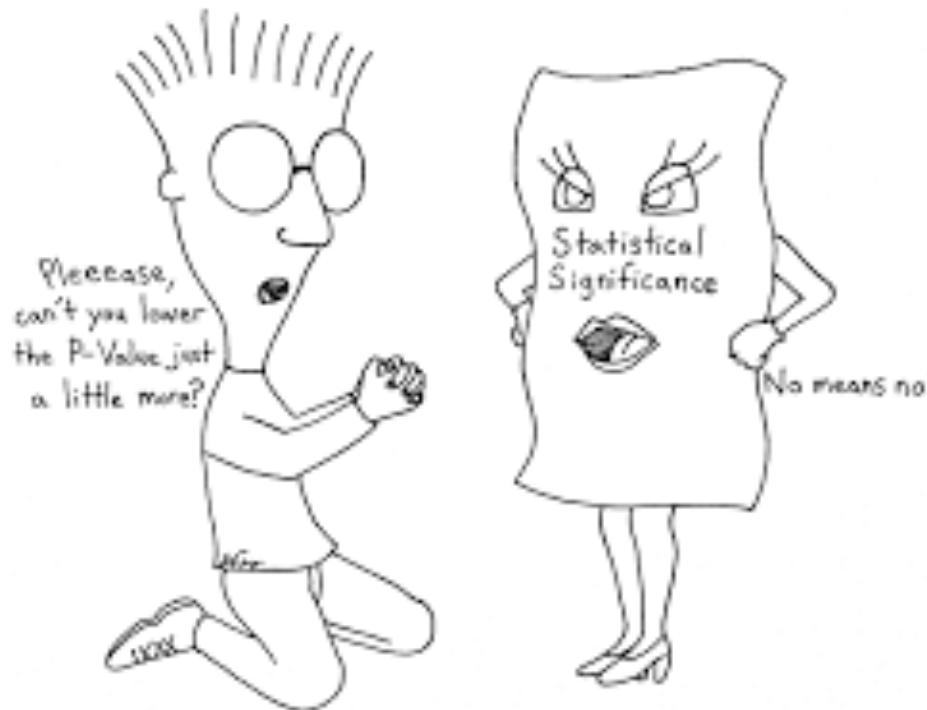
```
10 # Using function pnorm() in order to find the p-value:  
11 ````{R}  
12 pnorm(-1, mean = 0, sd = 1, lower.tail = TRUE)  
13 ````  
  
[1] 0.1586553
```

Interpretation of p-value

- The p-value is the conditional probability of extreme values (as or more extreme than what has been observed) of the test statistic assuming that the null hypothesis is true.
- When the p-value is small, say 0.01 for example, it is rare to find values as extreme as what we have observed.
- This means that the observed value of the test statistic is quite extreme if we were to believe the null hypothesis.
- As the p-value increases, it indicates that there is a good chance to find more extreme values (for the test statistic) than what has been observed.
- Then, the observed value does not seem that extreme any more.
- In this case, we think it is quite reasonable to believe that what we have observed was generated according to the null hypothesis, so we would be more reluctant to reject the null hypothesis.

Interpretation of p-value

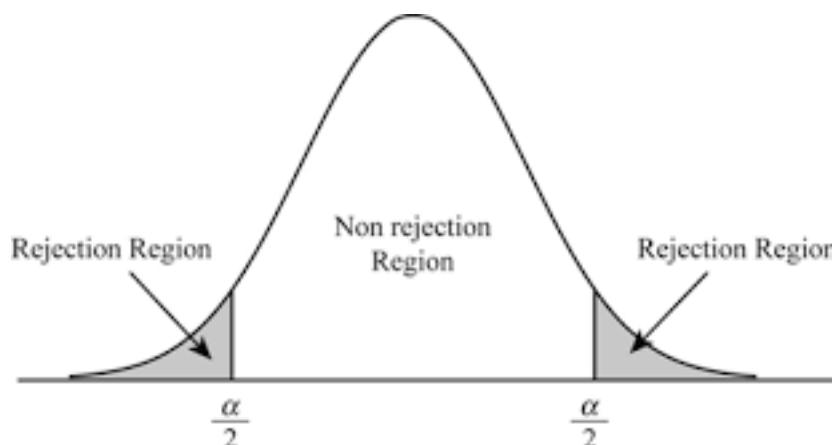
- A common mistake is to regard the p-value as the probability of the null hypothesis given the observed value of the test statistic: $P(H_0 | \bar{x})$.
- This is because intuitively it makes more sense to evaluate the null hypothesis by finding its probability given the data we have observed.
- However, this is not what the p-value provides.



<u>P-VALUE</u>	<u>INTERPRETATION</u>
0.001	HIGHLY SIGNIFICANT
0.01	
0.02	
0.03	
0.04	SIGNIFICANT
0.049	
0.050	OH CRAP. REDO CALCULATIONS.
0.051	
0.06	ON THE EDGE OF SIGNIFICANCE
0.07	
0.08	HIGHLY SUGGESTIVE, SIGNIFICANT AT THE P<0.10 LEVEL
0.09	
0.099	
≥0.1	HEY, LOOK AT THIS INTERESTING SUBGROUP ANALYSIS

Significance Level

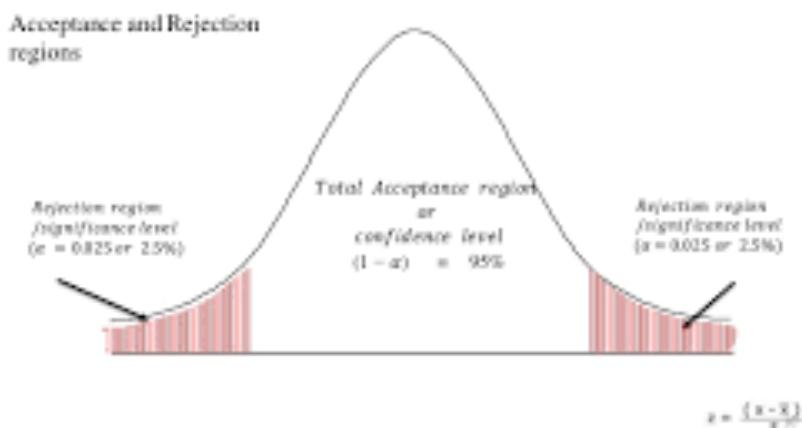
- In order to use the p-value to decide whether we should reject the null hypothesis, a convenient approach is to prespecify a cutoff for the p-value and reject the null hypothesis if pobs is below the cutoff (i.e., when the measure of agreement between the null hypothesis and observed data is less than an acceptable level).
- This cutoff is called the **significance level** or the size of the test.



Significance Level

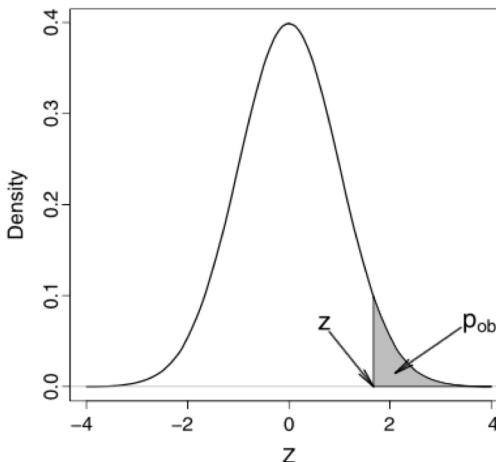
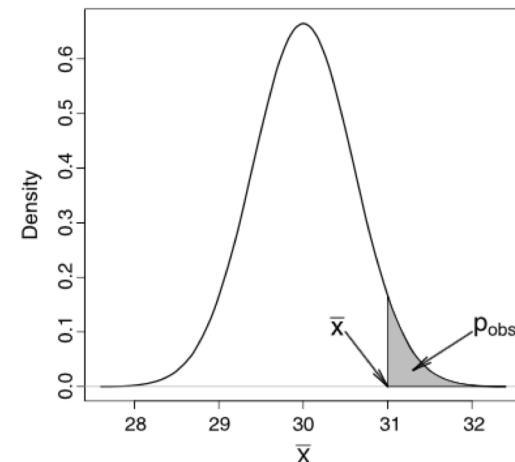
- The common significance levels are 0.01, 0.05, and 0.1.
- If p_{obs} is less than the assumed cutoff, we say that the data provides statistically significant evidence against H_0 , and we call the results statistically significant
- That is, the difference between the observed value of the test statistic (here, 98.4) and the value specified by the null hypothesis (here, 98.6) is statistically significant.

5% Significance level & 95% confidence level



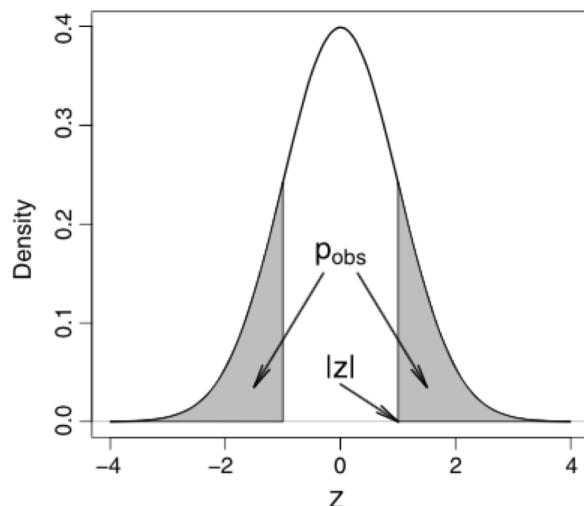
One-Sided Hypothesis Testing

- For the body temperature example, we tested the null hypothesis $H_0 : \mu = 98.6$ against the alternative $H_A : \mu < 98.6$.
- We refer to such tests as one-sided hypothesis testing, where the departure from the null is in one direction (here, in the direction of lower values than 98.6).
- In another example:
 - Suppose that we have observed that many Pima Indian women suffer from diabetes.
 - We know that obesity and diabetes are related; we might therefore hypothesize that this population is obese on average, where obesity is defined as BMI higher than 30.
 - If we denote the population mean of BMI for Pima Indian women, we can then express our hypothesis as $\mu > 30$.
 - In this case, the null hypothesis is $H_0: \mu = 30$; that is, $\mu_0 = 30$.



Two-Sided Hypothesis Testing

- For many hypothesis testing problems, we might be indifferent to the direction of departure from the null value.
- In such cases, we can express the null and alternative hypotheses as:
 - $H_0 : \mu = \mu_0$ and $H_A : \mu \neq \mu_0$, respectively.
- Then we consider both large positive values and small negative values of z-score as evidence against the null hypothesis, and our alternative hypothesis is referred to as two-sided.



Above the p-value for a two-sided hypothesis test of average normal body temperature, where $H_0 : \mu = 98.6$ and $H_A : \mu \neq 98.6$.
After standardizing, $p_{\text{obs}} = P(Z \leq -1) + P(Z \geq 1) = 2 \times 0.16 = 0.32$

Two-sided hypothesis

- For example, suppose we believe that the average normal body temperature is different from the accepted value 98.6°F, but we are not sure whether it is higher or lower than 98.6.
- Then the null hypothesis remains $H_0 : \mu = 98.6$, but the alternative hypothesis is expressed as $H_A : \mu \neq 98.6$.
- As before, we calculate the sample mean $\bar{x} = 98.4$ and standardize it to obtain the z-score, which is -1 .
- The p-value is still calculated as the probability of values as or more extreme than the observed z-score.
- However, in this case, extreme values are those whose distance from 0 is more than the distance of -1 from zero.
- These are values that are either less than -1 or greater than 1 . Therefore, to find the observed significance level, we need to add the probabilities for $Z \leq -1$ and $Z \geq 1$:

Two-sided hypothesis

- For the two-sided hypothesis, we multiply the above probability by 2.
- Similar approach is used for testing one-sided or two-sided hypothesis regarding population proportion.
- For the BMI example, z-score was 1.67.
- For the one-sided hypothesis of the form $H_0 : \mu > \mu_0$,
- We need to find the upper tail probability of 1.67 as follows:

```
17 - # For the BMI example, z-score was 1.67.  
18 - # For the one-sided hypothesis of the form  $H_0 : \mu > \mu_0$ ,  
19 - # We need to find the upper tail probability of 1.67 as follows:  
20 - ````{R}  
21 pnorm(1.67, mean = 0, sd = 1, lower.tail = FALSE)  
22 ````
```

```
[1] 0.04745968
```

- Remember to specify the option `lower.tail=FALSE` to get the upper tail probability

When Unknown variance

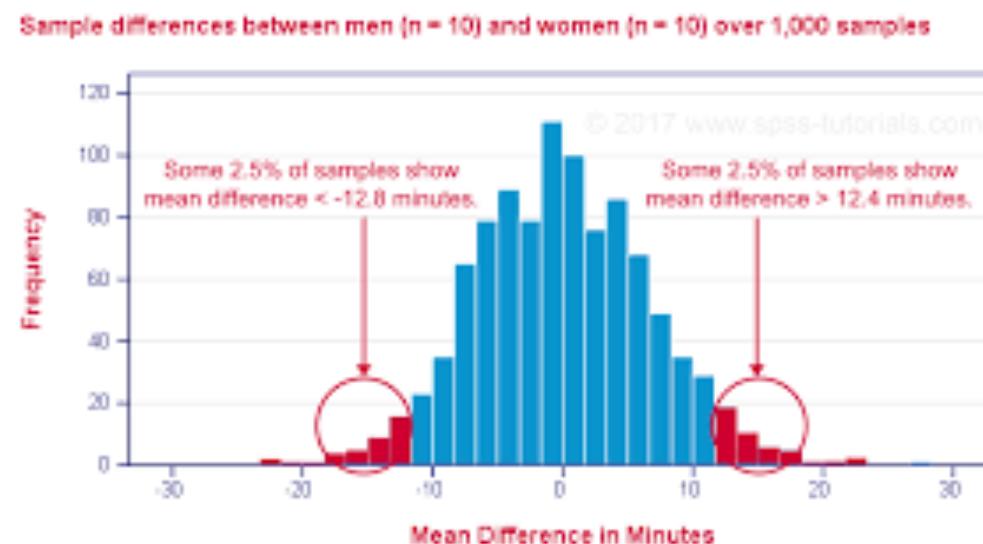
- When σ^2 is unknown and we need to use the data to estimate it separately, we use the t-test to evaluate hypotheses regarding the mean of a normal distribution.
- For the BMI example, we found t -score was $t = 5.33$. For the one-sided hypothesis of the form $H_0 : \mu > \mu_0$, we need to find the upper tail probability of 5.33 from a t distribution with $n - 1$ degrees of freedom, where $n = 200$ in this example.
- We use the pt () function:

```
24
25 # When σ² is unknown and we need to use the data to estimate it separately:
26 ````{R}
27 pt(5.33, df = 199, lower.tail = FALSE)
28 ````
```

[1] 1.324778e-07

Hypothesis Testing Using t-tests

- So far, we have assumed that the population variance σ^2 is known.
- Therefore, evaluating a hypothesis regarding the population mean did not involve estimating σ^2 .
- In reality, σ^2 is almost always unknown
- Thus, we need to estimate it from the data.
- As before, we estimate σ^2 using the sample variance S^2 .
- We would be of course uncertain about our estimate of σ^2 , and our hypothesis testing procedure should take this additional source of uncertainty into account.



Hypothesis Testing Using t-tests

- Similar to our approach for finding confidence intervals, we account for this additional source of uncertainty by using the t -distribution with $n - 1$ degrees of freedom instead of the standard normal distribution.
- The hypothesis testing procedure is then called the t-test.
- To perform a t-test , we use the following test statistic (instead of Z):

$$T = \frac{\bar{X} - \mu_0}{S/\sqrt{n}},$$

- where \bar{X} is the sample mean, n is the sample size, S is the sample standard deviation, and μ_0 is the null value. The test statistic, T , has a t -distribution with $n - 1$ degrees of freedom under the null.

Hypothesis Testing Using t-tests

- Suppose we hypothesize that the population mean of BMI among Pima Indian women is above 30: $H_A : \mu > 30$.
- The corresponding null hypothesis is $H_0 : \mu = 30$.
- The sample size is $n = 200$.
- The sample mean and standard deviation are $\bar{x} = 32.31$ and $s = 6.13$, respectively.
- The t -score is 5.33.

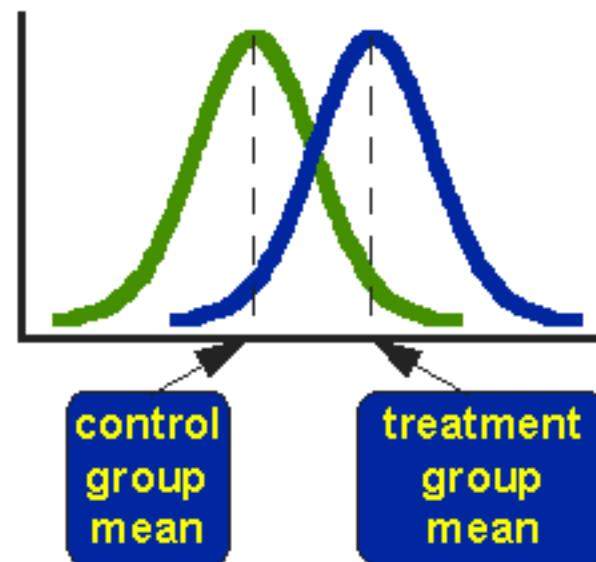
$$t = \frac{32.31 - 30}{6.13/\sqrt{200}} = 5.33.$$

- The resulting probability is 1.33×10^{-7} , which is shown as $1.33e-07$.
- This is quite small and leads us to conclude that the result is statistically significant.

Hypothesis Testing Using t-tests

Hypothesis Testing Using t-tests

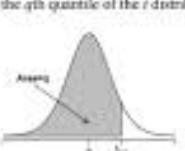
- At any reasonable significance level, there is strong evidence to reject the null hypothesis and conclude that the population mean of BMI among Pima Indian women is in fact greater than 30.
- Therefore, on average, the population has overweight.



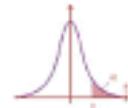
Hypothesis Testing Using t-tests

- To assess the null hypothesis $H_0 : \mu = \mu_0$ using the t -test, we first calculate the t -score based on the observed sample mean \bar{x} and sample standard deviation.
- Then we calculate the corresponding p-value as follows:
 - If $H_A: \mu < \mu_0$, $p_{obs} = P(T \leq t)$, if $H_A: \mu > \mu_0$, $p_{obs} = P(T \geq t)$
 - If $H_A: \mu \neq \mu_0$, $p_{obs} = 2 \times P(T \geq |t|)$
- Where T has a t-distribution with $n - 1$ degrees of freedom, and t is our observed t-score.
- This is known as the single-sample t-test.

Quartiles of the t Distribution
The table gives the value of $t_{n,q}$ - the qth quartile of the t distribution for n degrees of freedom.



$q = 0.6$	0.75	0.9	0.95	0.975	0.99	0.995	0.9975	0.999	0.9995	
1	0.5249	1.0000	3.078	6.314	12.706	31.821	63.857	127.321	318.309	636.633
2	0.2857	0.8385	1.886	2.920	4.303	6.965	9.925	14.089	22.327	31.599
3	0.2765	0.7445	1.838	2.353	3.182	4.543	5.841	7.453	10.715	12.924
4	0.2707	0.7407	1.533	2.132	2.776	3.747	4.604	5.598	7.175	8.610
5	0.2672	0.7267	1.426	2.015	2.571	3.365	4.032	4.771	5.898	6.868
6	0.2648	0.7176	1.480	1.943	2.487	3.143	3.707	4.317	5.208	5.958
7	0.2632	0.7111	1.415	1.895	2.365	2.958	3.499	4.023	4.785	5.408
8	0.2619	0.7064	1.337	1.666	2.336	2.896	3.355	3.813	4.501	5.041
9	0.2610	0.7027	1.383	1.833	2.262	2.821	3.250	3.699	4.297	4.781
10	0.2602	0.6998	1.372	1.812	2.228	2.764	3.168	3.581	4.144	4.587
11	0.2596	0.6974	1.383	1.796	2.201	2.718	3.108	3.487	4.025	4.457
12	0.2590	0.6955	1.356	1.782	2.179	2.683	3.055	3.423	3.930	4.318
13	0.2586	0.6939	1.359	1.789	2.189	2.699	3.063	3.439	3.956	4.338
14	0.2582	0.6926	1.345	1.763	2.145	2.624	2.977	3.326	3.787	4.140



	One-Tailed	10%	5%	2.5%	1%	0.5%	0.25%	0.1%	0.05%
	Two-Tailed	20%	10%	5%	2%	1%	0.5%	0.2%	0.1%
1	3.078	6.314	12.71	31.82	63.86	127.3	318.3	636.6	
2	1.886	2.920	4.203	6.965	9.925	14.09	22.33	31.60	
3	1.638	2.353	3.182	4.543	5.841	7.453	10.21	12.90	
4	1.533	2.132	2.776	3.747	4.604	5.598	7.175	8.610	
5	1.478	2.015	2.571	3.365	4.032	4.771	5.898	6.868	
6	1.440	1.943	2.447	3.143	3.707	4.317	5.208	5.958	
7	1.415	1.895	2.336	2.958	3.499	4.023	4.785	5.408	
8	1.397	1.860	2.306	2.896	3.355	3.813	4.501	5.041	
9	1.383	1.833	2.262	2.821	3.250	3.699	4.297	4.781	
10	1.372	1.812	2.228	2.764	3.168	3.581	4.144	4.587	

T-test
Used to compare two samples to determine if they came from the same population.



Are both of them humans?



Hypothesis Testing Using t-tests

- Alternatively, instead of calculating the t-score and finding the appropriate tail probabilities to obtain the p-value, we can use the function `t.test()`.
- For the BMI example, we use this function as follows:

```
32 # Alternatively, instead of calculating the t-score and finding the appropriate tail probabilities
33 # For the BMI example, we use this function as follows:
34
35 ````{R}
36 # install.packages("MASS")
37 library(MASS)
38
39 t.test(x = Pima.tr$bmi, mu = 30, alternative = "two.sided")
40 ````
```

One Sample t-test

```
data: Pima.tr$bmi
t = 5.3291, df = 199, p-value = 2.661e-07
alternative hypothesis: true mean is not equal to 30
95 percent confidence interval:
31.45521 33.16479
sample estimates:
mean of x
32.31
```

Hypothesis Testing Using t-tests

- Here, the argument x is a (nonempty) numeric vector of data values, and μ is the population mean according to the null hypothesis.
- For one-sided t-tests, set the argument alternative to either “greater”, or “less”.
- Notice that the output provides the t-score (t), the degrees of freedom (df), and the p-value.
- Additionally, it provides the sample mean $\bar{x} = 32.31$ and the 95% confidence interval for the population mean, [31.46, 33.16].
- We can estimate the interval at other confidence levels (instead of 0.95) by using the option `conf.level`:

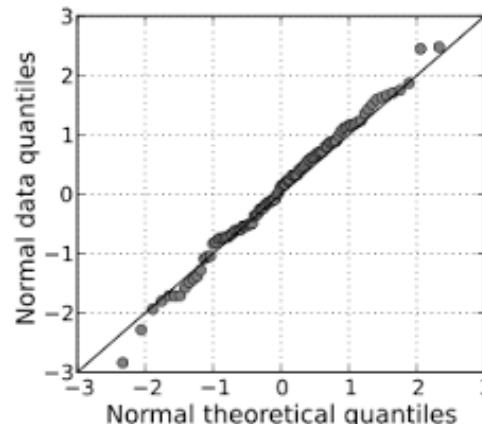
```
44 # Estimating the interval at other confidence levels (instead of 0.95) by using the option conf.level:  
45 ````{R}  
46 t.test(x = Pima.tr$bmi, mu = 30, conf.level = 0.9)  
47 ````
```

```
One Sample t-test  
  
data: Pima.tr$bmi  
t = 5.3291, df = 199, p-value = 2.661e-07  
alternative hypothesis: true mean is not equal to 30  
90 percent confidence interval:  
 31.59367 33.02633  
sample estimates:  
mean of x  
 32.31
```

Note that only the confidence interval estimate changes. The parts that are related to hypothesis testing remain as before.

Shapiro–Wilk test of normality

- In a previous class we create Q–Q plots to visually assess the appropriateness of normality assumption for random variables.
- The appropriateness of the normality assumption can be evaluated formally using a testing procedure such as the Shapiro–Wilk test of normality.
- More specifically, this test evaluates the null hypothesis that the distribution of the random variable is normal.
- As usual, we then either reject this hypothesis and conclude that the normality assumption is not appropriate, or fail to reject it and conclude that there is no strong evidence of deviation from normality.



Shapiro–Wilk test of normality

- Finally, to perform the Shapiro–Wilk test of normality in R, we use the function `shapiro.test()`.
- For example, if we assume that BMI among Pima Indian women is normally distributed, we can evaluate our assumption as follows:

```
48
49 # Shapiro-Wilk test of normality
50 ````{R}
51 shapiro.test(x = Pima.tr$bmi)
52 ````
```

Shapiro-Wilk normality test

data: Pima.tr\$bmi
W = 0.99104, p-value = 0.2523

In this case, the p-value is large, so we do not reject the null hypothesis, which states the distribution is normal, at commonly used significance levels. In other words, the test confirms our normality assumption.

Rmarkdown

```
~/Documents/R_working_directory/Rmarkdown_TRGN_599_Week_6_Lecture_1.html
```

Rmarkdown_TRGN_599_Week_6_Lecture_1

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Hypothesis Testing

Using function pnorm() in order to find the p-value:

```
pnorm(-1, mean = 0, sd = 1, lower.tail = TRUE)  
## [1] 0.1586553
```

For the BMI example, z-score was 1.67.

For the one-sided hypothesis of the form $H_0 : \mu > \mu_0$,

We need to find the upper tail probability of 1.67 as follows:

```
pnorm(1.67, mean = 0, sd = 1, lower.tail = FALSE)  
## [1] 0.04745968
```

When σ^2 is unknown and we need to use the data to estimate it separately:

```
pt(5.33, df = 199, lower.tail = FALSE)  
## [1] 1.324778e-07
```

Alternatively, instead of calculating the t-score and finding the appropriate tail probabilities to obtain the p-value, we can use the function t.test().

For the BMI example, we use this function as follows:

```
# install.packages("MASS")  
library(MASS)  
  
t.test(x = Pima.tr$bmi, mu = 30, alternative = "two.sided")  
  
##  
## One Sample t-test  
##  
## data: Pima.tr$bmi  
## t = 5.3291, df = 199, p-value = 2.661e-07  
## alternative hypothesis: true mean is not equal to 30  
## 95 percent confidence interval:  
## 31.45521 33.16479  
## sample estimates:  
## mean of x  
## 32.31
```