



# Statistical Inference

**Module 8:** T Confidence Intervals

**Module 9:** Hypothesis Testing

**Module 10:** P values

**Komlan Atitey, PhD**

Biostatistics and Computational Biology Branch  
(BCBB)

# Outline

## ➤ Confidence interval

- ☐ Constructing confidence interval for  $\mu$  with  $z$  quantiles
- ☐ Constructing confidence interval for  $\mu$  with  $t$  quantiles
- ☐ Computing the Confidence Interval for a Difference Between Two Means

## ➤ Hypothesis testing

- ☐ Errors in Hypothesis Testing
- ☐ level of significance
- ☐ Testing means of a normal population with known  $\sigma$
- ☐ Testing means of a small sample coming from a normal

## ➤ P-value

- ☐ P-value interpretation
- ☐ Calculate p-value
- ☐ Calculating a single p-value from a normal distribution
- ☐ Calculating a single p-value from a  $t$  distribution

## ➤ Quiz

# Module 8: Confidence Intervals

- A confidence interval, in statistics, refers to the probability that a population parameter will fall between a set of values for a certain proportion of times. Analysts often use confidence intervals that contain either 95% or 99% of expected observations.
- If several random samples were collected, the mean for that variable would be slightly different from one sample to another. Therefore, when researchers estimate population means, instead of providing only one value, they specify a range of values (or an interval) within which this mean is likely to be located.
- The confidence interval is obtained by adding and subtracting the margin of error from the sample mean. This result is the upper limit and the lower limit of the confidence interval.

## ❑ *Confidence interval (Ci)*

$$Ci = \text{Sample mean} \pm \text{Margin of error}$$

## ❑ *Margin of error (Me)*

- ✓ The margin of error is the range of values above and below the sample statistic in a confidence interval.
- ✓ It tells you how many percentage points your results will differ from the real population value.

$$\text{Margin of error} = \text{Critical value} \times \text{Standard deviation of the statistic}$$

$$\text{Margin of error} = \text{Critical value} \times \text{Standard error of the statistic}$$

# Module 8: Confidence Intervals

## ➤ Standard Normal distribution

- ❑ Consider  $X_1, \dots, X_n$  a sequence of *i.i.d.* random variables of size  $n$  with mean  $E(X) = \mu$ , and variance  $Var(X) = \sigma^2$
- ❑ The **standard Normal distribution** has mean  $\mu = 0$  and variance  $\sigma^2 = 1$ . A random variable with this distribution is usually denoted by  $Z$ . That is,

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

## ➤ Standardized sample mean

- ❑ Consider a standardization of the mean  $\mu = \bar{X}$ .
- ❑ We subtract off the mean of  $\bar{X}$ , and divide through by the standard deviation of  $\bar{X}$ , which is  $\frac{\sigma}{\sqrt{n}}$ , to obtain a standardized version of the sample mean:

$$\frac{\bar{X} - \mu}{\sigma/\sqrt{n}}$$

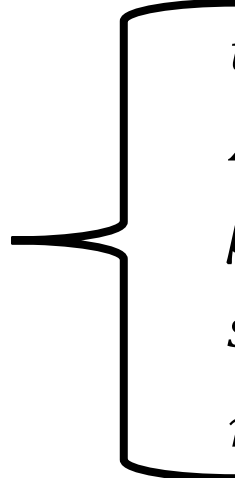
- ✓ Via simulation the application of the central limit theorem, it has been demonstrated that:

$$\frac{\bar{X} - \mu}{\sigma/\sqrt{n}} \sim N(0,1)$$

# Module 8: Confidence Intervals

## ➤ ***t*-distribution**

The *t*-distribution describes the standardized distances of sample means to the population mean when the population standard deviation is not known, and the observations come from a normally distributed population.

$$t = \frac{\bar{X} - \mu}{s/\sqrt{n}}$$


- $t$  = Student's *t*-distribution
- $\bar{X}$  = sample mean
- $\mu$  = population mean
- $s$  = sample standard deviation
- $n$  = sample size

## ➤ **Key difference between the *t*- and *z*-distributions**

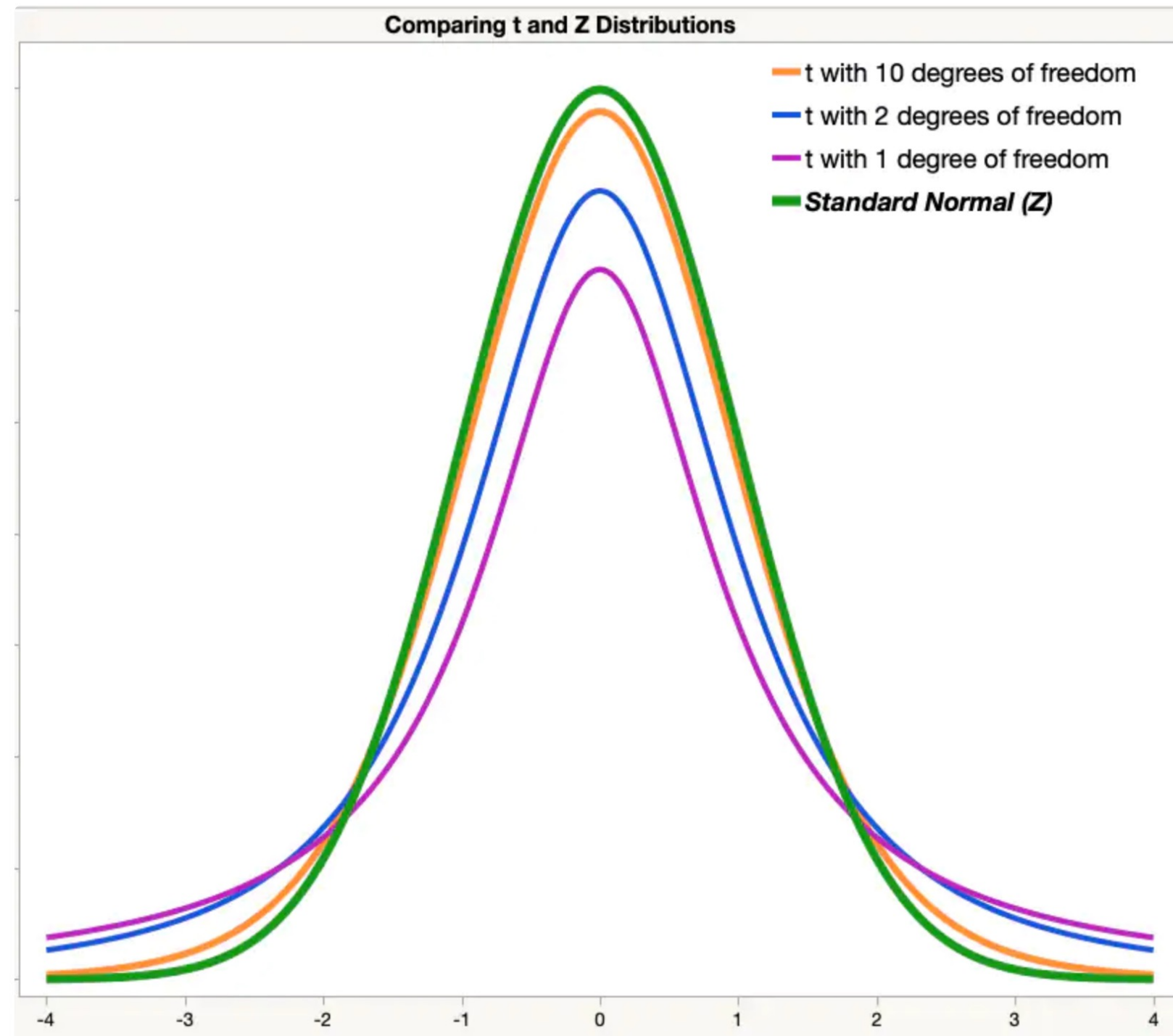
- ☐ The standard normal or *z*-distribution assumes that you know the population standard deviation.
- ☐ The *t*-distribution is based on the sample standard deviation.
- ☐ The *t*-distribution is most useful for small sample sizes, when the population standard deviation is not known, or both.

- ☐ The *t*-distribution is defined by the ***degrees of freedom***  $n - 1$   $t_{n-1} \sim \frac{\bar{X} - \mu}{s/\sqrt{n}}$

# Module 8: Confidence Intervals

## ➤ *t*-Distribution vs. normal distribution

- ☐ All of the distributions have a smooth shape.
- ☐ All are symmetric.
- ☐ All have a mean of zero.
- ☐ The shape of the *t*-distribution depends on the degrees of freedom.
- ☐ The curves with more degrees of freedom are taller and have thinner tails.
- ☐ All three *t*-distributions have “heavier tails” than the *z*-distribution.



# Module 8: Confidence Intervals

## ➤ Constructing confidence interval for $\mu$ with $z$ quantiles

A *z interval* is a specific type of confidence interval which tells you a range where you can expect a particular mean or proportion to fall. It can be calculated from a known standard deviation.

□ Assume  $X_1, \dots, X_n$  are *i. i. d.*  $\sim N(\mu, \sigma^2)$  and  $\sigma$  is known. Then we have an exact distributional result for a

standardized sample mean:  $\frac{\bar{X} - \mu}{\sigma/\sqrt{n}} \sim N(0,1)$

□ Let denote  $z_{1-\frac{\alpha}{2}}$  to be  $\left(1 - \frac{\alpha}{2}\right)$  *th* quantile of standard normal distribution  $N(0,1)$ .

The *q**th* quantile of a data set is defined as that value where a *q* fraction of the data is below that value and  $(1 - q)$  fraction of the data is above that value.

□ Due to  $N(0,1)$  is symmetric around 0, we have:  $z_{\frac{\alpha}{2}} = -z_{1-\frac{\alpha}{2}}$

We can then write:  $P\left(-z_{1-\frac{\alpha}{2}} \leq \frac{\bar{X} - \mu}{\sigma/\sqrt{n}} \leq z_{1-\frac{\alpha}{2}}\right) = P\left(\bar{X} - z_{1-\frac{\alpha}{2}} \frac{\sigma}{\sqrt{n}} \leq \mu \leq \bar{X} + z_{1-\frac{\alpha}{2}} \frac{\sigma}{\sqrt{n}}\right) = 1 - \alpha$

$\left[\bar{X} - z_{1-\frac{\alpha}{2}} \frac{\sigma}{\sqrt{n}}, \bar{X} + z_{1-\frac{\alpha}{2}} \frac{\sigma}{\sqrt{n}}\right]$  is a  $(1 - \alpha)$  confidence interval for a mean parameter  $\mu$

✓  $\alpha$  is the significance level used to compute the confidence interval

✓  $1 - \alpha$  is confidence coefficient

# Module 8: Confidence Intervals

## Example: Z confidence interval for a mean

Let's calculate 88 percent confidence interval for a data which is: 3,7,11,0,7,0,4,5,6,2 with a known standard deviation  $\sigma=2$ .

Since our confidence coefficient is 0.88 (corresponding to an 88 percent confidence interval) we have:

$$1 - \alpha = 0.88 \text{ and } \alpha = 0.12$$

The commands to find the confidence interval in R are the following:

```
> alpha <- 0.12
> s <- 2
> ### read in the data
> x <- c(3, 7, 11, 0, 7, 0, 4, 5, 6, 2) # data
> n <- length(x) # data size
> ### make a standard normal r.v.
> Z <- Normal(0, 1)
> ### left
> left <- mean(x) - quantile(Z, 1 - alpha/2) * s/sqrt(n)
> ### right
> right <- mean(x) + quantile(Z, 1 - alpha/2) * s/sqrt(n)
> ci <- c(left, right)
> ci
[1] 3.516675 5.483325
```

Use:  
library(distributions3)



# Module 8: Confidence Intervals

## ➤ Constructing confidence interval for $\mu$ with $t$ quantiles

$$t_{n-1} \sim \frac{\bar{X} - \mu}{s/\sqrt{n}} \quad \left\{ \begin{array}{l} t = \text{Student's } t\text{-distribution} \\ \bar{X} = \text{sample mean} \\ \mu = \text{population mean} \\ s = \text{sample standard deviation} \\ n = \text{sample size} \end{array} \right.$$

□ Let denote  $t_{n-1, 1-\frac{\alpha}{2}}$  to be a  $(n-1, 1-\frac{\alpha}{2})$ th quantile of  $t$ -distribution with  $n-1$  degrees of freedom.

The  $q$ th quantile of a data set is defined as that value where a  $q$  fraction of the data is below that value and  $(1-q)$  fraction of the data is above that value.

□ Due to  $t$  is symmetric around 0, we have

$$P\left(-t_{n-1, 1-\frac{\alpha}{2}} \leq \frac{\bar{X} - \mu}{s/\sqrt{n}} \leq t_{n-1, 1-\frac{\alpha}{2}}\right) = P\left(\bar{X} - t_{n-1, 1-\frac{\alpha}{2}} \frac{s}{\sqrt{n}} \leq \mu \leq \bar{X} + t_{n-1, 1-\frac{\alpha}{2}} \frac{s}{\sqrt{n}}\right) = 1 - \alpha$$

$\left[\bar{X} - t_{n-1, 1-\frac{\alpha}{2}} \frac{s}{\sqrt{n}}, \bar{X} + t_{n-1, 1-\frac{\alpha}{2}} \frac{s}{\sqrt{n}}\right]$  is a  $(1-\alpha)$  confidence interval for a mean parameter  $\mu$

# Module 8: Confidence Intervals

## Example: T confidence interval for a mean

Here, we will calculate an 88 percent confidence interval for the mean of a single sample. We'll use the same data we use for z-test, which was: 3,7,11,0,7,0,4,5,6,2

Since our confidence coefficient is 0.88 (corresponding to an 88 percent confidence interval) we have:

$$1 - \alpha = 0.88 \text{ and } \alpha = 0.12$$

The commands to find the confidence interval in R are the following:

```
> alpha <- 0.12
> s <- 2
> ### read in the data
> x <- c(3, 7, 11, 0, 7, 0, 4, 5, 6, 2)
> n <- length(x)
> ### compute the degree of freedom
> df <- n-1
> ### make T_9 random variable
> T_9 <- StudentsT(df = df)
> ### left
> left <- mean(x) - quantile(T_9, 1 - alpha/s) * sd(x) / sqrt(n)
> ### right
> right <- mean(x) + quantile(T_9, 1 - alpha/s) * sd(x) / sqrt(n)
> ### compute ci
> ci <- c(left, right)
> ci
[1] 2.631598 6.368402
```

# Module 8: Confidence Intervals

## ➤ Computing the Confidence Interval for a Difference Between Two Means

- ❑ The confidence interval will be computed using either the  $z$  or  $t$  distribution for the selected confidence level and the standard error of the point estimate.
- ❑ The use of  $z$  or  $t$  again depends on whether the sample sizes are large ( **$n_1 \geq 30$  and  $n_2 \geq 30$** ) or small.
- ❑ Compute the degree of freedom ( $df$ )

$$df = n_1 + n_2 - 2$$

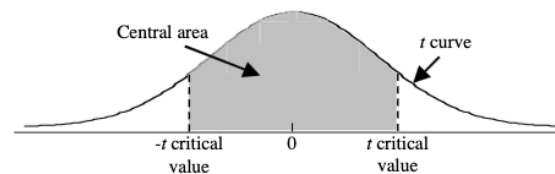
- ❑ Use  $z$ -table or  $t$ -table to find the corresponding critical values  $z_{cv}$ , or  $t_{cv}$  associated to the confidence level
  - ✓ If the sample sizes are larger, that is both  $n_1$  and  $n_2$  are greater than 30, then one uses the  $z$ -table.

$$Ci = (\bar{x}_1 - \bar{x}_2) \mp z_{cv} \sqrt{\left(\frac{s_1^2}{n_1}\right) + \left(\frac{s_2^2}{n_2}\right)} \quad \left\{ \begin{array}{l} \bar{x}_1: \text{Mean or average of the first sample} \\ \bar{x}_2: \text{Mean or average of the second sample} \\ s_1^2: \text{Variance of the first sample} \\ s_2^2: \text{Variance of the second sample} \end{array} \right.$$

- ✓ If either sample size is less than 30, then the  $t$ -table is used.

$$Ci = (\bar{x}_1 - \bar{x}_2) \mp t_{cv} \sqrt{\left(\frac{s_1^2}{n_1}\right) + \left(\frac{s_2^2}{n_2}\right)}$$

# *t critical values*



Confidence area captured:		0.90	0.95	0.98	0.99
Confidence level:		90%	95%	98%	99%
Degrees of Freedom	1	6.31	12.71	31.82	63.66
	2	2.92	4.30	6.97	9.93
	3	2.35	3.18	4.54	5.84
	4	2.13	2.78	3.75	4.60
	5	2.02	2.57	3.37	4.03
	6	1.94	2.45	3.14	3.71
	7	1.90	2.37	3.00	3.50
	8	1.86	2.31	2.90	3.36
	9	1.83	2.26	2.82	3.25
	10	1.81	2.23	2.76	3.17
	11	1.80	2.20	2.72	3.11
	12	1.78	2.18	2.68	3.06
	13	1.77	2.16	2.65	3.01
	14	1.76	2.15	2.62	2.98
	15	1.75	2.13	2.60	2.95
	16	1.75	2.12	2.58	2.92
	17	1.74	2.11	2.57	2.90
	18	1.73	2.10	2.55	2.88
	19	1.73	2.09	2.54	2.86
	20	1.73	2.09	2.53	2.85
	21	1.72	2.08	2.52	2.83
	22	1.72	2.07	2.51	2.82
	23	1.71	2.07	2.50	2.81
	24	1.71	2.06	2.49	2.80
	25	1.71	2.06	2.49	2.79
	26	1.71	2.06	2.48	2.78
	27	1.70	2.05	2.47	2.77
	28	1.70	2.05	2.47	2.76
	29	1.70	2.05	2.46	2.76
	30	1.70	2.04	2.46	2.75
	40	1.68	2.02	2.42	2.70
	60	1.67	2.00	2.39	2.66
	70	1.67	1.99	2.38	2.65
	80	1.66	1.99	2.37	2.64
	90	1.66	1.99	2.37	2.63
	100	1.66	1.98	2.36	2.63
	1000	1.65	1.96	2.33	2.58
z critical values	$\infty$	1.645	1.96	2.33	2.58
$\alpha$ for 2-tailed tests		0.10	0.05	0.02	0.01
$\alpha$ for 1-tailed tests		0.05	0.025	0.01	0.005

# Quiz 4

In a study of emergency room waiting times, investigators consider a new and the standard triage system. To test the systems, administrators selected 20 nights and randomly assigned the new triage system to be used on 10 nights. They calculated the nightly median waiting time (MWT) to see a physician. The average MWT for the new system was 3 hours with a variance of 0.60 while the average MWT for the old system was 5 hours with a variance of 0.68. Consider the 95% confidence interval estimate for the differences of the mean MWT associated with the new system. Assume a constant variance. What is the interval ? Subtract in this order (New System - Old System).

- [1.25,2.75]
- [-2.70,-1.29]
- [-2.75,-1.25]
- [1.29,2.70]

## Response 4

```
> mu.bar.new <- 3
> var.new <- 0.60
> mu.bar.old <- 5
> var.old <- 0.68
> n.new <- 10
> n.old <- 10
> ### degree of freedom
> df <- (n.new -1) + (n.old -1)
> df
[1] 18
> ### confidence interval
> tcv <- 2.101
> error <- tcv*sqrt((var.new/n.new) + (var.old/n.old))
> left <- (mu.bar.new-mu.bar.old) - error
> left
[1] -2.751677
> right <- (mu.bar.new-mu.bar.old) + error
> right
[1] -1.248323
```

# Module 9: Hypothesis Testing

A **statistical hypothesis test** is a method of statistical inference used to decide whether the data at hand sufficiently support a particular hypothesis. It allows us to make probabilistic statements about population parameters.

## ➤ Components of a Hypothesis Test

1. Formulate the hypothesis to be tested.
2. Determine the appropriate test statistic and calculate it using the sample data.
3. Comparison of test statistic to critical region to draw initial conclusions.
4. Calculation of p value.
5. Conclusion, written in terms of the original problem.

# Module 9: Hypothesis Testing

## ➤ Null vs Alternative Hypotheses

In any hypothesis testing problem, there are always two competing hypotheses under consideration:

- ❑ The Null hypothesis ( $H_o$ )
- ❑ The alternative hypothesis ( $H_a$ )
  - ✓ A null hypothesis determines there is no difference between two groups or conditions, while the alternative hypothesis determines that there is a difference.
  - ✓ The objective of hypothesis testing is to decide, based on sample information, if the alternative hypotheses is actually supported by the data.
  - ✓ If the sample does not strongly contradict  $H_o$ , we will continue to believe in the plausibility of the null hypothesis.
- ❑ The two possible conclusions:
  1. Reject  $H_o$
  2. Fail to reject  $H_o$

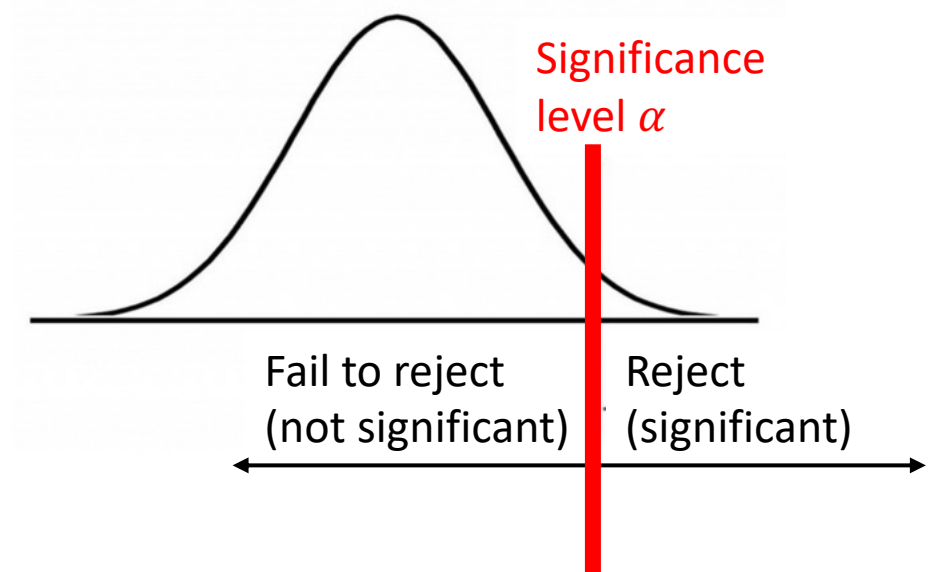
# Module 9: Hypothesis Testing

## ➤ Errors in Hypothesis Testing

- ❑ **Type I error** is when the null hypothesis is rejected, but it is true: ***False positive test***
- ❑ **Type II error** is not rejecting  $H_0$  when  $H_0$  is false: ***False negative test***

## ➤ level of significance

- ❑ The level of significance is the criteria or threshold value based on which one can reject the null hypothesis or fail to reject the null hypothesis.
- ❑ The level of significance determines whether the outcome of hypothesis testing is statistically significant or otherwise. The significance level is also called as **alpha level**.





# Module 9: Hypothesis Testing

## ➤ Testing means of a normal population with known $\sigma$

❑ Null hypothesis:  $H_o: \mu = \mu_o$

❑ Test statistic value:  $z = \frac{\bar{X} - \mu_o}{\sigma/\sqrt{n}}$

❑ Alternative hypothesis:  $H_a$

**Alternative Hypothesis:  $H_a$**

$$\mu > \mu_o$$

$$\mu < \mu_o$$

$$\mu \neq \mu_o$$

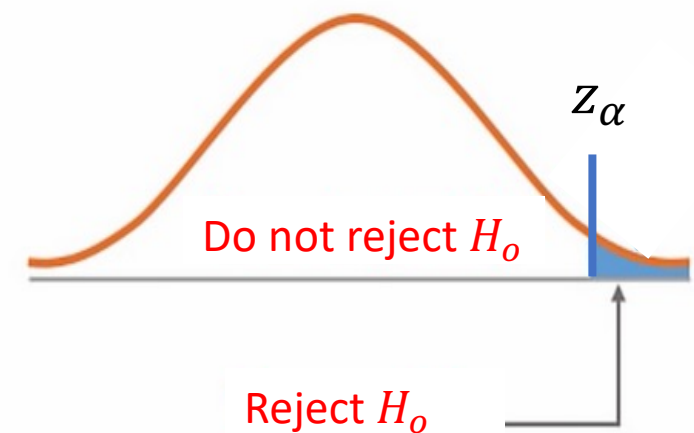
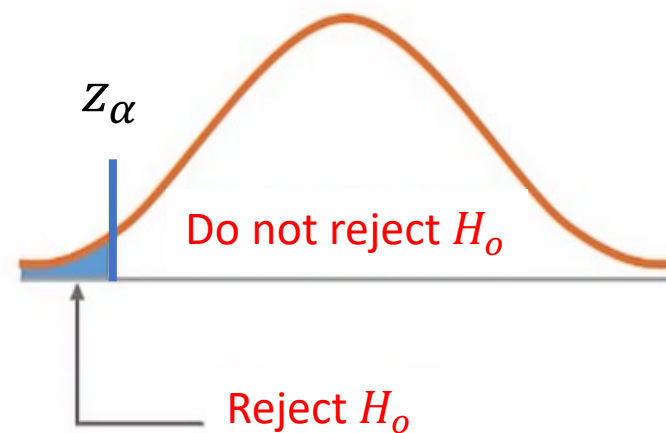
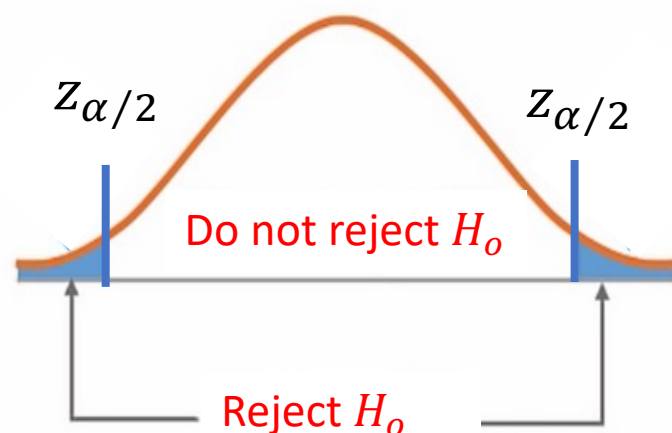
❑ Critical region

**Rejection Region for Level  $\alpha$  Test**

$z \geq z_\alpha$  (right-tailed test)

$z \leq -z_\alpha$  (left-tailed test)

either  $z \geq z_{\alpha/2}$  or  $z \leq -z_{\alpha/2}$  (two-tailed test)



# Module 9: Hypothesis Testing

## Problem

Suppose the food label on a cookie bag states that there is at most 2 grams of saturated fat in a single cookie. In a sample of 35 cookies, it is found that the mean amount of saturated fat per cookie is 2.1 grams. Assume that the population standard deviation is 0.25 grams. At .05 significance level, can we reject the claim on food label?

## Solution

```
> ### The null hypothesis is that  $\mu \leq 2$ . We begin with computing the test statistic.  
> xbar <- 2.1          # sample mean  
> mu0 <- 2            # hypothesized value  
> sigma <- 0.25        # population standard deviation  
> n <- 35              # sample size  
> z <- (xbar-mu0)/(sigma/sqrt(n))  
> z                    # test statistic  
[1] 2.366432  
> ### We then compute the critical value at .05 significance level  
> alpha <- .05  
> z.alpha <- qnorm(1-alpha) # critical value  
> z.alpha  
[1] 1.644854
```

## Answer

The test statistic 2.3664 is greater than the critical value of 1.6449. Hence, at .05 significance level, we reject the claim that there is at most 2 grams of saturated fat in a cookie.

# Module 9: Hypothesis Testing

## ➤ Testing means of a small sample coming from a normal

❑ Null hypothesis:  $H_o: \mu = \mu_o$

❑ Test statistic value:  $t = \frac{\bar{x} - \mu_o}{s/\sqrt{n}}$

❑ Alternative hypothesis:  $H_a$

### Alternative Hypothesis: $H_a$

$$\mu > \mu_o$$

$$\mu < \mu_o$$

$$\mu \neq \mu_o$$

### Rejection Region for Level $\alpha$ Test

$$t \geq t_{\alpha, n-1} \text{ (upper-tailed test)}$$

$$t \leq -t_{\alpha, n-1} \text{ (lower-tailed test)}$$

$$\text{either } t \geq z_{\alpha/2, n-1} \text{ or } t \leq -z_{\alpha/2, n-1} \text{ (two-tailed test)}$$

# Module 9: Hypothesis Testing

## Problem

Suppose the manufacturer claims that the mean lifetime of a light bulb is more than 10,000 hours. In a sample of 30 light bulbs, it was found that they only last 9,900 hours on average. Assume the sample standard deviation is 125 hours. At .05 significance level, can we reject the claim by the manufacturer?

## Solution

```
> ### The null hypothesis is that  $\mu \geq 10000$ . We begin with computing the test statistic.  
> xbar <- 9900           # sample mean  
> mu0 <- 10000          # hypothesized value  
> s <- 125              # sample standard deviation  
> n <- 30               # sample size  
> t <- (xbar-mu0)/(s/sqrt(n))  
> t                     # test statistic  
[1] -4.38178  
> ### We then compute the critical value at .05 significance level.  
> alpha <- .05  
> t.alpha <- qt(1-alpha, df=n-1)  
> -t.alpha              # critical value  
[1] -1.699127
```

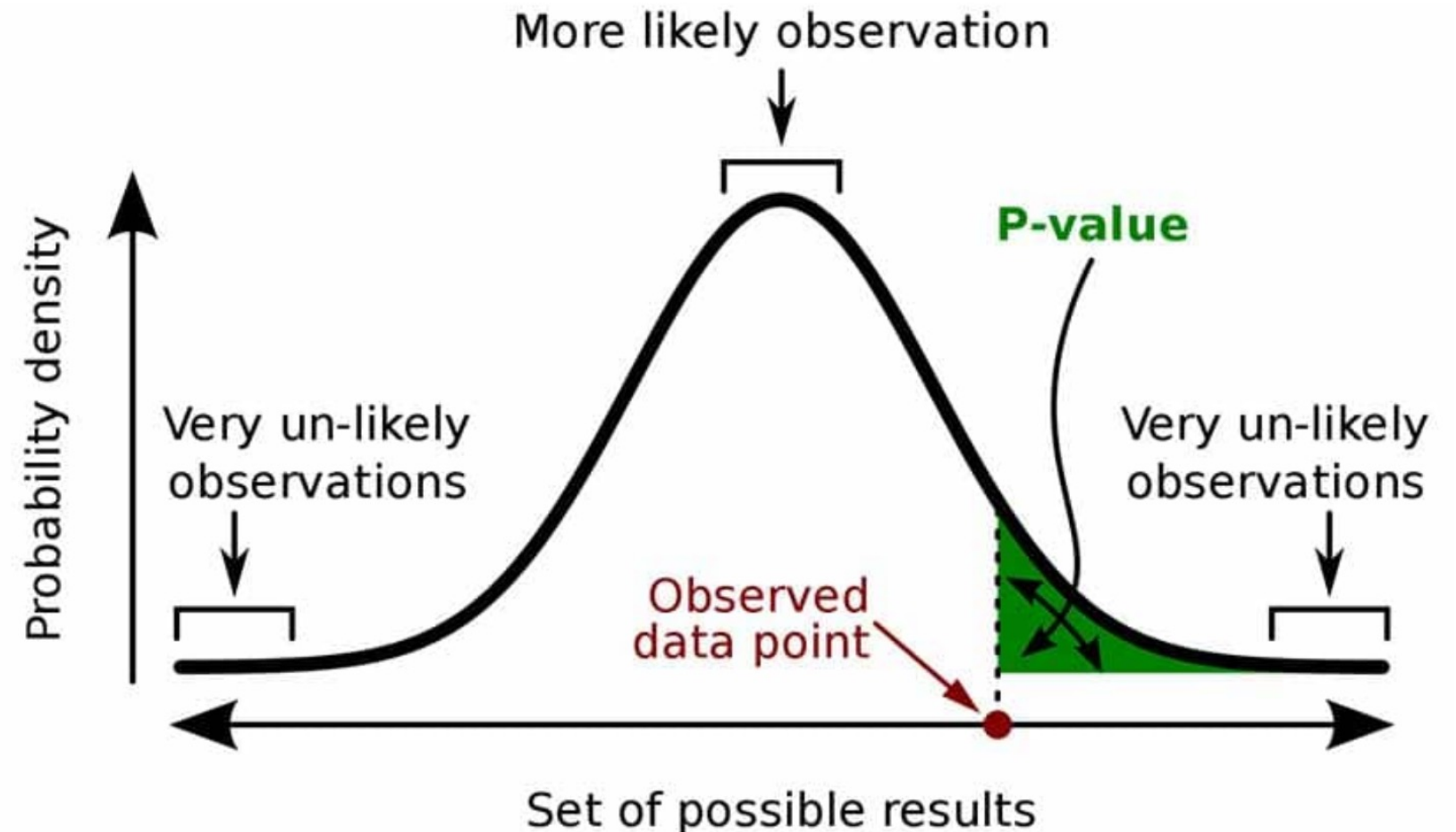
## Answer

The test statistic -4.3818 is less than the critical value of -1.6991. Hence, at .05 significance level, we can reject the claim that mean lifetime of a light bulb is above 10,000 hours.

# Module 10: P-values

- The ***p* value** is defined as the probability under the assumption of no effect or no difference (null hypothesis), of obtaining a result equal to or more extreme than what was actually observed.
- ❑ The ***p* value** is a number, calculated from a statistical test, that describes how likely you are to have found a particular set of observations if the null hypothesis were true.
- ❑ *P* values are used in hypothesis testing to help decide whether to reject the null hypothesis.
  - ✓ The smaller the *p* value, the more likely you are to reject the null hypothesis.

A ***p*-value** (shaded green area) is the probability of an observed (or more extreme) result assuming that the null hypothesis is true



# Module 10: P-values

## ➤ P-value interpretation

❑ A **p-value** less than or equal to your significance level (typically  $\leq 0.05$ ) is statistically significant.

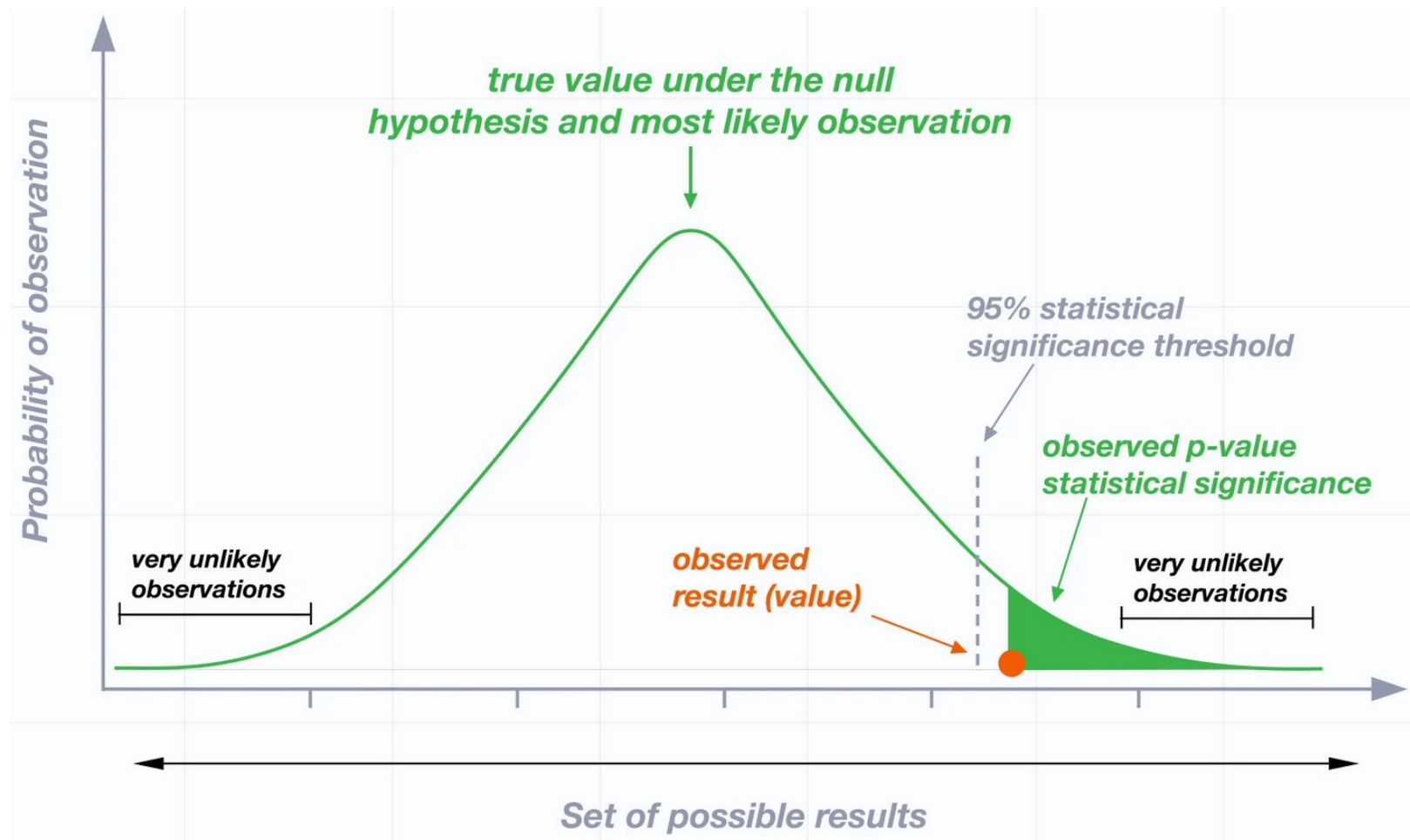
✓ For instance, if you set  $\alpha = 0.05$ , you would reject the null hypothesis if your **p-value**  $\leq 0.05$ .

✓ It indicates strong evidence against the null hypothesis, as there is less than a 5% probability the null is correct (and the results are random). Therefore, we reject the null hypothesis and accept the alternative hypothesis.

❑ A **p-value** more than the significance level (typically  $p > 0.05$ ) is not statistically significant and indicates strong evidence for the null hypothesis.

✓ This means we retain the null hypothesis and reject the alternative hypothesis.

✓ You should note that you cannot accept the null hypothesis; we can only reject it or fail to reject it.



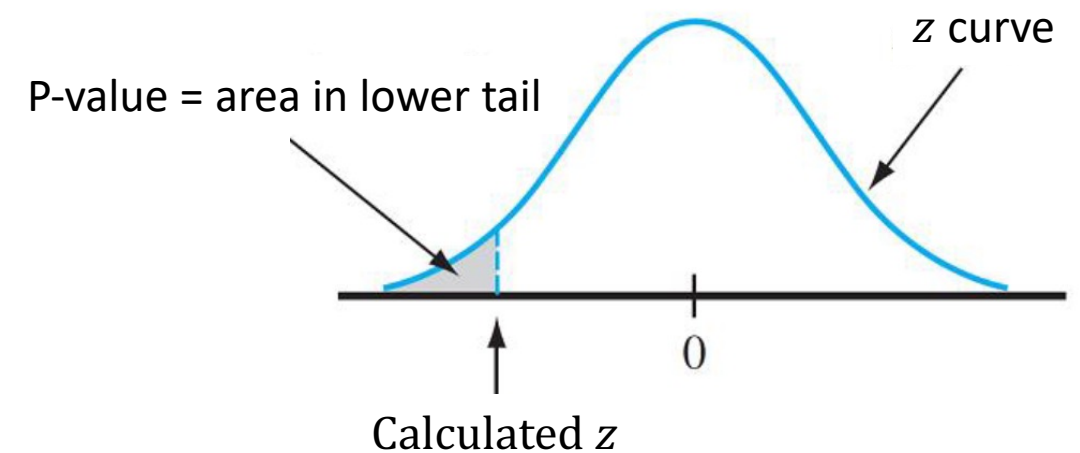
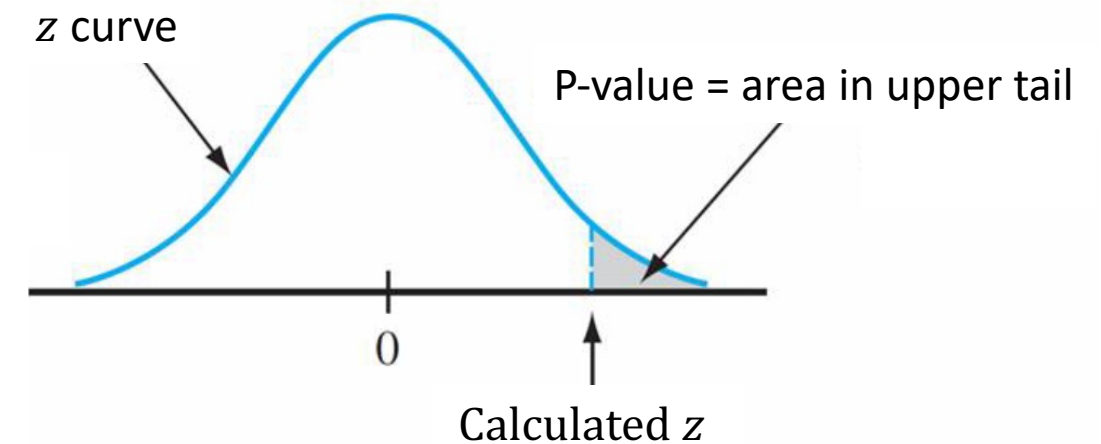
# Module 10: P-values

## ➤ Calculate *p*-value

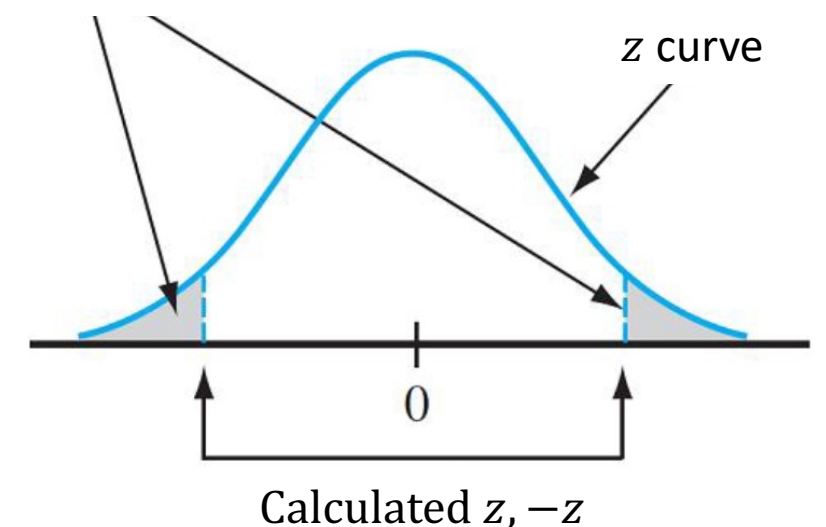
The calculation of the ***p*-value** depends on whether the test is upper , lower , or two tailed.

$$\text{p-value: } \begin{cases} P = 1 - \phi(z) & \text{for an upper-tailed z test} \\ P = \phi(z) & \text{for a lower-tailed z test} \\ P = 2[1 - \phi(|z|)] & \text{for a two-tailed z test} \end{cases}$$

Each of these is the probability of getting a value at least as extreme as what was obtained (assuming  $H_0$  true).



P-value = sum of area in two tails





# Module 10: P-values, Example

## Problem 1

In a left-tailed hypothesis test, let's say we wish to calculate the p-value associated with a z-score of -1.8.

## Solution 1

In R, we may use the ***pnorm()*** function to find the *p*-value associated with a z-score, which has the following syntax.

```
> P.value <- pnorm(q=-1.8, lower.tail=TRUE)
> P.value
[1] 0.03593032
```

## Answer 1

0.03593032 is the p-value. We would reject the null hypothesis based on a significance level of  $\alpha = 0.05$  because the p-value is less than 0.05.

## Problem 2

In a right-tailed hypothesis test, let's say we wish to calculate the p-value associated with a z-score of 1.8.

## Solution 2

```
> P.value <- pnorm(q=1.8, lower.tail=FALSE)
> P.value
[1] 0.03593032
```

## Answer 2

0.03593032 is the p-value. We would reject the null hypothesis if we used a significance level of  $\alpha = 0.05$  because the p-value is less than 0.05.



# Module 10: P-values, Example

## Problem 3

In a two-tailed hypothesis test, let's say we wish to calculate the p-value associated with a z-score of 1.24.

## Solution 3

```
> P.value <- 2*pnorm(q=1.24, lower.tail=FALSE)
> P.value
[1] 0.2149754
```

## Answer 3

0.2149 is the p-value. We would fail to reject the null hypothesis of our hypothesis test if we used a significance level of  $\alpha = 0.05$  because the p-value is not less than 0.05.

# Module 10: P-values, Example

## ➤ Calculating a single $p$ -value from a normal distribution

□ We look at the steps necessary to calculate the  $p$  value for a particular test. In the interest of simplicity we only look at a two-sided test, and we focus on one example.

□ Here we want to show that the mean is not close to a fixed value,  $a$ . 
$$\begin{cases} H_o : \mu_x = a \\ H_a : \mu_x \neq a \end{cases}$$

□ The  $p$  value is calculated for a particular sample mean. Here we assume that we obtained a sample mean,  $x$  and want to find its  $p$  value.

- ✓ It is the probability that we would obtain a given sample mean that is greater than the absolute value of its Z-score or less than the negative of the absolute value of its Z-score.
- ✓ We will use a value of  $a$  of 5, a standard deviation of 2, and a sample size of 20. We then find the  $p$  value for a sample mean of 7 in two different ways:

### First

```
> a <- 5
> s <- 2
> n <- 20
> xbar <- 7
> z <- (xbar-a)/(s/sqrt(n))
> z
[1] 4.472136
> P.value <- 2*pnorm(-abs(z))
> P.value
[1] 7.744216e-06
```

### Second

We now look at the same problem only specifying the mean and standard deviation within the *pnorm* command.

```
> a <- 5
> s <- 2
> n <- 20
> xbar <- 7
> P.value <- 2*(1-pnorm(xbar,mean=a,sd=s/sqrt(20)))
> P.value
[1] 7.744216e-06
```

# Module 10: P-values, Example

## ➤ Calculating a single $p$ -value from a $t$ distribution

❑ Finding the  $p$  value using a  $t$  distribution is very similar to using the Z-score as demonstrated above. The only difference is that you have to specify the number of degrees of freedom. Here we look at the same example but use the  $t$  distribution instead:

❑ Here we want to show that the mean is not close to a fixed value,  $\alpha$ . 
$$\begin{cases} H_o : \mu_x = \alpha \\ H_a : \mu_x \neq \alpha \end{cases}$$

❑ We will use a value of  $\alpha$  of 5, a standard deviation of 2, and a sample size of 20. We then find the  $p$  value for a sample mean of 7 as follow:

```
> a <- 5
> s <- 2
> n <- 20
> xbar <- 7
> t <- (xbar-a)/(s/sqrt(n))
> t
[1] 4.472136
> P.value <- 2*pt(-abs(t),df=n-1)
> P.value
[1] 0.0002611934
```

0.0002611934 is the  $p$ -value. We would reject the null hypothesis if we used a significance level of  $= 0.05$  because the  $p$ -value is less than 0.05.

# Quiz 1

In a a population of interest, a sample of 9 men yielded a sample average brain volume of 1,100cc and standard deviation of 30cc (cube centimeter). What is a 95% Students' T confidence interval for a mean brain volume in this new population?

- [1080,1120]
- [1077,1123]
- [1092,1108]
- [1031,1169]

## Response 1

```
> n <- 9
> mu_bar <- 1100
> s <- 30
> library(distributions3)
> error <- qt(0.975,df=n-1)*s/sqrt(n)
> left <- mu_bar-error
> left
[1] 1076.94
> right <- mu_bar+error
> right
[1] 1123.06
```

# Quiz 2

A diet pill is given to 9 subjects over six weeks. The average difference in weight (follow-up - baseline) is -2 pounds. What would the standard deviation of the difference in weight have to be for the upper endpoint of the 95% T confidence interval touch 0 ?

- 2.60
- 2.10
- 1.50
- 0.30

## Response 2

```
> n <- 9
> mu_bar <- -2
> right <- 0
> error <- -mu_bar
> s <- -mu_bar*sqrt(n)/qt(0.975,df=n-1)
> s
[1] 2.601903
```

# Quiz 3

In an effort to improve running performance, 5 runners were either given a protein supplement or placebo. Then, after a suitable washout period, they were given the opposite treatment. Their mile times were recorded under both the treatment and placebo, yielding 10 measurements with 2 subjects per period. The researchers intend to use a t-test and interval to investigate the treatment. Should they use a paired or independent group T test and interval ?

- A paired interval
- It's necessary to use both
- You could use either
- Independent groups, since all subjects were seen under both systems

## Response 3

### A paired t-test is appropriate when the same subjects are measured under different conditions or treatments. In this case, each runner is measured twice, once under the treatment condition (protein supplement or placebo) and once under the placebo condition (or vice versa). The measurements are paired because they come from the same individuals.

### By using a paired t-test, the researchers can compare the differences in mile times within each subject, which helps control for individual variations and provides a more precise evaluation of the treatment's effect on performance.

### The paired interval considers the paired nature of the data and provides a more accurate estimate of the treatment effect range.

# Quiz 5

Suppose that you create a 95% T confidence interval. You then create a 90% confidence interval using the same data. What can be said about the 90% interval with respect to the 95% interval ?

- The interval will be wider
- The interval will be of same width, but shifted
- The interval will be narrower
- It is impossible to tell

## Response 5

### In summary, the 90% confidence interval will be narrower than the 95% confidence  
### interval when using the same data, indicating a higher level of precision but also  
### a slightly lower level of confidence.

# Quiz 6

A pharmaceutical company is interested in testing a potential blood pressure lowering medication. Their first examination considers only subjects that received the medication at baseline then two weeks later, the data are as follows (SBP in mmHg):

Subject	Baseline	Week 2
1	140	132
2	138	135
3	150	151
4	148	146
5	135	130

Consider testing the hypothesis that there was a mean reduction in blood pressure, give the p-value for the associated two-sided T test.

(Hint: consider that the observations are paired).

- 0.087
- 0.05
- 0.10
- 0.043

## Response 6

```
> x0 <- c(140, 138, 150, 148, 135)
> x1 <- c(132, 135, 151, 146, 130)
> t.test(x0, x1, alternative="greater", paired=TRUE)

      Paired t-test

data:  x0 and x1
t = 2.2616, df = 4, p-value = 0.04326
alternative hypothesis: true mean difference is greater than 0
95 percent confidence interval:
 0.1951315      Inf
sample estimates:
mean difference
          3.4
```



# Quiz 7

A sample of 9 men yielded a sample average brain volume of 1,100cc and standard deviation of 30cc. What is the complete set of values of  $\mu_0$  that a test of  $H_0: \mu = \mu_0$  would fail to reject the null hypothesis in a two-sided 5% Students t-test?

- 1031 to 1169
- 1080 to 1120
- 1081 to 1119
- 1077 to 1123

## Response 7

```
> CI.lower <- 1100-qt(0.975, 8)*30/sqrt(9)
> CI.upper <- 1100+qt(0.975, 8)*30/sqrt(9)
> print(c(CI.lower, CI.upper))
[1] 1076.94 1123.06
```