7 One-Sample Hypothesis Tests (Cont'd)

MTH 3240 Environmental Statistics

Spring 2020

Objectives

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- State two options for testing hypotheses using non-normal data.
- Carry out a one-sample sign test for a population median.
- Decide which test (the one-sample t test or the sign test) is more appropriate for a given set of data.

Dealing With Non-Normal Data

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  2. Carry out a ***nonparametric*** test (i.e. one that doesn't require normality).

  We'll look at these two approaches one at a time.

Transforming Data to Normality

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- The next example illustrates **transforming right skewed** data (by taking their **logs**), then carrying out the t **test** using the transformed data.

Example

Here are **radiocesium** measurements (^{137}Cs, in pCi/L) in $n = 10$ water specimens from the Cactus Crater disposal site.

69, 77, 227, 215, 28, 153, 25, 325, 55, 42

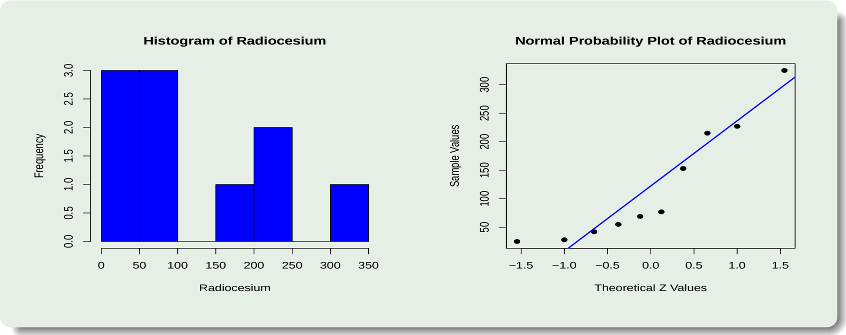
Suppose we want to test the hypotheses

$$\begin{aligned} H_0 : \mu &\geq 215 \\ H_a : \mu &< 215 \end{aligned}$$

where $\boldsymbol{\mu}$ is the (unknown) **population mean** ^{137}Cs concentration.

Because n isn't large, the *one-sample* t *test* would only be appropriate if the sample was from a **normal** population.

We check the **normality** assumption using a **histogram** and/or **normal probability plot.**



Histogram of Radiocesium

Normal Probability Plot of Radiocesium

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The **logs** of the data are:

$$4.2, \quad 4.3, \quad 5.4, \quad 5.4, \quad 3.3, \quad 5.0, \quad 3.2, \quad 5.8, \quad 4.0, \quad 3.7$$

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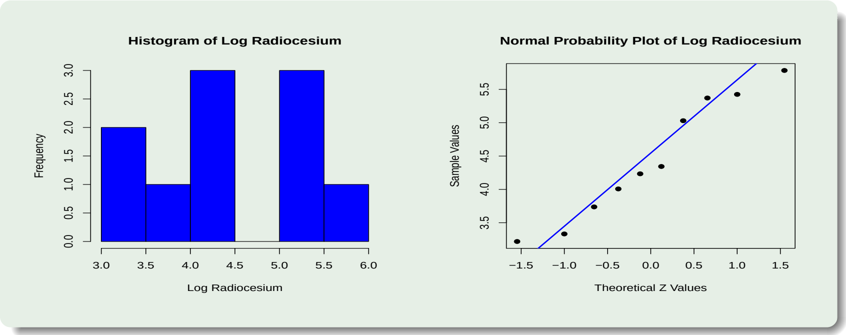
The **logs** of the data are:

4.2, 4.3, 5.4, 5.4, 3.3, 5.0, 3.2, 5.8, 4.0, 3.7

The **normality** assumption is (approximately) met for the **log** data (see next slide).


Histogram of Log Radiocesium
Frequency
0.0
0.5
1.0
1.5
2.0
2.5
3.0
3.0
3.5
4.0
4.5
5.0
5.5
6.0
Log Radiocesium
Normal Probability Plot of Log Radiocesium
Sample Values
3.5
4.0
4.5
5.0
5.5
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
Theoretical Z Values

So a **one-sample t test** is appropriate for the **log** data.

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$$\log(215) \;=\; 5.4\,,$$

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On the **log** pCi/L scale, the comparison value is no longer 215, but rather

$$\log(215) \;=\; 5.4\,,$$

so the hypotheses are now

$$\begin{aligned} H_0 : \mu &\geq 5.4 \\ H_a : \mu &< 5.4 \end{aligned}$$

where now μ is the true (unknown) **population mean *log*** ^{137}Cs concentration.

Using the **log** data, the **test statistic** is t **= -3.21** and the **p-value** is **0.005**.

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Thus we **reject** H_0 and conclude that the **population mean** ***log*** ^{137}Cs concentrationμ is less than 5.4

Carrying Out a Nonparametric Test

- The second approach to testing hypothesis with **non-normal** data is to use a ***nonparametric*** test, i.e. one that **doesn’t** rely on a normality assumption.

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- The second approach to testing hypothesis with **non-normal** data is to use a ***nonparametric*** test, i.e. one that **doesn't** rely on a normality assumption.

  The ***sign test*** (described next) is a **nonparametric** alternative to the *one-sample* t *test*.

One-Sample Sign Test

- The ***one-sample sign test*** is a **nonparametric** test for a **population *median*** $\tilde{\mu}$.

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- The ***one-sample sign test*** is a **nonparametric** test for a **population *median*** $\tilde{\mu}$.
- The **null hypothesis** is that $\tilde{\mu}$ is equal to some ***claimed value*** $\tilde{\mu}_0$.

Null Hypothesis:

$$H_0 : \tilde{\mu} \;=\; \tilde{\mu}_0.$$

- The **alternative hypothesis** is one of the following.

Alternative Hypothesis:

1. $H_a : \tilde{\mu} > \tilde{\mu}_0$ (**upper-tailed test**)
2. $H_a : \tilde{\mu} < \tilde{\mu}_0$ (**lower-tailed test**)
3. $H_a : \tilde{\mu} \neq \tilde{\mu}_0$ (**two-tailed test**)

depending on what we're trying to verify using the data.

Sign Test Statistic:

$$S^+ \ = \ \text{Number of } X_i\text{'s that are greater than } \tilde{\mu}_0.$$

(If any X_i's equal $\tilde{\mu}_0$, they're discarded, and n is diminished by the number of discarded X_i's.)

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(If any X_i's equal $\tilde{\mu}_0$, they're discarded, and n is diminished by the number of discarded X_i's.)

To compute S^+, we just **count** how many data values fall **above $\tilde{\mu}_0$.**

- **If H_0 was true**, the population median $\tilde{\mu}$ would be equal to $\tilde{\mu}_0$, ...

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  ... and because **half** of the population would fall above $\tilde{\mu}_0$ ...

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  ... in which case S^+ **would be close to $n/2$**.

- But **if $\boldsymbol{H_a}$ was true**, the population median $\tilde{\mu}$ would differ from $\tilde{\mu}_0$ in the direction specified by H_a, **...**

- But **if $\boldsymbol{H_a}$ was true**, the population median $\tilde{\mu}$ would differ from $\tilde{\mu}_0$ in the direction specified by H_a, ...

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  ... and we'd expect more or less than half of the sample to fall above $\tilde{\mu}_0$, depending on the direction of H_a, ...

  ... in which case S^+ **would differ from $\boldsymbol{n/2}$** in that **same direction.**

- Thus ...

- Thus ...
  1. S^+ will be approximately $n/2$ (most likely) if H_0 is true.
  2. It will **differ from** $n/2$ (most likely) in the direction specified by H_a if H_a is true.

1. *Large* values of S^+ (larger than $n/2$) provide evidence in favor of $H_a : \tilde{\mu} > \tilde{\mu}_0$.
2. *Small* values of S^+ (smaller than $n/2$) provide evidence in favor of $H_a : \tilde{\mu} < \tilde{\mu}_0$.
3. *Both large and small* values of S^+ (larger or smaller than $n/2$) provide evidence in favor of $H_a : \tilde{\mu} \neq \tilde{\mu}_0$.

- Now suppose our sample is from **any** (continuous) population whose median is $\tilde{\mu}$.

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Sampling Distribution of the Test Statistic Under H_0:
If S^+ is the one-sample sign test statistic, then when

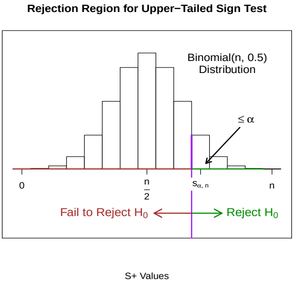
$$H_0 : \tilde{\mu} \ = \ \tilde{\mu}_0$$

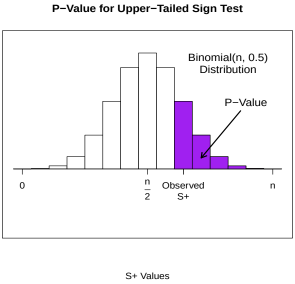
is true,

$$S^+ \ \sim \ \text{binomial}(n,\, 0.5).$$

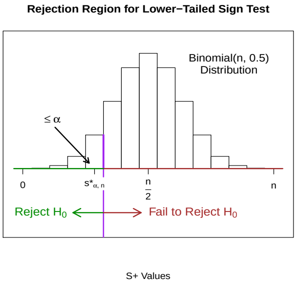
- **P-values** and **rejection regions** are obtained from the appropriate tail(s) of the **binomial**$(n,\, 0.5)$ **distribution**, as shown on the next slides.

1. $H_a : \tilde{\mu} > \tilde{\mu}_0$ (Upper-Tailed Test)

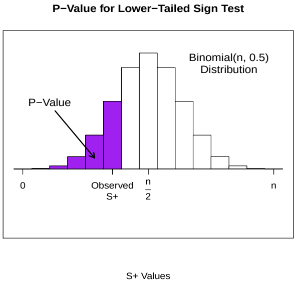

Rejection Region for Upper−Tailed Sign Test


P−Value for Upper−Tailed Sign Test

2. $H_a : \tilde{\mu} < \tilde{\mu}_0$ (Lower-Tailed Test)

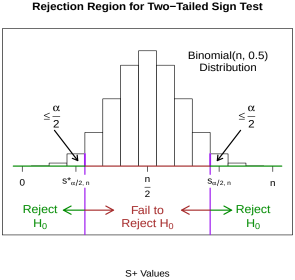


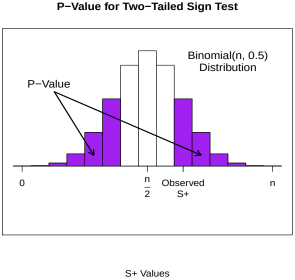
Rejection Region for Lower−Tailed Sign Test



P−Value for Lower−Tailed Sign Test

3. $H_a : \tilde{\mu} \neq \tilde{\mu}_0$ (Two-Tailed Test)


Rejection Region for Two−Tailed Sign Test


P−Value for Two−Tailed Sign Test

One-Sample Sign Test for $\tilde{\mu}$

Assumptions: $x_1, x_2, \ldots, x_n$ is a random sample from *any* continuous population.

Null hypothesis: $H_0 : \tilde{\mu} = \tilde{\mu}_0$.

Test statistic value: $s^+ =$ number of x_i's greater than $\tilde{\mu}_0$.

Decision rule: Reject H_0 if p-value $< \alpha$ or s^+ is in rejection region.

One-Sample Sign Test for $\tilde{\mu}$

Alternative hypothesis	P-value = tail probability of the binomial$(n, 0.5)$ distribution: *	Rejection region = s^+ values such that: **
$H_a : \tilde{\mu} > \tilde{\mu}_0$	to the right of (and including) s^+	$s^+ \geq s_{\alpha,n}$
$H_a : \tilde{\mu} < \tilde{\mu}_0$	to the left of (and including) s^+	$s^+ \leq s^*_{\alpha,n}$
$H_a : \tilde{\mu} \neq \tilde{\mu}_0$	$2\cdot$(the smaller of the tail probabilities to the right of (and including) s^+ and to the left of (and including) s^+)	$s^+ \leq s^*_{\alpha/2,n}$ or $s^+ \geq s_{\alpha/2,n}$

* For a given sample size (after deleting $\tilde{\mu}_0$-valued x_i's) n, the p-value for a one-tailed test is obtained from a binomial$(n,\ 0.5)$ distribution table by locating the upper or lower tail probability (depending on the direction of H_a) associated with the observed S^+ value. For a two-tailed test, locate both the upper and lower tail probabilities and multiply the smaller of these by two.

One-Sample Sign Test for $\tilde{\mu}$

** For a given sample size (after deleting $\tilde{\mu}_0$-valued x_i's) n and level of significance α, $s_{\alpha,n}$ is obtained from a binomial$(n,\,0.5)$ distribution table by locating the smallest s for which the upper tail probability is less than α. $s^*_{\alpha,n}$ is obtained by locating the largest s for which the lower tail probability is less than α. For the two-tailed test, $s_{\alpha/2,n}$ and $s^*_{\alpha/2,n}$ are defined analogously but with $\alpha/2$ used in place of α. In practice, due to the discreteness of the distribution, it's not always possible obtain a rejection region having exact probability α.

Example

Here again are **radiocesium** measurements (^{137}Cs, in pCi/L) in $n = 10$ water specimens.

69, 77, 227, 215, 28, 153, 25, 325, 55, 42

Instead of the t *test* on the *log* data (as in the earlier example), we could carry out a **sign test** on the **original** data.

In this case, the hypotheses are:

$$\begin{aligned} H_0 : \tilde{\mu} &= 215 \\ H_a : \tilde{\mu} &< 215 \end{aligned}$$

where $\tilde{\mu}$ is the (unknown) population **median** ^{137}Cs concentration.

In this case, the hypotheses are:

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where $\tilde{\mu}$ is the (unknown) population **median** ^{137}Cs concentration.

One of the data values **equals 215**, so before computing S^+, we **discard** it and diminish the sample size from $\boldsymbol{n = 10}$ to $\boldsymbol{n = 9}$.

This leaves us with **2** observations greater than **215**, out of the $n = 9$ that remain, so the **test statistic** is

$$S^+ \;=\; \mathbf{2}.$$

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From the sign test table, the **p-value** is **0.0898**, and we **fail to reject** H_0.

Exercise

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Nine lab technicians used the new method to measure SO_2 in an EPA audit cylinder containing a known concentration of **447 ppm**.

Their results are below.

SO_2 Measurements on EPA Audit Cylinder Containing 447 ppm

Technician	SO_2 Measurement
1	688
2	478
3	524
4	447
5	2135
6	434
7	712
8	464
9	478

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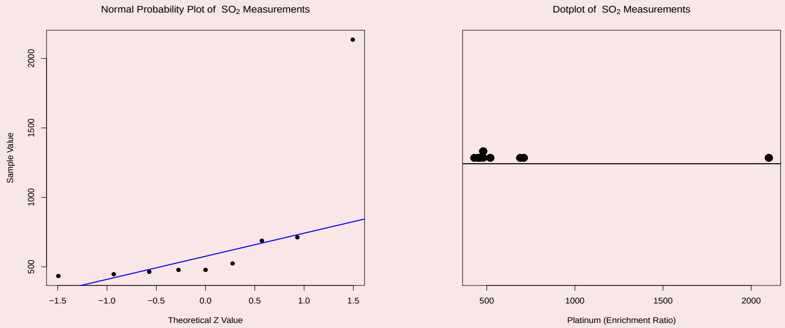
A **normal probability** plot and **dotplot** of the data are on the next slide.


Normal Probability Plot of SO$_2$ Measurements
Sample Value
500
1000
1500
2000
−1.5
−1.0
−0.5
0.0
0.5
1.0
1.5
Theoretical Z Value
Dotplot of SO$_2$ Measurements
500
1000
1500
2000
Platinum (Enrichment Ratio)

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Carry out a **sign test** to decide if there's evidence for bias in the new method. Use level of significance $\alpha = 0.05$.

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Hints: The hypotheses are

$$\begin{aligned} H_0 : \tilde{\mu} &= 447 \\ H_a : \tilde{\mu} &\neq 447 \end{aligned}$$

where $\tilde{\mu}$ is the (unknown) population **median** SO_2 measurement result at the lab.

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where $\tilde{\mu}$ is the (unknown) population **median** SO_2 measurement result at the lab.

(You should get $S^+ = \mathbf{7}$ and p-value = **0.0704**.)

The One-Sample *Z* Test

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  It's used with a **dichotomous** (**success/failure**) random sample of size n from a **population** whose (unknown) **proportion** of **successes** is p.

- The **null hypothesis** is that p is equal to some ***claimed value*** p_0.

Null Hypothesis:

$$H_0 : p \; = \; p_0.$$

- The **alternative hypothesis** is one of the following.

Alternative Hypothesis:

1. $H_a : p > p_0$ (**upper-tailed test**)
2. $H_a : p < p_0$ (**lower-tailed test**)
3. $H_a : p \neq p_0$ (**two-tailed test**)

depending on what we're trying to verify using the data.

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One-Sample Z Test Statistic (for a Proportion):

$$Z = \frac{\hat{P} - p_0}{\sigma_{\hat{P}}},$$

where

$$\sigma_{\hat{P}} = \sqrt{\frac{p_0(1-p_0)}{n}}.$$

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- Z indicates how many **standard errors** $\hat{P}$ is **away from p_0**, and in what direction (positive or negative).

- $\hat{P}$ is an estimate of p, so ...

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    - **If H_0 was true**, ...

- $\hat{\boldsymbol{P}}$ is an estimate of $\boldsymbol{p}$, so **...**
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    ... we'd expect $\hat{P}$ to be close p_0.

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  - But **if H_a was true**, ...

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  - **If H_0 was true**, ...

    ... we'd expect $\hat{P}$ to be close p_0.
  - But **if H_a was true**, ...

    ... we'd expect $\hat{P}$ to differ from p_0 in the direction specified by H_a.

- $\hat{P}$ is an estimate of p, so ...
  - **If H_0 was true**, ...

    ... we'd expect $\hat{P}$ to be close p_0.
  - But **if H_a was true**, ...

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- Thus ...

- $\hat{\boldsymbol{P}}$ is an estimate of $\boldsymbol{p}$, so ...
  - **If $\boldsymbol{H_0}$ was true**, ...

    ... we'd expect $\hat{P}$ to be close p_0.
  - But **if $\boldsymbol{H_a}$ was true**, ...

    ... we'd expect $\hat{P}$ to differ from p_0 in the direction specified by H_a.
- Thus ...
  1. Z will be approximately **zero** (most likely) if H_0 is true.
  2. It will **differ from zero** (most likely) in the direction specified by H_a if H_a is true.

1. *Large positive* values of Z provide evidence in favor of $H_a : p > p_0$.
2. *Large negative* values of Z provide evidence in favor of $H_a : p < p_0$.
3. *Both large positive and large negative* values of Z provide evidence in favor of $H_a : p \neq p_0$.

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Sampling Distribution of the Test Statistic Under H_0:
If Z is the one-sample Z test statistic (for a proportion), then when

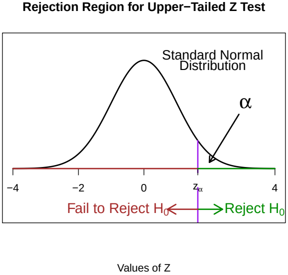
$$H_0 : \; p \; = \; p_0$$

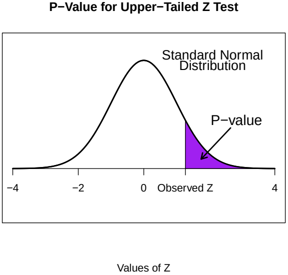
is true,

$$Z \; \sim \; \mathsf{N}(0, \, 1).$$

- **P-values** and **rejection regions** are obtained from the appropriate tail(s) of the **N$(0,\ 1)$ distribution**, as shown on the next slides.

1. $H_a : p > p_0$ (Upper-Tailed Test)


Rejection Region for Upper−Tailed Z Test


P−Value for Upper−Tailed Z Test

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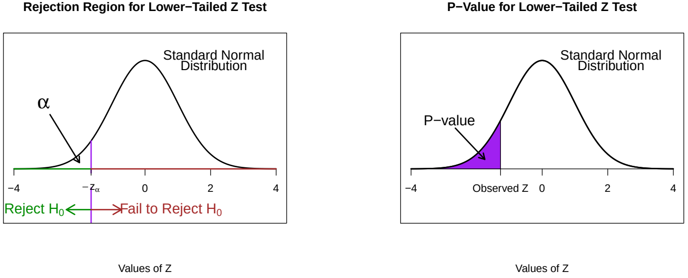
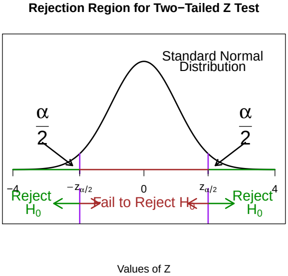
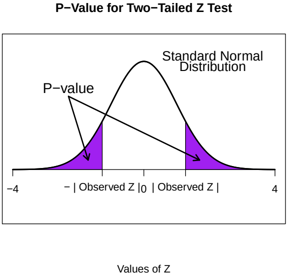


3. $H_a : p \neq p_0$ (Two-Tailed Test)





One-Sample Z Test for p

Assumptions: The data are a random sample of size n from a dichotomous population, and n is large (using the criteria $np_0 \geq 10$ and $n(1-p_0) \geq 10$).

Null hypothesis: $H_0 : p = p_0$.

Test statistic value: $z = \frac{\hat{p}-p_0}{\sqrt{\frac{p_0(1-p_0)}{n}}}$.

Decision Rule: Reject H_0 if p-value $< \alpha$ or z is in rejection region.

One-Sample Z Test for p

Alternative hypothesis	P-value = area under standard normal distribution:	Rejection region = z values such that:*
$H_a : p > p_0$	to the right of z	$z > z_\alpha$
$H_a : p < p_0$	to the left of z	$z < -z_\alpha$
$H_a : p \neq p_0$	to the left of $-\lvert z \rvert$ and right of $\lvert z \rvert$	$z > z_{\alpha/2}$ or $z < -z_{\alpha/2}$

* z_α is the $100(1-\alpha)$th percentile of the standard normal distribution.

Example

Farmers use biosolids (sludge) from wastewater treatment plants to fertilize soil.

A study was carried out to assess the risk of farmers' exposure to salmonella through the application of biosolids to farmlands.

In a sample of $n = 92$ biosolids specimens, **22** tested *positive* for salmonella.

Here’s a portion of the data set.

”Neg”, ”Neg”, ”Pos”, ”Pos”, ”Neg”, ”Neg”, ”Neg”,
”Neg”, ”Neg”, ”Neg”, ”Neg” ”Neg”, ”Neg”, ”Neg”,
”Neg”, ”Neg”, ”Pos”, ”Pos”, ”Neg”, ”Neg”, ”Neg”,
⋮
”Neg”, ”Neg”, ”Neg”, ”Neg”, ”Neg”, ”Neg”, ”Pos”,
”Neg”, ”Pos”, ”Pos”, ”Neg” ”Neg”, ”Neg”, ”Pos”,
”Neg”

We'll carry out a **one-sample z test** to decide if the true (unknown) **population proportion** of biosolids specimens that are **positive** for salmonella is **less than 0.25**.

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We'll use a level of significance $\alpha = 0.05$.

The **hypotheses** are

$$\begin{aligned} H_0 : p &= 0.25 \\ H_a : p &< 0.25 \end{aligned}$$

where p is the (unknown) **population proportion** of biosolids specimens that are **positive** for salmonella.

The **sample proportion** is

$$\hat{P} = \frac{22}{92} = \mathbf{0.24}\,.$$

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So the **test statistic** is

$$\begin{aligned}\boldsymbol{Z} \;&=\; \frac{\hat{P}-p_0}{\sqrt{p_0(1-p_0)/n}}\\ &=\; \frac{0.24-0.25}{\sqrt{0.25(1-0.25)/92}}\end{aligned}$$

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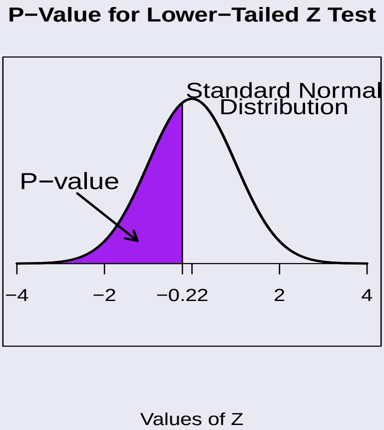
Thus the sample proportion, $\hat{\boldsymbol{P}} = \mathbf{0.24}$, is only **0.22 of a standard error below** the hypothesized value **0.25.**

The **p-value** is the area to the **left** of Z **= -0.22** under the **N**$(0,\ 1)$ curve, as shown on the next slide.


P−Value for Lower−Tailed Z Test
Standard Normal Distribution
P−value
−4
−2
−0.22
2
4
Values of Z

The **p-value** (obtained using statistical software) is **0.4129**.

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Thus, because the **p-value *isn't* less** than **0.05**, we **fail to reject H_0.**

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Thus, because the **p-value *isn't* less** than **0.05**, we **fail to reject H_0.**

There's **not** statistically significant **evidence** that the **population proportion** of biosolids specimens that are **positive** for salmonella is less than 0.25.