

## 7 One-Sample Hypothesis Tests (Cont'd)

MTH 3240 Environmental Statistics

Spring 2020

### Objectives

Objectives:

- 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

- The one-sample  $t$  procedures (and many others) require that the sample was drawn from a **normal** population (or that  $n$  is **large**).

If this **normality** assumption isn't met (and  $n$  isn't large), there are two possible remedies:

1. **Transform** the data to normality before carrying out the hypothesis test, or
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

- The first approach to testing hypothesis with **non-normal** data is to **transform** the data to normality first.
- 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 ( $^{137}\text{Cs}$ , 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

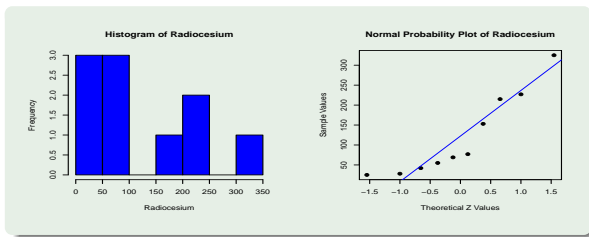
$$H_0 : \mu \geq 215$$

$$H_a : \mu < 215$$

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



The plots suggest the sample is from a **right skewed** population, so the **t test** might **not** be trustworthy.

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).

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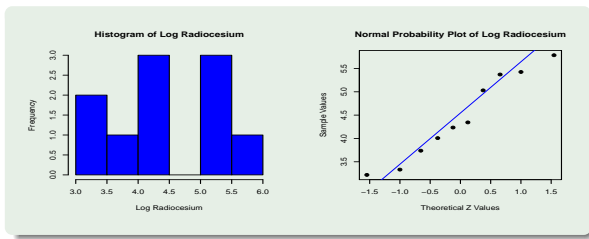
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So a **one-sample  $t$  test** is appropriate for the **log** data.

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

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

so the hypotheses are now

$$H_0 : \mu \geq 5.4$$

$$H_a : \mu < 5.4$$

where now  $\mu$  is the true (unknown) **population mean log**  $^{137}\text{Cs}$  concentration.

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

Thus we **reject  $H_0$**  and conclude that the **population mean log**  $^{137}\text{Cs}$  concentration  $\mu$  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.

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

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## One-Sample Sign Test

- 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.)

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  $\tilde{\mu}_0$ , ...  
... and because **half** of the population would fall above  $\tilde{\mu}_0$   
...  
... we'd expect about **half** of the sample to fall above  $\tilde{\mu}_0$ , ...  
... in which case  $S^+$  **would be close to  $n/2$** .

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- But if  $H_a$  was true, the population median  $\tilde{\mu}$  would differ from  $\tilde{\mu}_0$  in the direction specified by  $H_a$ , ...  
... 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  $n/2$  in that same direction.

- 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  $\tilde{\mu}$ .

The null distribution is as follows.

**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,

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

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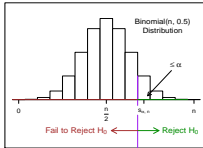
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- **P-values and rejection regions** are obtained from the appropriate tail(s) of the **binomial( $n, 0.5$ ) distribution**, as shown on the next slides.

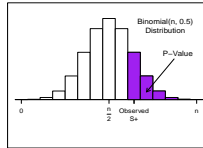
1.  $H_a : \tilde{\mu} > \tilde{\mu}_0$  (Upper-Tailed Test)

Rejection Region for Upper-Tailed Sign Test



S+ Values

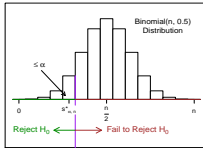
P-Value for Upper-Tailed Sign Test



S+ Values

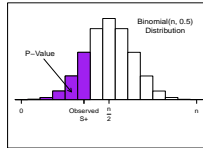
2.  $H_a : \tilde{\mu} < \tilde{\mu}_0$  (Lower-Tailed Test)

Rejection Region for Lower-Tailed Sign Test



S+ Values

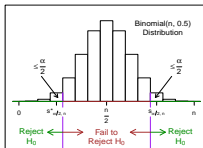
P-Value for Lower-Tailed Sign Test



S+ Values

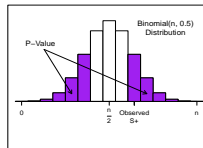
3.  $H_a : \tilde{\mu} \neq \tilde{\mu}_0$  (Two-Tailed Test)

Rejection Region for Two-Tailed Sign Test



S+ Values

P-Value for Two-Tailed Sign Test



S+ Values

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

**Assumptions:**  $x_1, x_2, \dots, x_n$  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.

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### 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 (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.

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### 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  $\alpha$ ,  $s_{\alpha, n}$  is obtained from a binomial( $n, 0.5$ ) distribution table by locating the smallest  $s$  for which the upper tail probability is less than  $\alpha$ .  $s_{\alpha, n}^*$  is obtained by locating the largest  $s$  for which the lower tail probability is less than  $\alpha$ . 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  $\alpha$ . In practice, due to the discreteness of the distribution, it's not always possible obtain a rejection region having exact probability  $\alpha$ .

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#### Example

Here again are **radiocesium** measurements ( $^{137}\text{Cs}$ , 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:

$$H_0 : \tilde{\mu} = 215$$

$$H_a : \tilde{\mu} < 215$$

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

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

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

$$S^+ = 2.$$

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

### Exercise

A study was carried out to determine the accuracy of a new a method developed by the U.S. EPA for measuring sulfur dioxide ( $\text{SO}_2$ ) emissions from coal burning power plants.

**Nine** lab technicians used the new method to measure  $\text{SO}_2$  in an EPA audit cylinder containing a known concentration of **447 ppm**.

Their results are below.

### SO<sub>2</sub> Measurements on EPA Audit Cylinder Containing 447 ppm

Technician	SO <sub>2</sub> Measurement
1	688
2	478
3	524
4	447
5	2135
6	434
7	712
8	464
9	478

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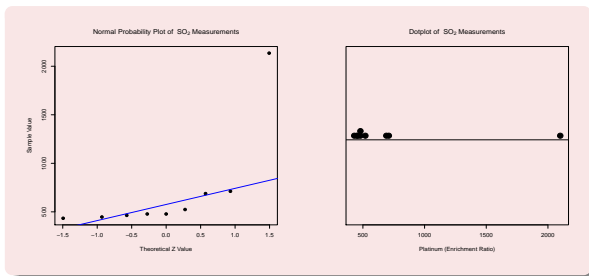
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(The very large SO<sub>2</sub> result may have been due to an equipment malfunction, but we'll leave it in the data set).

We want to decide if there's any statistically significant **evidence for bias** (in either direction) using the new method.

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



Due to the outlier, it **wouldn't** be reasonable to assume the data are a sample from a **normal** distribution. Also,  $n$  is small, so one-sample  **$t$  test** is **not** appropriate.

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

**Hints:** The hypotheses are

$$H_0 : \tilde{\mu} = 447$$

$$H_a : \tilde{\mu} \neq 447$$

where  $\tilde{\mu}$  is the (unknown) population **median** SO<sub>2</sub> measurement result at the lab.

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

## The One-Sample Z Test

- The **one-sample  $z$  test for  $p$**  is a hypothesis test for an (unknown) **population proportion  $p$** .

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:**

$$H_0 : p = p_0.$$

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- 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.

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

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

where

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

- $Z$  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 ...
  - **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  $H_a$ .
- 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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- Suppose we have a random sample from a **dichotomous** population.

If sample size  $n$  is large, the **null distribution** is as follows.

**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,

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

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

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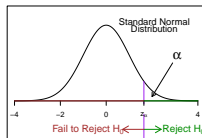
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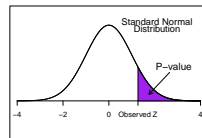
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**1.  $H_a : p > p_0$  (Upper-Tailed Test)**

Rejection Region for Upper-Tailed Z Test



P-Value for Upper-Tailed Z Test



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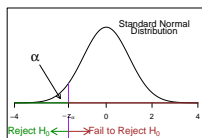
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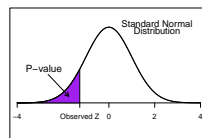
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**2.  $H_a : p < p_0$  (Lower-Tailed Test)**

Rejection Region for Lower-Tailed Z Test



P-Value for Lower-Tailed Z Test



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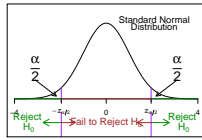
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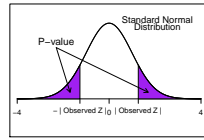
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### 3. $H_a : p \neq p_0$ (Two-Tailed Test)

Rejection Region for Two-Tailed Z Test



P-Value for Two-Tailed Z 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 $- z $ and right of $ z $	$z > z_{\alpha/2}$ or $z < -z_{\alpha/2}$

\*  $z_{\alpha}$  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.

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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"

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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**.

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

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The **hypotheses** are

$$H_0 : p = 0.25$$

$$H_a : p < 0.25$$

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

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The **sample proportion** is

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

So the **test statistic** is

$$\begin{aligned} Z &= \frac{\hat{P} - p_0}{\sqrt{p_0(1 - p_0)/n}} \\ &= \frac{0.24 - 0.25}{\sqrt{0.25(1 - 0.25)/92}} \\ &= -0.22. \end{aligned}$$

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

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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.

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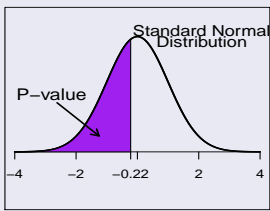
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P-Value for Lower-Tailed Z Test



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

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