Lecture - Inference Review

Sta102 / BME102

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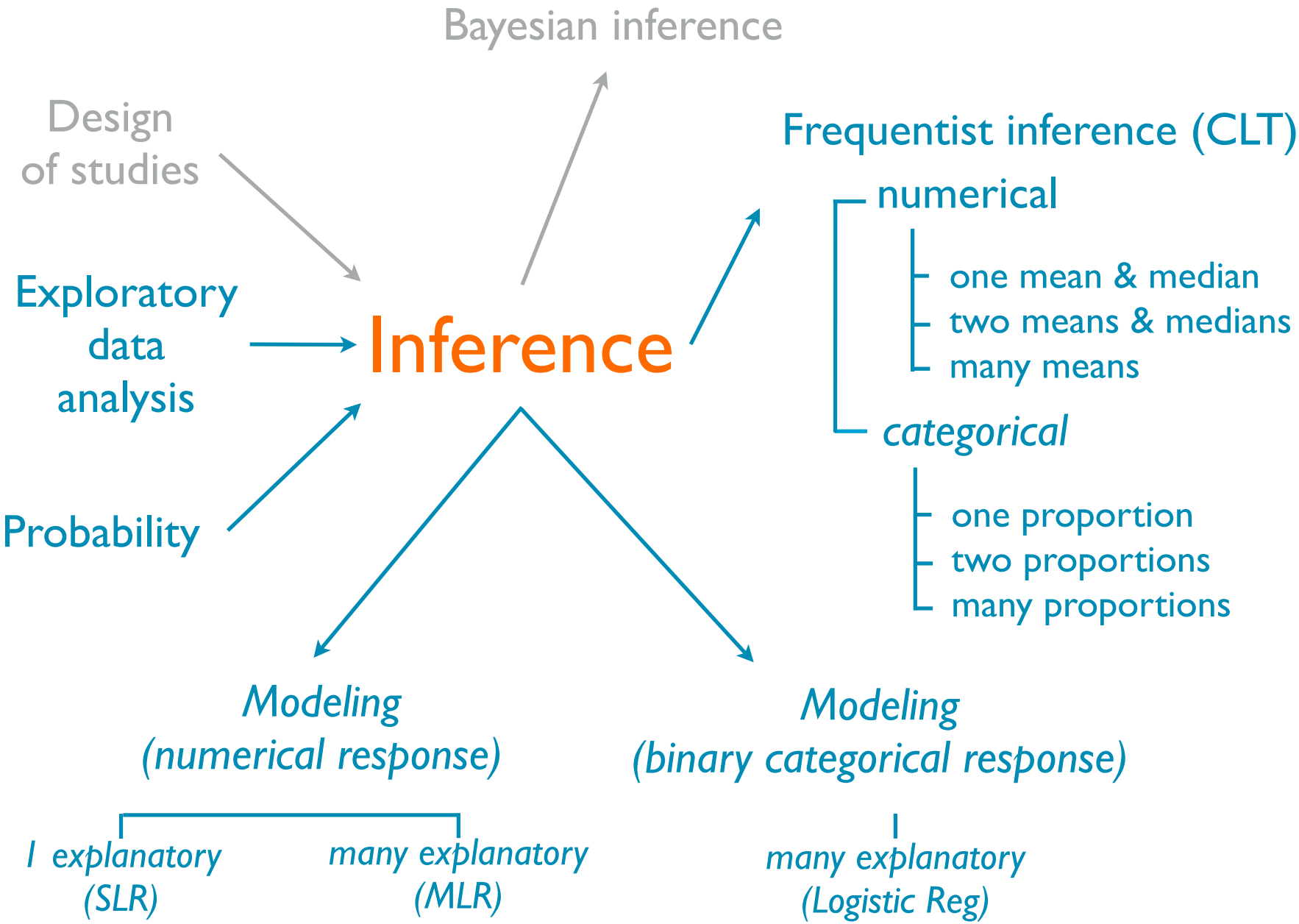
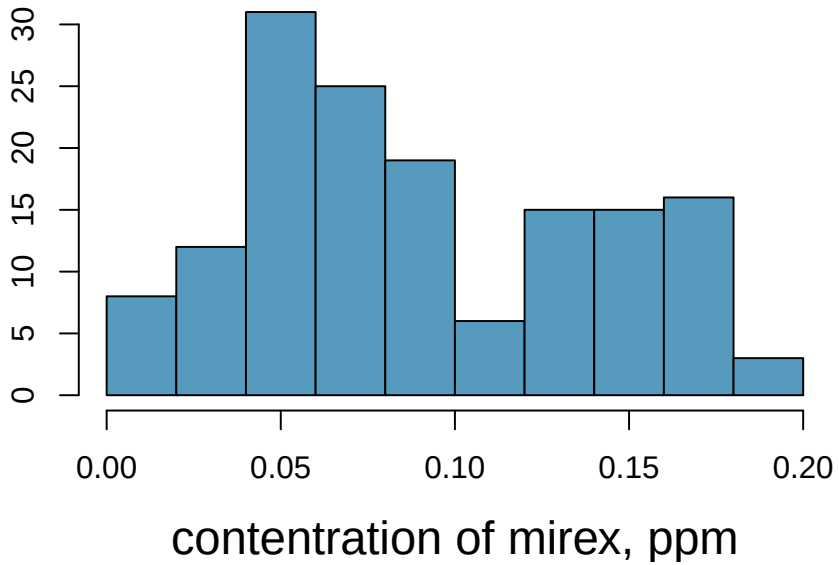

Bayesian inference
Design of studies
Exploratory data analysis
Probability
Inference
Frequentist inference (CLT)
numerical
one mean & median
two means & medians
many means
categorical
one proportion
two proportions
many proportions
Modeling (numerical response)
1 explanatory (SLR)
many explanatory (MLR)
Modeling (binary categorical response)
many explanatory (Logistic Reg)

Exploratory data analysis

variable(s)	visualization	summary statistics
categorical	bar plot	frequency table, relative frequency table, proportion
numerical	dot plot, histogram, box plot	mean, median, SD, z-score, range, IQR, five number summary (min, Q1, median, Q3, max)
categorical vs. categorical	segmented bar plot, mosaicplot	contingency table, difference in proportions
numerical vs. categorical	side-by-side box plots	statistics by group, difference in means
numerical vs. numerical	scatterplot	correlation

Example - Salmon contamination

Researchers tested 150 randomly selected farm raised salmon for organic contaminants. They found the mean concentration of carcinogenic insecticide mirex to be 0.0913 ppm, with standard deviation 0.0495 ppm. As a safety recommendation to recreational fishers, the EPA's recommended screening value for mirex is 0.08 ppm. Are farmed salmon contaminated beyond the level permitted by the EPA?



Salmon - set-up

$$n = 150,\ \bar{x} = 0.0913,\ s = 0.0495$$

- cases:

Salmon - set-up

$$n = 150,\ \bar{x} = 0.0913,\ s = 0.0495$$

- cases: 150 salmon
- variable(s):

Salmon - set-up

$$n = 150, \ \bar{x} = 0.0913, \ s = 0.0495$$

- cases: 150 salmon
- variable(s): only 1 - concentration of contaminant (numerical)
- parameter of interest:

Salmon - set-up

$$n = 150,\ \bar{x} = 0.0913,\ s = 0.0495$$

- cases: 150 salmon
- variable(s): only 1 - concentration of contaminant (numerical)
- parameter of interest: μ, true mean concentration of contaminant in all farmed salmon
- point estimate:

Salmon - set-up

$$n = 150,\ \bar{x} = 0.0913,\ s = 0.0495$$

- cases: 150 salmon
- variable(s): only 1 - concentration of contaminant (numerical)
- parameter of interest: μ, true mean concentration of contaminant in all farmed salmon
- point estimate: $\bar{x}$, mean concentration of contaminant in sampled farmed salmon
- test:

Salmon - set-up

$$n = 150,\ \bar{x} = 0.0913,\ s = 0.0495$$

- cases: 150 salmon
- variable(s): only 1 - concentration of contaminant (numerical)
- parameter of interest: μ, true mean concentration of contaminant in all farmed salmon
- point estimate: $\bar{x}$, mean concentration of contaminant in sampled farmed salmon
- test: test of population mean against a null value, Z test since $n > 30$, (T test will yield similar results)
  - independence: random sample, $150 < 10\%$ of all farmed salmon $\rightarrow$ concentration of contaminant in one salmon in the sample is independent of another
  - sample size/skew: the distribution isn't extremely skewed, and $n > 30$
- hypotheses:

Salmon - set-up

$$n = 150,\ \bar{x} = 0.0913,\ s = 0.0495$$

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  - sample size/skew: the distribution isn't extremely skewed, and $n > 30$
- hypotheses: $H_0 : \mu = 0.08$; $H_A : \mu > 0.08$

Salmon - p-value

- $H_A : \mu > 0.08 \rightarrow$ one-tailed

Salmon - p-value

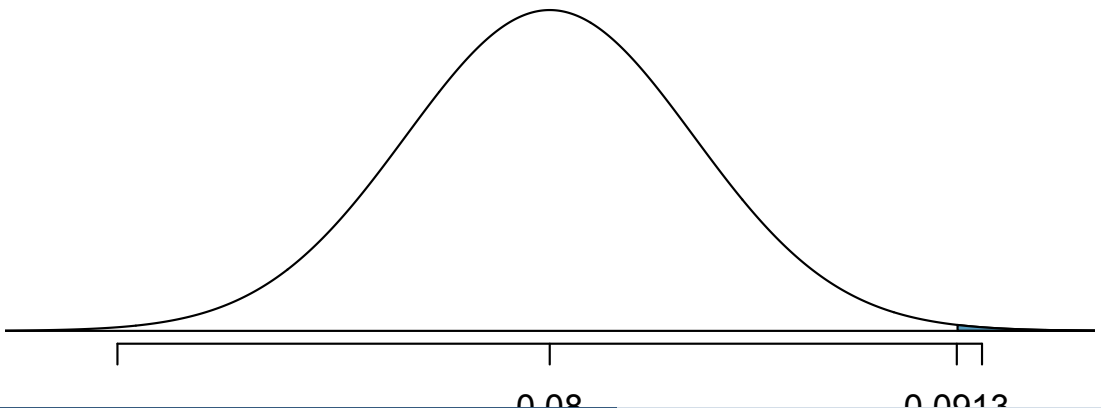
- $H_A : \mu > 0.08 \rightarrow$ one-tailed
- p-value: P(obtaining a random sample of 150 farmed salmon with an average concentration of contaminant ≥ 0.0913 ppm, if the true average concentration is 0.08 ppm)

Salmon - p-value

- $H_A : \mu > 0.08 \rightarrow$ one-tailed
- p-value: P(obtaining a random sample of 150 farmed salmon with an average concentration of contaminant ≥ 0.0913 ppm, if the true average concentration is 0.08 ppm)
- Since the sampling distribution is nearly normal (according to the CLT), we can find this probability using a Z score, which requires
  - an observed value (sample mean $= 0.0913$),
  - a true mean (null value that we assume to be true $= 0.08$), and
  - a measure of variability (SE $= 0.004$).

Salmon - p-value

- $H_A : \mu > 0.08 \rightarrow$ one-tailed
- p-value: P(obtaining a random sample of 150 farmed salmon with an average concentration of contaminant ≥ 0.0913 ppm, if the true average concentration is 0.08 ppm)
- Since the sampling distribution is nearly normal (according to the CLT), we can find this probability using a Z score, which requires
  - an observed value (sample mean $= 0.0913$),
  - a true mean (null value that we assume to be true $= 0.08$), and
  - a measure of variability (SE $= 0.004$).



Salmon - p-value

- $H_A : \mu > 0.08 \rightarrow$ one-tailed
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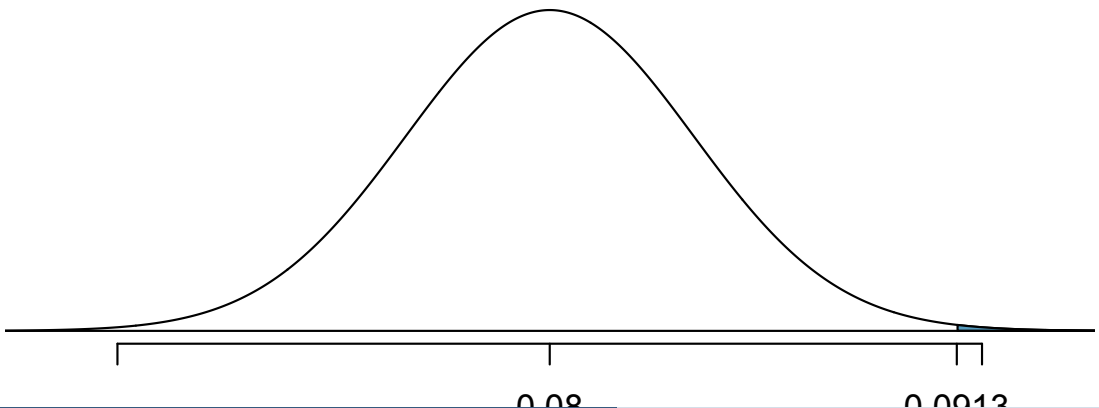
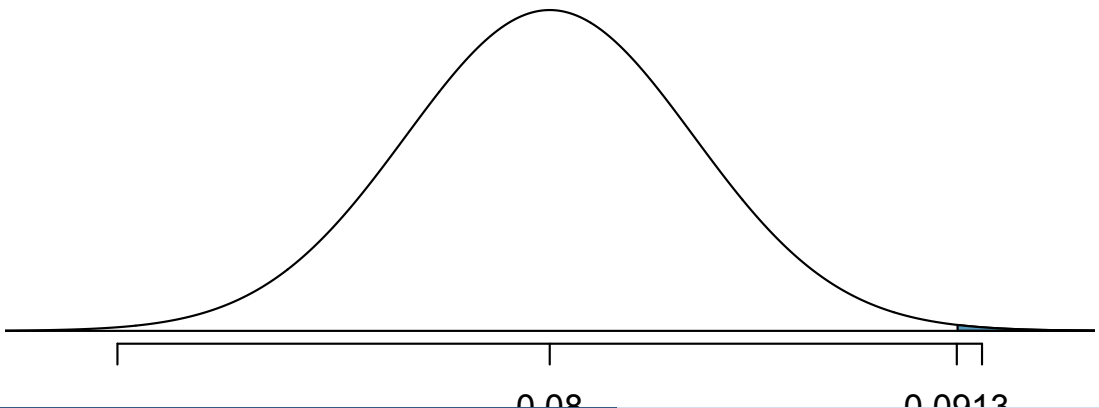


$$Z = \frac{0.0913 - 0.08}{0.004} = 2.83$$

Salmon - p-value

- $H_A : \mu > 0.08 \rightarrow$ one-tailed
- p-value: P(obtaining a random sample of 150 farmed salmon with an average concentration of contaminant ≥ 0.0913 ppm, if the true average concentration is 0.08 ppm)
- Since the sampling distribution is nearly normal (according to the CLT), we can find this probability using a Z score, which requires
  - an observed value (sample mean = 0.0913),
  - a true mean (null value that we assume to be true = 0.08), and
  - a measure of variability (SE = 0.004).



$$\begin{aligned} Z &= \frac{0.0913 - 0.08}{0.004} \\ &= 2.83 \\ p - value &= P(Z > 2.83) \\ &= 0.0023 \end{aligned}$$

Salmon - p-value (using R)

```
inference(salmon[,"Mirex"], est = "mean", type = "ht",
          method = "theoretical", null = 0.08,
          alternative = "greater")

## Single mean
## Summary statistics: mean = 0.0913 ;  sd = 0.0495 ;  n = 150
## H0: mu = 0.08
## HA: mu > 0.08
## Standard error = 0.004
## Test statistic: Z = 2.804
## p-value:  0.0025
```

*Results slightly different due to rounding.

Salmon - confidence interval

- Confidence level: 95%

Salmon - confidence interval

- Confidence level: 95%
- Theoretical: Using a critical value based on the normal distribution ($z^\star$):

$$\begin{aligned} &\text{point estimate} \pm ME \\ = &\text{point estimate} \pm z^\star \times SE \end{aligned}$$

Salmon - confidence interval

- Confidence level: 95%
- Theoretical: Using a critical value based on the normal distribution ($z^\star$):

$$\begin{aligned} &\text{point estimate} \pm ME \\ =\ &\text{point estimate} \pm z^\star \times SE \end{aligned}$$

$$0.0913 \pm 1.96 \times 0.004 \quad \approx \quad 0.0913 \pm 0.008$$

Salmon - confidence interval

- Confidence level: 95%
- Theoretical: Using a critical value based on the normal distribution ($z^\star$):

$$\begin{aligned} & \text{point estimate} \pm ME \\ = \ & \text{point estimate} \pm z^\star \times SE \end{aligned}$$

$$\begin{aligned} 0.0913 \pm 1.96 \times 0.004 &\approx 0.0913 \pm 0.008 \\ &= (0.0833, 0.0993) \end{aligned}$$

Salmon - confidence interval (using R)

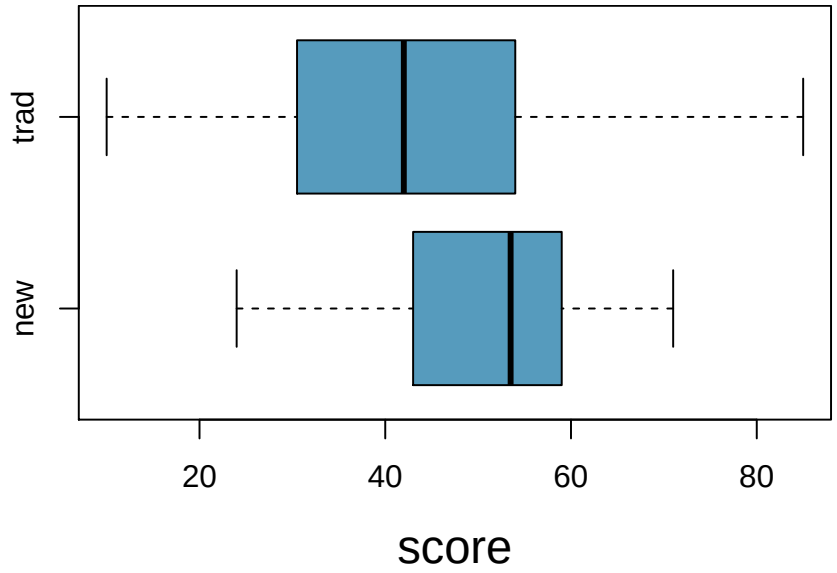
```
inference(salmon[,"Mirex"], est = "mean", type = "ci",
          method = "theoretical")

## Single mean
## Summary statistics: mean = 0.0913 ;  sd = 0.0495 ;  n = 150
## Standard error = 0.004
## 95 % Confidence interval = ( 0.0834 , 0.0993 )
```

*Results are slightly different due to rounding.

Example - Reading

An educator believes that new reading activities for elementary school children will improve reading comprehension scores. She randomly assigns third graders to an 8-week program in which some will use these activities (18 students) and others will experience traditional teaching methods (20 students). At the end of the experiment, both groups can take a reading comprehension exam. The distributions of their scores are shown below. Is there a difference between the average reading scores of students subjected to new and traditional methods?



Reading - set-up

- cases:

Reading - set-up

- cases: 38 students
- variable(s):

Reading - set-up

- cases: 38 students
- variable(s): (1) score - numerical, (2) treatment - categorical
- parameter of interest:

Reading - set-up

- cases: 38 students
- variable(s): (1) score - numerical, (2) treatment - categorical
- parameter of interest: $\mu_{new} - \mu_{trad}$, difference between average scores of all students subjected to new and traditional methods
- point estimate:

Reading - set-up

- cases: 38 students
- variable(s): (1) score - numerical, (2) treatment - categorical
- parameter of interest: $\mu_{new} - \mu_{trad}$, difference between average scores of all students subjected to new and traditional methods
- point estimate: $\bar{x}_{new} - \bar{x}_{trad}$, difference between average scores of students in this study subjected to new and traditional methods
- test:

Reading - set-up

- cases: 38 students
- variable(s): (1) score - numerical, (2) treatment - categorical
- parameter of interest: $\mu_{new} - \mu_{trad}$, difference between average scores of all students subjected to new and traditional methods
- point estimate: $\bar{x}_{new} - \bar{x}_{trad}$, difference between average scores of students in this study subjected to new and traditional methods
- test: compare two population means of independent groups (unpaired)
- hypotheses:

Reading - set-up

- cases: 38 students
- variable(s): (1) score - numerical, (2) treatment - categorical
- parameter of interest: $\mu_{new} - \mu_{trad}$, difference between average scores of all students subjected to new and traditional methods
- point estimate: $\bar{x}_{new} - \bar{x}_{trad}$, difference between average scores of students in this study subjected to new and traditional methods
- test: compare two population means of independent groups (unpaired)
- hypotheses: (two-tailed)

$$H_0 : \mu_{new} = \mu_{trad}$$
$$H_A : \mu_{new} \neq \mu_{trad}$$

- test statistic:

Reading - set-up

- cases: 38 students
- variable(s): (1) score - numerical, (2) treatment - categorical
- parameter of interest: $\mu_{new} - \mu_{trad}$, difference between average scores of all students subjected to new and traditional methods
- point estimate: $\bar{x}_{new} - \bar{x}_{trad}$, difference between average scores of students in this study subjected to new and traditional methods
- test: compare two population means of independent groups (unpaired)
- hypotheses: (two-tailed)

$$H_0 : \mu_{new} = \mu_{trad}$$
$$H_A : \mu_{new} \neq \mu_{trad}$$

- test statistic: T since $n_1 < 30$ and $n_2 < 30$

Reading - p-value

```
Test statistic: T = 2.254
Degrees of freedom: 17
```

one tail	0.100	0.050	0.025	0.010	0.005
two tails	0.200	0.100	*0.050*	*0.020*	0.010
df 16	1.34	1.75	2.12	2.58	2.92
17	1.33	1.74	*2.11*	*2.57*	2.90
18	1.33	1.73	2.10	2.55	2.88
19	1.33	1.73	2.09	2.54	2.86
20	1.33	1.72	2.09	2.53	2.85

```
p-value: between 0.01 and 0.05
```

Reading - p-value (using R)

```
inference(reading[,"score"], group = reading[,"treatment"],
          est = "mean", type = "ht", method = "theoretical",
          null = 0, alternative = "twosided")

## Response variable: numerical, Explanatory variable: categorical
## Difference between two means
## Summary statistics:
## n_new = 18, mean_new = 16.7778, sd_new = 6.6999
## n_trad = 20, mean_trad = 11.55, sd_trad = 7.5983
## Observed difference between means (new-trad) = 5.2278
##
## H0: mu_new - mu_trad = 0
## HA: mu_new - mu_trad != 0
## Standard error = 2.32
## Test statistic: T =  2.254
## Degrees of freedom:  17
## p-value =  0.0378
```

Reading - confidence interval

- Confidence level: 95%

Reading - confidence interval

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- Theoretical: Using a critical value based on the t distribution ($t^\star$):

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Reading - confidence interval

- Confidence level: 95%
- Theoretical: Using a critical value based on the t distribution ($t^\star$):

$$\begin{aligned} &\text{point estimate} \pm ME \\ =\ &\text{point estimate} \pm t^\star \times SE \end{aligned}$$

$$5.23 \pm 2.11 \times 2.32 \quad \approx \quad 5.23 \pm 4.90$$

Reading - confidence interval

- Confidence level: 95%
- Theoretical: Using a critical value based on the t distribution ($t^\star$):

$$\begin{aligned} & \text{point estimate} \pm ME \\ = \ & \text{point estimate} \pm t^\star \times SE \end{aligned}$$

$$\begin{aligned} 5.23 \pm 2.11 \times 2.32 &\approx 5.23 \pm 4.90 \\ &= (0.33, 10.13) \end{aligned}$$

Reading - confidence interval (using R)

```
inference(reading[,"score"], group = reading[,"treatment"],
          est = "mean", type = "ci", method = "theoretical")

## Response variable: numerical, Explanatory variable: categorical
## Difference between two means
## Summary statistics:
## n_new = 18, mean_new = 16.7778, sd_new = 6.6999
## n_trad = 20, mean_trad = 11.55, sd_trad = 7.5983
## Observed difference between means (new-trad) = 5.2278
##
## Standard error = 2.3196
## 95 % Confidence interval = ( 0.3339 , 10.1217 )
```

Example - Breast Cancer

A survey was conducted in the US of 10,000 women with ages between 50-54 whose mothers had been diagnosed with breast cancer at some point in their life. 400 of the survey respondents reported themselves as also having had breast cancer. If the prevalence rate of breast cancer for US women in this age group is about 2% does this survey show evidence for the heritability of breast cancer?

Breast Cancer - set-up

$$n = 10000, \hat{p} = 0.04$$

- cases:

Breast Cancer - set-up

$$n = 10000, \hat{p} = 0.04$$

- cases: 10000 women whose mothers had breast cancer
- variable(s):

Breast Cancer - set-up

$$n = 10000, \hat{p} = 0.04$$

- cases: 10000 women whose mothers had breast cancer
- variable(s): only 1 - respondent's breast cancer status (categorical)
- parameter of interest:

Breast Cancer - set-up

$$n = 10000, \hat{p} = 0.04$$

- cases: 10000 women whose mothers had breast cancer
- variable(s): only 1 - respondent's breast cancer status (categorical)
- parameter of interest: p, true proportion of women with breast cancer (whose mothers also had breast cancer)
- point estimate:

Breast Cancer - set-up

$$n = 10000, \hat{p} = 0.04$$

- cases: 10000 women whose mothers had breast cancer
- variable(s): only 1 - respondent's breast cancer status (categorical)
- parameter of interest: p, true proportion of women with breast cancer (whose mothers also had breast cancer)
- point estimate: $\hat{p}$, proportion of women with breast cancer in survey sample
- hypotheses:

Breast Cancer - set-up

$$n = 10000, \hat{p} = 0.04$$

- cases: 10000 women whose mothers had breast cancer
- variable(s): only 1 - respondent's breast cancer status (categorical)
- parameter of interest: p, true proportion of women with breast cancer (whose mothers also had breast cancer)
- point estimate: $\hat{p}$, proportion of women with breast cancer in survey sample
- hypotheses: $H_0 : p = 0.02$; $H_A : p > 0.02$

Breast Cancer - p-value

- $H_A : p > 0.02 \rightarrow$ one-tailed

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- $H_A : p > 0.02 \rightarrow$ one-tailed
- p-value: P(obtaining a sample of 10000 women where 400 or more have had breast cancer, if the true prevalence breast cancer is 0.02)

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- Conditions: **expected** number of success (200) and failures (9800) ≥ 10

Breast Cancer - p-value

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- p-value: P(obtaining a sample of 10000 women where 400 or more have had breast cancer, if the true prevalence breast cancer is 0.02)
- Conditions: **expected** number of success (200) and failures (9800) ≥ 10
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- Conditions: **expected** number of success (200) and failures (9800) ≥ 10
- Since the sampling distribution is nearly normal (according to the CLT), we can find this probability using a Z score
- Because we are conducting a hypothesis test on a proportion,

$$SE = \sqrt{p_0(1-p_0)/n} = \sqrt{0.02(1-0.02)/10000} = 0.0014$$

Breast Cancer - p-value

- $H_A : p > 0.02 \rightarrow$ one-tailed
- p-value: P(obtaining a sample of 10000 women where 400 or more have had breast cancer, if the true prevalence breast cancer is 0.02)
- Conditions: **expected** number of success (200) and failures (9800) ≥ 10
- Since the sampling distribution is nearly normal (according to the CLT), we can find this probability using a Z score
- Because we are conducting a hypothesis test on a proportion,

$$SE = \sqrt{p_0(1-p_0)/n} = \sqrt{0.02(1-0.02)/10000} = 0.0014$$

$$Z = \frac{\hat{p} - p_0}{\sqrt{p_0(1-p_0)/n}} = \frac{0.04 - 0.02}{0.0014} = 14.29$$

Breast Cancer - p-value

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- Because we are conducting a hypothesis test on a proportion,

$$SE = \sqrt{p_0(1-p_0)/n} = \sqrt{0.02(1-0.02)/10000} = 0.0014$$

$$Z = \frac{\hat{p} - p_0}{\sqrt{p_0(1-p_0)/n}} = \frac{0.04 - 0.02}{0.0014} = 14.29$$

$$\text{p-value} = P(Z > 14.29) \approx 0$$

Breast Cancer - p-value (using R)

```
inference(bc, est = "proportion", type = "ht",
          method = "theoretical", null = 0.02,
          alternative = "greater", success="yes")

## Single proportion -- success: yes
## Summary statistics: p_hat = 0.04 ;  n =  10000
## H0: p = 0.02
## HA: p > 0.02
## Check conditions: number of expected successes = 200 ; number of
## Standard error = 0.0014
## Test statistic: Z =  14.286
## p-value =  0
```

Breast Cancer - confidence interval

- Confidence level: 99%

Breast Cancer - confidence interval

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- Conditions: **observed** number of success (400) and failures (9600) ≥ 10

Breast Cancer - confidence interval

- Confidence level: 99%
- Conditions: **observed** number of success (400) and failures (9600) ≥ 10
- Theoretical: Using a critical value based on the Z distribution ($z^\star$):

$$\begin{aligned} &\text{point estimate} \pm ME \\ =\ &\text{point estimate} \pm z^\star \times SE \end{aligned}$$

Breast Cancer - confidence interval

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- Conditions: **observed** number of success (400) and failures (9600) ≥ 10
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For a confidence interval,

$$SE = \sqrt{\hat{p}(1-\hat{p})/n} = 0.00196$$

Breast Cancer - confidence interval

- Confidence level: 99%
- Conditions: **observed** number of success (400) and failures (9600) ≥ 10
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For a confidence interval,

$$SE = \sqrt{\hat{p}(1-\hat{p})/n} = 0.00196$$

$$0.04 \pm 2.58 \times 0.00196 \quad \approx \quad 0.04 \pm 0.0050$$

Breast Cancer - confidence interval

- Confidence level: 99%
- Conditions: **observed** number of success (400) and failures (9600) ≥ 10
- Theoretical: Using a critical value based on the Z distribution ($z^\star$):

$$\begin{aligned} & \text{point estimate} \pm ME \\ = \ & \text{point estimate} \pm z^\star \times SE \end{aligned}$$

For a confidence interval,

$$SE = \sqrt{\hat{p}(1-\hat{p})/n} = 0.00196$$

$$\begin{aligned} 0.04 \pm 2.58 \times 0.00196 &\approx 0.04 \pm 0.0050 \\ &= (0.035, 0.045) \end{aligned}$$

Reading - confidence interval (using R)

```
inference(bc, est = "proportion", type = "ci",
          method = "theoretical", success="yes",
          conflevel = 0.99)

Single proportion -- success: yes
Summary statistics: p_hat = 0.04 ;  n =  10000
Check conditions: number of successes = 400 ; number of failures = 9
Standard error = 0.002
99 % Confidence interval = ( 0.035 , 0.045 )
```

Example - Breast Cancer & Age

It is theorized that an important risk factor for breast cancer is age at first birth. An international study was set up to test this hypothesis. Breast-cancer cases were identified among women in selected hospitals in the United States, Greece, Yugoslavia, Brazil, Taiwan, and Japan. Controls were chosen from women of comparable age who were in the hospital at the same time as the cases but who did not have breast cancer. All women were asked about their age at first birth.

The set of women with at least one birth was arbitrarily divided into two categories: (1) women whose age at first birth was less than or equal to 29 years and (2) women whose age at first birth was 30 years. The following results were found among women with at least one birth: 683 of 3220 (21.2%) women with breast cancer (case women) and 1498 of 10,245 (14.6%) women without breast cancer (control women) had an age at first birth greater than 30. How can we assess whether this difference is significant or simply due to chance?

Breast Cancer & Age - set-up

We are comparing two categorical variables (breast cancer status vs. age at first birth), this can be summarized by a contingency table.

	Breast Cancer (case)	No Breast Cancer (Controls)	Total
≤ 29			
≥ 30			
Total			

Breast Cancer & Age - set-up

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We are given 683 of 3220 (21.2%) women with breast cancer (case women) and 1498 of 10,245 (14.6%) women without breast cancer (control women) had an age at first birth greater than 30.

	Breast Cancer (case)	No Breast Cancer (Controls)	Total
≤ 29			
≥ 30	683		
Total	3220		

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	Breast Cancer (case)	No Breast Cancer (Controls)	Total
≤ 29	2537		
≥ 30	683		
Total	3220		

Breast Cancer & Age - set-up

We are comparing two categorical variables (breast cancer status vs. age at first birth), this can be summarized by a contingency table.

We are given 683 of 3220 (21.2%) women with breast cancer (case women) and 1498 of 10,245 (14.6%) women without breast cancer (control women) had an age at first birth greater than 30.

	Breast Cancer (case)	No Breast Cancer (Controls)	Total
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	Breast Cancer (case)	No Breast Cancer (Controls)	Total
≤ 29	2537	8747	11284
≥ 30	683	1498	2181
Total	3220	10245	13465

Breast Cancer & Age - set-up

$$n_{case} = 3220, \;\; n_{ctrl} = 10245, \;\; \hat{p}_{case} = 0.212, \;\; \hat{p}_{ctrl} = 0.146$$

- cases:

Breast Cancer & Age - set-up

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Breast Cancer & Age - set-up

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Breast Cancer & Age - set-up

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- parameter of interest: $p_{case} - p_{ctrl}$
- point estimate:

Breast Cancer & Age - set-up

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- point estimate: $\hat{p}_{case} - \hat{p}_{ctrl}$
- test: compare two population proportion of independent groups
- hypotheses:

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- variable(s): (1) breast cancer status - categorical, (2) age at first birth - categorical
- parameter of interest: $p_{case} - p_{ctrl}$
- point estimate: $\hat{p}_{case} - \hat{p}_{ctrl}$
- test: compare two population proportion of independent groups
- hypotheses: (two-tailed)

  $H_0 : p_{case} = p_{ctrl}$
  $H_A : p_{case} \neq p_{ctrl}$
- Note: $p_{case} = P(age \geq 30 | case)$ and $p_{ctrl} = P(age \geq 30 | ctrl)$

Breast Cancer & Age - p-value

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  - case: **expected** number of successes (522) and failures (2698) are ≥ 10
  - control: **expected** number of successes (1659) and failures (8586) are ≥ 10

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  - control: **expected** number of successes (1659) and failures (8586) are ≥ 10
- The sampling distribution is nearly normal (according to the CLT), we can find this probability using a Z score
- Because we are conducting a hypothesis test on the difference of two proportions,

$$SE = \sqrt{\hat{p}(1-\hat{p})\left(1/n_{case} + 1/n_{ctrl}\right)} = 0.0074$$

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$$\text{p-value} = P(Z > 8.92) + P(Z < -8.92) \approx 0$$

Breast Cancer & Age - p-value (using R)

```
inference(z[,"age"],group=z[,"bc"],
          est = "proportion", type = "ht",
          method = "theoretical", null = 0.02,
          alternative = "greater", success=">30")

## Response variable: categorical, Explanatory variable: categorical
## Two categorical variables
## Difference between two proportions -- success: >30
## Summary statistics:
##       group
## data    case  ctrl   Sum
##   <29   2537  8747 11284
##   >30    683  1498  2181
##   Sum   3220 10245 13465
## Observed difference between proportions (case-ctrl) = 0.0659

...
```

Breast Cancer & Age - p-value (using R)

```
inference(z[,"age"],group=z[,"bc"],
          est = "proportion", type = "ht",
          method = "theoretical", null = 0,
          alternative = "greater", success=">30")
```

```
...
```

```
## H0: p_case - p_ctrl = 0
## HA: p_case - p_ctrl > 0
## Pooled proportion = 0.162
## Check conditions:
##    case : number of expected successes = 522 ; number of expected failur
##    ctrl : number of expected successes = 1659 ; number of expected failu
## Standard error = 0.007
## Test statistic: Z =  8.853
## p-value =  0
```

Breast Cancer & Age - confidence interval

- Confidence level: 98%

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- Theoretical: Using a critical value based on the Z distribution ($z^\star$):

$$\begin{aligned} &\text{point estimate} \pm ME \\ =\ &\text{point estimate} \pm z^\star \times SE \end{aligned}$$

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$$\begin{aligned} &\text{point estimate} \pm ME \\ &= \text{point estimate} \pm z^\star \times SE \end{aligned}$$

For a confidence interval,

$$\begin{aligned} SE &= \sqrt{\hat{p}_{case}(1-\hat{p}_{case})/n_{case} + \hat{p}_{ctrl}(1-\hat{p}_{ctrl})/n_{ctrl}} \\ &= \sqrt{0.212(1-0.212)/3220 + 0.146(1-0.146)/10245} \\ &= 0.008 \end{aligned}$$

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$$(0.212 - 0.146) \pm 2.33 \times 0.008 \quad \approx \quad 0.066 \pm 0.0186$$

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$$\begin{aligned} (0.212 - 0.146) \pm 2.33 \times 0.008 &\approx 0.066 \pm 0.0186 \\ &= (0.0474,\ 0.0846) \end{aligned}$$

Breast Cancer & Age - confidence interval (using R)

```
inference(z[,"age"],group = z[,"bc"],
          est = "proportion", type = "ci",
          method = "theoretical", success=">30",
          conflevel = 0.98)

## Response variable: categorical, Explanatory variable: categorical
## Two categorical variables
## Difference between two proportions -- success: >30
## Summary statistics:
##       group
## data    case  ctrl   Sum
##   <29   2537  8747 11284
##   >30    683  1498  2181
##   Sum   3220 10245 13465
## Observed difference between proportions (case-ctrl) = 0.0659
##
## Check conditions:
##    case : number of successes = 683 ; number of failures = 2537
##    ctrl : number of successes = 1498 ; number of failures = 8747
## Standard error = 0.008
## 98 % Confidence interval = ( 0.0473 , 0.0845 )
```