

INFERENCE GUIDE

CONFIDENCE INTERVALS

Use **confidence intervals** to **estimate** a parameter with a particular **confidence level, C**.

IDENTIFY: Interval name, parameter, and C level

CHECK: Check that conditions for the procedure are met.

CALCULATE:

CI: point estimate \pm critical value \times SE of estimate

df = (if applicable)
(____, ____)

CONCLUDE:

We are C% confident that the interval (__, __) contains the true [parameter]. (Put the parameter in *context*.)

We have evidence that [...], because [...]. OR
We do not have evidence that [...], because [...].

When the parameter is: **a single proportion p**

IDENTIFY: **1-Sample Z-Interval** for a population proportion or **1-Sample Z-Test** for a population proportion

CHECK:

- Data come from a random sample or process
- If sampling without replacement, $n \leq 10\%$ of N
- For CI: $n\hat{p} \geq 10$ and $n(1 - \hat{p}) \geq 10$
For Test: $np_0 \geq 10$ and $n(1 - p_0) \geq 10$

CALCULATE: (Desmos; TI 1-PropZInt, 1-PropZTest)

point estimate: sample proportion \hat{p}

SE of estimate: for CI: use $\sqrt{\frac{\hat{p}(1-\hat{p})}{n}}$; for Test: use $\sqrt{\frac{p_0(1-p_0)}{n}}$

When the parameter is: **a difference in proportions $p_1 - p_2$**

IDENTIFY: **2-Sample Z-Interval** for diff in population props. or **2-Sample Z-Test** for diff in population proportions

CHECK:

- Data come from 2 independent random samples or 2 randomly assigned treatments.
- If sampling w/o repl., $n_1 \leq 10\%$ of N_1 and $n_2 \leq 10\%$ of N_2
- For CI: $n_1\hat{p}_1 \geq 10$, $n_1(1 - \hat{p}_1) \geq 10$,
 $n_2\hat{p}_2 \geq 10$, $n_2(1 - \hat{p}_2) \geq 10$
For Test: use \hat{p}_c , the pooled proportion, in place of \hat{p}_1 and \hat{p}_2 above

CALCULATE: (Desmos; TI 2-PropZInt, 2-PropZTest)

point estimate: difference of sample proportions $\hat{p}_1 - \hat{p}_2$

SE of estimate:

CI: use $\sqrt{\frac{\hat{p}_1(1-\hat{p}_1)}{n_1} + \frac{\hat{p}_2(1-\hat{p}_2)}{n_2}}$; Test: use $\sqrt{\hat{p}_c(1-\hat{p}_c)\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}$

HYPOTHESIS TESTS

Use **hypothesis tests** to **test** H_0 versus H_A at a particular **significance level, α** .

IDENTIFY: Test name, parameter, hypotheses, and α

CHECK: Check that conditions for the procedure are met.

CALCULATE:

standardized test statistic = $\frac{\text{point estimate} - \text{null value}}{\text{SE of estimate}}$

df = (if applicable)
p-value =

CONCLUDE:

p-value $\leq \alpha$, so we reject H_0 .

We have evidence that [H_A]. (Put H_A in *context*.)

OR

p-value $> \alpha$, so we do NOT reject H_0 .

We do NOT have evidence that [H_A]. (Put H_A in *context*.)

When the parameter is: **a single mean μ**

IDENTIFY: **1-Sample T-Interval** for a population mean or **1-Sample T-Test** for a population mean

CHECK:

- Data come from a random sample or process
- If sampling without replacement, $n \leq 10\%$ of N
- $n \geq 30$ OR population distribution is nearly normal OR sample data is free from strong skewness and outliers

CALCULATE: (Desmos; TI TInterval, T-Test)

point estimate: sample mean \bar{x}

SE of estimate: $\frac{s}{\sqrt{n}}$

$df = n - 1$

When the parameter is: **a difference in means $\mu_1 - \mu_2$**

IDENTIFY: **2-Sample T-Interval** for diff in population means or **2-Sample T-Test** for diff in population means

CHECK:

- Data come from 2 independent random samples or 2 randomly assigned treatments.
- If sampling w/o repl., $n_1 \leq 10\%$ of N_1 and $n_2 \leq 10\%$ of N_2
- $n_1 \geq 30$ and $n_2 \geq 30$ OR both population distributions nearly normal OR both sample data sets are free from strong skewness and outliers

CALCULATE: (Desmos; TI 2-SampTInt, 2-SampTTest)

point estimate: difference of sample means $\bar{x}_1 - \bar{x}_2$

SE of estimate: $\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}$

df : use technology

The χ^2 Hypothesis Tests for categorical variables: $\text{chi-square statistic} = \sum \frac{(\text{observed} - \text{expected})^2}{\text{expected}}$

*When comparing the distribution of **one categorical variable to a fixed/specified population distribution**

IDENTIFY: χ^2 Goodness of Fit Test

CHECK:

- Data come from a random sample or process.
- If sampling without replacement, $n \leq 10\%$ of N
- All expected counts ≥ 5 . (To calculate expected counts for each category, multiply the sample size by the expected proportion under H_0 .)

CALCULATE: (Desmos or TI χ^2 GOF-Test)

$$\chi^2 =$$

$$df = \# \text{ of categories} - 1$$

When comparing the distribution of a **categorical variable across 2 or more populations/treatments**

IDENTIFY: χ^2 Test for Homogeneity

CHECK:

- Data come from 2 or more independent random samples or 2 or more randomly assigned treatments.
- If sampling without replacement, each n should $\leq 10\%$ of each corresponding N
- All expected counts ≥ 5 . (Calculate expected counts and verify this to be true.)

CALCULATE: (Desmos; TI χ^2 -Test, then 2ND MATRIX, EDIT, 2: [B] to find expected counts)

$$\chi^2 =$$

$$df = (\# \text{ of rows} - 1)(\# \text{ of cols} - 1)$$

When looking for **association or dependence between two categorical variables**

IDENTIFY: χ^2 Test for Independence

CHECK:

- Data come from a random sample or process.
- If sampling without replacement, $n \leq 10\%$ of N
- All expected counts ≥ 5 . (Calculate expected counts and verify this to be true.)

CALCULATE: (Desmos; TI χ^2 -Test, then 2ND MATRIX, EDIT, 2: [B] to find expected counts)

$$\chi^2 =$$

$$df = (\# \text{ of rows} - 1)(\# \text{ of cols} - 1)$$

See also CALCULATE instructions using NumWorks calculator, Casio calculator, or R commands.

*Not tested on the AP[®] Exam.