CONFIDENCE INTERVALS AND SAMPLE SIZES
CHAPTER 7 – One Population

CONFIDENCE INTERVALS: point estimate ± margin of error

C.I. around mean (sec 7.1, p. 359)

(σ known; data normal or n ≥ 30)

$$C.I._{1-\alpha} = \bar{X} \pm z_{\alpha/2}\left(\frac{\sigma}{\sqrt{n}}\right)$$

C.I. around mean (sec 7.2, p. 371)

(σ unknown; data normal or n ≥ 30)

$$C.I._{1-\alpha} = \bar{X} \pm t_{\alpha/2,df}\left(\frac{s}{\sqrt{n}}\right)$$

df = n - 1

C.I. around proportion (sec 7.3, p. 378)

($n\hat{p} \geq 5$ and $n\hat{q} \geq 5$)

$$C.I._{1-\alpha} = \hat{p} \pm z_{\alpha/2}\sqrt{\frac{\hat{p}\hat{q}}{n}}$$

$\hat{p}$ = sample ppt

SAMPLE SIZES (always round up to nearest integer)

Estimate of mean (p. 369)

$$n = \left(\frac{z_{\alpha/2} \times \sigma}{E}\right)^2$$

E = error bound

σ can = s

Estimate of proportion (p. 379)

$$n = \hat{p}\hat{q}\left(\frac{z_{\alpha/2}}{E}\right)^2$$

E = error bound

σ can = s

NOTE : if $\hat{p}$ is unknown, use $\hat{p} = \hat{q} = .50$ in formula above

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COMMON Z VALUES		
$1-\alpha$	α	$z_{\alpha/2}$
.90		
.95		
.96		
.98		
.99		

HINTS:

1. For "… how large a sample…" use sample size formulas.
2. For "…find …confidence interval…" use C.I. formulas
3. Use **normal** for mean.
   Use **binomial** for proportion, ratio, percent

ROUNDING:

C.I. normal

– **if using raw data**, round CI values to one decimal place more than the raw data size.

- **if using given mean**, round CI values to same size as the mean.

C.I. binomial – usually 3 decimal places

Sample sizes – round UP to next integer

CONFIDENCE INTERVALS AND SAMPLE SIZES
CHAPTER 9 – Two Populations

CONFIDENCE INTERVALS

C.I. around difference between two means

(sec 9.1, p. 474) **(**σ_1 and σ_2 known; n_1, $n_2 \geq 30$ or pops. normal**)**

$$C.I._{1-\alpha} = \left(\bar{X}_1 - \bar{X}_2\right) \pm z_{\alpha/2}\sqrt{\left(\frac{\sigma_1^2}{n_1} + \frac{\sigma_2^2}{n_2}\right)}$$

C.I. around difference of two means

independent samples (sec. 9.2, p. 485)

(σ_1 and σ_2 unknown; pops. normal or $n_1,n_2 \geq 30$

$$C.I._{1-\alpha} = \left(\bar{x}_1 - \bar{x}_2\right) \pm t_{\alpha/2,df}\sqrt{\left(\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}\right)}$$

df = smaller of ($n_1 - 1$) or ($n_2 - 1$)
variances are assumed unequal

C.I. around difference of two means

dependent or paired samples (sec. 9.3, p. 498)

$$C.I._{1-\alpha} = \bar{D} \pm t_{\alpha/2,df}\frac{s_D}{\sqrt{n}}$$

$\bar{D}$ = mean of differences

s_D = st. dev. of differences

n = number of pairs

$df = n - 1$

C.I. around difference of two proportions

(sec. 9.4, p. 507)

$$C.I._{1-\alpha} = \left(\hat{p}_1 - \hat{p}_2\right) \pm z_{\alpha/2}\sqrt{\left(\frac{\hat{p}_1 \cdot \hat{q}_1}{n_1} + \frac{\hat{p}_2 \cdot \hat{q}_2}{n_2}\right)}$$

HYPOTHESIS TESTING (ch. 8 and 9)

A. DETERMINE H_0 and H_1.

one mean			**one proportion**			**two means***	**two proportions***
$H_0: \mu =$	$H_0: \mu =$	$H_0: \mu =$	$H_0: p =$	$H_0: p =$	$H_0: p =$	$H_0: \mu_1 = \mu_2$	$H_0: p_1 = p_2$
$H_1: \mu \neq$	$H_1: \mu <$	$H_1: \mu >$	$H_1: p \neq$	$H_1: p <$	$H_1: p >$	$H_1: \mu_1 \neq \mu_2$	$H_1: p_1 \neq p_2$
2–tailed	left tailed	right tailed	2–tailed	left tailed	right tailed	2–tailed	2 - tailed

*** also have left tailed and right tailed forms**

NOTE: two means, dependent samples use H_O: $\mu_D = 0$ versus $\mu_D \neq 0$, $\mu_D < 0$, $\mu_D > 0$

B. CHOOSE α LEVEL AND DETERMINE EFFECT OF TYPE I ERROR.

Type I (or α level) error: Your sample suggests that you reject the null hypothesis when it is really true within the population.

α = maximum probability of committing a Type I error

C. DETERMINE CRITICAL VALUE (based on μ or p, n value, 1- or 2-tailed test)

One mean:

σ known (sec. 8.2) – use **z value**

σ unknown (sec. 8.3) – use **t value** (d.f. = n – 1)

One proportion (sec 8.4):

$np_0(1-p_0) \geq 10$ - always use **z value**

Two means:

σ_1, σ_2 known (sec. 9.1) – use **z value**

σ_1, σ_2 unknown, independent samples (sec. 9.2) – use **t value** (d.f. = n – 1 for smaller n)

dependent samples (sec 9.3) – use **t value** (d.f. = n – 1)

Two proportions (sec. 9.4): always use **z value**

COMMON Z VALUES		
α	1 tailed	2 tailed
.01	2.33	2.58
.02	2.05	2.33
.05	1.65	1.96
.10	1.28	1.65

D. DETERMINE TEST VALUE (based on data and μ or p from H_0)

one mean: $$\text{t.v.} = \frac{(\bar{X} - \mu)}{(\sigma/\sqrt{n})} = \frac{(\bar{X} - \mu)}{(s/\sqrt{n})}$$

(sec 8.2 and sec 8.3) μ = population mean

one proportion: $$\text{t.v.} = \frac{(\hat{p} - p)}{\sqrt{\left(\frac{p \cdot q}{n}\right)}}$$

(sec 8.4) $\hat{p} = \frac{X}{n}$ p = population proportion two means: $\begin{cases} \sigma \text{ known (sec. 9.1) use } z \text{ and } \sigma \\ \sigma \text{ unknown (sec. 9.2) use } t \text{ and } s \\ \quad \text{with (df} = n-1 \text{ for smallest } n) \end{cases}$

$$t.v. = \frac{\left[\left(\bar{X}_1 - \bar{X}_2\right) - \left(\mu_1 - \mu_2\right)\right]}{\sqrt{\left(\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}\right)}}$$

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two means with dependent samples (matched pairs – sec. 9.3):

$$t.v. = \frac{\left(\bar{D} - \mu_D\right)}{\left(s_D / \sqrt{n}\right)}$$

μ_D = mean of differences

s_D = st. dev. of differences

n = number of pairs

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two proportions (sec 9.4) - assume samples independent with $n \cdot p$ and $n \cdot q \geq 5$

$$t.v. = \frac{\left[\left(\hat{p}_1 - \hat{p}_2\right) - \left(p_1 - p_2\right)\right]}{\left[\sqrt{(\bar{p}\bar{q})}\sqrt{\left(\frac{1}{n_1} + \frac{1}{n_2}\right)}\right]}$$

$\bar{p} = \frac{(x_1 + x_2)}{(n_1 + n_2)}$ $\qquad \hat{p}_1 = \frac{x_1}{n_1}$

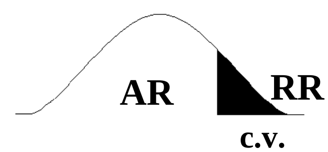
$\bar{q} = 1 - \bar{p}$ $\qquad \hat{p}_2 = \frac{x_2}{n_2}$

E. MAKE A DECISION – classical approach (see next page for p-value approach)
(based on right, left, or two tailed test, test value (t.v.) and critical value c.v.).

AR is acceptance (do not reject) region **RR** is rejection region

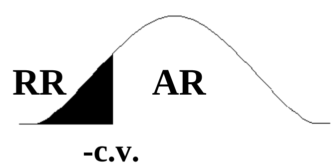
Right tailed

Reject H_0 if t.s. > c.v.; do not reject H_0 otherwise.



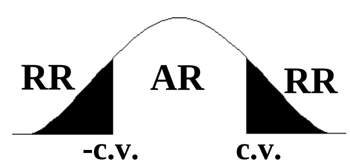
Left tailed

Reject H_0 if t.s. < - c.v.; do not reject H_0 otherwise.



Two tailed

Reject H_0 if t.s. > c.v. or t.s. < - c.v.;
do not reject H_0 otherwise.



P-value (using STAT – TESTS on calculator)

If $p < \alpha$, reject H_0
If $p \geq \alpha$, do not reject H_0

SEE PAGE 417 FOR WORDING OF DECISION EXPLANATION