In one population, 29.2% are omnivorous ($p_1 = 0.292$). In a second population, 78.3% are omnivorous ($p_2 = 0.783$). When random samples of sizes 5000 and 100 are taken from the first and second populations respectively, what is the chance that $\hat{P}_2 - \hat{P}_1$ is at most 0.497?

Check if we expect the $\hat{P}_2 - \hat{P}_1$ sampling to follow a normal distribution. The random sampling from two (presumably very large) populations allows us to assume independence. The inequalities are also satisfied:

$$n_1p_1 > 10$$
 $n_1(1-p_1) > 10$
 $n_2p_2 > 10$
 $n_2(1-p_2) > 10$

So, we do expect $\hat{P}_2 - \hat{P}_1$ sampling to follow a normal distribution.

$$\hat{P}_2 - \hat{P}_1 \sim \mathcal{N}(p_2 - p_1, SE)$$

Calculate the expected difference.

$$p_2 - p_1 = 0.783 - 0.292$$
$$= 0.491$$

Calculate the standard error.

$$SE = \sqrt{\frac{p_1(1-p_1)}{n_1} + \frac{p_2(1-p_2)}{n_2}}$$

$$= \sqrt{\frac{0.292(1-0.292)}{5000} + \frac{0.783(1-0.783)}{100}}$$

$$= 0.0417$$

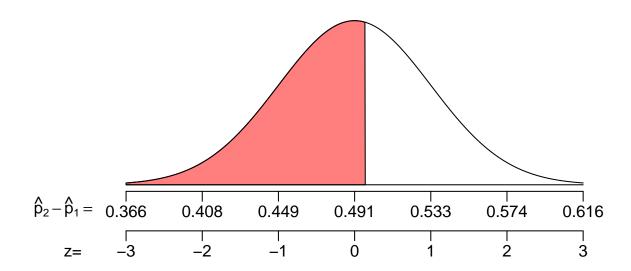
We have the parameters for $\hat{P}_2 - \hat{P}_1$ sampling.

$$\hat{P}_2 - \hat{P}_1 \sim \mathcal{N}(0.491, \, 0.0417)$$

Determine a z score for the boundary $\hat{p}_2 - \hat{p}_1 = -0.427$.

$$Z = \frac{(\hat{p}_2 - \hat{p}_1) - (p_2 - p_1)}{SE}$$
$$= \frac{(0.497) - (0.491)}{0.0417}$$
$$= 0.14$$

Draw a sketch. The phrase "at most 0.497" suggests finding a left area.



Use a z table.

$$\Pr\left(\hat{P}_2 - \hat{P}_1 < 0.497\right) = \Pr(Z < 0.14)$$
$$= \Phi(0.14)$$
$$= 0.5557$$

Thus, we conclude that there is a 55.57% chance that $\hat{P}_2 - \hat{P}_1$ is at most 0.497.

In one population, 68.9% are abysmal ($p_1 = 0.689$). In a second population, 63.8% are abysmal ($p_2 = 0.638$). When random samples of sizes 1000 and 800 are taken from the first and second populations respectively, what is the chance that $\hat{P}_2 - \hat{P}_1$ is more than -0.04?

Check if we expect the $\hat{P}_2 - \hat{P}_1$ sampling to follow a normal distribution. The random sampling from two (presumably very large) populations allows us to assume independence. The inequalities are also satisfied:

$$n_1p_1 > 10$$
 $n_1(1-p_1) > 10$
 $n_2p_2 > 10$
 $n_2(1-p_2) > 10$

So, we do expect $\hat{P}_2 - \hat{P}_1$ sampling to follow a normal distribution.

$$\hat{P}_2 - \hat{P}_1 \sim \mathcal{N}(p_2 - p_1, SE)$$

Calculate the expected difference.

$$p_2 - p_1 = 0.638 - 0.689$$
$$= -0.051$$

Calculate the standard error.

$$SE = \sqrt{\frac{p_1(1-p_1)}{n_1} + \frac{p_2(1-p_2)}{n_2}}$$

$$= \sqrt{\frac{0.689(1-0.689)}{1000} + \frac{0.638(1-0.638)}{800}}$$

$$= 0.0224$$

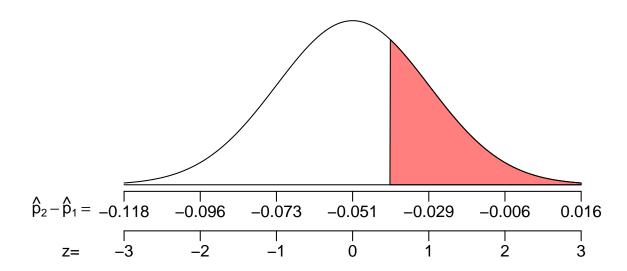
We have the parameters for $\hat{P}_2 - \hat{P}_1$ sampling.

$$\hat{P}_2 - \hat{P}_1 \sim \mathcal{N}(-0.051, 0.0224)$$

Determine a z score for the boundary $\hat{p}_2 - \hat{p}_1 = -0.04$.

$$Z = \frac{(\hat{p}_2 - \hat{p}_1) - (p_2 - p_1)}{SE}$$
$$= \frac{(-0.04) - (-0.051)}{0.0224}$$
$$= 0.49$$

Draw a sketch. The phrase "more than -0.04" suggests finding a right area.



Use a z table.

$$Pr(\hat{P}_2 - \hat{P}_1 > -0.04) = Pr(Z > 0.49)$$

= 1 - \Phi(0.49)
= 0.3121

Thus, we conclude that there is a 31.21% chance that $\hat{P}_2 - \hat{P}_1$ is more than -0.04.

In one population, 56% are angry ($p_1=0.56$). In a second population, 21.2% are angry ($p_2=0.212$). When random samples of sizes 2000 and 900 are taken from the first and second populations respectively, what is the chance that $\hat{P}_2-\hat{P}_1$ is between -0.38 and -0.316?

Check if we expect the $\hat{P}_2 - \hat{P}_1$ sampling to follow a normal distribution. The random sampling from two (presumably very large) populations allows us to assume independence. The inequalities are also satisfied:

$$n_1p_1 > 10$$
 $n_1(1-p_1) > 10$
 $n_2p_2 > 10$
 $n_2(1-p_2) > 10$

So, we do expect $\hat{P}_2 - \hat{P}_1$ sampling to follow a normal distribution.

$$\hat{P}_2 - \hat{P}_1 \sim \mathcal{N}(p_2 - p_1, SE)$$

Calculate the expected difference.

$$p_2 - p_1 = 0.212 - 0.56$$

= -0.348

Calculate the standard error.

$$SE = \sqrt{\frac{p_1(1-p_1)}{n_1} + \frac{p_2(1-p_2)}{n_2}}$$

$$= \sqrt{\frac{0.56(1-0.56)}{2000} + \frac{0.212(1-0.212)}{900}}$$

$$= 0.0176$$

We have the parameters for $\hat{P}_2 - \hat{P}_1$ sampling.

$$\hat{P}_2 - \hat{P}_1 \sim \mathcal{N}(-0.348, 0.0176)$$

Determine *z* scores of the boundaries.

$$Z_{lower} = \frac{(\hat{p}_2 - \hat{p}_1)_{lower} - (p_2 - p_1)}{SE}$$

$$= \frac{(-0.38) - (-0.348)}{0.0176}$$

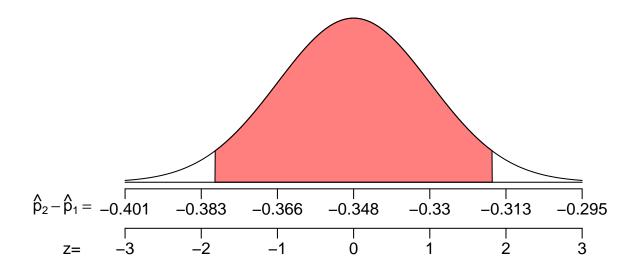
$$= -1.82$$

$$Z_{upper} = \frac{(\hat{p}_2 - \hat{p}_1)_{upper} - (p_2 - p_1)}{SE}$$

$$= \frac{(-0.316) - (-0.348)}{0.0176}$$

$$= 1.82$$

Draw a sketch. The phrase "between -0.38 and -0.316" suggests finding a central area.



Use a z table.

$$\Pr\left(-0.38 < \hat{P}_2 - \hat{P}_1 < -0.316\right) = \Pr(|Z| < 1.82)$$
$$= 2 \cdot \Phi(1.82) - 1$$
$$= 0.9312$$

Thus, we conclude that there is a 93.12% chance that $\hat{P}_2 - \hat{P}_1$ is between -0.38 and -0.316.

In one population, 38.6% are preoccupied (p_1 = 0.386). In a second population, 27.9% are preoccupied (p_2 = 0.279). When random samples of sizes 900 and 9000 are taken from the first and second populations respectively, what is the chance that $\hat{P}_2 - \hat{P}_1$ is outside the interval (-0.143, -0.071)?

Check if we expect the $\hat{P}_2 - \hat{P}_1$ sampling to follow a normal distribution. The random sampling from two (presumably very large) populations allows us to assume independence. The inequalities are also satisfied:

$$n_1p_1 > 10$$
 $n_1(1-p_1) > 10$
 $n_2p_2 > 10$
 $n_2(1-p_2) > 10$

So, we do expect $\hat{P}_2 - \hat{P}_1$ sampling to follow a normal distribution.

$$\hat{P}_2 - \hat{P}_1 \sim \mathcal{N}(p_2 - p_1, SE)$$

Calculate the expected difference.

$$p_2 - p_1 = 0.279 - 0.386$$
$$= -0.107$$

Calculate the standard error.

$$SE = \sqrt{\frac{p_1(1-p_1)}{n_1} + \frac{p_2(1-p_2)}{n_2}}$$

$$= \sqrt{\frac{0.386(1-0.386)}{900} + \frac{0.279(1-0.279)}{9000}}$$

$$= 0.0169$$

We have the parameters for $\hat{P}_2 - \hat{P}_1$ sampling.

$$\hat{P}_2 - \hat{P}_1 \sim \mathcal{N}(-0.107, 0.0169)$$

Determine z scores of boundaries.

$$Z_{lower} = \frac{(\hat{p}_2 - \hat{p}_1)_{lower} - (p_2 - p_1)}{SE}$$

$$= \frac{(-0.143) - (-0.107)}{0.0169}$$

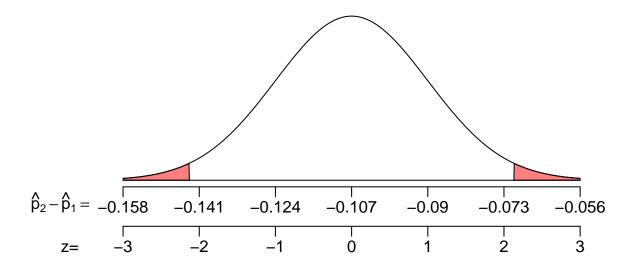
$$= -2.13$$

$$Z_{upper} = \frac{(\hat{p}_2 - \hat{p}_1)_{upper} - (p_2 - p_1)}{SE}$$

$$= \frac{(-0.071) - (-0.107)}{0.0169}$$

$$= 2.13$$

Draw a sketch. The phrase "outside the interval (-0.143, -0.071)" suggests finding a two-tail area.



Use a z table.

$$\Pr\left(\hat{P}_2 - \hat{P}_1 < -0.143 \text{ OR } \hat{P}_2 - \hat{P}_1 > -0.071\right) = \Pr(|Z| > 2.13)$$

$$= 2 \cdot \Phi(-2.13)$$

$$= 0.0332$$

Thus, we conclude that there is a 3.32% chance that $\hat{P}_2 - \hat{P}_1$ is outside the interval (-0.143, -0.071).

In one sample of 40 cases, 38.2% are reclusive ($\hat{p}_1 = 0.382$). In a second sample of 300 cases, 61.1% are reclusive ($\hat{p}_2 = 0.611$). Determine a 95% confidence interval of $p_2 - p_1$.

- (a) Determine the lower bound.
- (b) Determine the upper bound.

Determine the point estimate of $p_2 - p_1$ (our best guess for this population parameter is the corresponding sample statistic).

$$\hat{p}_2 - \hat{p}_1 = 0.611 - 0.382$$
$$= 0.229$$

Determine the critical z^* value such that $P(|Z| < z^*) = 0.95$.

$$z^* = 1.96$$

Determine the standard error.

$$SE = \sqrt{\frac{\hat{p}_1(1-\hat{p}_1)}{n_1} + \frac{\hat{p}_2(1-\hat{p}_2)}{n_2}}$$

$$= \sqrt{\frac{(0.382)(0.618)}{40} + \frac{(0.611)(0.389)}{300}}$$

$$= 0.0818$$

Determine the lower bound.

$$LB$$
 = point estimate $-ME$
= $(\hat{p}_2 - \hat{p}_1) - z^*SE$
= $0.229 - (1.96)(0.0818)$
= 0.0687

Determine the upper bound.

$$UB$$
 = point estimate + ME
= $(\hat{p}_2 - \hat{p}_1) + z^*SE$
= 0.229 + (1.96)(0.0818)
= 0.389

We are 95% confident that $p_2 - p_1$ is between 0.0687 and 0.389.

- (a) The lower bound = 0.0687
- (b) The upper bound = 0.389

In one sample of 1000 cases, 11.1% are fluorescent ($\hat{p}_1 = 0.111$). In a second sample of 90 cases, 43.6% are fluorescent ($\hat{p}_2 = 0.436$). Determine a 80% confidence interval of $p_2 - p_1$.

- (a) Determine the lower bound.
- (b) Determine the upper bound.

Determine the point estimate of $p_2 - p_1$ (our best guess for this population parameter is the corresponding sample statistic).

$$\hat{p}_2 - \hat{p}_1 = 0.436 - 0.111$$
$$= 0.325$$

Determine the critical z^* value such that $P(|Z| < z^*) = 0.8$.

$$z^* = 1.28$$

Determine the standard error.

$$SE = \sqrt{\frac{\hat{p}_1(1-\hat{p}_1)}{n_1} + \frac{\hat{p}_2(1-\hat{p}_2)}{n_2}}$$

$$= \sqrt{\frac{(0.111)(0.889)}{1000} + \frac{(0.436)(0.564)}{90}}$$

$$= 0.0532$$

Determine the lower bound.

$$LB$$
 = point estimate $-ME$
= $(\hat{p}_2 - \hat{p}_1) - z^*SE$
= $0.325 - (1.28)(0.0532)$
= 0.257

Determine the upper bound.

UB = point estimate + ME
=
$$(\hat{p}_2 - \hat{p}_1) + z^*SE$$

= 0.325 + (1.28)(0.0532)
= 0.393

We are 80% confident that $p_2 - p_1$ is between 0.257 and 0.393.

- (a) The lower bound = 0.257
- (b) The upper bound = 0.393

An experiment is run with a control group of size 62 and a treatment group of size 91. The results are summarized in the table below.

	treatment	control
angry	20	45
not angry	42	46

Using a significance level of 0.05, determine whether the treatment causes an effect on the proportion of cases that are angry.

- (a) Determine a *p*-value.
- (b) Does the treatment have a significant effect? (yes or no)

State the hypotheses.

$$H_0: p_2 - p_1 = 0$$

 $H_A: p_2 - p_1 \neq 0$

Determine the sample proportions.

$$\hat{p}_1 = \frac{20}{62} = 0.323$$

$$\hat{p}_2 = \frac{45}{91} = 0.495$$

Determine the difference of sample proportions.

$$\hat{p}_2 - \hat{p}_1 = 0.495 - 0.323 = 0.172$$

Determine the pooled proportion (because the null assumes the population proportions are equal).

$$\hat{p} = \frac{20 + 45}{62 + 91} = 0.425$$

Determine the standard error.

$$SE = \sqrt{\frac{\hat{p}(1-\hat{p})}{n_1} + \frac{\hat{p}(1-\hat{p})}{n_2}}$$
$$= \sqrt{\frac{(0.425)(0.575)}{62} + \frac{(0.425)(0.575)}{91}}$$
$$= 0.0814$$

We can be more specific about what the null hypothesis claims.

$$H_0: \hat{P}_2 - \hat{P}_1 \sim \mathcal{N}(0, 0.0814)$$

We want to describe how unusual our observation is under the null by finding the p-value. To do so, first find the z score.

$$Z = \frac{(\hat{p}_2 - \hat{p}_1) - (p_2 - p_1)_0}{SE}$$
$$= \frac{(0.495 - 0.323) - 0}{0.0814}$$
$$= 2.11$$

Determine the *p*-value.

$$p$$
-value = $2 \cdot \Phi(-|z|)$
= $2 \cdot \Phi(-2.11)$
= 0.0348

Compare the *p*-value to the signficance level.

p-value
$$< \alpha$$

So, we reject the null hypothesis. Thus the difference in proportions is significant.

- (a) The *p*-value = 0.0348
- (b) We reject the null, so yes

An experiment is run with a control group of size 105 and a treatment group of size 104. The results are summarized in the table below.

	treatment	control
special	63	76
not special	42	28

Using a significance level of 0.04, determine whether the treatment causes an effect on the proportion of cases that are special.

- (a) Determine a *p*-value.
- (b) Does the treatment have a significant effect? (yes or no)

State the hypotheses.

$$H_0: p_2 - p_1 = 0$$

 $H_A: p_2 - p_1 \neq 0$

Determine the sample proportions.

$$\hat{p}_1 = \frac{63}{105} = 0.6$$

$$\hat{p}_2 = \frac{76}{104} = 0.731$$

Determine the difference of sample proportions.

$$\hat{p}_2 - \hat{p}_1 = 0.731 - 0.6 = 0.131$$

Determine the pooled proportion (because the null assumes the population proportions are equal).

$$\hat{p} = \frac{63 + 76}{105 + 104} = 0.665$$

Determine the standard error.

$$SE = \sqrt{\frac{\hat{p}(1-\hat{p})}{n_1} + \frac{\hat{p}(1-\hat{p})}{n_2}}$$
$$= \sqrt{\frac{(0.665)(0.335)}{105} + \frac{(0.665)(0.335)}{104}}$$
$$= 0.0653$$

We can be more specific about what the null hypothesis claims.

$$H_0: \hat{P}_2 - \hat{P}_1 \sim \mathcal{N}(0, 0.0653)$$

We want to describe how unusual our observation is under the null by finding the p-value. To do so, first find the z score.

$$Z = \frac{(\hat{p}_2 - \hat{p}_1) - (p_2 - p_1)_0}{SE}$$
$$= \frac{(0.731 - 0.6) - 0}{0.0653}$$
$$= 2.01$$

Determine the *p*-value.

$$p$$
-value = $2 \cdot \Phi(-|z|)$
= $2 \cdot \Phi(-2.01)$
= 0.0444

Compare the *p*-value to the signficance level.

p-value
$$> \alpha$$

So, we retain the null hypothesis. Thus the difference in proportions is not significant.

- (a) The *p*-value = 0.0444
- (b) We retain the null, so no