Homework 10

Your name and student ID

Today's date

```
BEGIN ASSIGNMENT
requirements: requirements.R
generate: true
```

```
library(testthat)
```

Homeworks are for practice only this semester. Solutions will be released by the end of August 10

Helpful hints:

- Every function you need to use was taught during lecture! So you may need to revisit the lecture code to help you along by opening the relevant files on Datahub. Alternatively, you may wish to view the code in the condensed PDFs posted on the course website. Good luck!
- Knit your file early and often to minimize knitting errors! If you copy and paste code for the slides, you are bound to get an error that is hard to diagnose. Typing out the code is the way to smooth knitting! We recommend knitting your file each time after you write a few sentences/add a new code chunk, so you can detect the source of knitting errors more easily. This will save you and the GSIs from frustration! **You must knit correctly before submitting.**
- If your code runs off the page of the knitted PDF then you will LOSE POINTS! To avoid this, have a look at your knitted PDF and ensure all the code fits in the file (you can easily view it on Gradescope via the provided link after submitting). If it doesn't look right, go back to your .Rmd file and add spaces (new lines) using the return or enter key so that the code runs onto the next line.

You would like to conduct a survey of highschool students to determine the proportion who are current e-cigarettes users. Before you conduct your survey, you need to determine how large of a sample size. Suppose that you would like the width of the 95% confidence interval to be 5 percentage points.

1. [1 point] Determine the most conservative sample size you would require and assign it to object p1. Recall that to do this, you need to use a p^* of 0.5.

```
BEGIN QUESTION
name: p1
manual: false
points: 1
```

```
p1 <- "YOUR ANSWER HERE"
# remember to remove " " if you want to store a number

# BEGIN SOLUTION NO PROMPT
p1 <- ceiling((1.96/0.025)^2*0.5*(1-0.5))
p1
```

```
## [1] 1537
```

```
# END SOLUTION
```

```
## Test ##
test_that("p1", {
  expect_true(all.equal(p1, 1537, tol = 0.00001))
  print("Checking: sample size calculated")
})
```

```
## [1] "Checking: sample size calculated"
## Test passed
```

$n = (z * /m)^2 p * (1 - p*)$ $n = (1.96/0.025)^2 \times 0.5 \times (1 - 0.5) = 1536.64 = 1537$

Thus, we would need a sample size of 1537 high school students to obtain a margin of error of 2.5 percentage points if we assume the true prevalence is 50%.

2. [1 point] You've seen a recent publication from the Annals of Internal Medicine that estimated that 9.2% of individuals aged 18 to 24 years old are current e-cigarette users. What is the sample size estimate assuming that $p^* = 0.092$.

```
BEGIN QUESTION
name: p2
manual: false
points: 1
```

```
p2 <- "YOUR ANSWER HERE"
# remember to remove " " if you want to store a number

# BEGIN SOLUTION NO PROMPT
p2 <- ceiling((1.96/0.025)^2*0.092*(1-0.092))
p2
```

```
## [1] 514
```

```
# END SOLUTION
```

```
## Test ##
test_that("p2", {
  expect_true(all.equal(p2, 514, tol = 0.00001))
  print("Checking: sample size calculated")
})
```

```
## [1] "Checking: sample size calculated"
## Test passed
```

$n = (z * /m)^2 p * (1 - p*)$ $n = (1.96/0.025)^2 \times 0.092 \times (1 - 0.092) = 513.459 = 514$

Thus, we would need a sample size of 514 high school students to obtain a margin of error of 2.5 percentage points if we assume the true prevalence is 9.2%.

3. [1 point] The recent publication referenced in the previous question only looked at adults (aged 18+), but observed that the rate of current use was inversely related to age among the population they surveyed. Because of this finding would you suppose that the sample size estimated in part (b) is too low or too high?

```
BEGIN QUESTION
name: p3
manual: false
points: 1
```

```r
# Uncomment one of the following options:
# p3 <- "Too low"
# p3 <- "Too high"

# BEGIN SOLUTION NO PROMPT
p3 <- "Too low"
# END SOLUTION
```

```r
## Test ##
test_that("p3", {
  expect_true(p3 == "Too low")
  print("Checking: selected choice")
})
```

```
## [1] "Checking: selected choice"
## Test passed
```

I would suppose that the estimated sample size is too low because the true prevalence among highschool students is likely higher than among 18-24 year olds. If that is the case, then using a higher $p*$ in the sample size calculation would increase the sample size required.

Exclusive breastfeeding during the first six months of life is recommended for optimal infant growth and development. Suppose that you conducted a survey of randomly chosen women from California and found that 775 out of 5615 new mothers exclusively breast fed their infants.

Perform all four of the methods discussed in lecture and during lab to create a 95% confidence interval for the proportion of infants exclusively breast fed.

```
library(tidyverse)
library(tibble)
```

Store your answer to p4-p7 using the following format:

```
pX <- c(lowerbound, upperbound)

# For example, if lowerbound = 10, upperbound = 20:
pX <- c(10, 20)
```

4. [1 point] Use the large sample method of constructing a 95% CI.

```
BEGIN QUESTION
name: p4
manual: false
points: 1
```

```
# YOUR CODE HERE

# Replace "lowerbound" and "upperbound" with your answer
# If your answer is a number, make sure it doesn't have quotes around it
p4 <- c("lowerbound", "upperbound")

# BEGIN SOLUTION NO PROMPT
num_successes <- 775
sample_size <- 5615

p_hat <- num_successes/sample_size # estimate proportion
se <- sqrt(p_hat*(1-p_hat)/sample_size) # standard error
p4 <- c(p_hat - 1.96*se, p_hat + 1.96*se) # CI
p4
```

```
## [1] 0.1290011 0.1470452
```

```
# END SOLUTION
```

```
## Test ##
test_that("p4a", {
  expect_true(all.equal(p4[1], 0.1290011, tol = 0.001))
  print("Checking: lowerbound to 3 decimal places")
})
```

```
## [1] "Checking: lowerbound to 3 decimal places"
## Test passed
## Test ##
test_that("p4b", {
  expect_true(all.equal(p4[2], 0.1470452, tol = 0.001))
  print("Checking: upperbound to 3 decimal places")
})
```

```
## [1] "Checking: upperbound to 3 decimal places"
## Test passed
```

5. [1 point] Use the Clopper Pearson (Exact) method of constructing a 95% CI.

```
BEGIN QUESTION
name: p5
manual: false
points: 1
```

```
# YOUR CODE HERE

# Replace "lowerbound" and "upperbound" with your answer
# If your answer is a number, make sure it doesn't have quotes around it
p5 <- c("lowerbound", "upperbound")

# BEGIN SOLUTION NO PROMPT
exact_out <- binom.test(num_successes, sample_size, p=0.5)
p5 <- c(exact_out$conf.int[1], exact_out$conf.int[2])
p5
```

```
## [1] 0.1291020 0.1473222
```

```
# END SOLUTION
```

```
## Test ##
test_that("p5a", {
  expect_true(all.equal(p5[1], 0.1291020 , tol = 0.001))
  print("Checking: lowerbound to 3 decimal places")
})
```

```
## [1] "Checking: lowerbound to 3 decimal places"
## Test passed
```

```
## Test ##
test_that("p5b", {
  expect_true(all.equal(p5[2], 0.1473222, tol = 0.001))
  print("Checking: upperbound to 3 decimal places")
})
```

```
## [1] "Checking: upperbound to 3 decimal places"
## Test passed
```

6. [1 point] Use the Wilson Score method of constructing a 95% CI with a continuity correction.

```
BEGIN QUESTION
name: p6
manual: false
points: 1
```

```
# YOUR CODE HERE

# Replace "lowerbound" and "upperbound" with your answer
# If your answer is a number, make sure it doesn't have quotes around it
p6 <- c("lowerbound", "upperbound")

# BEGIN SOLUTION NO PROMPT
wilson_out <- prop.test(num_successes, sample_size, p=0.5)
p6 <-  c(wilson_out$conf.int[1], wilson_out$conf.int[2])
p6
```

```
## [1] 0.1291619 0.1473842
```

```
# END SOLUTION
```

```
## Test ##
test_that("p6a", {
  expect_true(all.equal(p6[1], 0.1291619, tol = 0.001))
  print("Checking: lowerbound to 3 decimal places")
})
```

```
## [1] "Checking: lowerbound to 3 decimal places"
## Test passed
```

```
## Test ##
test_that("p6b", {
  expect_true(all.equal(p6[2], 0.1473842, tol = 0.001))
  print("Checking: upperbound to 3 decimal places")
})
```

```
## [1] "Checking: upperbound to 3 decimal places"
## Test passed
```

7. [1 point] Use the Plus Four method of constructing a 95% CI.

```
BEGIN QUESTION
name: p7
manual: false
points: 1
```

```
# YOUR CODE HERE

# Replace "lowerbound" and "upperbound" with your answer
# If your answer is a number, make sure it doesn't have quotes around it
p7 <- c("lowerbound", "upperbound")
```

```
# BEGIN SOLUTION NO PROMPT
p_tilde <- (num_successes + 2)/(sample_size + 4)
se <- sqrt(p_tilde*(1 - p_tilde)/sample_size) # standard error
p7 <- c(p_tilde - 1.96*se, p_tilde + 1.96*se) # CI
p7
```

```
## [1] 0.1292517 0.1473099
```

```
# END SOLUTION
```

```
## Test ##
test_that("p7a", {
  expect_true(all.equal(p7[1], 0.1292517, tol = 0.001))
  print("Checking: lowerbound to 3 decimal places")
})
```

```
## [1] "Checking: lowerbound to 3 decimal places"
## Test passed
```

```
## Test ##
test_that("p7b", {
  expect_true(all.equal(p7[2], 0.1473099, tol = 0.001))
  print("Checking: upperbound to 3 decimal places")
})
```

```
## [1] "Checking: upperbound to 3 decimal places"
## Test passed
```

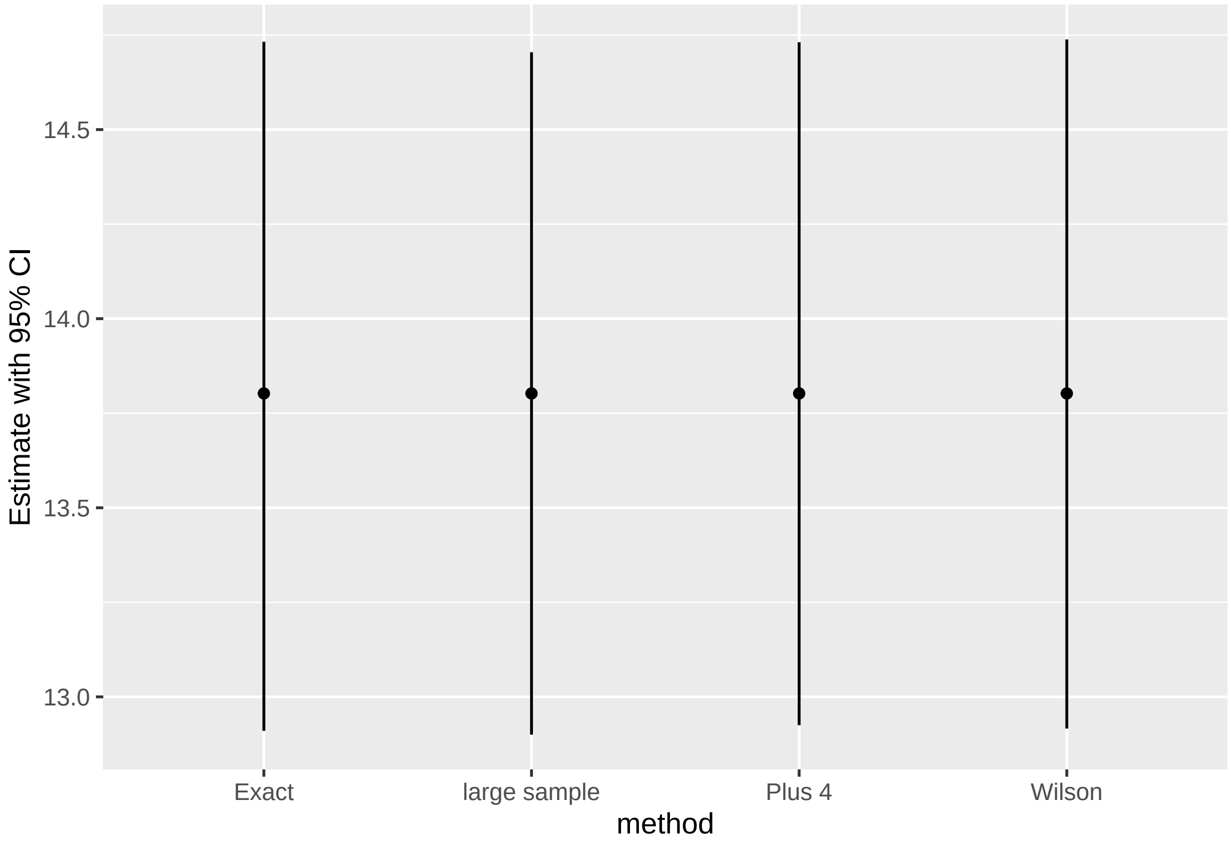
8. [2 points] Create a plot comparing the confidence intervals. If you are stuck, refer back to the example code presented in Lab 10.

```
BEGIN QUESTION
name: p8
manual: true
```

```
p8 <- "YOUR ANSWER HERE"

# BEGIN SOLUTION NO PROMPT
breastfeed_CIs <- tibble(method   =    c("large sample", "Exact",     "Wilson",      "Plus 4"),
                         lower_CI = c(12.90011     , 12.91020   ,  12.91619   ,  12.92517),
                         upper_CI = c(14.70452     , 14.73222   ,  14.73842   ,  14.73099),
                         estimate = c(p_hat*100    , p_hat*100   ,  p_hat*100   ,  p_hat*100)
                         )

p8 <- ggplot(data = breastfeed_CIs, aes(x = method, y = estimate)) +
  geom_point() +
  geom_segment(aes(x = method, xend = method, y = lower_CI, yend = upper_CI)) +
  labs(y = "Estimate with 95% CI")
p8
```



```
# END SOLUTION

# NO AG FOR THIS QUESTION
```

9. [1 point] Do the methods produce confidence intervals that are basically the same or very different? Why?

```
BEGIN QUESTION
name: p9
manual: true
```

The plot comparing the 4 CIs is below. They are nearly identical. This is because the sample size is large enough such that the CLT holds, implying that the large sample method is good, and so are all the other methods. When the sample size is large enough, all the CIs should agree.

10. [1 point] Suppose that in 2010, the rate of exclusive breastfeeding in California was known to be 18.6%. Based on the 95% CIs calculated in questions 4-7, is there evidence against the null hypothesis that the underlying rate is equal to 18.6% in favor of the alternative that the rate is different from 18.6%?

```
BEGIN QUESTION
name: p10
manual: true
```

18.6% falls far above all of the CIs. Because 18.6 is outside of the range of the CIs, we can conclude that the p-value for the corresponding hypothesis test would be $< 5\%$ and conclude that yes, there is evidence in favor of the alternative hypothesis that the rate differs from 18.6%

To confirm your answer to Problem 9, perform a two-sided hypothesis test and interpret the p-value.

11. [1 point] State the null and alternative hypotheses:

```
BEGIN QUESTION
name: p11
manual: true
```

$H_0 : \mu = 18.6\%$ vs. $H_a : \mu \neq 18.6\%$

12. [1 point] Calculate the test statistic:

```
BEGIN QUESTION
name: p12
manual: false
points: 1
```

```
p12 <- "YOUR ANSWER HERE"

# BEGIN SOLUTION NO PROMPT
n <- 5615
p0 <- 0.186

p12 <- ((p_hat - p0) / sqrt(p0 * (1-p0) / n))
p12
```

```
## [1] -9.239275
```

```
# END SOLUTION
```

```
## Test ##
test_that("p12", {
  expect_true(all.equal(p12, -9.239275, tol = 0.001))
  print("Checking: test statistic to 3 decimal places")
})
```

```
## [1] "Checking: test statistic to 3 decimal places"
## Test passed
```

z-test for one-sample test for a proportion:

$$z = \frac{\hat{p} - p_0}{\sqrt{\frac{p_0(1-p_0)}{n}}} = \frac{0.1380232 - .186}{\sqrt{\frac{.186(1-.186)}{5615}}} = -9.239266$$

The test statistic is equal to -9.239266.

13. [1 point] Calculate the p-value:

```
BEGIN QUESTION
name: p13
manual: false
points: 1
```

```
p13 <- "YOUR ANSWER HERE"

# BEGIN SOLUTION NO PROMPT
p13 <- pnorm(p12, lower.tail = T) * 2
p13
```

```
## [1] 2.48172e-20
```

```
# END SOLUTION
```

```
## Test ##
test_that("p13", {
  expect_true(all.equal(p13, 2.48172e-20, tol = 0.001))
  print("Checking: p-value to 3 decimal places")
})
```

```
## [1] "Checking: p-value to 3 decimal places"
## Test passed
```

14. [1 point] Interpret the p-value:

```
BEGIN QUESTION
name: p14
manual: true
```

The p-value is very very tiny, much less than 0.0001%. This implies that the chance of seeing a proportion of 13.8% (or one even more different in magnitude) from the null value of 18.6% is $< 0.0001\%$. Thus, there is evidence against the null hypothesis, in favor of the alternative hypothesis that the proportion differs from 18.6%.

The quadrivalent HPV vaccine was introduced to Canada in 2007, and was given to girls in Ontario, Canada who were enrolled in grade 8 (13-14 year olds). Before 2007, no girls recieved the vaccine, while in the 4 years after it was introduced nearly 40% of girls recieved the vaccine each year. One concern that some people had was that the vaccine itself would increase promiscuity if the girls felt a false sense of protection, which could thereby increase the prevalence of other sexually transmitted infections (STIs) among vaccinated girls. This paper examines this question using an advanced method called the "regression discontinuity" design which harnesses the abrupt change in vaccination status across cohorts of girls to estimate the causal effect of vaccination against HPV on the occurrence of other STIs.

Read only the abstract of the paper, and don't worry about the details because these are advanced methods. Note that the term "RD" is the difference in risk of STIs between girls exposed and unexposed to HPV vaccination. We can therefore think of this risk difference as the difference between two proportions.

15. [1 point] Interpret this result from the abstract: We identified 15 441 (5.9%) cases of pregnancy and sexually transmitted infection and found no evidence that vaccination increased the risk of this composite outcome: RD per 1000 girls -0.61 (95% confidence interval [CI] -10.71 to 9.49).

In particular, what does -0.61 estimate?

```
BEGIN QUESTION
name: p15
manual: true
```

-0.61 is the estimated difference in the proportions of girls with an STI comparing girls who were vaccinated vs. girls who were not vaccinated.

16. [1 point] The 95% confidence interval includes 0. What can you conclude about the p-value for a two-sided test of the difference between vaccinated and unvaccinated girls and their risk of sexually transmitted diseases?

```
BEGIN QUESTION
name: p16
manual: true
```

Given that the null value for the H_0 that there is no difference is included in the 95% CI, we know that the corresponding two-sided test of the difference between the underlying proportions would be greater than 5%.

An allergy to peanuts is increasingly common in Western countries. A randomized controlled trial enrolled infants with a diagnosed peanut sensitivity. Infants were randomized to either avoid peanuts or to consume them regularly until they reached age 5. At the end of the study, 18 out of the 51 randomized to avoid peanuts were tested to be allergic to peanuts. Only 5 out of the 47 randomized to consuming them regularly were tested to be allergic to peanuts.

17. [1 point] Estimate the difference between the two proportions.

```
BEGIN QUESTION
name: p17
manual: false
points: 1
```

```
p17 <- "YOUR ANSWER HERE"

# BEGIN SOLUTION NO PROMPT
succ1 <- 18
n1 <- 51

succ2 <- 5
n2 <- 47

p17 <- (18/51) - (5/47) # 35.3% - 10.6%
p17
```

```
## [1] 0.2465582
```

```
# END SOLUTION
```

```
## Test ##
test_that("p17", {
  expect_true(all.equal(p17, 0.2465582, tol = 0.001))
  print("Checking: estimate to 3 decimal places")
})
```

```
## [1] "Checking: estimate to 3 decimal places"
## Test passed
```

18. [1 point] Use the plus four method to find a 99% confidence interval for the difference between the two groups. Store the upper and lower bounds into an object called p18.

```
BEGIN QUESTION
name: p18
manual: false
points: 1
```

```
# YOUR CODE HERE

# Replace "lowerbound" and "upperbound" with your answer
# If your answer is a number, make sure it doesn't have quotes around it
p18 <- c("lowerbound", "upperbound")

# BEGIN SOLUTION NO PROMPT
p1_tilde <- (succ1 + 1)/(n1 + 2)
p2_tilde <- (succ2 + 1)/(n2 + 2)
se <- sqrt((p1_tilde*(1 - p1_tilde)/(n1 + 2)) + (p2_tilde*(1 - p2_tilde)/(n2 + 2)))

p18 <- c((p1_tilde - p2_tilde) - 2.576 * se, (p1_tilde - p2_tilde) + 2.576 * se)
p18
```

```
## [1] 0.02784538 0.44423779
```

```
# END SOLUTION
```

```
## Test ##
test_that("p18a", {
  expect_true(all.equal(p18[1], 0.02784538 , tol = 0.001))
  print("Checking: lowerbound to 3 decimal places")
})
```

```
## [1] "Checking: lowerbound to 3 decimal places"
## Test passed
```

```
## Test ##
test_that("p18b", {
  expect_true(all.equal(p18[2], 0.44423779, tol = 0.001))
  print("Checking: upperbound to 3 decimal places")
})
```

```
## [1] "Checking: upperbound to 3 decimal places"
## Test passed
```

Solution: The 99% confidence interval for the difference is 2.78% to 44.4%.

19. [1 point] Why would it have been inappropriate to use the large sample method to create a 99% CI?

```
BEGIN QUESTION
name: p19
manual: true
```

Because the number of “successes” was 5 in the group who consumed peanuts regularly. Since $5 < 10$, it is not appropriate to use the large sample method.

Perform a two-sided hypothesis test for the difference between the groups. Start by stating the null and alternative hypotheses, then calculate the test statistic, the p-value, and conclude with your interpretation of the p-value.

20. [1 point] State the null and alternative hypotheses:

```
BEGIN QUESTION
name: p20
manual: true
```

$H_0 : p_1 = p_2$ vs. $H_A : p_1 \neq p_2$

21. [1 point] Calculate the test statistic:

```
BEGIN QUESTION
name: p21
manual: false
points: 1
```

```
p21 <- "YOUR ANSWER HERE"

# BEGIN SOLUTION NO PROMPT
phat <- (succ1 + succ2)/(n1 + n2)
p21 <- (succ1/n1 - succ2/n2)/sqrt(phat*(1- phat)*(1/n1 + 1/n2))
p21
```

```
## [1] 2.877213
```

```
# END SOLUTION
```

```
## Test ##
test_that("p19", {
  expect_true(all.equal(p19, 2.877213, tol = 0.001))
  print("Checking: test statistic to 3 decimal places")
})
```

```
## -- Error (<text>:3:3): p19 -----------------------------------------------------
## Error: object 'p19' not found
## Backtrace:
##  1. testthat::expect_true(all.equal(p19, 2.877213, tol = 0.001))
##  4. base::all.equal(p19, 2.877213, tol = 0.001)
```

First, calculate $\hat{p}$, the estimated probability of having a peanut allergy assuming that the proportions are the same: $\hat{p} = \frac{18+5}{51+47} = 0.2346939$

Then, the test statistic is: $\frac{\hat{p_1}-\hat{p_2}}{\sqrt{\hat{p}(1-\hat{p})\left(\frac{1}{n_1}+\frac{1}{n_2}\right)}} = \frac{0.3529412-0.106383}{\sqrt{0.2346939(1-0.2346939)\left(\frac{1}{51}+\frac{1}{47}\right)}} = 2.877213$

22. [1 point] Calculate the p-value:

```
BEGIN QUESTION
name: p22
manual: false
points: 1
```

```r
p22 <- "YOUR ANSWER HERE"

# BEGIN SOLUTION NO PROMPT
p22 <- pnorm(p21, lower.tail = F) * 2
p22
```

```
## [1] 0.004012052
```

```r
# END SOLUTION
```

```r
## Test ##
test_that("p22", {
  expect_true(all.equal(p22, 0.004012052, tol = 0.001))
  print("Checking: test statistic to 3 decimal places")
})
```

```
## [1] "Checking: test statistic to 3 decimal places"
## Test passed
```

23. [1 point] Interpret the p-value:

```
BEGIN QUESTION
name: p23
manual: true
```

The p-value is < 0.001. Because the p-value is so small there is evidence against the null hypothesis in favor of the alternative that there is a difference between the groups.

24. [1 point] Suppose you were testing the hypotheses $H_0 : \mu_d = 0$ and $H_a : \mu_d \neq 0$ in a paired design and obtain a p-value of 0.21. Which one of the following could be a possible 95% confidence interval for μ_d?

```
BEGIN QUESTION
name: p24
manual: false
points: 1
```

```
# Uncomment one of the following choices:
# p24 <- "-2.30 to -0.70"
# p24 <- "-1.20 to 0.90"
# p24 <- "1.50 to 3.80"
# p24 <- "4.50 to 6.90"

# BEGIN SOLUTION NO PROMPT
p24 <- "-1.20 to 0.90"
# END SOLUTION
```

```
## Test ##
test_that("p24", {
  expect_true(p24 == "-1.20 to 0.90")
  print("Checking: choice for p24")
})
```

```
## [1] "Checking: choice for p24"
## Test passed
```

25. [1 point] Suppose you were testing the hypotheses $H_0 : \mu_d = 0$ and $H_a : \mu_d \neq 0$ in a paired design and obtain a p-value of 0.02. Also suppose you computed confidence intervals for μ_d. Based on the p-value which of the following are true?

```
BEGIN QUESTION
name: p25
manual: false
points: 1
```

```
# Uncomment one of the following choices:
# p25 <- "Both a 95% CI and a 99% CI will contain 0."
# p25 <- "A 95% CI will contain 0, but a 99% CI will not."
# p25 <- "A 95% CI will not contain 0, but a 99% CI will."
# p25 <- "Neither a 95% CI nor a 99% CI interval will contain 0."

# BEGIN SOLUTION NO PROMPT
p25 <- "A 95% CI will not contain 0, but a 99% CI will."
# END SOLUTION
```

```
## Test ##
test_that("p25", {
  expect_true(p25 == "A 95% CI will not contain 0, but a 99% CI will.")
  print("Checking: choice for p25")
})
```

```
## [1] "Checking: choice for p25"
## Test passed
```