QSCI 482 Story 3

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Question 1

```r
rm(list = ls())
library(glue)
lengths <- read.csv('DaphneHybrids.csv')$Lengths
samp_n <- length(lengths)
samp_var <- var(lengths)
samp_se <- sqrt(samp_var / samp_n)
samp_dof <- samp_n-1
alpha <- 0.05
delta <- 2
n <- 50
delta = 3
for (i in 1:10){
  t <- qt(1-alpha/2, df = n-1)
  n <- ceiling(  (samp_var*t^2) / delta^2  )
}
glue('choose n = {n} to achieve 95% confidence interval of 3mm')
```

```
## choose n = 16 to achieve 95% confidence interval of 3mm
```

Question 2

a. If we want to detect an increase in shell length from 310 to 320 μm with a significance level of 0.05 and power of 0.90, what sample size is needed under the new protocol?

```r
# H_0: shell_delta >= 10 microns
# H_A: shell_delta < 10 microns
# One tailed alpha
rm(list = ls())
alpha <- 0.05
power <- 0.90
beta <- 1 - power
delta <- 10     # Want to see an increase from 310 to 320
df <- read.csv('WhiskeyCreekAfter.csv')
samp_var <- var(df$ShellLengths)
samp_n <- length(df$ShellLengths)
n <- 50
for (i in {1:10}){
  t_a <- qt(1-alpha, df = n-1, lower.tail = F)
  t_b <- qt(1-beta, df = n-1, lower.tail = F)
```

```
  n <- ceiling(  (samp_var / delta^2) * (t_a + t_b)^2  )
}
glue('to detect growth of at least 10 microns we need a sample size of {n}')
```

```
## to detect growth of at least 10 microns we need a sample size of 112
```

b. What sample size is needed for the same requirements as in (a), except with a power of 0.99?

```
# H_0: shell_delta >= 10 microns
# H_A: shell_delta < 10 microns
# One tailed alpha

alpha <- 0.05
power <- 0.99
beta <- 1 - power
delta <- 10      # Want to see an increase from 310 to 320
n <- 50
for (i in {1:10}){
  t_a <- qt(1-alpha, df = n-1, lower.tail = F)
  t_b <- qt(1-beta, df = n-1, lower.tail = F)
  n <- ceiling(  (samp_var / delta^2) * (t_a + t_b)^2  )
}
glue('to detect growth of at least 10 microns with power 0.99 we need a sample
      size of {n}')
```

```
## to detect growth of at least 10 microns with power 0.99 we need a sample
## size of 206
```

c. What sample size is needed for the same requirements as in (a), except with a significance level of 0.10?

```
# H_0: shell_delta >= 10 microns
# H_A: shell_delta < 10 microns
# One tailed alpha

alpha <- 0.10
power <- 0.90
beta <- 1 - power
delta <- 10      # Want to see an increase from 310 to 320
n <- 50
for (i in {1:10}){
  t_a <- qt(1-alpha, df = n-1, lower.tail = F)
  t_b <- qt(1-beta, df = n-1, lower.tail = F)
  n <- ceiling(  (samp_var / delta^2) * (t_a + t_b)^2  )
}
glue('to detect growth of at least 10 microns with alpha = 0.10 and power = 0.90
      we need a sample size of {n}')
```

```
## to detect growth of at least 10 microns with alpha = 0.10 and power = 0.90
## we need a sample size of 86
```

d. What sample size is needed for the same requirements as in (a), if we need only detect an increase in shell length from 310 to 330 μm

```
# H_0: shell_delta >= 10 microns
# H_A: shell_delta < 10 microns
# One tailed alpha

alpha <- 0.05
power <- 0.90
beta <- 1 - power
delta <- 20      # Want to see an increase from 310 to 330
n <- 50

for (i in {1:10}){
  t_a <- qt(1-alpha, df = n-1, lower.tail = F)
  t_b <- qt(1-beta, df = n-1, lower.tail = F)
  n <- ceiling(  (samp_var / delta^2) * (t_a + t_b)^2  )
}
glue('to detect growth of at least 20 microns with alpha = 0.05 and power = 0.90
     we need a sample size of {n}')
```

```
## to detect growth of at least 20 microns with alpha = 0.05 and power = 0.90
## we need a sample size of 30
```

Question 3

Using the data in Question 2, and the same scenario, with a significance level of 0.05, what is the minimum detectable difference in shell length, that can be detected 90% of the time, if

a. You take a random sample of the shell lengths of 15 baby oysters?

```
alpha <- 0.05
power <- 0.90
beta <- 1-power
samp_n <- 15     # given sample n
t_a <- qt(1-alpha, df = samp_n -1, lower.tail = F)
t_b <- qt(1-beta, df = samp_n - 1, lower.tail = F)
delta <- sqrt(samp_var / samp_n) * (t_a + t_b)
glue('With a sample size of 15 we can detect a minimum difference of
     {signif(delta,3)} microns')
```

```
## With a sample size of 15 we can detect a minimum difference of
## -28.8 microns
```

b. You take a random sample of the shell lengths of 500 baby oysters?

```
alpha <- 0.05
power <- 0.90
beta <- 1-power
samp_n <- 500    # given sample n
delta <- sqrt(samp_var / samp_n) * (t_a + t_b)
glue('With a sample size of 500 we can detect a minimu difference of
     {signif(delta,3)} microns')
```

```
## With a sample size of 500 we can detect a minimu difference of
```

```
## -4.98 microns
```

Question 4

Consider the data and scenario in Question 2, with a significance level of 0.05. It turns out the new protocol actually increases shell growth more than expected, resulting in mean shell length increasing from 310 to 345 μm. What is the power to detect this difference if:

a. You take a random sample of the shell lengths of 20 baby oysters?

```
alpha <- 0.05
delta <- 35
samp_n <- 20
se <- sqrt(samp_var / samp_n)
t_a <- qt(1-alpha, df = samp_n - 1)
t_b <- (delta / se) - t_a
power <-1 - pt(t_b,df = samp_n - 1,lower.tail = F)
glue('estimated power is {signif(power,3)}')
```

```
## estimated power is 0.992
```

b. You take a random sample of the shell lengths of 40 baby oysters?

```
alpha <- 0.05
delta <- 35
samp_n <- 40
se <- sqrt(samp_var / samp_n)
t_a <- qt(1-alpha, df = samp_n - 1)
t_b <- (delta / se) - t_a
power <-1 - pt(t_b,df = samp_n - 1,lower.tail = F)
glue('estimated power is {signif(power,3)}')
```

```
## estimated power is 1
```