1. When conducting the work of Lab 11, we conducted the test that uses the Central Limit Theorem even though the sample size was "small" (i.e., $n < 30$). It turns out, that how "far off" the t-test is can be computed using a first-order Edgeworth approximation for the error. Below, we will do this for the the further observations.

   (a) Boos and Hughes-Oliver (2000) note that

   $$P(T \leq t) \approx F_Z(t) + \underbrace{\frac{\text{skew}}{\sqrt{n}} \frac{(2t^2 + 1)}{6} f_Z(t)}_{\text{error}},$$

   where $f_Z(\cdot)$ and $F_Z(\cdot)$ are the Gaussian PDF and CDF and skew is the skewness of the data. What is the potential error in the computation of the p-value when testing $H_0 : \mu_X = 0; H_a : \mu_X < 0$ using the zebra finch further data?

   ```
   skew <- skewness(finches_data$further)
   n <- 25
   t <- t.test(finches_data$further, mu = 0,
                    conf.level = 0.95, alternative = "less")$statistic
   fz <- dnorm(t)
   Fz <- pnorm(t)

   (potential_error <- Fz+(skew/sqrt(n))*(((2*t^2)+1)/6)*fz)

   ##               t
   ## -1.189164e-13
   ```

   The potential error is -1.189164e-13 which is approximately zero.

   (b) Compute the error for t statistics from -10 to 10 and plot a line that shows the error across t. Continue to use the skewness and the sample size for the zebra finch further data.

Potential Error vs. t from −10 to 10
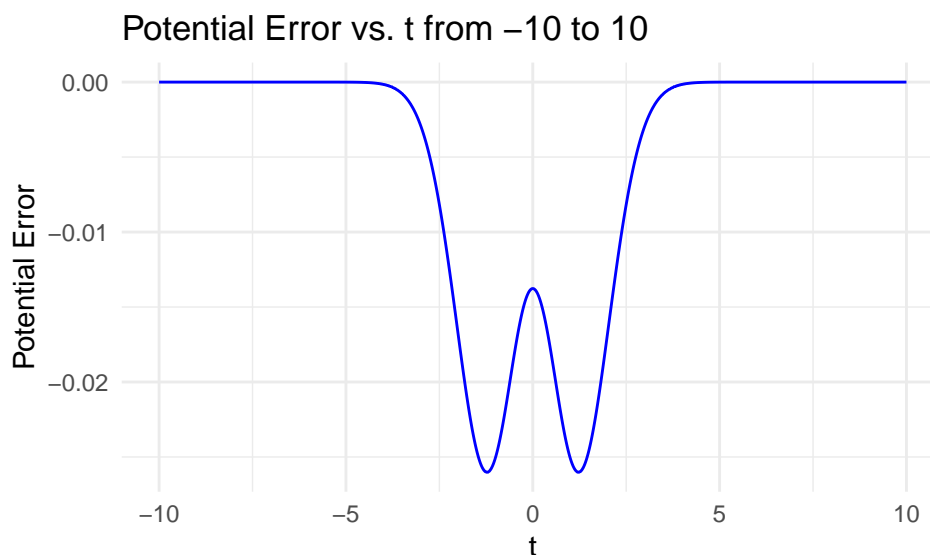
   (c) Suppose we wanted to have a tail probability within 10% of the desired $\alpha = 0.05$. Recall we did a left-tailed test using the further data. How large of a sample size would we need? That is, we need to solve the error formula equal to 10% of the desired left-tail probability:

   $$0.10\alpha \stackrel{set}{=} \underbrace{\frac{\text{skew}}{\sqrt{n}} \frac{(2t^2 + 1)}{6} f_Z(t)}_{\text{error}},$$

1

which yields

$$n = \left(\frac{\text{skew}}{6(0.10\alpha)} (2t^2 + 1) f_Z(t) \right)^2 .$$

```
skew <- skewness(finches_data$further)
a <- 0.05

t <- qnorm(0.05)
fz <- dnorm(t)

(n <- ((skew/(6*0.10*a))*((2*t^2)+1)*fz)^2)

## [1] 520.8876
```

A sample size of 520.8876 would be required. Since we cannot have a fraction of a sample, we would realistically need a sample of 521.

2. Complete the following steps to revisit the analyses from lab 11 using the bootstrap procedure.

   (a) Now, consider the zebra finch data. We do not know the generating distributions for the closer, further, and difference data, so perform resampling to approximate the sampling distribution of the T statistic:

   $$T = \frac{\bar{x}_r - 0}{s/\sqrt{n}},$$

   where $\bar{x}_r$ is the mean computed on the rth resample and s is the sample standard deviation from the original samples. At the end, create an object called `resamples.null.closer`, for example, and store the resamples shifted to ensure they are consistent with the null hypotheses at the average (i.e., here ensure the shifted resamples are 0 on average, corresponding to $t = 0$, for each case).

```
# resamples.null.closer

n <- 25
R <- 10000
resamples.null.closer <- tibble(t = rep(NA, R))

for(i in 1:R){
  curr.resample <- sample(finches_data$closer,
                          size = nrow(finches_data),
                          replace = T)

  resamples.null.closer$t[i] <- (mean(curr.resample))/(sd(finches_data$closer)/sqrt(n))
}
# Center
resamples.null.closer <- (resamples.null.closer)$t
resamples.null.closer.shifted <- resamples.null.closer - mean(resamples.null.closer)
(mean(resamples.null.closer.shifted))

## [1] 1.449368e-16

# resamples.null.further

n <- 25
R <- 10000
resamples.null.further <- tibble(t = rep(NA, R))
```

```r
for(i in 1:R){
  curr.resample <- sample(finches_data$further,
                          size = nrow(finches_data),
                          replace = T)

  resamples.null.further$t[i] <- (mean(curr.resample))/(sd(finches_data$further)/sqrt(n))
}
# Center
resamples.null.further <- (resamples.null.further)$t
resamples.null.further.shifted <- resamples.null.further - mean(resamples.null.further)
(mean(resamples.null.further.shifted))

## [1] -3.621881e-16

# resamples.null.diff

n <- 25
R <- 10000
resamples.null.diff <- tibble(t = rep(NA, R))

for(i in 1:R){
  curr.resample <- sample(finches_data$diff,
                          size = nrow(finches_data),
                          replace = T)

  resamples.null.diff$t[i] <- (mean(curr.resample))/(sd(finches_data$diff)/sqrt(n))
}
# Center
resamples.null.diff <- (resamples.null.diff)$t
resamples.null.diff.shifted <- resamples.null.diff - mean(resamples.null.diff)
(mean(resamples.null.diff.shifted))

## [1] 5.700163e-16
```

(b) Compute the bootstrap p-value for each test using the shifted resamples. How do these compare to the t-test p-values?

```r
# Closer
t_closer <- t.test(finches_data$closer, mu = 0,
                   conf.level = 0.95, alternative = "two.sided")$statistic
(p_closer <- mean(resamples.null.closer.shifted >= t_closer))

## [1] 0

# Further
t_further <- t.test(finches_data$further, mu = 0,
                    conf.level = 0.95, alternative = "two.sided")$statistic
(p_further <- mean(resamples.null.further.shifted <= t_further))

## [1] 0

# Diff
t_diff <- t.test(finches_data$diff, mu = 0,
                 conf.level = 0.95, alternative = "two.sided")$statistic
low <- -(t_diff)
high <- (t_diff)
```

```
p.low = mean(resamples.null.diff.shifted <= low)
p.high = mean(resamples.null.diff.shifted >= high)
(p_diff = p.low + p.high)

## [1] 0
```

All three of the p-values are 0 which is what we expected. In lab 11, all three of the t-test p-values were also virtually zero.

(c) What is the 5th percentile of the shifted resamples under the null hypothesis? Note this value approximates $t_{0.05,n-1}$. Compare these values in each case.

```
# Closer
(firth_percentile_closer <- quantile(resamples.null.closer.shifted, .05))

##        5%
## -1.582595

(firth_percentile_closer_t <- qt(0.05, df=length(finches_data$closer-1)))

## [1] -1.708141

# Further
(firth_percentile_further <- quantile(resamples.null.further.shifted, .05))

##        5%
## -1.636823

(firth_percentile_further_t <- qt(0.05, df=length(finches_data$further-1)))

## [1] -1.708141

# Diff
(firth_percentile_diff <- quantile(resamples.null.diff.shifted, .05))

##        5%
## -1.602875

(firth_percentile_diff_t <- qt(0.05, df=length(finches_data$diff-1)))

## [1] -1.708141
```

In all three cases the values are very similar to one another which is what we expected.

(d) Compute the bootstrap confidence intervals using the resamples. How do these compare to the t-test confidence intervals?

```
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 10000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = boots.closer, type = "bca")
##
## Intervals :
## Level       BCa
## 95%    ( 0.1455,  0.3395 )
## Calculations and Intervals on Original Scale
## Warning : BCa Intervals used Extreme Quantiles
## Some BCa intervals may be unstable
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
```

```
## Based on 10000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = boots.further, type = "bca")
##
## Intervals :
## Level       BCa
## 95%   (-0.6028, -0.0423 )
## Calculations and Intervals on Original Scale
## BOOTSTRAP CONFIDENCE INTERVAL CALCULATIONS
## Based on 10000 bootstrap replicates
##
## CALL :
## boot.ci(boot.out = boots.diff, type = "bca")
##
## Intervals :
## Level       BCa
## 95%   ( 0.1513,  0.9319 )
## Calculations and Intervals on Original Scale
```

The 95 percent closer confidence interval is (0.1542, 0.3395), which we can compare to the t-value closer confidence interval of 0.1173875, 0.1950586). The boot-strap confidence interval is much bigger than the t-test one which was not expected. The 95 percent further confidence interval is (-0.6028, -0.0545), which we can compare to the t-value closer confidence interval of (-0.2565176, -0.1489313). The boot-strap confidence interval again is much bigger than the t-test one which was not expected. Finally, the 95 percent diff confidence interval is (0.1513, 0.9319), which we can compare to the t-value closer confidence interval of (0.2719028, 0.4459921). The boot-strap confidence interval again is much bigger than the t-test one which was not expected.

3. Complete the following steps to revisit the analyses from lab 11 using the randomization procedure.

   (a) Now, consider the zebra finch data. We do not know the generating distributions for the closer, further, and difference data, so perform the randomization procedure

```
# Randomization Test Closer

rand.closer <- tibble(t = rep(NA, R))

for(i in 1:R){
  curr.rand <- resamples.null.closer.shifted *
    sample(x = c(-1, 1),
           size = length(resamples.null.closer.shifted),
           replace = T)

  rand.closer$t[i] <- mean(curr.rand)
}
# Thinking is hard
rand.closer.shifted <- rand.closer |>
  mutate(t = t + mean(resamples.null.closer)) # shifting back

# Randomization Test Further

rand.further <- tibble(t = rep(NA, R))

for(i in 1:R){
```

```
    curr.rand <- resamples.null.further.shifted *
      sample(x = c(-1, 1),
             size = length(resamples.null.further.shifted),
             replace = T)

  rand.further$t[i] <- mean(curr.rand)
}
# Thinking is hard
rand.further.shifted <- rand.further |>
  mutate(t = t + mean(resamples.null.further)) # shifting back

# Randomization Test Diff

rand.diff <- tibble(t = rep(NA, R))

for(i in 1:R){
  curr.rand <- resamples.null.diff.shifted *
    sample(x = c(-1, 1),
           size = length(resamples.null.diff.shifted),
           replace = T)

  rand.diff$t[i] <- mean(curr.rand)
}
# Thinking is hard
rand.diff.shifted <- rand.diff |>
  mutate(t = t + mean(resamples.null.diff)) # shifting back
```

(b) Compute the randomization test p-value for each test.

```
# closer randomization p-value
(p_closer_randomization <- mean(rand.closer >= t_closer))

## [1] 0

# further randomization p-value
(p_further_randomization <- mean(rand.further <= t_further))

## [1] 0

# diff randomization p-value
low <- -(t_diff)
high <- (t_diff)
p.low.rand = mean(rand.diff <= low)
p.high.rand = mean(rand.diff >= high)
(p_diff_rand = p.low.rand + p.high.rand)

## [1] 0
```

(c) Compute the randomization confidence interval by iterating over values of μ_0.
  Hint: You can "search" for the lower bound from Q_1 and subtracting by 0.0001, and the upper bound using Q_3 and increasing by 0.0001. You will continue until you find the first value for which the two-sided p-value is greater than or equal to 0.05.

6

References

Boos, D. D. and Hughes-Oliver, J. M. (2000). How large does n have to be for z and t intervals? *The American Statistician*, 54(2):121–128.