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) **?** note that

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

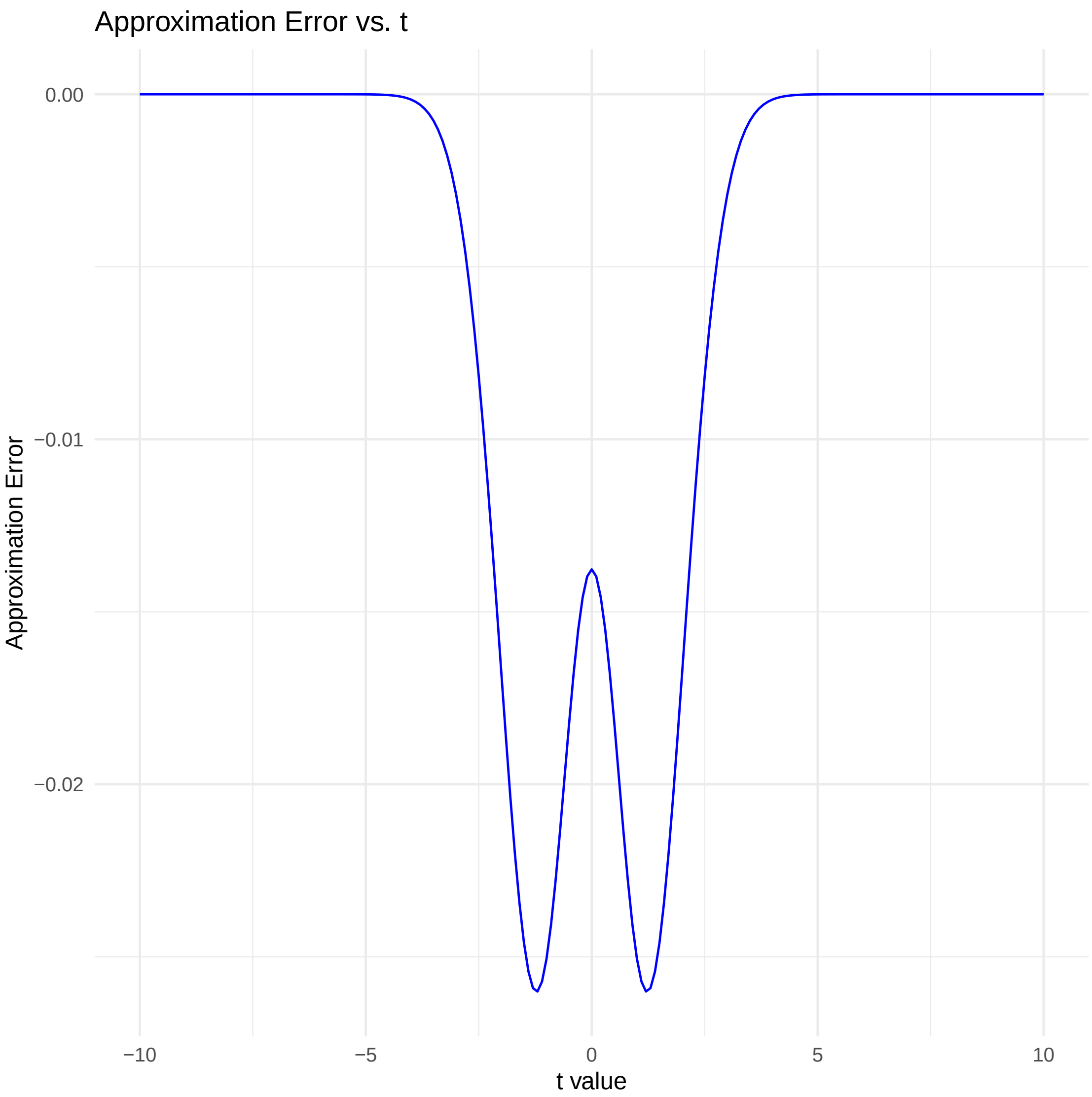
   where $f_Z(\cdot)$ and $F_Z(\cdot)$ are the Gaussian PDF and CDF and skew is the skewness of the data. What is the potential error in the computation of the p-value when testing $H_0 : \mu_X = 0; H_a : \mu_X < 0$ using the zebra finch further data?

```r
library(e1071)
finch_data = read_csv("zebrafinches.csv")
# View(finch_data)
further = finch_data$further
n = length(further)
t = mean(further) / (sd(further)/sqrt(n))

error = (skewness(further) / sqrt(n)) * ((2*t^2 + 1) / 6) * dnorm(t)
error

## [1] -1.226006e-13
```

   The small error value (error $\approx -1.226e-13$) indicates almost no additional error suggesting that the t-test is reliable in this case.

   (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.

```r
library(ggplot2)
library(e1071)
finch_data = read_csv("zebrafinches.csv")
further = finch_data$further
n = length(further)
t_vals = seq(-10, 10, by = 0.1)
error_vals = (skewness(further) / sqrt(n)) * ((2*t_vals^2 + 1) / 6) * dnorm(t_vals)
# error_vals
df = data.frame(t_vals, error_vals)

ggplot(df, aes(x = t_vals, y = error_vals)) +
  geom_line(color = "blue") +
  labs(title = "Approximation Error vs. t",
       x = "t value",
       y = "Approximation Error") +
  theme_minimal()
```



The graph shows how much skewness might affect the approximation error at various t-values. The two peaks of errors show where the t-test accuracy is the worst.

(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:

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

which yields

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

```
library(e1071)

finch_data = read_csv("zebrafinches.csv")
```

```
# View(finch_data)
further = finch_data$further
alpha = 0.05
t = qnorm(alpha)
skewness(further)

## [1] -1.035507

n = ((skewness(further)/(6*0.1*0.05)) * (2*t^2 + 1) * dnorm(t))^2
n

## [1] 520.8876
```

For the t-test's approximation to be accurate within 10% of the p-value, we need approximately 521 samples.

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).

```
library(e1071)

finch_data = read_csv("zebrafinches.csv")
further = finch_data$further
closer = finch_data$closer
diff = finch_data$diff
n = nrow(finch_data)
m0 = 0

set.seed(123)
R <- 10000
further_resamples <- tibble(t.stats=rep(NA, R))
closer_resamples = tibble(t.stats=rep(NA, R))
diff_resamples = tibble(t.stats=rep(NA, R))
for(i in 1:R){
  new_further_resample = sample(further,
                       size = n,
                       replace = T)

  new_closer_resample = sample(closer,
                       size = n,
                       replace = T)

  new_diff_resample = sample(diff,
                       size = n,
                     replace = T)

further_resamples$t.stats[i] <- mean(new_further_resample)/(sd(further)/sqrt(n))
closer_resamples$t.stats[i] = mean(new_closer_resample)/(sd(closer)/sqrt(n))
diff_resamples$t.stats[i] = mean(new_diff_resample)/(sd(diff)/sqrt(n))
}
# View(further_resamples)

resamples.null.farther = further_resamples$t.stats - mean(further_resamples$t.stats)
resamples.null.closer = closer_resamples$t.stats - mean(closer_resamples$t.stats)
resamples.null.diff = diff_resamples$t.stats - mean(diff_resamples$t.stats)
```

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

```
## [1] 0
## [1] 0
## [1] 0
```

All the bootstrap p-values are 0, suggesting strong evidence against the null in all the data.

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

```
## [1] "-1.68480212921038 is the 5th percentile of the shifted further data resamples"
## [1] "-1.59314617071328 is the 5th percentile of the shifted closer data resamples"
## [1] "-1.56409157711738 is the 5th percentile of the shifted diff data resamples"
## [1] -1.710882
```

The data has a $t_{0.05,n-1} = -1.711$ which is more extreme than all three of the bootstrapped critical values. This suggests that the boostrap method might be better to use than the t-test. This is because the values indicate the bootstrap has a tighter distribution.

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

```
library(e1071)

finch_data = read_csv("zebrafinches.csv")
further = finch_data$further
closer = finch_data$closer
diff = finch_data$diff
n = nrow(finch_data)
m0 = 0

set.seed(123)
R <- 10000
further_resamples <- tibble(t.stats=rep(NA, R))
closer_resamples = tibble(t.stats=rep(NA, R))
diff_resamples = tibble(t.stats=rep(NA, R))
for(i in 1:R){
  new_further_resample = sample(further,
                     size = n,
                     replace = T)

  new_closer_resample = sample(closer,
                     size = n,
                     replace = T)

  new_diff_resample = sample(diff,
                     size = n,
                     replace = T)

further_resamples$t.stats[i] <- mean(new_further_resample)/(sd(further)/sqrt(n))
closer_resamples$t.stats[i] = mean(new_closer_resample)/(sd(closer)/sqrt(n))
diff_resamples$t.stats[i] = mean(new_diff_resample)/(sd(diff)/sqrt(n))
}
# View(further_resamples)

resamples.null.further = further_resamples$t.stats - mean(further_resamples$t.stats)
resamples.null.closer = closer_resamples$t.stats - mean(closer_resamples$t.stats)
resamples.null.diff = diff_resamples$t.stats - mean(diff_resamples$t.stats)

CI_further = quantile(resamples.null.further, c(0.025, 0.975))
CI_closer = quantile(resamples.null.closer, c(0.025, 0.975))
CI_diff = quantile(resamples.null.diff, c(0.025, 0.975))

CI_further_t = mean(further) + c(-1, 1) * qt(0.975, df = n-1) * sd(further)/sqrt(n)
CI_closer_t = mean(closer) + c(-1, 1) * qt(0.975, df = n-1) * sd(closer)/sqrt(n)
CI_diff_t = mean(diff) + c(-1, 1) * qt(0.975, df = n-1) * sd(diff)/sqrt(n)
#Should I use resamples.null.data or just the data
CI_further

##      2.5%     97.5%
## -2.033830  1.826771

CI_further_t

## [1] -0.2565176 -0.1489313

CI_closer

##      2.5%     97.5%
## -1.878078  1.926030

CI_closer_t

## [1] 0.1173875 0.1950586

CI_diff

##      2.5%     97.5%
## -1.857155  2.032365

CI_diff_t

## [1] 0.2719028 0.4459921
```

the Bootstrap CIs are wider than the t-CIs.

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 = function(data, mu0 = 0, R = 10000){
  x_shift = data-m0
  rand = tibble(xbars = rep(NA, R))

  for (i in 1:R){
    curr.rand = x_shift * sample(c(-1,1),
                                 length(x_shift),
                                 replace = T)
    rand$xbars[i] = mean(curr.rand)
  }

  rand = rand |>
    mutate(
      xbars = xbars + mu0
    )
  return(rand$xbars)
}

finch_data = read_csv("zebrafinches.csv")

rand_further = randomization_test(finch_data$further)
rand_closer = randomization_test(finch_data$closer)
rand_diff = randomization_test(finch_data$diff)
```

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

```
randomization_test = function(data, mu0 = 0, R = 10000){
  x_shift = data-mu0
  rand = tibble(xbars = rep(NA, R))

  for (i in 1:R){
    curr.rand = x_shift * sample(c(-1,1),
                                 size = length(x_shift),
                                 replace = T)
    rand$xbars[i] = mean(curr.rand)
  }

  rand = rand |>
    mutate(
      xbars = xbars + mu0
    )
  return(rand$xbars)
}

finch_data = read_csv("zebrafinches.csv")

rand_further = randomization_test(finch_data$further)
rand_closer = randomization_test(finch_data$closer)
rand_diff = randomization_test(finch_data$diff)

pval_randomization = function(data, rand_samples, mu0 = 0){
  delta = abs(mean(data) - mu0)
  low = mu0 - delta
  high = mu0 + delta
  mean(rand_samples <= low) + mean(rand_samples >= high)
}

pval_further = pval_randomization(finch_data$further, rand_further)
pval_closer = pval_randomization(finch_data$closer, rand_closer)
pval_diff = pval_randomization(finch_data$diff, rand_diff)

pval_further

## [1] 0

pval_closer

## [1] 0

pval_diff

## [1] 0
```

Because all three p-values are 0, there is strong evidence against the null hypothesis across all the data.

(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.

```
## [1] -0.2627244 -0.1427244
## [1] 0.1162231 0.1962231
## [1] 0.2689475 0.4589475
```

4. **Optional Challenge:** In this lab, you performed resampling to approximate the sampling distribution of the T statistic using

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

I'm curious whether it is better/worse/similar if we computed the statistics using the sample standard deviation of the resamples (s_r), instead of the original sample (s)

$$T = \frac{\bar{x}_r - 0}{s_r/\sqrt{n}}.$$

(a) Perform a simulation study to evaluate the Type I error for conducting this hypothesis test both ways.

(b) Using the same test case(s) as part (a), compute bootstrap confidence intervals and assess their coverage – how often do we 'capture' the parameter of interest?