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?

```
library(tidyverse)
#Load in Data
dat.finch = read.csv("zebrafinches.csv")

#Question 1
library(moments)#used for calculating statistics
library(ggplot2)

n <- length(dat.finch$further)
x_bar <- mean(dat.finch$further)
s <- sd(dat.finch$further)
t_obs <- x_bar / (s / sqrt(n)) #t-value
skew <- skewness(dat.finch$further)

#Could use this instead shows same thing
#(ttest <- t.test(x = dat.finch£further,
                # mu = 0,
                # alternative = "less"))
# Gaussian PDF and CDF at t
fz <- dnorm(t_obs)
Fz <- pnorm(t_obs)

# Edgeworth approximation error
edgeworth_error <- (skew / sqrt(n)) * ((2 * t_obs^2 + 1) / 6) * fz
```

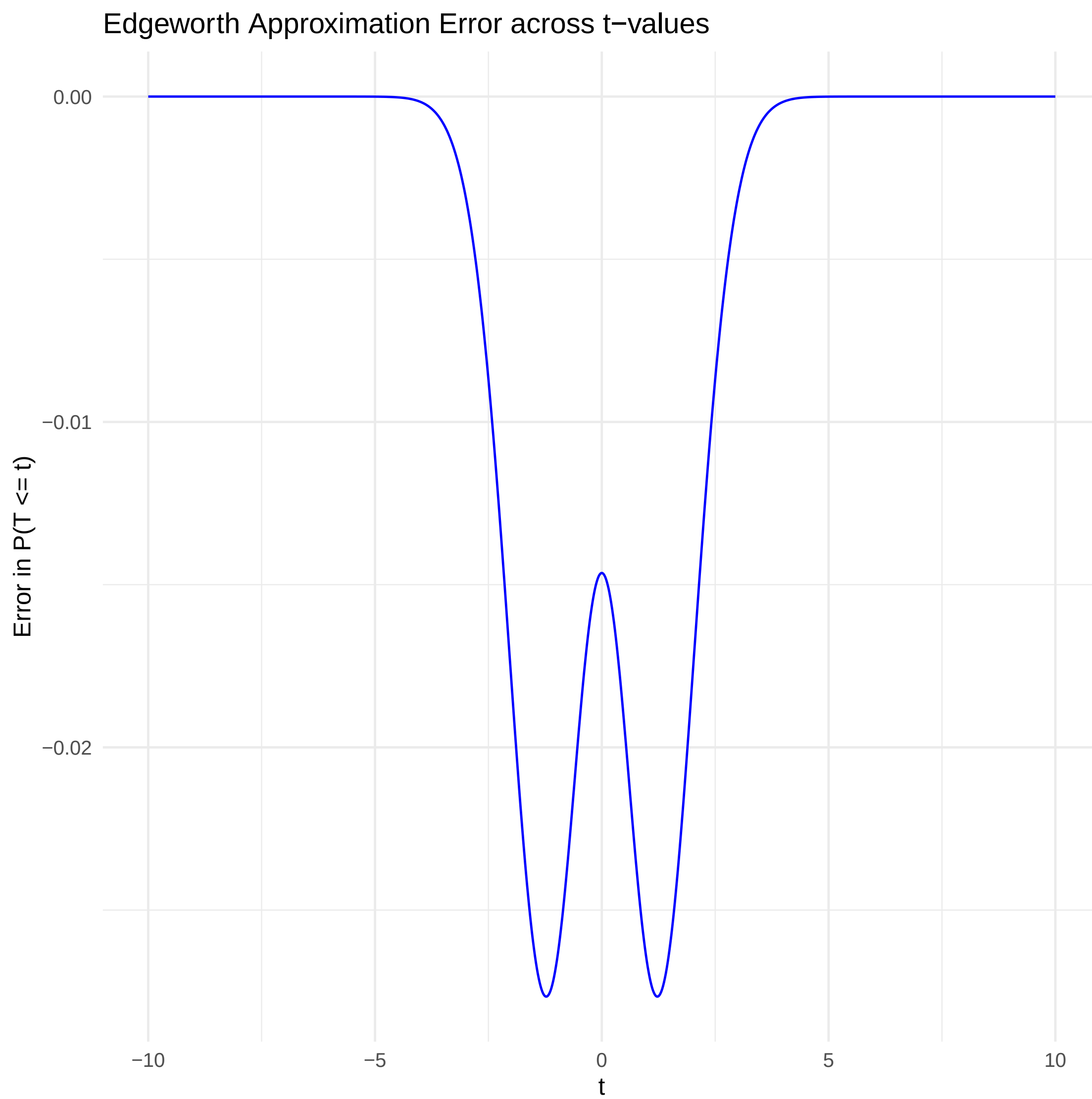
   The Edgeworth error in p-value estimate: -1.303424e-13. This means the potential error is very small only changing the p value by 1.303424e-11 percent which is not important.

   (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.

```
t_vals <- seq(-10, 10, length.out = 1000)
fz_vals <- dnorm(t_vals)
error_vals <- (skew / sqrt(n)) * ((2 * t_vals^2 + 1) / 6) * fz_vals

error_df <- data.frame(t = t_vals, error = error_vals)

ggplot(error_df, aes(x = t, y = error)) +
  geom_line(color = "blue") +
  labs(title = "Edgeworth Approximation Error across t-values",
       x = "t", y = "Error in P(T <= t)") +
  theme_minimal()
```



(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:

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

which yields

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

```
alpha <- 0.05
target_error <- 0.10 * alpha  # 10% of alpha
t_alpha <- qnorm(alpha)  # for left-tailed test
fz_alpha <- dnorm(t_alpha)
```

```r
# Solve for n
numerator <- skew * (2 * t_alpha^2 + 1) * fz_alpha
n_required <- (numerator / (6 * target_error))^2
```

The required sample size to keep the Edgeworth approximation error within 10% of the tail probability $\alpha = 0.05$ is approximately $n = 589$.

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

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.