

- 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.

- Boos and Hughes-Oliver (2000) note that

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

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?

**Solution:** The potential error in the computation of the  $p$ -value is  $-1.226006e - 13$

```
finch.dat = read.csv('./zebrafinches.csv')

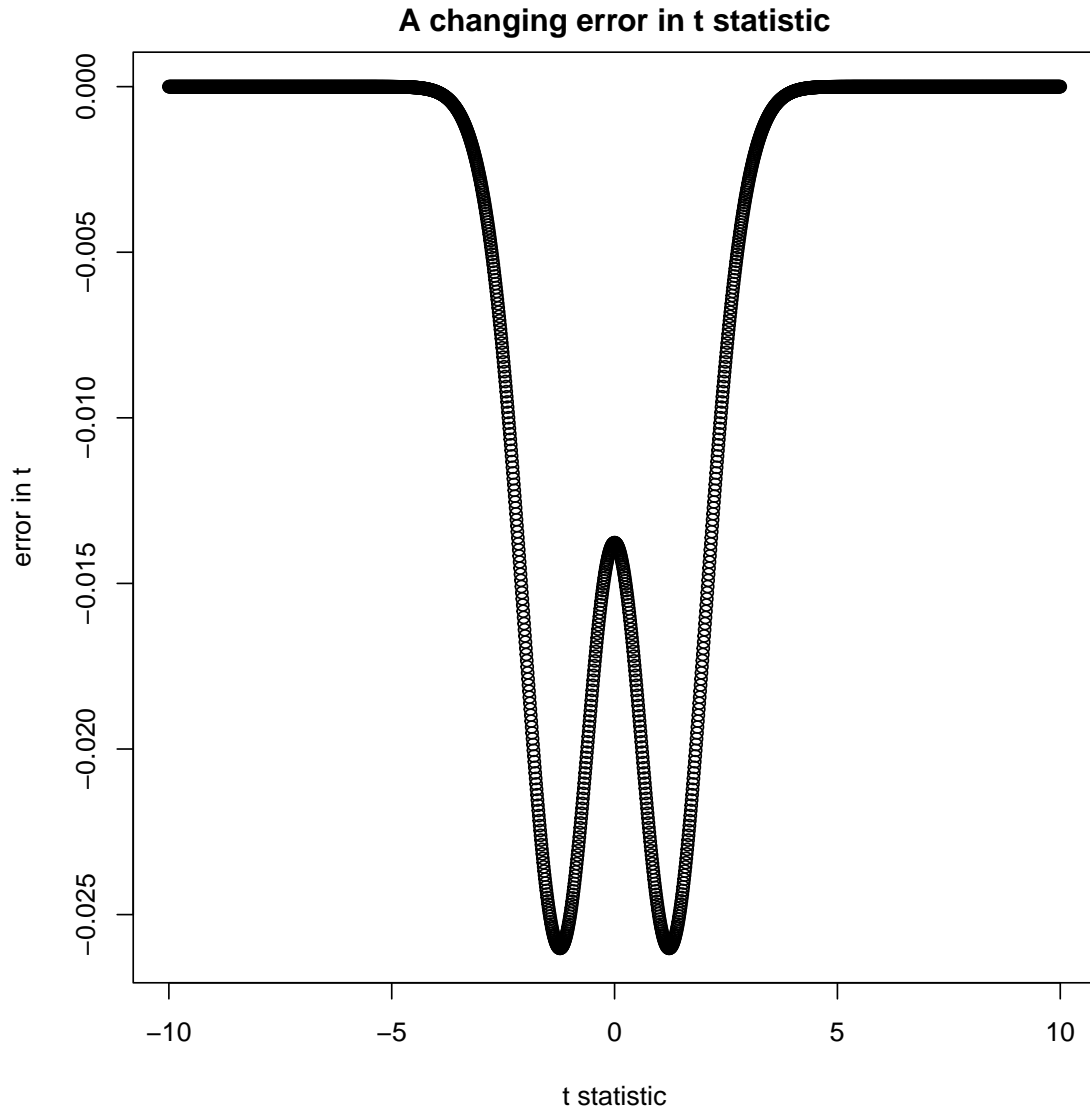
#potential error in p-value
n = length(finch.dat$furthere)
t.furthere = t.test(finch.dat$furthere, alternative = 'less',
                    mu = 0)$statistic[1]
gauss.pdf = dnorm(t.furthere)
finch.skew = skewness(finch.dat$furthere)

error = gauss.pdf*finch.skew*(2*t.furthere^2 + 1)/(sqrt(n)*6)
```

- 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.

**Solution:**

```
#t-statistic error from -10 to 10
t.errors = c()
for (i in seq(-10, 10, by = 0.01)){
  t = i
  gauss.pdf = dnorm(t)
  error = gauss.pdf*finch.skew*(2*t^2 + 1)/(sqrt(n)*6)
  t.errors = append(t.errors, error)
}
par(mar = c(4, 4, 2, 1))
plot(seq(-10, 10, by = 0.01), t.errors,
     xlab = 't statistic',
     ylab = 'error in t',
     main = 'A changing error in t statistic')
```



- (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:

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

which yields

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

**Solution:** Calculating  $n$  with the given formula, we get a value very close to zero (on the order of  $10^{-20}$ ). That means that our data is so far from the null hypothesis of 0, that any datapoint over here will be beyond that 0.05 threshold.

```
#Sample size needed
a= 0.05
gauss.pdf = dnorm(t.further)
n = ((finch.skew/(6*0.10*a))*(2*t.further^2 + 1)*gauss.pdf)^2
n
```

```
##          t
## 1.503091e-20
```

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  $r^{\text{th}}$  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).

**Solution:** In the below code, the mean of the shifted `resamples.null.closer` is approximately 0

```
R <- 10000
resamples <- tibble(xbars = rep(NA, R))

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

  resamples$xbars[i] <- mean(curr.resample)
}
#Shifted Resamples
delta = mean(resamples$xbars)
resamples.null.closer = data.frame(xbars.shifted = resamples$xbars - delta)
```

- (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 5<sup>th</sup> 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  $\mu_0$ .  
**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.