Lab 07 Jackie Stephens

Q1: What is the sample size, n? Show the code you used for the calculation and remember to check for missing data. **N = 219L**

```
dat_Gentoo = subset(penguins, species != "Gentoo")

n = sum(!is.na(dat_Gentoo$bill_length_mm))
```

Q2: What is the sample standard deviation? Show the code you used for the calculation.

```
sd(dat_Gentoo$bill_length_mm, na.rm = TRUE) = 5.477062
```

Q3: What are the critical t-values? Show the R code you used for the calculation.

```
t_crit = abs(qt(alpha / 2, df = n - 1))
```

-1.97 and 1.97

Q4: What is the sample standard error? Show the R code you used for the calculation.

```
sse = sd(dat_Gentoo$bill_length_mm, na.rm = TRUE)/sqrt(n) = 0.370
```

Q5: Finally, construct the CI and show the R code you used for the calculation.

CI = 0.2660114 and 1.724898

```
GentooBL_ci = c(
  lower = mean(dat_Gentoo$bill_length_mm) - ci_radius,
  upper = mean(dat_Gentoo$bill_length_mm) + ci_radius)
```

Q6: What is the CI?

41.19909, 42.65024

Q7: Show the r code you used to call the boot() function.

```
Gentoo_boot = boot( data = dat_Gentoo$bill_length_mm, statistic = boot_mean, R = 10000)
```

Q8: Show the r code you used to calculate the upper and lower 2.5% quantiles.

```
quantile(Gentoo_boot$t, c(0.025, 0.975))
```

Q9: Show your completed rarefaction_sampler() function.

```
rarefaction_sampler = function(input_dat, n_iterations)
{
  n_input_rows = nrow(input_dat)
  n = n_input_rows
  results_out = matrix(
    nrow = n_iterations,
    ncol = n_input_rows)
  for(i in 1:n_iterations)
  {
    for(j in 1:n)
    {
      rows_j = sample(n, size = j, replace=TRUE)
      t1 = input_dat[rows_j, ]
      t2 = apply(t1, 2, sum)
      results_out[i, j] = sum(t2 > 0)
    }
  }
  return(results_out)
}
```

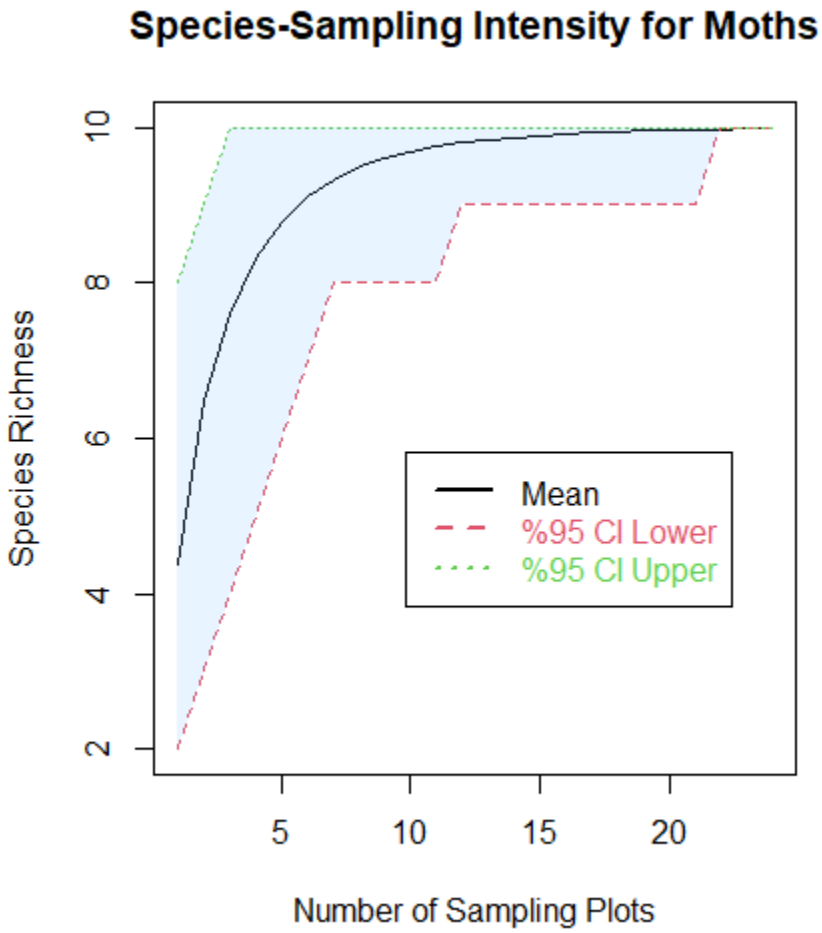
Q10: What did you find most difficult about building the function?

I found trying to understand how the loops worked the most difficult when building the function. Also, trying to identify what to set n to was difficult because it seemed incorrect to say it to a variable that was already defined.

Q11: Show the code you used to perform the simulations and construct the curve.

```
moths = read.csv(here("data", "moths.csv"))

rarefact = rarefaction_sampler(moths[,-1], 10000)

head(rarefact)

rare_mean = apply(rarefact, 2, mean)

rare_quant = apply(rarefact, 2, quantile, probs=c(0.025, 0.975))

rare = t(rbind(rare_mean, rare_quant))

head(rare)

matplot(

  rare,

  type='l',

  xlab='Number of Sampling Plots',

  ylab='Species Richness',

  main="Species-Sampling Intensity for Moths")

polygon(x = c(1:24,24:1),y = c(rare[,2],rev(rare[,3])),

        col= adjustcolor("dodgerblue", alpha.f = 0.10),

                    border= NA)

legend(

  'bottomright',

  legend=c('Mean','%95 CI Lower','%95 CI Upper'),

  lty=c(1,2,3),lwd=c(2,2,2), col=c(1,2,3), inset=c(0.1,0.25),

  text.col = c(1,2,3))
```

Q12: Include your rarefaction curve plot in your report. Show the R-code you used to create your plot.



Q13: About how many sites should you visit if you want to see all of the moth species? Explain your reasoning using your rarefaction curve figure.

If you wanted to see all the moth species, you would most likely want to visit at least 15 sites if not all 20. I say this because the curve shows that the confidence intervals don't start to narrow until you visit more sites. Even though the 95% CIs do not guarantee that you have a 95% chance of seeing all 10 at more sampling plots, the proximity to the mean is convincing.