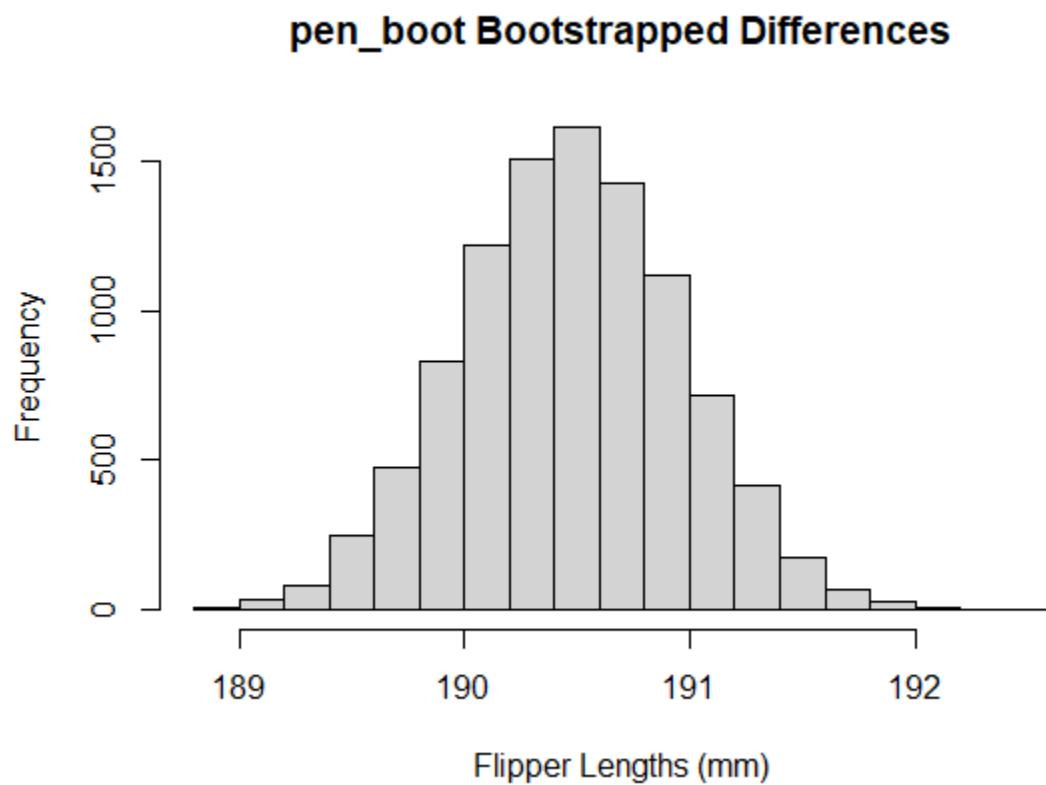


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1.  
`sd(pen_boot$t)`  
0.4877053

2.



3.  
`quantile(pen_boot$t, c(0.025, 0.975))`  
**2.5% 97.5%**  
189.5311 191.4227

4. No, I do not think that the resampled differences follow a skewed distribution. With a mean of 190.47, a median of 190.47, and the center point of the histogram appearing almost exactly at ~190.5, this suggests a characteristic normal distribution.

5.  
`pen_ecdf <- ecdf(pen_boot$t)`

6. There is 100% likelihood of observing a difference in means greater than -4.5

```
1 - pen_ecdf(-4.5)
```

7. There is a zero percent likelihood of observing a difference in means *less* than -8

```
pen_ecdf(-8)
```

8.

$H_0$ : The difference in mean flipper lengths between the two sampled groups is equal to zero

$H_a$ : The difference in mean flipper lengths between the two sampled groups is greater **or** less than zero

9.

```
wilcox.test(pine ~ treatment, dat = dat_tree)
```

10. (-28.84, -2.95 )

```
pine <- veg %>%  
  select(block, plot, date, treatment, pine)
```

```
ctrl_pine <- pine %>%  
  filter(treatment == "control")  
clip_pine <- pine %>%  
  filter(treatment == "clipped")
```

```
tree_boot <- two.boot(ctrl_pine$pine,  
                      clip_pine$pine,  
                      mean, R = 10000,  
                      na.rm = T)  
boot.ci(tree_boot)
```

11. No, they fall outside of the bootstrap range

```
2.5% 97.5%  
-29.75 -4.00
```

12. The Simpson Diversity index describes the relative amount of species richness within a sampled population.

13.

```
dat_all$s.sidi.standardized <- ((dat_all$s.sidi - s_sidi_mean)/ s_sidi_sd)
```

14.

```
n = 10000
```

```
result_mc = numeric(n)
```

```
set.seed(42)
```

```
for(i in 1:n)
```

```
{
```

```
  index_1 = sample(nrow(dat_1), replace = T)
```

```
  index_2 = sample(nrow(dat_1), replace = T)
```

```
  dat_1_resample =
```

```
    data.frame(
```

```
      b.sidi = dat_1$b.sidi[index_1],
```

```
      s.sidi = dat_1$s.sidi[index_2]
```

```
    )
```

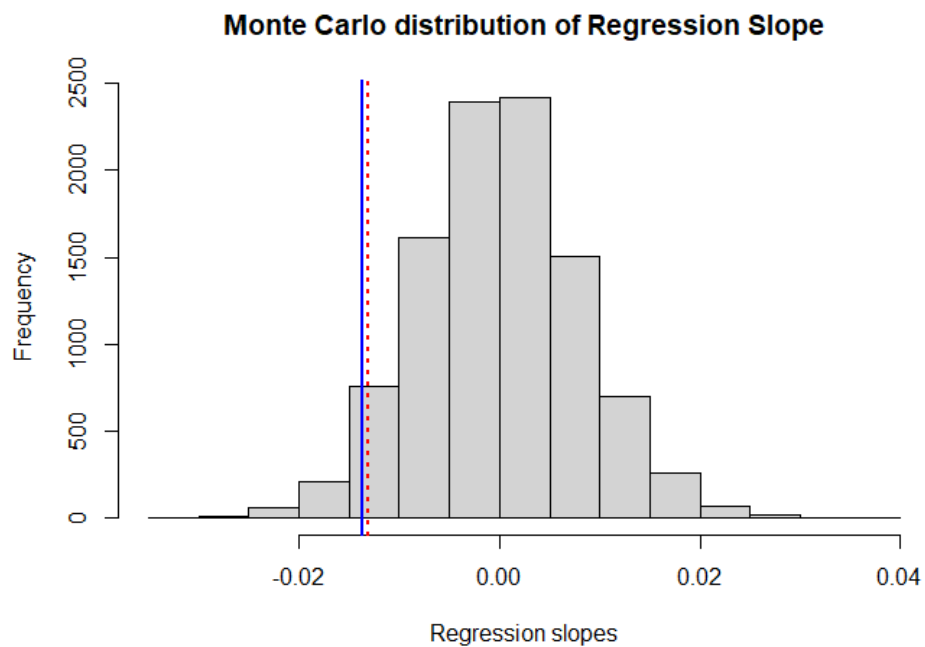
```
  fit_1_resampled <- lm(b.sidi ~ s.sidi, data = dat_1_resample)
```

```
  slope_resampled = coef(fit_1_resampled)[2]
```

```
  result_mc[i] = coef(fit_1_resampled)[2]
```

```
}
```

15.



16. The critical value was -0.01312608 , which was slightly higher than the observed value

17. My conclusion regarding the evidence for a negative relationship between vegetation cover diversity and bird diversity is that it seems plausible. The closeness of the critical value and resampled slopes could suggest that the initially sampled negative slope is less likely to be an anomaly.

18.

```
n = 10000
```

```
result <- numeric(n)
```

```
set.seed(42)
```

```
for (i in 1:n)
```

```
{
```

```
  index <- sample(nrow(dat_1),  
                  replace = T)
```

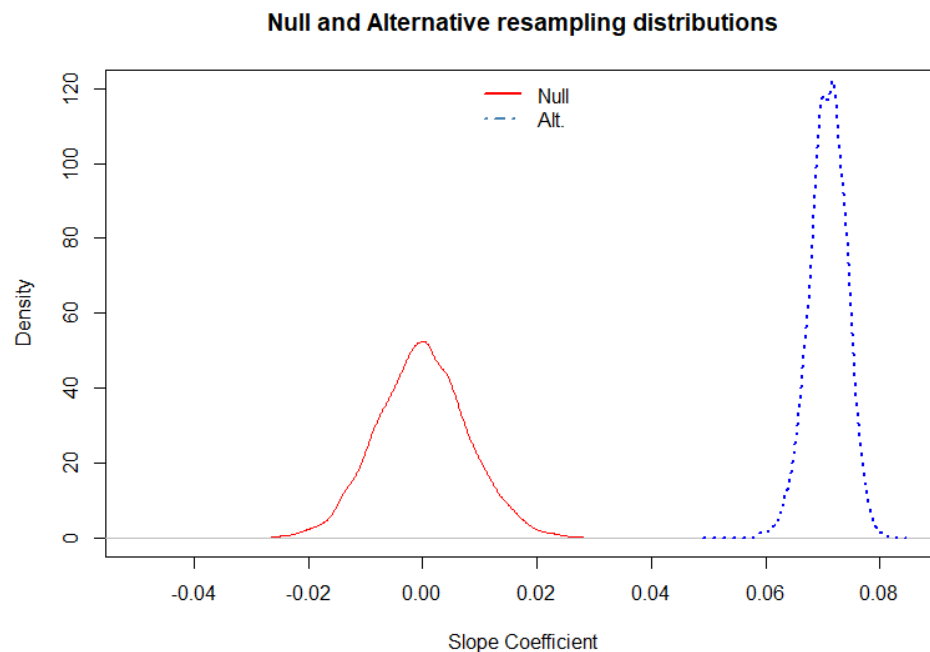
```
  dat_boot_resample = dat_1[index,]  
  head(dat_boot)
```

```
  fit_boot = lm(b.sidi ~ s.sidi,  
                data = dat_boot_resample)
```

```
  result[i] <- coef(fit_boot)
```

```
}
```

19.



20. The values in the region that includes both curves is the distribution of plausible slope coefficients that are possible given that the null hypothesis is true.

