

Juliana Berube

Lab 08

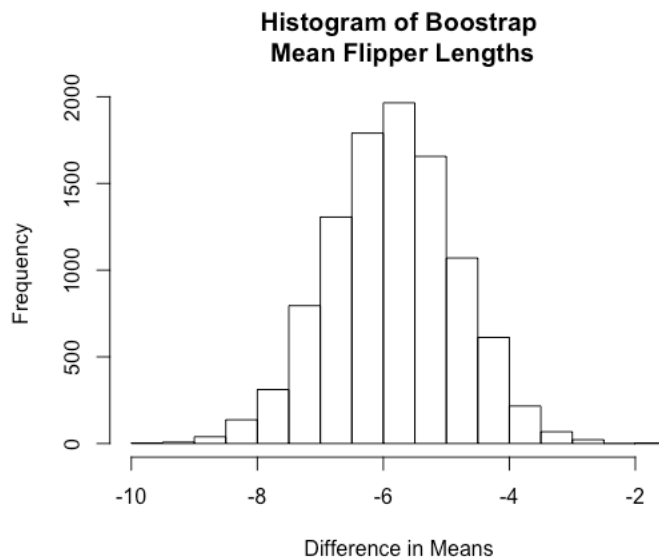
11/7/21

*Worked with Jessica Bonin

1. 1.009681

```
sd(pen_boot$t, na.rm=TRUE)
```

2.



3. 2.5% 97.5%

```
-7.845902 -3.898597
```

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

4. I do not think that the resampled data follows a skewed distribution. This is because the mean and median of the resampled data are very similar, so there is not much difference in the distribution of the data. In addition, the histogram follows a normal bell-shaped distribution, and does not express a heavy skew.

5. `pen_ecdf=ecdf(pen_boot$t)`

6. 0.092

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

7. 0.0187

```
pen_ecdf(-8)
```

8. Null: There is no difference in means of the mean flipper length between the two species is equal to 0
Alternative: There is a significant difference in the means of the mean flipper length between the two species, which is not equal to 0

9. p-value = 0.1005
`wilcox.test(pine ~ treatment, data = dat_trees, exact=FALSE)`

10. 2.5% 97.5%
 4.00000 29.50312

11. 15.91619
Yes, it falls within the 95% quantile

12. The Simpson diversity index measures the diversity of species in a community. It quantifies the diversity of species in association with another variables.

13. `s_sidi_mean = mean(dat_all$s.sidi, na.rm = TRUE)`
`s_sidi_sd = sd(dat_all$s.sidi, na.rm = TRUE)`
`dat_all$s.sidi.standardized = (dat_all$s.sidi - s_sidi_mean)/s_sidi_sd`
`mean(dat_all$s.sidi.standardized)`
`sd(dat_all$s.sidi.standardized)`

14. `dat_bird = read.csv(here("data", "bird.sub.csv"))`
`dat_habitat = read.csv(here("data", "hab.sub.csv"))`
`dat_all = merge(dat_bird, dat_habitat, by = c("basin", "sub"))`
`dat_1 = subset(dat_all, select = c(b.sidi, s.sidi))`

`m = 10000`
`result = numeric(m)`

`for(i in 1:m)`
`{`
`index_1 = sample(nrow(dat_1), replace = TRUE)`
`index_2 = sample(nrow(dat_1), replace = TRUE)`

`fit_1 = lm(b.sidi ~ s.sidi, data = dat_all)`
`coef(fit_1)`
`slope_observed = coef(fit_1)[2]`

`dat_resampled_i =`
`data.frame(`
`b.sidi = dat_1$b.sidi[index_1],`
`s.sidi = dat_1$s.sidi[index_2]`

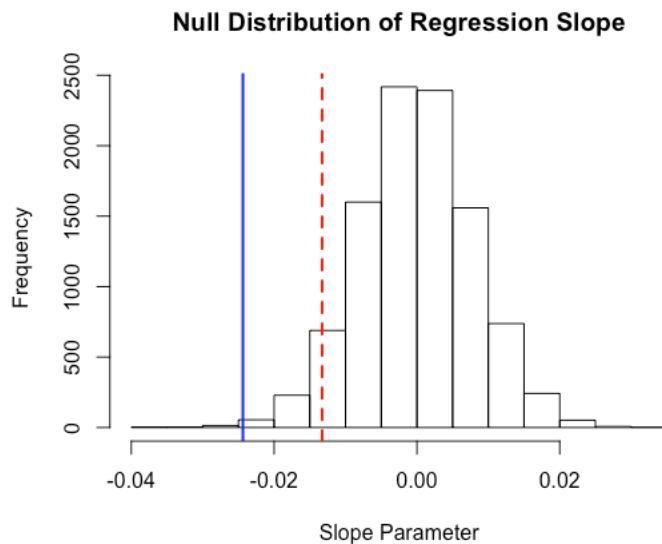
)

```
fit_resampled_i = lm(b.sidi ~ s.sidi, data = dat_resampled_i)
```

```
result[i] = coef(fit_resampled_i)[2]
```

```
}
```

15.



16. The critical value was -0.01327932. The slope observed is -0.02437131. The observed slope is greater and more negative than the critical value.

17. We have evidence that bird species declines with an increase in vegetation diversity, because our observed slope is further away from 0 than our critical value. If there were no relationship or a positive relationship, the observed slope would match or be greater than the critical value. Since the slope is much more negative, we can see a distinct negative relationship.