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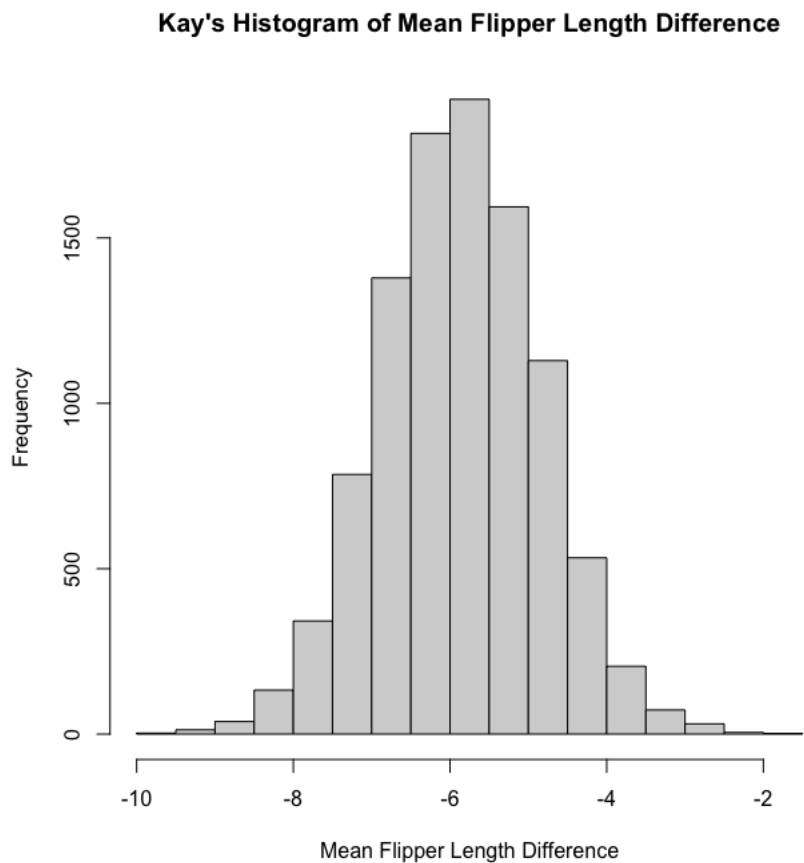
November 2, 2022

ECo 634: Michael France Nelson

Lab 8

1. `sd(pen_boot$t)`

1.018



2.

3. `boot.ci(pen_boot)`

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

2.5% 97.5%

-7.854141 -3.907780

4. The resamples differences in means do not follow a skewed distribution, rather it is relatively normally distributed based on the shape of the graph. Additionally, the mean (-

5.872) and median (-5.880) are very close, so the data is central as opposed to skewed to the left or right.

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

6. `1-pen_ecdf(-4.5)`
0.085

7. `pen_ecdf(-8)`
0.019

8. Null hypothesis: There is no difference in mean flipper length between two penguin species.

Alternative: There is a difference in mean flipper length between two penguin species.

9. `wilcox.test(pine ~ treatment, data = dat_tree, alternative = "two.sided")`
p-value = 0.1005

10. `tree_boot <- two.boot(clipped_sample, control_sample, FUN= mean, R=1000, na.rm= TRUE)`
`quantile(tree_boot$t, c(0.025, 0.975))`
2.5% 97.5%
4.496875 29.753125

11. The observed difference in mean tree counts is 16, and it does fall within the 95% bootstrap CI.

12. Simpson diversity index is a measure of diversity used to quantify biodiversity of an index by taking the number of species present into account

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

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

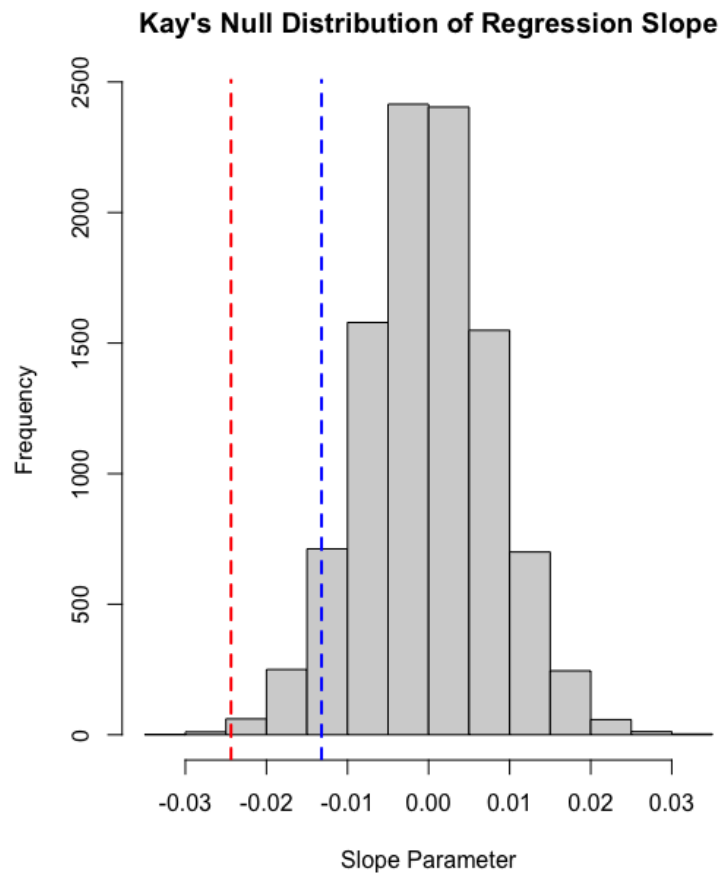
 `dat_resampled_i =`
 `data.frame(`
 `b.sidi = dat_1$b.sidi[index_1],`
 `s.sidi = dat_1$s.sidi[index_2]`

```

)
fit_resampled_i = lm(b.sidi ~ s.sidi, data = dat_resampled_i)
slope_resampled_i = coef(fit_resampled_i)[2]

result_mc[i] = coef(fit_resampled_i)[2]
}

```



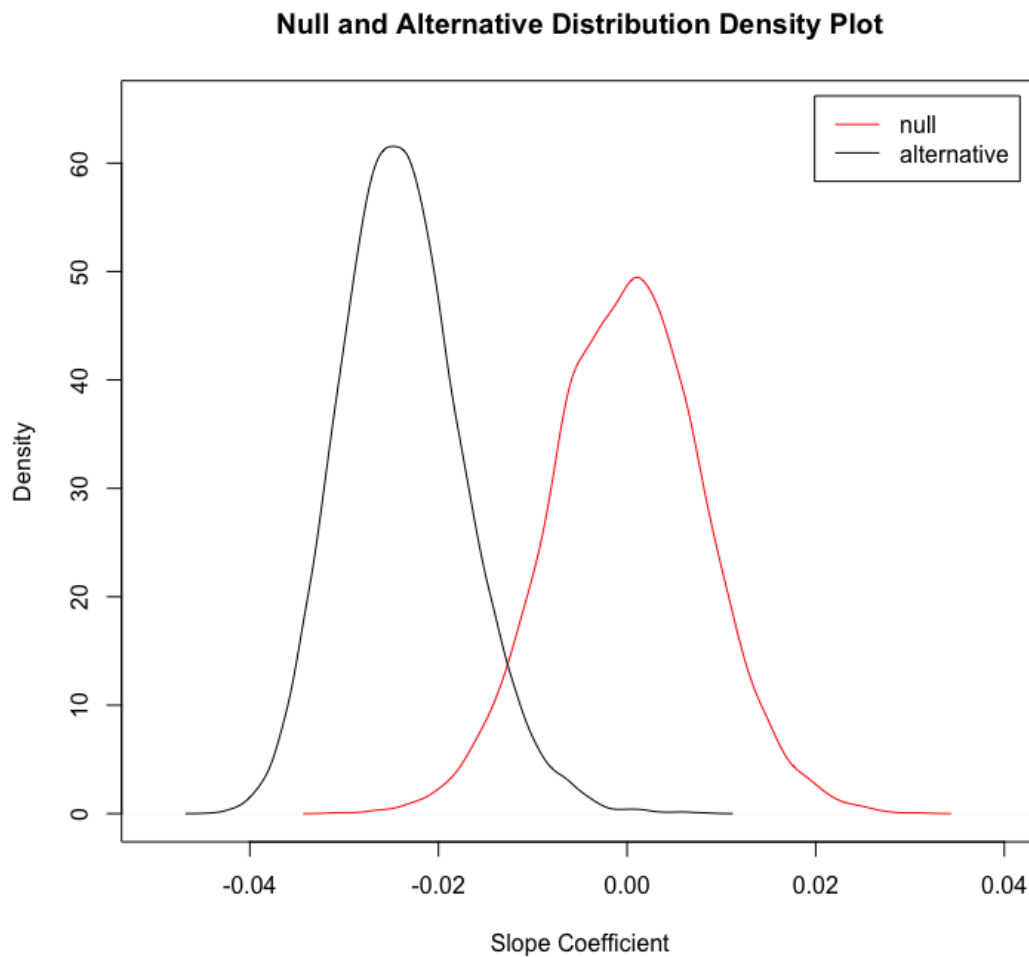
- 15.
16. The critical value was -0.01320388, and the observed slope is less than the critical value.
17. My conclusion is that there is strong evidence of a negative relationship between vegetation cover and bird diversity because the observed slope is much lower than the critical value. In this analysis, we are testing the null distribution, so we are rejecting the null hypothesis that there is no relationship based on the observed and critical value.
18. plot(

density(result_mc),
 main = "Null and Alternative Distribution Density Plot",

```

xlab = "Slope Coefficient", ylim = c(0,65), xlim = c(-0.05, 0.04), col = "red")
lines(density(result_boot), col = "black")
legend("topright",
      legend= c("null", "alternative"), lty= c(1,1),
      col = c("red", "black"), inset = c(0.02, 0.02))

```



19.

20. You cannot clearly assume anything about the region that falls under both the bootstrap and Monte Carlo curves. This region is ambiguous and doesn't necessarily have any significance.