Julia Vineyard

Worked with: Andrew Gordon, Juliana Berube, Jessica Bonin

Lab 8: Modeling 1

1. sd= 1.002531

sd(pen\_boot$t)

1. Chart, histogram

   Description automatically generated
2. 2.5%= -7.838642, 97.5%= -3.891121

quantile(pen\_boot$t, c(0.025, 0.975))

1. No, the resampled differences in means does not follow a skewed distribution. The histogram resembles a normal distribution, and when observing the mean and median the data is centered around both. (mean= -5.871841, median= -5.867501)
2. pen\_ecdf= ecdf(pen\_boot$t)
3. The probability of observing a mean difference of -4.5 or greater is 0.0822.

pen\_ecdf(-4.5)

1. The probability of observing a mean difference of -8 or smaller is 0.0177.

pen\_ecdf(-8)

1. The null hypothesis: the difference in mean flipper length between Adeline and Chinstrap penguins is equal to 0. The alternative hypothesis: the difference in mean flipper length between Adelie and Chinstrap penguins is not equal to 0.
2. p-value=0.1005

veg= read.csv(here("data", "vegdata.csv"))

dat\_tree= droplevels(subset(veg, treatment %in% c("control", "clipped")))

wilcox.test(pine ~ treatment, data=dat\_tree)

1. 3.871875. 30.250000

tree\_boot= two.boot(subset(dat\_tree, treatment == "clipped")$pine,

subset(dat\_tree, treatment == "control")$pine,

FUN=mean, R=1000, na.rm=TRUE)

quantile(tree\_boot$t, c(0.025, 0.975))

1. 16.26138 Yes it falls within the 95% bootstrap CI
2. Simpson’s Diversity Index is a measure of biodiversity that takes into account the number of species present and the relative abundance of each species.
3. 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

1. m = 10000

result = numeric(m)

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))

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)

result[i]=coef(fit\_resampled\_i)[2]

}

print(result[i])

1. Chart, histogram

   Description automatically generated
2. Critical value= -0.01338145. The observed slope is lower than the critical value. Slope observed= -0.02437131
3. Since our critical value is negative we can infer that there is a negative relationship between vegetation cover diversity and bird diversity, meaning that as vegetation cover diversity increases the bird diversity decreases.