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Lab #8

Mike Nelson

Q1: pen\_boot = two.boot(dat\_adel$flipper\_length\_mm,

dat\_chin$flipper\_length\_mm, FUN = mean, R = 10000,

na.rm = TRUE)

str(pen\_boot)

sd(pen\_boot$t)

Chart, histogram

Description automatically generatedQ2:

Q3: -6.53

quantile(pen\_boot$t)

Q4: The resampled means do not follow a skewed distribution because both the mean and the median are similar to each other. The histogram looks evenly distributed.

Q5: pen\_ecdf = ecdf(pen\_boot$t)

Q6: The probability is 0. 906

pen\_ecdf(-4.5)

Q7: The probability is 0.0155

pen\_ecdf

Q8: The null hypothesis is that there is no difference in mean flipper lengths between the two penguin species. The alternative hypothesis is that there is a difference between the mean flipper length between the two species, Adelie and Chinstrap.

Q9: The p-value is 0.05583

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

Q10: The endpoints were -2.25 and 20.50.

quantile(tree\_boot$t)

Q11: The observed difference in mean tree counts is around 16 and it does fall within the 95% confidence interval.

Q12: The Simpson diversity index is gauging a population from 0 to 1. This index quantifies diversity in a community/population. Commonly used to quantify biodiversity.

Q13: # Calculate the sample mean and sd:

b\_sidi\_mean = mean(dat\_all$b.sidi, na.rm = TRUE)

b\_sidi\_sd = sd(dat\_all$b.sidi, na.rm = TRUE)

# Use the subset-by-name symbol ($) to create a

# new column of z-standardized values.

dat\_all$b.sidi.standardized = (dat\_all$b.sidi - b\_sidi\_mean)/b\_sidi\_sd

mean(dat\_all$b.sidi.standardized)

sd(dat\_all$b.sidi.standardized)

Q14: 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]

print(slope\_resampled\_i)

Chart, histogram

Description automatically generated

Q15:

Q16: Critical value was 0.01. My critical value was less than the slope.

Q17: More vegetation cover diversity would cause less bird diversity according to my results. I know this because the value from my SDI shows that bird diversity is lower at ranges of high veg. cover.