Jahiya Clark

Prof. Nelson

Lab 7

10/28/2021

Lab 7

1. N= 123

dat\_pen = subset(penguins, species == "Gentoo")

sum(as.numeric(is.na(dat\_pen$bill\_length\_mm)))

n\_pen <- length(dat\_pen$bill\_length\_mm) - 1

1. Sample standard deviation is 3.081857

sd\_pen <- sd(dat\_pen$bill\_length\_mm, na.rm = TRUE)

1. T critical is -1.9796, 1.9796

pen\_crit <- qt(c(0.025, 0.975), df = n\_pen-1)

pen\_crit

1. SSE is 0.2778817

sse\_pen <- (sd\_pen)/sqrt(n\_pen)

sse\_pen

1. The parametric CI is 47.50488 ± 0.5500946

radius\_pen <- pen\_crit \* sse\_pen

gen\_pen <- mean(dat\_pen$bill\_length\_mm, na.rm = TRUE)

ci\_pen <-gen\_pen + radius\_pen

ci\_pen

1. Lower: 47.06523 Upper: 48.00394

7.

boot\_mean = function(x, i)

{

return(mean(x[i], na.rm = TRUE))

}

require(boot)

billboot = boot(

data = dat\_pen$bill\_length\_mm,

statistic = boot\_mean,

R = 10000)

print(billboot)

8.

quantile(

billboot$t,

c(0.025, 0.975))

2.5% 97.5%

46.96195 48.05366

9.

moths = read.csv(here("data", "moths.csv"))

moth\_dat = moths[,-1]

rarefaction\_sampler = function(input\_dat, n\_iterations)

{

n\_input\_rows = nrow(input\_dat)

results\_out = matrix(

nrow = n\_iterations,

ncol = n\_input\_rows)

for(i in 1:n\_iterations)

{

for(j in 1:n)

{

rows\_j = sample(n, size = j, replace=TRUE)

t1 = input\_dat[rows\_j, ]

t2 = apply(t1, 2, sum)

results\_out[i, j] = sum(t2 > 0)

}

}

return(results\_out)

}

10. I wasn’t able to add shading to the confidence envelope.

11.

rarefact = rarefaction\_sampler(moths[,-1], 10000)

rarefact

rare\_mean = apply(rarefact, 2, mean)

rare\_quant = apply(rarefact, 2, quantile, probs=c(0.025, 0.975))

rare = t(rbind(rare\_mean, rare\_quant))

Diagram

Description automatically generated

matplot(

rare,

type='l',

xlab='Number of Sample sites',

ylab='Number of Moth Species',

main='Range of Number of Moth Speices

by Sampling Site',

col = 6:8)

legend(

'bottom',

legend=c('mean','2.5%','97.5%'),

lty=c(6,7,8),col=c(6,7,8), inset=c(.1,.1))

1. I would visit 20 sites to guarantee that I will see all the moth species. At 20 sites, the lower and upper quantile meet with the mean.