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Lab07

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\*worked with Jessica Bonin

1. 123

gentoo=penguins[which(penguins$species=='Gentoo'),]

gentoo2=gentoo[complete.cases(gentoo$bill\_length\_mm),]

nrow(gentoo2)

1. 3.081857

sd(gentoo2$bill\_length\_mm)

1. -1.9796 1.9796

qt(c(.025, .975), df=122)

1. 0.2778817

sse\_mean(gentoo2$bill\_length\_mm)

1. 48.05 46.95

(qt(.975, df=122))\* (sse\_mean(gentoo2$bill\_length\_mm))

mean(gentoo2$bill\_length\_mm)

47.50 + 0.55

47.50 - 0.55

1. 46.96667 48.06179
2. require(boot)

#boot(data, statistic, R)

#Finding boot mean

boot\_mean = function(x, i)

{

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

}

myboot =

boot(

data = gentoo2$bill\_length\_mm,

statistic = boot\_mean,

R = 10000)

print(myboot)

1. quantile(

myboot$t,

c(0.025, 0.975))

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

{

n= nrow(input\_dat)

results\_out = matrix(

nrow = n\_iterations,

ncol = n)

# The outer loop: runs once for each bootstrap iteration. index variable is i

for(i in 1:n\_iterations)

{

# The inner loop: simulates increasing sampling intensity

# Sampling intensity ranges from 1 site to the complete count of

# sites in the input data (n)

for(j in 1:n)

{

# sample the input data row indices, with replacement

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

# Creates a new data matrix

t1 = input\_dat[rows\_j, ]

# Calculates the column sums

t2 = apply(t1, 2, sum)

# Counts the number of columns in which any moths were observed

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

}

}

return(results\_out)}

1. The most difficult part was finding what was missing and being sure that the fix I made is correct.
2. rarefact = rarefaction\_sampler(moth\_dat, 10000)

head(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))

![Chart

Description automatically generated]()

matplot(

rare,

type='l',

xlab='Number of sampling plots',

ylab='Moth Species richness',

main='Rarefaction Curve:\n Number of Species Found per Number of Sampling Plots',

lty=c(1,6,4),col=c(1,"aquamarine3","coral1"))

legend(

'bottomright',

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

lty=c(1,6,4),col=c(1,"aquamarine3","coral1"), inset=c(.1,.1))

1. If you want to see all the moth species, then you should visit all 20 plots. Only when you reach 20 plots does the mean number of moths meet the maximum species richness.