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Lab07
10/31/21
*worked with Jessica Bonin

1. 123
   gentoo=penguins[which(penguins$species=='Gentoo'),]
   gentoo2=gentoo[complete.cases(gentoo$bill_length_mm),]
   nrow(gentoo2)

2. 3.081857
   sd(gentoo2$bill_length_mm)

3. -1.9796 1.9796
   qt(c(.025, .975), df=122)

4. 0.2778817
   sse_mean(gentoo2$bill_length_mm)

5. 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

6. 46.96667 48.06179

7. 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)


8.  quantile(
      myboot$t,
      c(0.025, 0.975))


9.  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)}
```

10. The most difficult part was finding what was missing and being sure that the fix I made is
    correct.

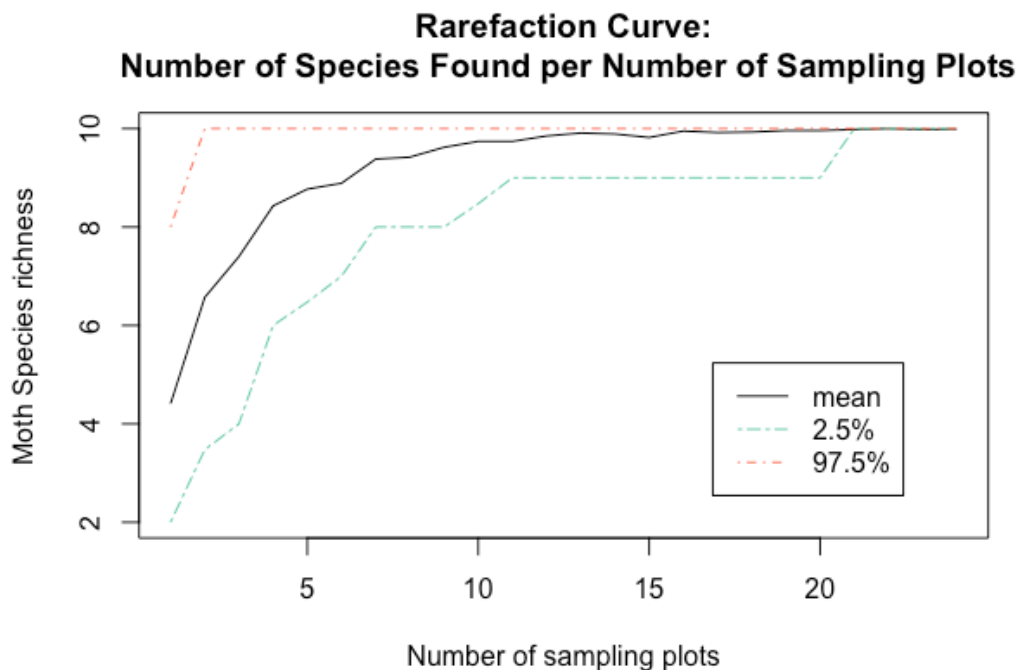11. rarefact = rarefaction_sampler(moth_dat, 10000)
    head(rarefact)

    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))

12.

Rarefaction Curve:
Number of Species Found per Number of Sampling Plots

```
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))
```

13. 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.