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Analysis of Environmental Data Lab

Lab 7

1.
   ```
   require(palmerpenguins)
   penguins_gentoo= penguins[penguins$species == 'Gentoo',]

   n = sum(!is.na(penguins_gentoo$bill_length_mm))
   print(n)
   [1] 123
   ```

2.
   ```
   std_dev= sd(penguins_gentoo$bill_length_mm, na.rm = TRUE)
   print(std_dev)
   [1] 3.081857
   ```

3.
   ```
   t_crit = abs(qt(alpha / 2, df = n - 1))
    print(t_crit)
   [1] 1.9796
   ```

4.
   ```
   sse = sd(penguins_gentoo$bill_length_mm, na.rm = TRUE) / sqrt(n)
   print(sse)
   [1] 0.2778817
   ```

5.
   ```
   ci_radius = sse * t_crit
   gentoo_bill_ci = c(
     lower = mean(penguins_gentoo$bill_length_mm, na.rm= TRUE) - ci_radius,
     upper = mean(penguins_gentoo$bill_length_mm, na.rm = TRUE) + ci_radius)
   print(round(gentoo_bill_ci, 4))
   lower   upper
   46.9548 48.0550
   ```

6. NA

7.
   ```
   boot_mean = function(x, i)
   {
     return(mean(x[i], na.rm = TRUE))
   }

   myboot =
   ```

```
    boot(
      data = penguins_gentoo$bill_length_mm,
      statistic = boot_mean,
      R = 10000)
```

8.
```
   quantile(
    myboot$t,
    c(0.025, 0.975))
  2.5%    97.5%
  46.97071 48.05285
```

9.
```
  rarefaction_sampler = function(input_dat, n_iterations)
  {
    n = nrow(moth_dat) #number of rows or sample observations
    n_input_rows = nrow(input_dat)

    results_out = matrix(
      nrow = n_iterations,
      ncol = n_input_rows)

    # 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. Understanding what the inner and outer loops are doing

11.

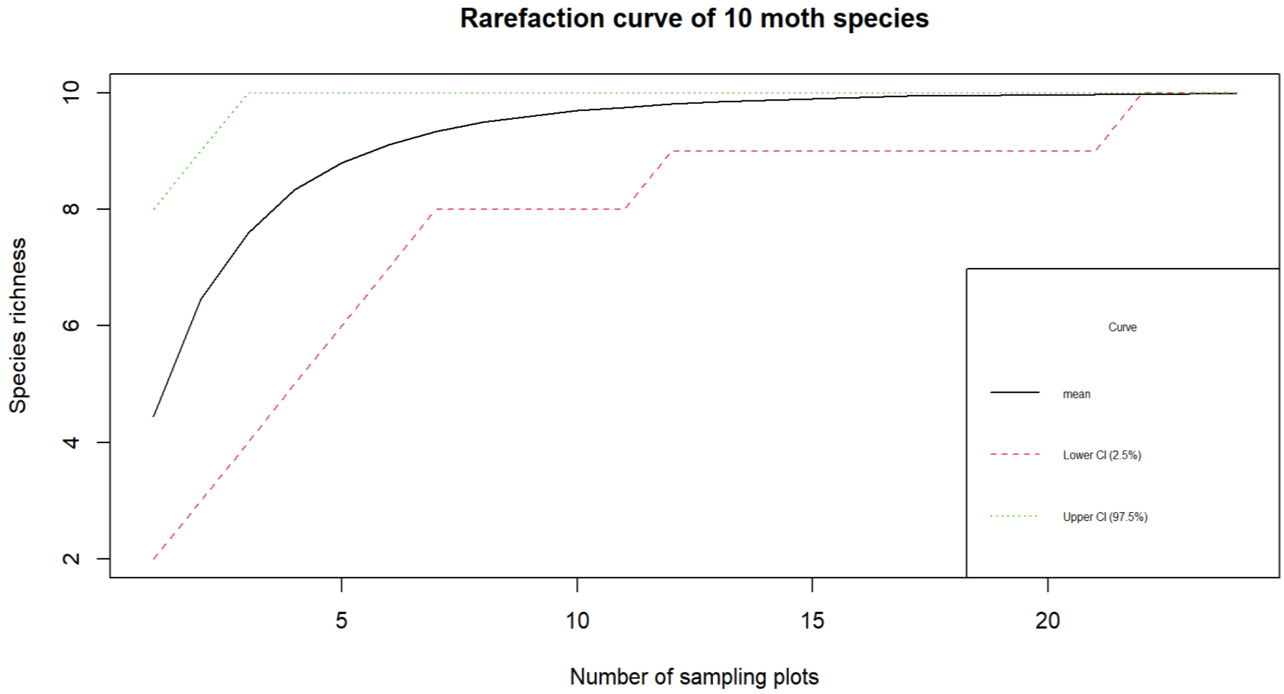
```
moths = read.csv(here("data", "moths.csv"))
rarefact = rarefaction_sampler(moths[,-1], 10000)

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.

```
matplot(
  rare,
  type='l',
  xlab='Number of sampling plots',
  ylab='Species richness',
  main="Rarefaction curve of 10 moth species")

legend(
  'bottomright',
  legend=c('mean','Lower CI (2.5%)','Upper CI (97.5%)'),
  lty=c(1,2,3),col=c(1,2,3), cex= 0.5, title= "Curve")
```



13. Chances are pretty good that you see all ten species after visiting 10 sampling plots, the curve gets very flat after this point indicating that you don’t have a very good chance of observing more species with each additional plot.