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ECo 634: Michael France Nelson

Lab 7

1. `n = 123`
`n = sum(!is.na(dat_pen$bill_length_mm))`
2. `sd(dat_pen$bill_length_mm, na.rm= TRUE)`
`sd = 3.081857`
3. `t_crit = qt(c(0.025, 0.975), df = length(dat_pen$bill_length_mm - 1))`
`t_crit = +/- 1.97928`
4. `sse = sd(dat_pen$bill_length_mm, na.rm = TRUE) / sqrt(n)`
`sse = 0.2778817`
5. `dat_pen_ci = c(`
`lower = mean(dat_pen$bill_length_mm, na.rm = TRUE) - ci_radius,`
`upper = mean(dat_pen$bill_length_mm, na.rm = TRUE) + ci_radius)`
`print(round(dat_pen_ci, 4))`
`lower = 46.9548 upper = 48.0550`
6. `CI lower = 46.97236 upper = 48.05530`
7. `boot_mean = function(x, i)`
`{`
`return(mean(x[i], na.rm = TRUE))`
`}`
`myboot =`
`boot(`
`data = dat_pen$bill_length_mm,`
`statistic = boot_mean,`
`R = 10000)`
8. `sd(myboot$t)`
`quantile(`
`myboot$t,`

```
c(0.025, 0.975))
```

9. rarefaction_sampler = function(input_dat, n_iterations)

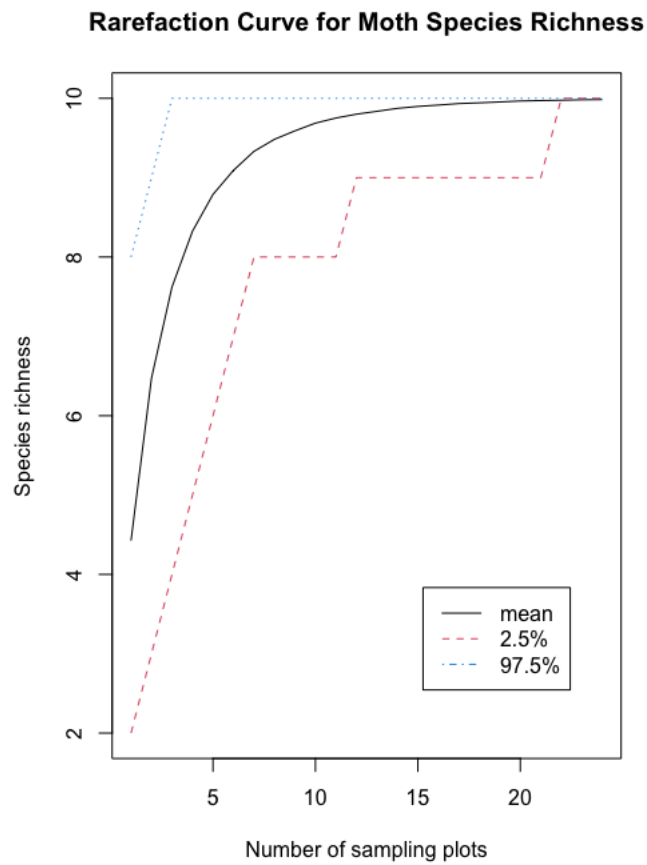
```
{  
  n_input_rows = nrow(input_dat)  
  
  results_out = matrix(  
    nrow = n_iterations,  
    ncol = n_input_rows)  
  
  for(i in 1:n_iterations)  
  {  
    for(j in 1:n)  
    {  
  
      rows_j = sample(n, size = j, replace=TRUE)  
  
      t1 = input_dat[rows_j, ]  
      t2 = apply(t1, 2, sum)  
  
      results_out[i, j] = sum(t2 > 0)  
    }  
  }  
  return(results_out)  
}
```

10. The most difficult part about building the function was understanding what each part of the function was doing.

11. 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',  
  col = c(1, 2, 4),  
  main="Rarefaction Curve for Moth Species Richness")
```

```
legend(  
  'bottomright',  
  legend=c('mean','2.5%','97.5%'),  
  lty=c(1,2,3),col=c(1,2,3), inset=c(.1,.1))
```

13. You should visit about 20 sites if you want to see all of the moth species because the rarefaction curve shows us that the maximum number of species richness occurs at around twenty sites. If you visit less than twenty sites, the species richness will be lower than the maximum. Furthermore, the maximum number of species richness cannot be surpassed, so if you visit more than 20 sites, there won't be any new species to see.