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ECO 634
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1. 119
gentoo <- penguins %>%
 filter(species == "Gentoo") %>%
 drop.na()

length(gentoo\$bill_length_mm)
2. 3.106116
sd(gentoo\$bill_length_mm, na.rm = TRUE)
3. 1.9802722
alpha = 0.05
t_crit = abs(qt(alpha / 2, df = n - 1))
4. 0.2859411
sse = sd(gentoo\$bill_length_mm, na.rm = TRUE) / sqrt(n)
5. 47.5 +/- 0.5662412
summary(gentoo\$bill_length_mm)
low_ci <- 47.5 - ci_radius
up_ci <- 47.5 + ci_radius
6. 47.56807 +/- 0.55378
7.
boot_rep <- function(x, r, statistic) {
 boot <- boot(
 data = x,
 statistic = statistic,
 R = r)
 print(boot)
}
boot_rep(gentoo\$bill_length_mm, 10000, boot_mean)
8. quantile(gentoo_boot\$t, c(0.025, 0.975))
9.
rarefaction <- function(input, reps) {

```

input <- as.data.frame(input)

r = reps
n = nrow(input)

results_out <- matrix(nrow = r,
                      ncol = n)
for (i in 1:r)
{
  for (j in 1:n)
  {
    #samples input data row indices w/ replace
    rows_j = sample(n, size = j, replace = TRUE)

    #new matrix from resampled rows
    t1 = as.matrix(input[rows_j,])

    #calc column sums of new matrix
    t2 = apply(t1, 2, sum)

    #count number of columns w/ observations
    results_out[i, j] = sum(t2 > 0)
  }
}
return(results_out)
}

```

10. I found troubleshooting the errors the most difficult part of constructing the function

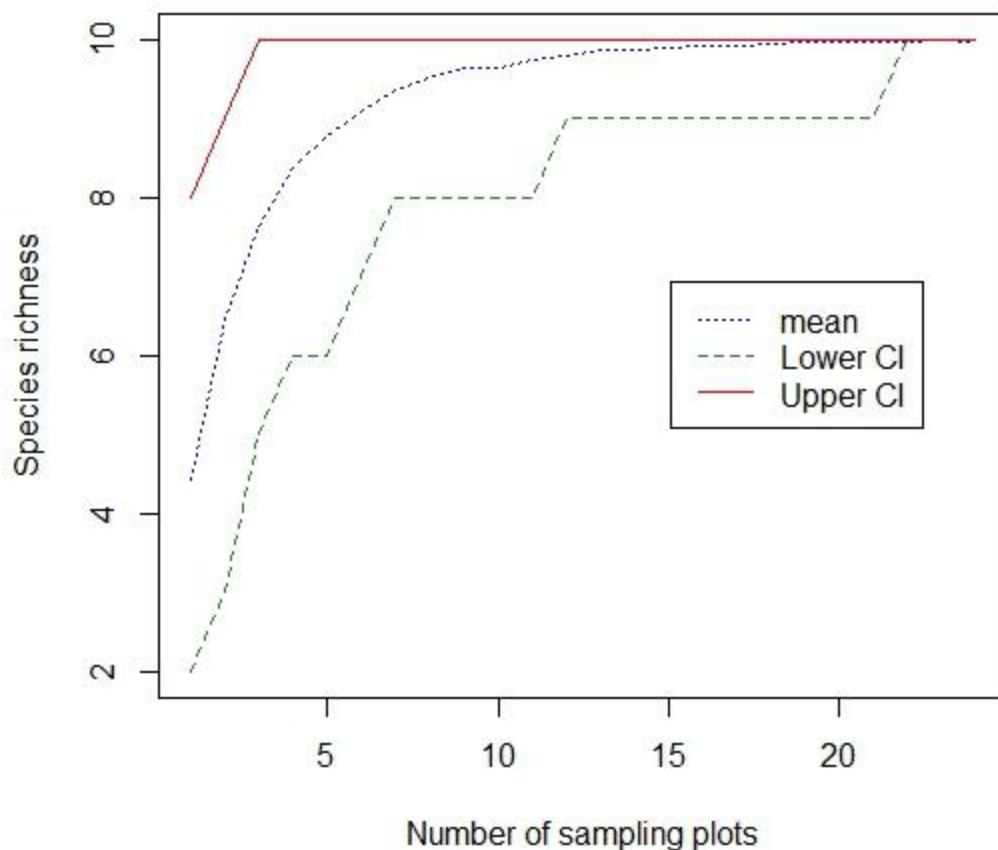
```

11. Moth_rare <- rarefaction(moths[,-1], 1000)
    rare_mean = apply(moth_rare, 2, mean)
    rare_quant = apply(moth_rare, 2, quantile, probs=c(0.025, 0.975))
    rare = t(rbind(rare_mean, rare_quant))

```

12.

Evan's Moth Rarefaction Curve



```
matplot(
  rare,
  type='l',
  lty = c("dotted", "dashed", "solid"),
  col = c("blue", "forestgreen", "red"),
  xlab='Number of sampling plots',
  ylab='Species richness',
  main="Evan's Moth Rarefaction Curve")
```

```
legend(
  'right',
  legend=c('mean','Lower CI','Upper CI'),
  lty = c("dotted", "dashed", "solid"),col=c("blue", "forestgreen", "red"), inset=c(.1,.1))
```

13. The rate of increase in species richness levels off after ~12 sites. To observe all of the species, you'd likely have to visit at least 12 sites.