

Lab 3: Mark-Recapture Introduction

Put your name here

Turn in via Canvas next Friday by the end of the day. Submit either a knitted pdf, html, or doc file. Knit frequently as you go. It's easier to trouble shoot along the way rather than when you have lots of untested code.

Do not print full dataframes unless I ask for them or I will not read your homework

Your instructor will provide instruction about R-projects and working directories.

For this lab we will be using turtle Mark-Recapture data from the C&O Canal in Cumberland, MD collected by Frostburg State University students. The data are collected using a robust design spatial capture-recapture approach with turtles receiving individual marks.

Your instructor will provide more details about the study.

We will use these data for a variety of mark-recapture labs to examine the details and inference we get from different study designs. This week we will pretend that the data were collected using a closed population design. In later labs we will allow for population change explicitly and more complicated individual capture history information.

First, we will read in the full turtle data from the first three primary session (summer 2018, fall 2018, spring 2019). Then we will summarize the data as if we just batch marked the turtles:

```
library(dplyr)
turtles <- read.csv("Data/turtle_scr.csv", stringsAsFactors = FALSE)
# str(turtles)

turtle_lp <- turtles %>%
  group_by(species, primary, secondary, batch_recap) %>%
  summarise(count = n())

# turtle_lp
```

1. Use the data above to fill out this table for Painted Turtles (CPIC):

PP	Day	C_t	R_t	New Marks	M_t
1	1				
1	2				
1	3				
1	4				
2	1				
2	2				
3	1				
3	2				
3	3				

2. Use these data to estimate the population size (\hat{N}) in each primary period with the Lincoln-Peterson Estimator.
3. Now use these data to estimate \hat{N} using the Chapman Method for each primary period.
4. Finally, use these data to estimate \hat{N} with the Schnabel Method for each primary period.
5. Make a plot of estimated abundances (y-axis) over time (x-axis = primary period) with one line for each method.
6. Compare and contrast the estimates from each method and describe the pros and cons of each and differences in inference from the different methods. (Discuss your results).
7. Write out the probability for this capture history assuming that $p(.) = c(.)$ for a closed population (see page 98-99 in the textbook along with class notes):

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8. Write out the probability for this capture history assuming that $p(.) \neq c(.)$ for a closed population:

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9. Write out the probability for this capture history assuming that $p(t) = c(t)$ for a closed population:

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10. Write out the probability for this capture history assuming that $p(t) \neq c(t)$ for a closed population:

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Next week I will add more questions about calculating closed populations from individually marked animals (not batch marked) using maximum likelihood. We will continue to use the turtle data to see how the estimates compare as our data collection becomes more detailed. Maximum likelihood will also provide us with information about the uncertainty in our estimates, which you will notice wasn't estimated with any of these current batch-mark methods.