

# 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.

```
getwd()

setwd("C:/Users/djhocking/Documents/Quant_Vert_Pop/")
```

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-Petersen Estimator. Just use the first 2 days of each primary period, pretending that we did a traditional Lincoln-Petersen design with just two sampling days (secondary sessions).

3. Now use these data to estimate  $\hat{N}$  using the Chapman Method for each primary period. Again only use the first two secondary sessions (days) for the Chapman method.

4. Finally, use these data to estimate  $\hat{N}$  with the Schnabel Method for each primary period. For this method you will use all secondary sessions within a 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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11. Using the `simple_closed1.inp` data, run a closed population Huggins model in program MARK assumming  $p(\cdot) = c(\cdot)$ . Display the results on the true scale.
12. Using the `simple_closed1.inp` data, run a closed population Huggins model in program MARK assumming  $p(\cdot), c(\cdot)$ . Display the results on the true scale.
13. Using the `simple_closed1.inp` data, run a closed population Huggins model in program MARK assumming  $p(t) = c(t)$ . Display the results on the true scale.
14. Using the `simple_closed1.inp` data, run a closed population Huggins model in program MARK assumming  $p(t), c(t)$ . Display the results on the true scale.
15. Thoroughly describe and interpret the results of numbers 11-14. Compare and contrast the results and the results of the different models and do multimodel comparison using AIC.