## Lab 3: Mark-Recapture Introduction

## Answers

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 receving 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.

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)</pre>
```

```
'data.frame':
                    194 obs. of 30 variables:
##
                        21 58 44 1201 1164 42 1143 4 27 1095 ...
   $ line
                 : int
##
   $ page
                        1 2 2 42 41 2 39 1 1 37 ...
##
                        "2018-06-08" "2018-06-10" "2018-06-10" "2019-04-22" ...
   $ date
                 : chr
##
   $ primary
                 : int
                        1 1 1 3 3 1 2 1 1 2 ...
   $ secondary
##
                        2 4 4 1 2 4 2 1 3 1 ...
                 : int
##
   $ period
                        2 4 4 7 8 4 6 1 3 5 ...
                 : int
                        "A" "A" "A" "A" ...
##
   $ site
                 : chr
##
   $ batch recap: int
                        0 1 1 0 1 0 0 0 1 0 ...
                        "17" "17" "18" "18" ...
##
   $ mark final : chr
##
   $ mark 1
                 : int
                        17 17 18 18 18 23 23 24 24 24 ...
                        1 4 7 5 3 6 3 8 3 8 ...
##
   $ trap
                   int
                        "CPIC" "CPIC" "CPIC" ...
##
   $ species
                 : chr
##
   $ subspecies : chr
                        "marginata" "marginata" "hybrid" ...
                        "M" "M" "M" "M" ...
##
   $ sex
                 : chr
   $ A
##
                 : int
                        NA NA NA NA NA NA NA NA NA ...
##
   $ B
                 : int
                        NA NA NA NA NA NA NA NA NA ...
##
   $ carapace
                 : int
                        112 113 143 143 144 150 150 135 135 135 ...
##
   $ car_max
                        112 113 145 NA NA 150 150 135 135 135 ...
                 : int
##
   $ plastron
                        103 102 132 130 133 140 141 123 123 123 ...
                 : int
##
                        39 39 49 30 45 52 51 46 46 25 ...
   $ depth
                 : int
                        180 180 330 310 340 425 450 270 280 300 ...
##
   $ mass
                 : int
##
   $ leeches
                        O O 1 NA NA O NA O O NA ...
                 : int
                        "N" "R" "N" "R" ...
##
   $ recap
                 : chr
##
   $ X
                        NA NA NA NA NA ...
                 : logi
   $ X.1
                 : logi
                        NA NA NA NA NA ...
                        "Y" "Y" "Y" "N" ...
##
   $ picture
                 : chr
```

```
## $ blood : chr "Y" "N" "Y" "N" ...
## $ smear : chr "Y" "N" "Y" "N" ...
## $ comments : chr "missing 2 claws on front left limb" "3 left front claws missing" "" "" ...
## $ FLAG : logi NA NA NA NA NA ...

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

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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