Mark-Recapture Estimates of Abundance

1 Initialization

```
> library(FSA)
> setwd("C://aaaWork/Class Materials//MnDNR_ShortCourse//Readings//MarkRecapture//")
```

2 Summarizing Capture Histories

2.1 Data Recorded in Capture History Format

```
> data(PikeNYPartial1)
> str(PikeNYPartial1)
'data.frame':
                   57 obs. of 5 variables:
$ id : int 2001 2002 2003 2004 2005 2006 2007 2008 2009 2010 ...
$ first : int  1 1 1 1 1 1 1 1 1 ...
$ second: int 0000000000...
$ third : int  0 0 0 0 0 0 0 0 0 ...
$ fourth: int 0000000000...
> rhead(PikeNYPartial1)
    id first second third fourth
46 2046 0 0 1
11 2011
                0
18 2018
         1
                0
                       0
23 2023
          1
                 1
                       0
                              0
55 2055
           0
                  0
                        0
56 2056
                  0
> pikech1 <- caphist.sum(PikeNYPartial1, cols = 2:5)</pre>
> str(pikech1)
List of 4
$ caphist.sum : 'table' int [, 1:10] 5 8 2 12 1 2 21 1 2 3
  ..- attr(*, "dimnames")=List of 1
  ....$ : chr [1:10] "0001" "0010" "0011" "0100" ...
 $ schnabel.sum:'data.frame':
                                 4 obs. of 4 variables:
 ..$ n: int [1:4] 27 18 14 9
 ..$ m: num [1:4] 0 3 4 4
 ..$ R: num [1:4] 27 18 14 0
  ..$ M: num [1:4] 0 27 42 52
 \ methodB.top : int [1:4, 1:4] NA NA NA NA 3 NA NA NA 2 2 ...
$ methodB.bot : num [1:4, 1:4] 0 27 27 27 3 15 18 18 4 10 ...
 ..- attr(*, "dimnames")=List of 2
 .. ..$ : chr [1:4] "m" "u" "n" "R"
 .. ..$ : NULL
 - attr(*, "class")= chr "CapHist"
```

```
0001 0010 0011 0100 0101 0110 1000 1001 1010 1100
  5 8 2 12 1 2 21 1 2
> pikech1$schnabel.sum
  n m R M
1 27 0 27 0
2 18 3 18 27
3 14 4 14 42
4 9 4 0 52
  Data Recorded in Capture-by-Date Format
> data(PikeNYPartial2)
> rhead(PikeNYPartial2)
  sample id
65 fourth 2054
48 fourth 2027
50 third 2041
7 first 2007
60 third 2051
28 second 2028
> ch.tab <- table(PikeNYPartial2$id, PikeNYPartial2$sample)</pre>
> head(ch.tab)
      first fourth second third
 2001
        1 0 0
 2002
               0
                      0
         1
                           0
       1
 2003
              0
                     0
      1
1
              0
                    0
 2004
                           0
 2005
              0
                    0
                          0
 2006
        1
              0
                    0
> ch.df1 <- as.data.frame(ch.tab)</pre>
> rhead(ch.df1)
   Var1 Var2 Freq
167 2053 second
222 2051 third
                1
213 2042 third
                 0
204 2033 third
                 0
202 2031 third
                0
78 2021 fourth
> ch.df2 <- unstack(ch.df1, Freq ~ Var2)</pre>
> rhead(ch.df2)
  first fourth second third
57 0 1 0 0
```

> pikech1\$caphist.sum

0

34

0

1

```
35
           0
      0
                  1
                         0
3
                   0
      1
             0
12
                         0
             0
                   0
39
> ch.df2 <- ch.df2[, c(1, 3, 4, 2)]
> rhead(ch.df2)
  first second third fourth
33
     0
            1
                  0
26
      1
            0
                   1
38
      0
             1
7
      1
            0
                   0
4
      1
             0
                   0
                         0
28
      0
> pikech2 <- caphist.sum(ch.df2)</pre>
> pikech2$caphist.sum
0001 0010 0011 0100 0101 0110 1000 1001 1010 1100
  5 8 2 12 1 2
                              21
```

3 Closed Population Single Sample – Jackson Lake Bluegill

3.1 Petersen Method

```
> data(BluegillJL)
> str(BluegillJL)
                    277 obs. of 2 variables:
 $ first : int  1 0 1 0 1 1 1 1 1 1 ...
 $ second: int 0 1 0 1 0 0 0 0 0 0 ...
> rhead(BluegillJL)
   first second
80
      0
269
        1
               0
81
        1
117
        1
              0
270
              0
       1
110
       1
> bgch <- caphist.sum(BluegillJL)</pre>
> bgch$caphist.sum
 01 10 11
81 187
> mr1 <- mr.closed1(196, 90, 9)
> summary(mr1)
```

```
Used the 'naive' Petersen method.
Observed inputs of: M=196, n=90, and m=9.
Resulted in a population estimate (N) of 1960.
> confint(mr1)
The Poisson method was used to construct the CI for N.
95% LCI 95% UCI
975.4 3448.4
> confint(mr1, citype = "hypergeom")
The hypergeom method was used to construct the CI for N.
95% LCI 95% UCI
1101 4151
```

3.2 Chapman Modification

```
> mr2 <- mr.closed1(196, 90, 9, type = "C")
> summary(mr2)

Used Chapman's modification of the Petersen method.
Observed inputs of: M=196, n=90, and m=9.
Resulted in a population estimate (N) of 1792.

> confint(mr2)

The Poisson method was used to construct the CI for N.
95% LCI 95% UCI
990.3 3503.5
```

4 Closed Population Multiple Samples – New York Pike

4.1 Capture Summaries Already Known

```
> n <- c(27, 18, 14, 9)
> m <- c(0, 3, 4, 4)
> R <- c(27, 18, 14, 0)
> ex1 <- mr.closed2(n, m, R, type = "S")
> summary(ex1)

Used the Schnabel method with Chapman modification.
Resulted in a population estimate (N) of 128.

> confint(ex1)

The Poisson method was used to construct the CI for N.
95% LCI 95% UCI
74.6 237.6
```

4.2 Capture Histories were Recorded

This (re)uses the the PikeNYPartial1 data frame and pikech1 object introduced in a previous section.

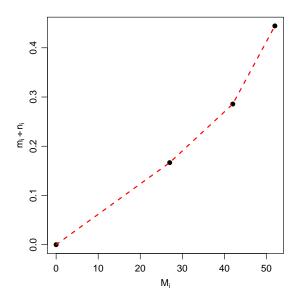
```
> ex2 <- mr.closed2(pikech1)
> summary(ex2)

Used the Schnabel method with Chapman modification.
Resulted in a population estimate (N) of 128.

> confint(ex2)

The Poisson method was used to construct the CI for N.
95% LCI 95% UCI
74.6 237.6

> plot(ex2, loess = TRUE)
```



4.3 Schumacher-Eschmeyer Method

```
> ex3 <- mr.closed2(pikech1, type = "SE")
> summary(ex3)

Used the Schumacher-Eschmeyer method.
Resulted in a population estimate (N) of 136.

> confint(ex3)

The normal method was used to construct the CI for N.
95% LCI 95% UCI
96.6 229.8
```

5 Open Population Multiple Samples

5.1 Capture Histories Given

```
> data(CutthroatAL)
> rhead(CutthroatAL)
    ID first second third
277 277
           0
                  1
56
   56
           0
                  0
328 328
          0
                  1
310 310
           0
                  1
11
           0
                  0
    11
                        1
81
           0
                  0
    81
                        1
> ch1 <- caphist.sum(CutthroatAL, cols = -1)</pre>
> ch1$methodB.top
     [,1] [,2] [,3]
[1,]
      NA
          17
                75
[2,]
           NA
[3,]
      NA
           NA
                NA
> ch1$methodB.bot
  [,1] [,2] [,3]
    0
       17
       244 198
   75
   75 261 277
n
  75 261
> ex1 <- mr.open(ch1)
> summary(ex1)
Observables
  m n R r z
1 0 75 75 21 NA
2 17 261 261 75 4
3 79 277
         O NA NA
Estimates
    M M.se
                         phi phi.se B B.se
              N N.se
  NA NA
                    NA 0.411 0.098 NA
              NA
2 30.8
        6 448.2 108.2
                          NA
                                 NA NA
                                         NA
              NA
                          NA
                                 NA NA
        NA
                    NA
Standard error of phi includes sampling and individual variability.
> confint(ex1)
The Jolly method was used to construct confidence intervals.
 N.lci N.uci phi.lci phi.uci B.lci B.uci
    NA
         NA 0.218 0.603
                                NA
2 236.1 660.2
                  NA
                          NA
                                NA
                                      NA
```

NA

NA

NA NA

NA

NA

5.2 Summaries Known, Must Be Entered into Vectors

```
> s1 <- rep(NA, 5)
> s2 <- c(6, rep(NA, 4))
> s3 \leftarrow c(7, 3, rep(NA, 3))
> s4 \leftarrow c(7, 4, 6, NA, NA)
> s5 \leftarrow c(4, 3, 6, 9, NA)
> mb.top <- cbind(s1, s2, s3, s4, s5)
> mb.top
     s1 s2 s3 s4 s5
[1,] NA 6 7 7 4
[2,] NA NA 3 4 3
[3,] NA NA NA 6 6
[4,] NA NA NA NA 9
[5,] NA NA NA NA NA
> m < -c(0, 6, 10, 17, 22)
> u <- c(28, 21, 22, 17, 11)
> n <- c(28, 27, 32, 34, 33)
> R \leftarrow c(28, 27, 32, 34, 0)
> mb.bot <- rbind(m, u, n, R)</pre>
> mb.bot
  [,1] [,2] [,3] [,4] [,5]
            10 17
   0
       6
    28
         21
              22
                   17
                        11
   28
        27
              32
                   34
n
R 28
       27
            32 34
                       0
> ex2 <- mr.open(mb.top, mb.bot)</pre>
> summary(ex2)
Observables
  m n R r z
1 0 28 28 24 NA
2 6 27 27 10 18
3 10 32 32 12 18
4 17 34 34 9 13
5 22 33 O NA NA
Estimates
    M M.se
               N N.se phi phi.se
                                      B B.se
              NA NA 1.851 0.460
                                     NA NA
2 51.8 14.5 207.3 89.3 0.765 0.246
                                      8.6 66.8
3 55.7 13.6 167.1 56.1 0.804 0.266 -12.9 37.4
4 62.5 17.2 121.5 37.5 NA
                               NA
                                     NA NA
  NA NA
            NA NA
                          NA
                                NA
                                       NA
                                            NA
Standard error of phi includes sampling and individual variability.
> confint(ex2)
The Jolly method was used to construct confidence intervals.
  N.lci N.uci phi.lci phi.uci B.lci B.uci
```

1	NA	NA	0.949	2.752	NA	NA
2	32.2	382.3	0.283	1.247	-122.4	139.5
3	57.2	277.0	0.283	1.326	-86.3	60.5
4	47.9	195.1	NA	NA	NA	NA
5	NA	NA	NA	NA	NA	NA

6 Analyses with Rcapture Package

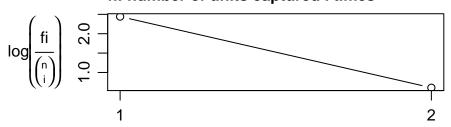
The "program MARK" is the industry standard for analyze capture-recapture data in a log-linear framework. This software depends on data organized in capture history format as illustrated in these notes. Recently the Rcapture package was introduced as a means of fitting the log-linear capture-recapture models in R. This package is available for download from CRAN and an article describing how to use Rcapture can be found in the April 2007 issue of the on-line Journal of Statistical Software (http://www.jstatsoft.org).

For those of you familiar with "program MARK" you may recognize some of the output below.

```
> library(Rcapture)
> d <- descriptive(PikeNYPartial1[, 2:5])
> plot(d)
```

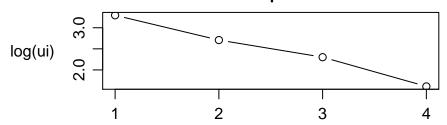
Exploratory Heterogeneity Graph

fi: number of units captured i times



i: number of captures

ui: number of units captured for the first time on (



i: capture occasion identification number

> r <- closedp(PikeNYPartial1[, 2:5])
> r

Number of captured units: 57

Abundance estimations and model fits:

	abundance	stderr	deviance	df	AIC
MO	145.7	35.7	15.756	13	51.235
Mt	139.0	33.5	4.201	10	45.680
Mh Chao	145.7	35.7	15.756	13	51.235
Mh Poisson2	57.0	20.2	13.752	12	51.230
Mh Darroch	57.0	0.0	13.752	12	51.230
Mth Chao	139.0	33.5	4.201	10	45.680
Mth Poisson2	57.0	19.5	2.310	9	45.788
Mth Darroch	57.0	0.0	2.310	9	45.788
Mb	64.5	5.4	4.271	12	41.750
Mbh	64.9	8.5	4.265	11	43.744

Note: 2 eta parameters has been set to zero in the Mh Chao model Note: 2 eta parameters has been set to zero in the Mth Chao model

> r1 <- openp(PikeNYPartial1[, 2:5])</pre>

> r1

Model fit:

 $\begin{array}{ccc} & \text{deviance} & \text{df} & \text{AIC} \\ \text{fitted model} & 2.683 & 7 & 50.162 \end{array}$

Test for trap effect:

Capture probabilities:

estimate stderr
period 1 -- -period 2 0.1429 0.0830
period 3 0.2222 0.1821
period 4 -- --

Survival probabilities:

estimate stderr
period 1 -> 2 0.7778 0.4647
period 2 -> 3 0.5000 0.4098
period 3 -> 4 -- --

Abundances:

estimate stderr
period 1 -- -period 2 126 67.9
period 3 63 49.5
period 4 -- --

Number of new arrivals:

Total number of units who ever inhabited the survey area: estimate stderr

all periods 132 56.1

Total number of captured units: 57

Note: 1 gamma parameter has been set to zero