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R Handout - R Mark Recapture

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1 Handout

```
> library(FSA) # mrClosed, capHistSum, BluegillJL
```

1.1 Single Census, Closed Population

```
> data(BluegillJL)
                     # data from FSA package
> view(BluegillJL)
   first second
29
       0
58
       0
              1
      1
             0
146
188
      0
             1
243
       0
              1
251
> bgtbl <- table(BluegillJL$first,BluegillJL$second)
> addmargins(bgtbl)
          1 Sum
       0
       0 81 81
     187 9 196
 1
 Sum 187 90 277
> mr1 <- mrClosed(M=196,n=90,m=9,type="Chapman")</pre>
> summary(mr1)
Used Chapman's modification of the Petersen method with M=196, n=90, and m=9.
```

```
N
[1,] 1792
> confint(mr1)
The Poisson method was used.
```

```
95% LCI 95% UCI
[1,] 990 3504

> bgch <- capHistSum(BluegillJL)
> bgch$caphist

01 10 11
81 187 9

> mr2 <- mrClosed(bgch,type="Chapman")
> summary(mr2)
```

Used Chapman's modification of the Petersen method with M=196, n=90, and m=9.

N [1,] 1792

1.2 Single Census, Closed Population, Size Classes

The following table appeared in the grey literature article "A mark recapture experiment to estimate the escapement of chinook salmon in the Keta River, 2000".

Table 1.-Numbers of chinook salmon marked in the Keta River and inspected for marks on the spawning grounds in 2000, by length group.

	550-659 mm	≥660 mm	Total
Event 1: Released with marks (M)	70	200	270
Event 2: Captured (C)	52	172	224
Recaptured (R)	9	37	46
R/C	17.3%	21.5%	20.5%

```
> marked <- c(70,200)
> num <- c(52,172)
> recaps <- c(9,37)
> lbls <- c("550-659 mm",">=660 mm")
> mr3 <- mrClosed(M=marked,n=num,m=recaps,type="Chapman",labels=lbls)
> summary(mr3,incl.SE=TRUE,incl.all=TRUE)

Used Chapman's modification of the Petersen method with observed inputs of:
550-659 mm- M=70, n=52, and m=9.
>=660 mm- M=200, n=172, and m=37.
```

```
N SE

550-659 mm 375 94.7

>=660 mm 914 116.6

All 1289 150.2

> confint(mr3)

550-659 mm - The binomial method was used.
>=660 mm - The binomial method was used.
```

```
95% LCI 95% UCI
550-659 mm 228 639
>=660 mm 700 1216
```

1.3 Multiple Census, Closed Population, Capture History Data

```
> data(PikeNYPartial1)
> view(PikeNYPartial1)
     id first second third fourth
1 2001 1 0 0
15 2015 1 0 0
31 2031 0 1 0
47 2047 0 0 1
53 2053 0 0 0
56 2056 0 0 0
                               1
> pikech <- capHistSum(PikeNYPartial1,cols=-1)</pre>
> pikech$caphist
0001 0010 0011 0100 0101 0110 1000 1001 1010 1100
   5 8 2 12 1 2 21 1 2 3
> pikech$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
> mr4 <- mrClosed(pikech,type="Schnabel")</pre>
> summary(mr4)
Used the Schnabel method with Chapman modification.
```

```
N
[1,] 128
> confint(mr4)
The Poisson method was used.
```

```
95% LCI 95% UCI
[1,] 75 238
```

1.4 Multiple Census, Closed Population, Summarized Data

```
> mr5 <- mrClosed(n=c(16,19,16),m=c(0,7,7),R=c(16,19,0),type="Schnabel")
> summary(mr5)
Used the Schnabel method with Chapman modification.
```

```
N
[1,] 50
> confint(mr5)
The Poisson method was used.
```

95% LCI 95% UCI [1,] 31 87