Preliminaries

```
> library(FSA)  # for mrClosed(), capHistSum()
> setwd("C:/aaaWork/Web/fishR/courses/Vermont2014/CourseMaterial/") # Derek's Computer
```

Single Census, Closed Population

```
> bg <- read.csv("Data/BluegillJL.csv",header=TRUE)
> view(bg)
    first second
24      1      0
79      1      0
124     1      0
167     1      0
242     0      1
273     0      1
> bgtbl <- xtabs(~first+second,data=bg)
> addmargins(bgtbl)
      second
first   0   1 Sum
  0     0  81  81
  1   187   9 196
  Sum 187  90 277
> mr1 <- mrClosed(M=196,n=90,m=9,type="Chapman")
> summary(mr1)
        N
[1,] 1792
> confint(mr1)
     95% LCI 95% UCI
[1,]     990    3504
```

```
> bgch <- capHistSum(bg)
> bgch$caphist

 01  10  11
 81 187   9
> mr2 <- mrClosed(bgch,type="Chapman")
> summary(mr2)
        N
[1,] 1792
```

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%**

```
> mr3 <- mrClosed(M=c(70,200),n=c(52,172),m=c(9,37),type="Chapman",
                  labels=c("550-659 mm",">=660 mm"))
> summary(mr3,incl.SE=TRUE,incl.all=TRUE)
              N    SE
550-659 mm  375  94.7
>=660 mm    914 116.6
All        1289 150.2
> confint(mr3)
             95% LCI 95% UCI
550-659 mm       228     639
>=660 mm         700    1216
```

Multiple Census, Closed Population, Capture History Data

```
> np <- read.csv("Data/PikeNYPartial1.csv",header=TRUE)
> view(np)
     id first second third fourth
7  2007     1      0     0      0
12 2012     1      0     0      0
14 2014     1      0     0      0
28 2028     0      1     0      0
44 2044     0      0     1      0
46 2046     0      0     1      0
> npch <- capHistSum(np,cols=-1)
> npch$caphist

0001 0010 0011 0100 0101 0110 1000 1001 1010 1100
   5    8    2   12    1    2   21    1    2    3
> npch$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(npch,type="Schnabel")
> summary(mr4)
      N
[1,] 128

> confint(mr4)
     95% LCI 95% UCI
[1,]      75     238
```

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)
     N
[1,] 50

> confint(mr5)
     95% LCI 95% UCI
[1,]      31      87
```