1 R Terminology Assignment Key

1. Load the data in the **RuffeBio.csv** file into a data frame in R.

```
> ## setwd("C:/aaaWork/Web/fishR/courses/Midwest2012/CourseMaterial")
> ruf <- read.csv("RuffeBio.csv")
> str(ruf)

'data.frame':	40 obs. of  10 variables:
 $ fishID  : int  60 61 62 63 64 65 66 67 68 69 ...
 $ locShort: Factor w/ 1 level "St. Louis R. (2007)": 1 1 1 1 1 1 1 1 1 1 ...
 $ year    : int  2007 2007 2007 2007 2007 2007 2007 2007 2007 2007 ...
 $ month   : int  9 9 9 9 9 9 9 9 9 9 ...
 $ day     : int  20 20 20 20 20 20 20 20 20 20 ...
 $ date    : Factor w/ 1 level "9/20/2007": 1 1 1 1 1 1 1 1 1 1 ...
 $ tl      : int  134 111 110 115 92 88 95 90 99 107 ...
 $ wt      : num  24.6 14.7 12.3 16 8.3 7.8 9.7 8.2 11.7 13 ...
 $ sex     : Factor w/ 3 levels "female","male",..: 1 1 1 1 1 1 1 1 1 1 ...
 $ maturity: Factor w/ 3 levels "","immature",..: 3 3 2 3 3 3 3 3 3 3 ...

> ruf$tl[17]

[1] 114
```

   (a) There are 10 variables in this data frame.
   (b) Data was recorded on 40 ruffe in this data frame.
   (c) The *tl* variable is a numeric variable type.
   (d) The *maturity* variable is a factor variable type.
   (e) The *tl* for the 17th measured individual is 114 mm.

2. For each situation below, create a new data frame (from the original) and record how many fish are in that data frame.

   (a) Just female ruffe.

```
> ruf1 <- Subset(ruf,sex=="female")
> nrow(ruf1)
[1] 31
```

   (b) Just ruffe greater than 110 mm.

```
> ruf2 <- Subset(ruf,tl>110)
> nrow(ruf2)
[1] 7
```

   (c) Just ruffe between 80 and 110 mm.

```
> ruf3 <- Subset(ruf,tl>80 & tl<110)
> nrow(ruf3)
[1] 25
```

   (d) Excluding all fish of an “unknown” sex.

```
> ruf5 <- Subset(ruf,sex!="unknown")
> nrow(ruf5)
[1] 39
```

3. Create new variables in the original data frame for the following situations.

   (a) Fulton's condition factor (The weight of the fish divided by the cubed length of the fish).

```
> ruf$fult <- ruf$wt/(ruf$tl^3)*10000
```

4. If you have time ...

   (a) Create a length variable that is the total length in inches.

```
> ruf$tlin <- ruf$tl/25.4
```

   (b) Create a subset of just male ruffe with a total length less than 80 mm.

```
> ruf4 <- Subset(ruf,sex=="male" & tl<80)
Warning:  The resultant data.frame has 0 rows.  Try str() on the result.
> nrow(ruf4)
[1] 0
```

   (c) What is the *tl* for all but the 10th individual?

```
> ruf$tl[-10]
 [1] 134 111 110 115  92  88  95  90  99  NA  99 102 105  90 102 114  NA  56  90 101 109
[22] 110 111 101  95  84 105 120 104 102  99  84  87  81  81  65  42  NA 115
```

   (d) Show all recorded information for the 11th individual.

```
> ruf[11,]
   fishID            locShort year month day      date tl  wt    sex maturity fult tlin
11     70 St. Louis R. (2007) 2007     9  20 9/20/2007 NA 9.7 female   mature   NA   NA
```

2 R Summarization Assignment Key

1. Load the data in the **LakeTroutALTER.xls** file into a data frame in R.

```
> ## setwd("C:/aaaWork/Web/fishR/courses/Midwest2012/CourseMaterial")
> lkt <- read.csv("LakeTroutALTER.csv")
> str(lkt)

'data.frame': 86 obs. of  8 variables:
 $ id    : int  18 512 307 52 84 37 80 36 17 59 ...
 $ tl    : int  225 247 256 268 285 288 295 324 328 330 ...
 $ fl    : int  202 226 235 241 262 265 270 295 297 299 ...
 $ sl    : int  185 212 209 228 240 244 243 273 278 280 ...
 $ w     : int  76 138 120 170 185 182 205 275 285 297 ...
 $ otorad: num  0.84 0.879 0.843 0.944 0.99 ...
 $ age   : int  8 6 6 9 7 9 7 10 7 10 ...
 $ sex   : Factor w/ 2 levels "F","M": 1 1 1 1 1 1 1 1 1 1 ...
```

   (a) There are 8 variables in this data frame.
   (b) Data was recorded on 86 ruffe in this data frame.
   (c) The *age* variable is a numeric variable type.
   (d) The *sex* variable is a factor variable type.

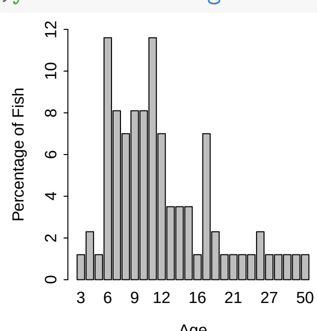
2. Summarize age in the following ways:

   (a) Construct age-frequency (number-at-age) and age-percentage (percentage-at-age) tables.

```
> ( agetbl <- table(lkt$age) )

 3  4  5  6  7  8  9 10 11 12 13 14 15 16 17 18 19 21 23 24 25 27 32 34 43 50
 1  2  1 10  7  6  7  7 10  6  3  3  3  1  6  2  1  1  1  1  2  1  1  1  1  1
> ( ageptbl <- round(prop.table(agetbl)*100,1) )

   3    4    5    6    7    8    9   10   11   12   13   14   15   16   17   18   19   21
 1.2  2.3  1.2 11.6  8.1  7.0  8.1  8.1 11.6  7.0  3.5  3.5  3.5  1.2  7.0  2.3  1.2  1.2
  23   24   25   27   32   34   43   50
 1.2  1.2  2.3  1.2  1.2  1.2  1.2  1.2
```

   (b) Construct a bar chart of the age-percentage table.

```
> barplot(ageptbl,xlab="Age",ylab="Percentage of Fish",ylim=c(0,12))
```



   (c) Construct an age-percentage table separated by sex (e.g., what percentage of males were age-17?).

```
> agetbl2 <- table(lkt$sex,lkt$age)
> round(prop.table(agetbl2,margin=1)*100,1)
```

```
      3    4    5    6    7    8    9   10   11   12   13   14   15   16   17   18   19
  F 0.0  0.0  0.0  8.5  8.5  8.5 10.6 10.6  8.5 10.6  6.4  2.1  2.1  2.1  8.5  4.3  2.1
  M 2.6  5.1  2.6 15.4  7.7  5.1  5.1  5.1 15.4  2.6  0.0  5.1  5.1  0.0  5.1  0.0  0.0

     21   23   24   25   27   32   34   43   50
  F 2.1  0.0  0.0  0.0  2.1  0.0  0.0  2.1  0.0
  M 0.0  2.6  2.6  5.1  0.0  2.6  2.6  0.0  2.6
```

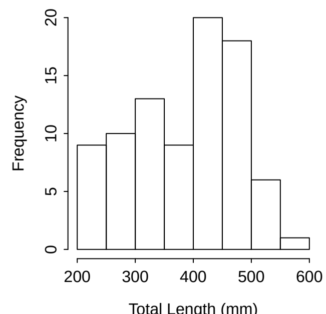
3. Summarize total length in the following ways:

   (a) Compute summary statistics of total length for all fish.

```
> Summarize(~tl,data=lkt,digits=1)
       n     mean       sd      min       Q1   median       Q3      max percZero
    86.0    387.0     92.5    206.0    325.0    415.0    461.0    567.0      0.0
```

   (b) Construct a histogram of total length using 50-mm length increments.

```
> hist(~tl,data=lkt,right=TRUE,breaks=seq(200,600,50),xlab="Total Length (mm)")
```

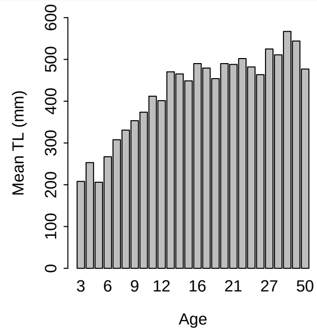


   (c) Compute summary statistics of total length separately for each age.

```
> ( smrzTL <- Summarize(tl~age,data=lkt,digits=1) )
   age  n  mean   sd min  Q1 median  Q3 max percZero
1    3  1 208.0   NA 208 208    208 208 208        0
2    4  2 253.0 45.3 221 237    253 269 285        0
3    5  1 206.0   NA 206 206    206 206 206        0
4    6 10 267.0 52.0 215 228    252 314 344        0
5    7  7 307.7 37.0 280 284    295 314 383        0
6    8  6 330.8 64.1 225 311    335 362 415        0
7    9  7 353.3 59.8 268 318    356 394 425        0
8   10  7 373.7 40.6 324 345    368 401 432        0
9   11 10 411.9 45.2 312 394    418 433 482        0
10  12  6 401.3 52.4 331 361    420 430 462        0
11  13  3 470.3 34.4 443 451    459 484 509        0
12  14  3 465.3 28.9 432 456    480 482 484        0
13  15  3 448.7  5.0 444 446    448 451 454        0
14  16  1 490.0   NA 490 490    490 490 490        0
15  17  6 479.3 28.9 424 478    488 494 505        0
16  18  2 454.0 15.6 443 448    454 460 465        0
17  19  1 490.0   NA 490 490    490 490 490        0
18  21  1 488.0   NA 488 488    488 488 488        0
19  23  1 502.0   NA 502 502    502 502 502        0
20  24  1 482.0   NA 482 482    482 482 482        0
21  25  2 463.5 12.0 455 459    464 468 472        0
22  27  1 525.0   NA 525 525    525 525 525        0
23  32  1 511.0   NA 511 511    511 511 511        0
24  34  1 567.0   NA 567 567    567 567 567        0
25  43  1 544.0   NA 544 544    544 544 544        0
26  50  1 477.0   NA 477 477    477 477 477        0
```

(d) Construct a bar plot of mean length-at-age.

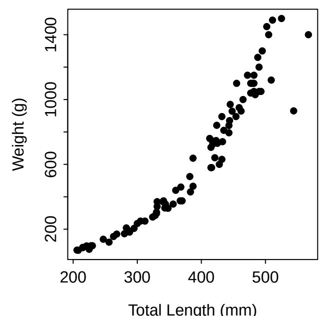
```
> plotH(mean~age,data=smrzTL,xlab="Age",ylab="Mean TL (mm)",ylim=c(0,600))
```



4. Examine the following relationships (graphically and, if appropriate, numerically):

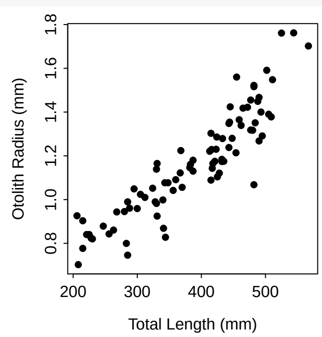
   (a) Between total length and weight.

```
> plot(w~tl,data=lkt,xlab="Total Length (mm)",ylab="Weight (g)",pch=16)
```



   (b) Between total length and otolith radius.

```
> plot(otorad~tl,data=lkt,xlab="Total Length (mm)",ylab="Otolith Radius (mm)",pch=16)
```



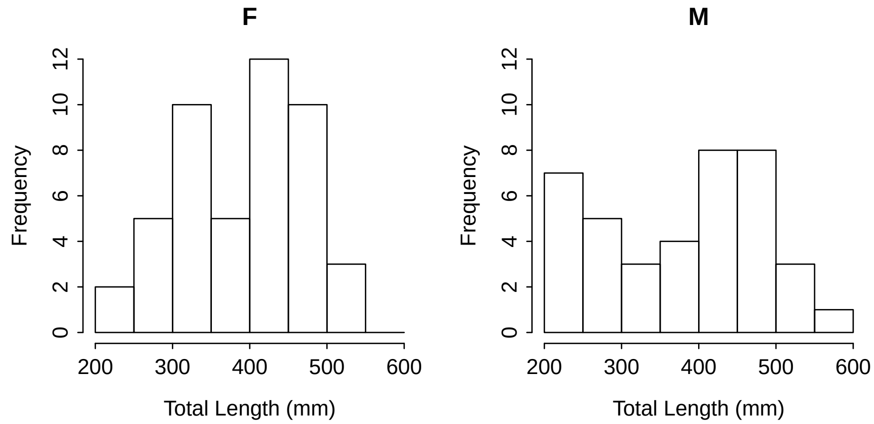
5. If you have time ...

   (a) Compute summary statistics of total length separated by sex of the fish.

```
> Summarize(tl~sex,data=lkt,digits=1)
  sex  n  mean    sd min  Q1 median  Q3 max percZero
1   F 47 396.0  80.6 225 331    415 460 544        0
2   M 39 376.3 105.2 206 284    413 464 567        0
```

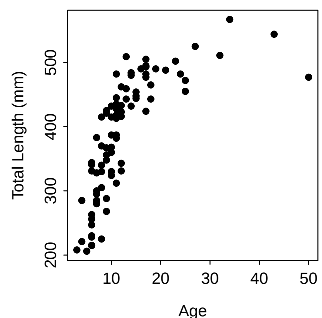
   (b) Construct separate histograms of total length for males and females.

```
> hist(tl~sex,data=lkt,right=TRUE,breaks=seq(200,600,50),xlab="Total Length (mm)")
```



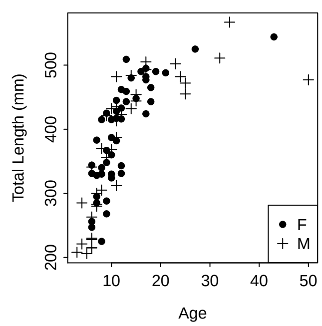
(c) Examine the relationship between age and total length.

```
> plot(tl~age,data=lkt,xlab="Age",ylab="Total Length (mm)",pch=16)
```



(d) Examine the relationship between age and total length with separate symbols for different sexes.

```
> pts <- c(16,3)
> plot(tl~age,data=lkt,xlab="Age",ylab="Total Length (mm)",pch=pts[sex])
> legend("bottomright",pch=pts,legend=levels(lkt$sex))
```



3 R Size Structure Assignment Key

1. Load the data in the **Lab1a.csv** file into a data frame in R (this is the same data used in the handout).

```
> ## setwd("C:/aaaWork/Web/fishR/courses/Midwest2012/CourseMaterial")
> lab1 <- read.csv("Lab1a.csv")
> lab1$len <- lab1$inches*25.4
```

2. Compute the PSD value for walleye.

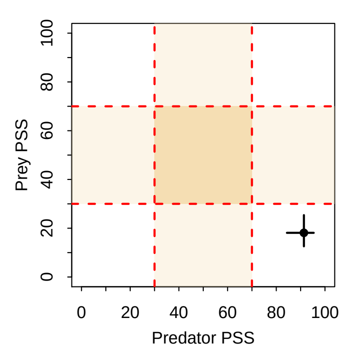
```
> pssVal("Walleye",units="mm")

     zero      stock    quality preferred memorable     trophy
        0        250        380       510       630        760

> wae <- Subset(lab1,species=="WAE")
> wae <- lencat(~len,data=wae,startcat=250,w=10)
> wae.lf <- table(wae$LCat)
> wae.rc <- rcumsum(wae.lf)
> wae.rc["380"]/wae.rc["250"]

   380
0.9135
```

3. Compute the PSD value for yellow perch.

```
> pssVal("Yellow perch",units="mm")

     zero      stock    quality preferred memorable     trophy
        0        130        200       250       300        380

> yep <- Subset(lab1,species=="YEP")
> yep <- lencat(~len,data=yep,startcat=70,w=10)
> yep.lf <- table(yep$LCat)
> yep.rc <- rcumsum(yep.lf)
> yep.rc["200"]/yep.rc["130"]

   200
0.1812
```

4. Construct a tic-tac-toe graph with a point for walleye and yellow perch on it.

```
> tictactoe()
> tictactoeAdd(c(wae.rc["380"],wae.rc["250"]),c(yep.rc["200"],yep.rc["130"]),
 pt.col="black")
```



```
Predator PSS was 91 with a 95% CI of (84.4,95.4).
Prey PSS was 18 with a 95% CI of (12.6,25.4).
```

5. If you have time ...

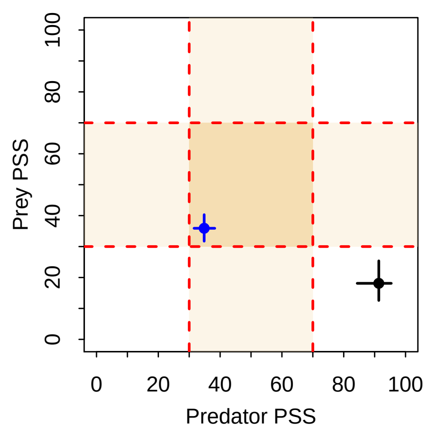
   (a) Compute the RSD-500 for walleye.

```
> wae.rc["500"]/wae.rc["250"]
   500
0.3269
```

   (b) Construct a tic-tac-toe graph with two points – one for walleye and yellow perch and one for largemouth bass and bluegill. [Note: you can copy the code for the largemouth bass and bluegill from the handout.]

```
> source("03_PSD.R")
```

```
> tictactoe()
> tictactoeAdd(c(wae.rc["380"],wae.rc["250"]),c(yep.rc["200"],yep.rc["130"]),
 pt.col="black")
Predator PSS was 91 with a 95% CI of (84.4,95.4).
Prey PSS was 18 with a 95% CI of (12.6,25.4).
> tictactoeAdd(c(lmb.rcum["300"],lmb.rcum["200"]),c(bg.rcum["200"],bg.rcum["150"]),
 pt.col="blue")
Predator PSS was 35 with a 95% CI of (31.6,38.3).
Prey PSS was 36 with a 95% CI of (31.7,40.3).
```



4 R Catch Curve Assignment Key

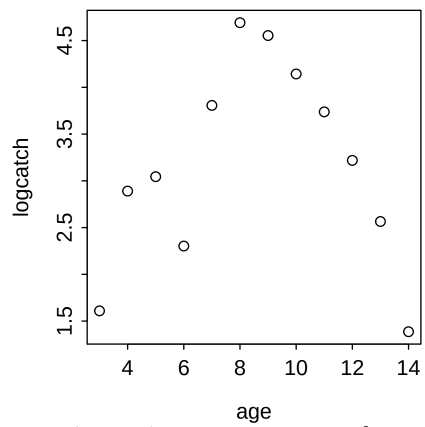
1. The population biology of Lake Superior lake trout ....

   (a) Enter the data into vectors and then combine into a data frame.

```
> lkt <- data.frame(age=3:14,catch=c(5,18,21,10,45,109,95,63,42,25,13,4))
> lkt$logcatch <- log(lkt$catch)
```

   (b) Plot log(catch) versus age. Which ages best represent the descending portion of the catch-curve?

```
> plot(logcatch~age,data=lkt)
```



   (c) Fit the linear model required to estimate instantaneous total mortality to these data with `lm()`. [Note: it may be easiest to combined the raw data into a data frame and then use `Subset()` to create a new data frame with just the ages on the descending limb.] What is an estimate of the instantaneous total mortality rate?

```
> lkt1 <- Subset(lkt,age>=9 & age <14)
> lm1 <- lm(logcatch~age,data=lkt1)
> coef(lm1)
(Intercept)         age
     9.0360     -0.4902
> ( z <- -coef(lm1)[2] )
   age
0.4902
```

   (d) Find the instantaneous total mortality rate using catchCurve(). Do these results match your results in the previous question?

```
> cc2 <- catchCurve(catch~age,data=lkt,9:13)
> summary(cc2)
  Estimate Std. Error t value  Pr(>|t|)
Z   0.4902    0.03044   16.11 0.0005207
A  38.7503         NA      NA        NA
```

2. Curtis (1990) examined the population dynamics ....

   (a) Estimate, with 95% confidence interval, the instantaneous total mortality rate of fish caught in 1963. Describe which ages of fish you used to make your estimate and why you chose those ages.

```
> cr63 <- data.frame(age=6:14,ct=c(129,339,331,192,70,16,0.5,0.5,0.5))
> cc63c <- catchCurve(ct~age,data=cr63,8:11)
> summary(cc63c)
  Estimate Std. Error t value Pr(>|t|)
Z     1.01     0.1472   6.857  0.02061
A    63.57         NA      NA       NA
```

   (b) Estimate, with 95% confidence interval, the instantaneous total mortality rate for fish of the 1963 year-class. Describe which ages of fish you used to make your estimate and why you chose those ages.

```
> long63 <- data.frame(age=c(6,10:14),ct=c(45,491,163,117,18,7))
> cc63l <- catchCurve(ct~age,data=long63,10:14)
> summary(cc63l)
  Estimate Std. Error t value Pr(>|t|)
Z     1.07     0.1205   8.883 0.003009
A    65.71         NA      NA       NA
```

5 R Growth Assignment Key

1. The length and otolith age of sculpins captured in the Arctic Long-Term Ecological Research area were recorded in **SculpinALTER.xls**. Use the total length and age data to answer the following questions.

   (a) Load these data into an R data frame.

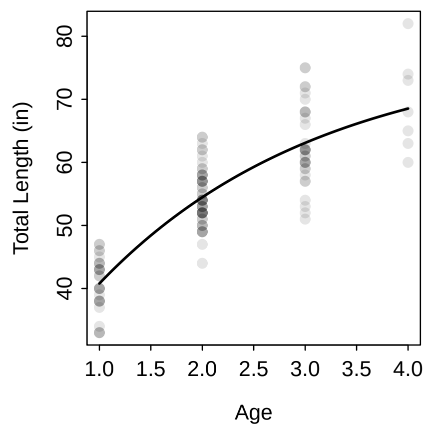
```
> ## setwd("C:/aaaWork/Web/fishR/courses/Midwest2012/CourseMaterial")
> sc <- read.csv("SculpinALTER.csv")
> str(sc)
'data.frame': 117 obs. of  3 variables:
 $ w  : num  0.9 1.15 1.5 1.25 1.35 1.95 2.3 0.9 0.4 0.3 ...
 $ tl : int  52 53 58 57 56 62 65 49 38 33 ...
 $ age: int  2 2 2 2 2 3 4 2 1 1 ...
```

   (b) Compute estimates for the three parameters of a "traditional" von Bertalanffy growth model.

```
> svb1 <- vbStarts(tl~age,data=sc,type="typical")
> vb1 <- vbFuns("typical",simple=TRUE)
> fit1 <- nls(tl~vb1(age,Linf,K,t0),data=sc,start=svb1)
> coef(fit1)
   Linf       K      t0
77.8280  0.4608 -0.6114
```

   (c) Construct a plot of length versus age with the best-fit von Bertalanffy growth model superimposed.

```
> fitPlot(fit1,xlab="Age",ylab="Total Length (in)",main="",
         col.pt=rgb(0,0,0,0.1),col.mdl="black")
```



2. If you have time ...

   (a) Compute estimates for the three parameters of a "Galucci and Quinn" parameterization of the von Bertalanffy growth model.

```
> vb2 <- vbFuns("GalucciQuinn",simple=TRUE)
> svb2 <- vbStarts(tl~age,data=sc,type="GalucciQuinn")
> fit2 <- nls(tl~vb2(age,omega,K,t0),data=sc,start=svb2)
> coef(fit2)
  omega       K      t0
35.8642  0.4608 -0.6114
```

   (b) Construct a length-weight regression model for these sculpins.

```
> sc$logTL <- log(sc$tl)
> sc$logW <- log(sc$w)
> lm1 <- lm(logW~logTL,data=sc)
> summary(lm1)

Call:
lm(formula = logW ~ logTL, data = sc)

Residuals:
    Min      1Q  Median      3Q     Max
-0.2951 -0.1011 -0.0014  0.0593  0.8035

Coefficients:
            Estimate Std. Error t value Pr(>|t|)
(Intercept) -12.2863     0.3047   -40.3   <2e-16
logTL         3.1260     0.0765    40.9   <2e-16

Residual standard error: 0.161 on 115 degrees of freedom
Multiple R-squared:  0.936,Adjusted R-squared:  0.935
F-statistic: 1.67e+03 on 1 and 115 DF,  p-value: <2e-16
```

6 R Mark-Recapture Assignment Key

1. Warren *et al.* (2004) examined the population of rainbow trout in the Upper Niagara Springs pond in 2000. Fish were captured at two times by using an electrofishing unit attached to a driftboat. The capture histories of all fish examined in the two samples are recorded in **RBTroutUNSP.xls**. Load these data into a data frame in R and answer the following questions.

   (a) Create a summary of the capture histories.

   ```
   > ## setwd("C:/aaaWork/Web/fishR/courses/Midwest2012/CourseMaterial")
   > rbt <- read.csv("RBTroutUNSP.csv")
   > str(rbt)
   'data.frame': 173 obs. of  3 variables:
    $ fish  : int  1 2 3 4 5 6 7 8 9 10 ...
    $ first : int  1 1 1 1 1 1 1 1 1 1 ...
    $ second: int  1 0 0 0 0 0 0 0 1 0 ...
   > q2.ch <- capHistSum(rbt,cols=-1)
   > q2.ch$caphist

   01 10 11
   99 63 11
   ```

   (b) From your capture history summary assign values to each of these symbols (M, n, m).

   ```
   > q2 <- mrClosed(M=74,n=110,m=11,type="Chapman")
   ```

   (c) Construct an appropriate population estimate, with a 95% confidence interval, for Upper Niagara Springs pond in 2000. State which method you used to construct the confidence interval and explain why you chose that method.

   ```
   > summary(q2)
   Used Chapman's modification of the Petersen method with M=74, n=110, and m=11.
   ```

   ```
          N
   [1,] 693
   > confint(q2)
   The  Poisson  method was used.
   ```

   ```
        95% LCI 95% UCI
   [1,]     402    1282
   ```

2. Mraz (1968) examined the population dynamics of ....

```
> n1 <- c(321,412,178,415,367)
> m1 <- c(0,45,55,93,113)
> R1 <- c(n1[1:4],0)
> mr1 <- mrClosed(n=n1,m=m1,R=R1,type="Schnabel")
> summary(mr1)
Used the Schnabel method with Chapman modification.
```

```
        N
[1,] 3280
> confint(mr1)
The normal method was used.
```

```
     95% LCI 95% UCI
[1,]    2776    4009
```

Reproducibility Information

Version Information

- **Compiled Date:** Mon Dec 16 2013
- **Compiled Time:** 11:13:18 AM

R Information

- **R Version:** R version 3.0.2 (2013-09-25)
- **System:** Windows, i386-w64-mingw32/i386 (32-bit)
- **Base Packages:** base, datasets, graphics, grDevices, methods, stats, utils
- **Other Packages:** FSA_0.4.3, knitr_1.5.15, nlstools_0.0-15, plotrix_3.5-2
- **Loaded-Only Packages:** bitops_1.0-6, car_2.0-19, caTools_1.16, cluster_1.14.4, evaluate_0.5.1, formatR_0.10, Formula_1.1-1, gdata_2.13.2, gplots_2.12.1, grid_3.0.2, gtools_3.1.1, highr_0.3, Hmisc_3.13-0, KernSmooth_2.23-10, lattice_0.20-24, MASS_7.3-29, multcomp_1.3-1, mvtnorm_0.9-9996, nlme_3.1-113, nnet_7.3-7, quantreg_5.05, sandwich_2.3-0, sciplot_1.1-0, SparseM_1.03, splines_3.0.2, stringr_0.6.2, survival_2.37-4, tools_3.0.2, zoo_1.7-10
- **Required Packages:** FSA, nlstools and their dependencies (car, gdata, gplots, Hmisc, knitr, multcomp, nlme, plotrix, quantreg, sciplot, stats)