R Handout - K-Pass Removal

Dr. Derek Ogle
Northland College

Mar 2014, Vermont CFWRU Workshop

Preliminaries

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

Single Removal Estimates

```
> d <- c(71,48,40)
> res <- removal(d,type="CarleStrub")
> summary(res)
The Carle & Strub's K-Pass Removal Method method was used.
   Estimate Std. Error
No 252.0000    46.3817
p    0.2809     0.0719
> confint(res)
   95% LCI  95% UCI
No  161.09 342.9065
p     0.14   0.4218
```

Multiple Removal Estimates – Data in Wide Format

```
> d <- read.csv("Data/JonesStockwell2.csv",header=TRUE)
> head(d)
  species site   age0 first second third
1 rainbow  A15 Age-1+    17     10     7
2 rainbow   A9  Age-0    17     12     8
3 rainbow  A10  Age-0    25     10     8
4 rainbow   B1  Age-0    69     43    23
5 rainbow   B1 Age-1+     6      2     1
6 rainbow Bio1  Age-0    38     20    20
```

```
> ( res <- apply(d[,4:6],MARGIN=1,FUN=removal,type="CarleStrub",just.ests=TRUE) )
         [,1]    [,2]    [,3]      [,4]   [,5]      [,6]    [,7]      [,8]    [,9]
No    41.0000 48.0000 48.0000 165.00000 9.0000 109.00000 31.0000 930.00000 31.0000
p      0.4304  0.3776  0.5119   0.42994 0.6923   0.33766  0.4737   0.26271  0.5185
No.se  7.0691 10.5594  4.7448  14.21881 0.6903  20.56207  4.7616 102.15821  3.6697
p.se   0.1303  0.1334  0.1037   0.06499 0.1726   0.09617  0.1382   0.03914  0.1275
         [,10]   [,11]     [,12]   [,13]     [,14]     [,15]     [,16]   [,17]
No    252.0000 11.0000 341.00000 46.0000 145.00000 148.00000 124.00000 14.0000
p       0.2809  0.6471   0.42266  0.4270   0.41786   0.36066   0.33969  0.5200
No.se  46.3817  1.0198  21.35046  7.6421  14.33083  20.63412  21.63915  2.4450
p.se    0.0719  0.1700   0.04584  0.1238   0.07094   0.07865   0.08978  0.1892
       [,18]  [,19]  [,20] [,21]   [,22]   [,23]   [,24]     [,25]   [,26]  [,27]
No    3.0000 3.0000 7.0000     2 14.0000 38.0000 24.0000 140.00000 24.0000 4.0000
p     0.7500 0.7500 0.7000     1  0.5417  0.4714  0.5897   0.71354  0.7059 0.8000
No.se 0.2659 0.2659 0.5783     0  2.1563  5.3417  2.1307   2.35888  1.0292 0.2052
p.se  0.2659 0.2659 0.1928   NaN  0.1820  0.1254  0.1276   0.04197  0.1029 0.2052
       [,28]    [,29]    [,30]  [,31] [,32]   [,33]     [,34]     [,35]   [,36]  [,37]
No    8.0000 13.0000 15.0000 2.0000     1 13.0000 546.00000 192.00000 17.0000 1.0000
p     0.6667  0.8125  0.3235 0.3333     1  0.5217   0.09486   0.38083  0.2326 0.5000
No.se 0.7687  0.3308  8.3835 2.8664     0  2.3325 487.43490  20.69024 17.5787 0.7338
p.se  0.1922  0.1103  0.2673 0.7166   NaN  0.1957   0.09356   0.06628  0.3133 0.7338
       [,38] [,39]  [,40]
No    5.0000     1 6.0000
p     0.5556     1 0.6000
No.se 1.1886     0 1.0024
p.se  0.2972   NaN 0.2506
```

```
> # transpose the result and make as a data.frame, add specific info from d, add CIs
> res <- data.frame(t(res))
> res <- cbind(d[,1:3],res)
> res <- within(res,{
   No.LCI <- No-1.96*No.se
   No.UCI <- No+1.96*No.se
 })
> head(res)                  # first 6 rows
  species site   age0  No      p   No.se    p.se No.UCI  No.LCI
1 rainbow  A15 Age-1+  41 0.4304  7.0691 0.13027  54.86  27.145
2 rainbow   A9  Age-0  48 0.3776 10.5594 0.13343  68.70  27.304
3 rainbow  A10  Age-0  48 0.5119  4.7448 0.10367  57.30  38.700
4 rainbow   B1  Age-0 165 0.4299 14.2188 0.06499 192.87 137.131
5 rainbow   B1 Age-1+   9 0.6923  0.6903 0.17257  10.35   7.647
6 rainbow Bio1  Age-0 109 0.3377 20.5621 0.09617 149.30  68.698
```