R Handout - R Size Structure (PSD/RSD)   Dr. Derek Ogle

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```
> library(FSA) # view, Subset, Summarize, lencat, rcumsum, pssVal, binCI, tictactoe, tictactoeAdd
```

0.1 Keuska Lake Data

```
> ## setwd("C:/aaaWork/Web/fishR/courses/Midwest2012/CourseMaterial/")
> d <- read.csv("lab1a.csv")
> str(d)

'data.frame': 2391 obs. of  8 variables:
 $ species  : Factor w/ 4 levels "BG","LMB","WAE",..: 1 1 1 1 1 1 1 1 1 1 ...
 $ date     : Factor w/ 12 levels "3/31/1999","4/1/1999",..: 6 6 6 6 4 4 6 6 6 6 ...
 $ geartype : Factor w/ 2 levels "BOOM SHOCKER",..: 1 1 1 1 1 1 1 1 1 1 ...
 $ sex      : Factor w/ 3 levels "F","M","U": NA NA NA NA NA NA NA NA NA NA ...
 $ inches   : num  0.9 1 1 1 1 1 1.1 1.1 1.1 1.1 ...
 $ grams    : int  0 0 0 0 1 1 0 0 0 0 ...
 $ age      : int  NA NA NA NA NA NA NA NA NA NA ...
 $ agestruct: Factor w/ 2 levels "SCALE","SPINE": NA NA NA NA NA NA NA NA NA NA ...
> d$len <- d$inches*25.4
> levels(d$species)

[1] "BG"  "LMB" "WAE" "YEP"
> lmb <- Subset(d,species=="LMB")
> str(lmb)

'data.frame': 981 obs. of  9 variables:
 $ species  : Factor w/ 1 level "LMB": 1 1 1 1 1 1 1 1 1 1 ...
 $ date     : Factor w/ 9 levels "3/31/1999","4/1/1999",..: 6 4 4 4 4 4 4 4 4 6 ...
 $ geartype : Factor w/ 2 levels "BOOM SHOCKER",..: 1 1 1 1 1 1 1 1 1 1 ...
 $ sex      : Factor w/ 0 levels: NA NA NA NA NA NA NA NA NA NA ...
 $ inches   : num  3.2 3.3 3.6 3.6 3.7 4 4 4.2 4.2 4.4 ...
 $ grams    : int  6 NA 8 8 NA NA NA 9 14 15 ...
 $ age      : int  NA NA NA NA NA NA NA NA NA NA ...
 $ agestruct: Factor w/ 2 levels "SCALE","SPINE": NA NA NA NA NA NA NA NA NA NA ...
 $ len      : num  81.3 83.8 91.4 91.4 94 ...
```

0.2 Length Frequency − Largemouth Bass

```
> Summarize(lmb$len,digits=1)
      n     mean       sd      min       Q1   median       Q3      max percZero
  981.0    260.8     67.3     81.3    224.0    267.0    305.0    521.0      0.0
> lmb1 <- lencat(~len,data=lmb,startcat=75,w=25)
> view(lmb1)
     species      date      geartype  sex inches grams age agestruct   len LCat
1182     LMB 4/28/1999 BOOM SHOCKER <NA>    5.4     NA  NA      <NA> 137.2  125
1477     LMB 4/28/1999 BOOM SHOCKER <NA>    9.5    165  NA      <NA> 241.3  225
1587     LMB 4/28/1999 BOOM SHOCKER <NA>   10.2    245  NA      <NA> 259.1  250
1653     LMB 4/15/1999 BOOM SHOCKER <NA>   10.5     NA  NA      <NA> 266.7  250
2078     LMB 3/31/1999     FYKE NET <NA>   13.7    576  NA      <NA> 348.0  325
2096     LMB 4/15/1999 BOOM SHOCKER <NA>   14.0    557   7     SCALE 355.6  350
```
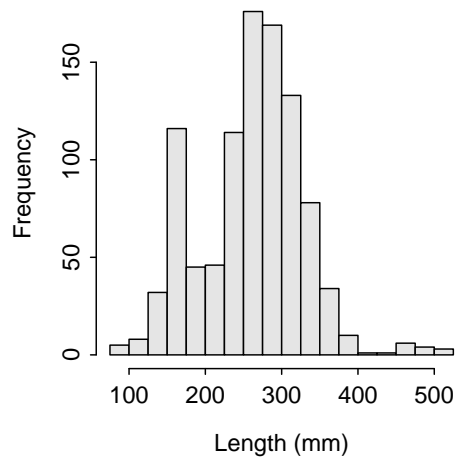
```
> hist(lmb$len,breaks=seq(75,525,25),right=FALSE,main="",xlab="Length (mm)",col="gray90")
> ( lmb.tbl <- table(lmb1$LCat) )

 75 100 125 150 175 200 225 250 275 300 325 350 375 400 425 450 475 500
  5   8  32 116  45  46 114 176 169 133  78  34  10   1   1   6   4   3
```


0.3 PSD – Largemouth Bass I

```
> pssVal("Largemouth bass",units="mm")
     zero     stock   quality preferred memorable    trophy
        0       200       300       380       510       630
> ( lmb.rcum <- rcumsum(lmb.tbl) )

 75 100 125 150 175 200 225 250 275 300 325 350 375 400 425 450 475 500
981 976 968 936 820 775 729 615 439 270 137  59  25  15  14  13   7   3
> ( lmb.stock <- lmb.rcum["200"] )
200
775
> ( lmb.qual <- lmb.rcum["300"] )
300
270
> lmb.qual/lmb.stock
   300
0.3484
> binCI(lmb.qual,lmb.stock)
 95% LCI 95% UCI
  0.3157  0.3826
```

0.4 Length Frequency – Bluegill

```
> bg <- Subset(d,species=="BG")
> Summarize(bg$len,digits=1)
```

```
          n        mean          sd         min          Q1      median          Q3         max percZero
     1160.0       130.0        59.4        22.9        73.7       130.0       183.0       267.0         0.0
> bg1 <- lencat(~len,data=bg,startcat=20,w=10)
> hist(bg$len,breaks=seq(20,270,10),right=FALSE,main="",xlab="Length (mm)",col="gray90")
> bg.tbl <- table(bg1$LCat)
> pssVal("Bluegill",units="mm")
     zero       stock    quality preferred memorable      trophy
        0          80        150        200        250         300
> ( bg.rcum <- rcumsum(bg.tbl) )

   20    30    40    50    60    70    80    90   100   110   120   130   140   150   160   170   180
 1160  1149  1085  1008   938   886   851   826   795   745   653   578   523   479   438   383   313
  190   200   210   220   230   240   250   260
  241   172   100    37     9     3     3     1
> bg.stock <- bg.rcum["150"]
> bg.qual <- bg.rcum["200"]
> bg.qual/bg.stock
    200
0.3591
> binCI(bg.qual,bg.stock)

 95% LCI 95% UCI
  0.3174    0.403
```
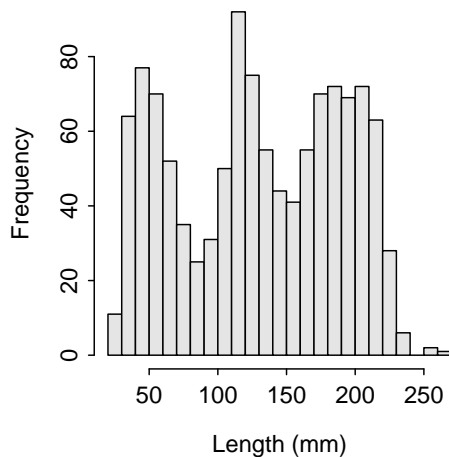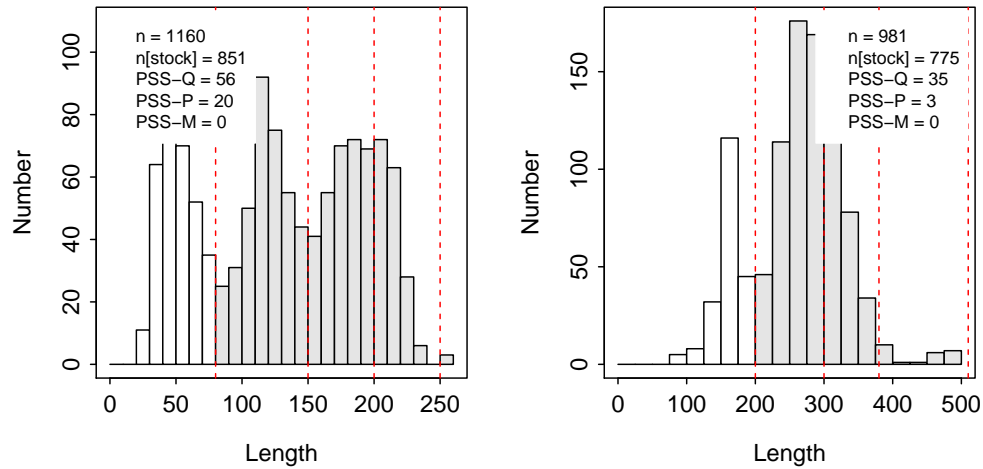
0.5 Summary Graphics

```
> pssPlot(~len,data=bg,species="Bluegill",units="mm",w=10,ylim=c(0,110),legend.pos="topleft")
> pssPlot(~len,data=lmb,species="Largemouth bass",units="mm",startcat=75,w=25)  # right
```



```
> tictactoe()
> tictactoeAdd(c(lmb.qual,lmb.stock),c(bg.qual,bg.stock),pt.col="black")

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).
```