Proportional Stock Density

1 Initialization

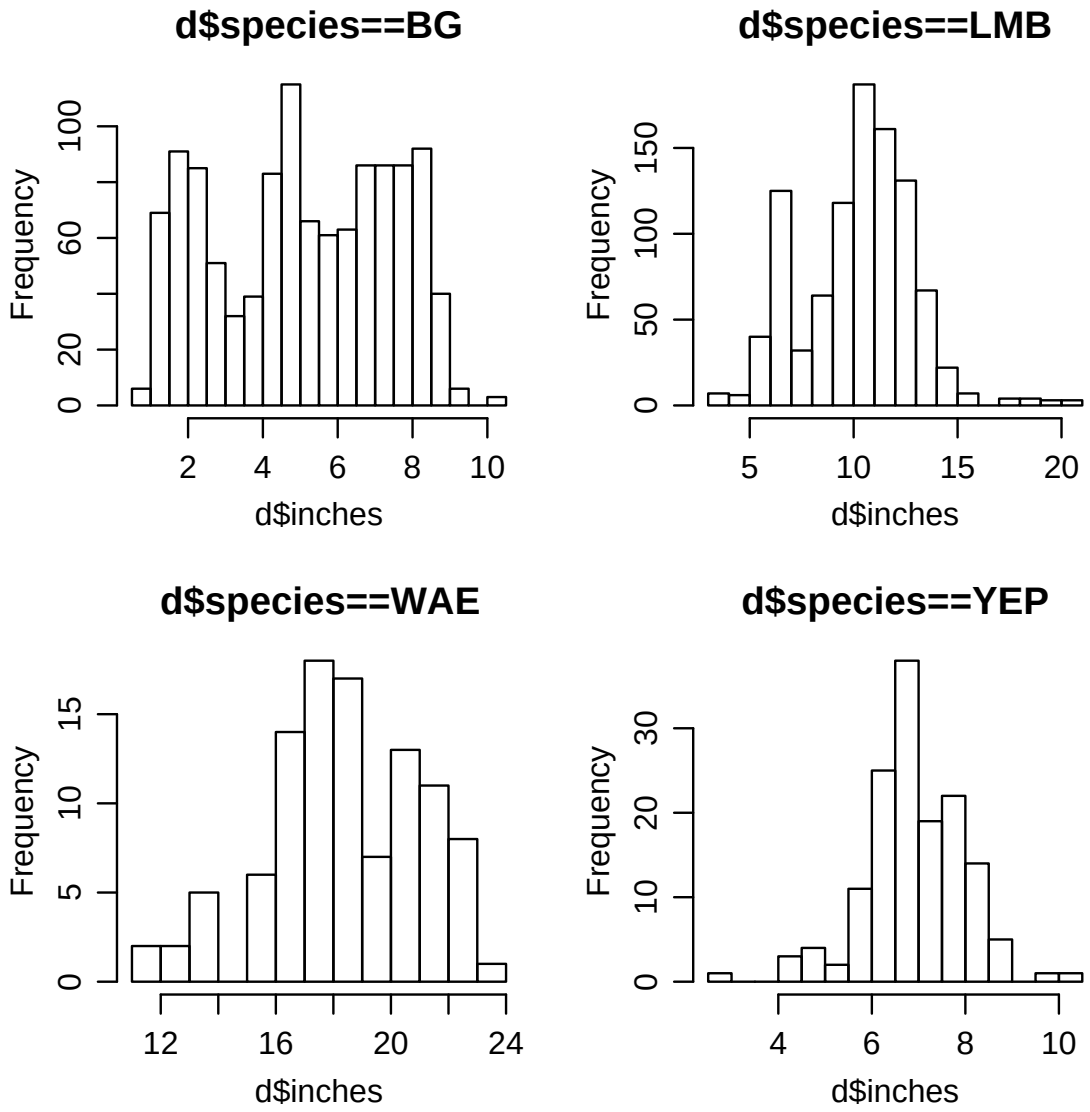
```
> library(FSA)
> library(xlsReadWrite)
> setwd("C://aaaWork/Class Materials//MnDNR_ShortCourse//Readings//PSD//")
```

2 Data

```
> d <- read.xls("lab1a.xls", colClasses = c("factor", "isodate", "factor",
+     "factor", "numeric", "numeric", "numeric", "factor"))
> 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     : chr  "1999-04-28" "1999-04-28" "1999-04-28" "1999-04-28" ...
 $ geartype : Factor w/ 2 levels "BOOM SHOCKER",..: 1 1 1 1 1 1 1 1 1 1 ...
 $ sex      : Factor w/ 4 levels "","F","M","U": 1 1 1 1 1 1 1 1 1 1 ...
 $ inches   : num  0.9 1 1 1 1 1 1.1 1.1 1.1 1.1 ...
 $ grams    : num  0 0 0 0 1 1 0 0 0 0 ...
 $ age      : num  NA NA NA NA NA NA NA NA NA NA ...
 $ agestruct: Factor w/ 3 levels "","SCALE","SPINE": 1 1 1 1 1 1 1 1 1 1 ...

> levels(d$species)

[1] "BG"  "LMB" "WAE" "YEP"

> lmb <- subset(d, species == "LMB")
> dim(lmb)

[1] 981   8

> bg <- subset(d, species == "BG")
> dim(bg)

[1] 1160    8

> wae <- subset(d, species == "WAE")
> dim(wae)

[1] 104   8

> yep <- subset(d, species == "YEP")
> dim(yep)

[1] 146   8
```

3 Summaries and Visualizations

```
> mhist(d$inches ~ d$species, same.breaks = FALSE, same.ylim = FALSE,
+     breaks = 15)
```




```
> tapply(d$inches, d$species, FUN = Summary, numdigs = 2)
```

```
$BG
       n      NAs  Valid n     Mean St. Dev.     Min.  1st Qu.   Median  3rd Qu.     Max.
 1160.00     0.00  1160.00     5.12     2.34     0.90     2.90     5.10     7.20    10.50

$LMB
       n      NAs  Valid n     Mean St. Dev.     Min.  1st Qu.   Median  3rd Qu.     Max.
  981.00     0.00   981.00    10.27     2.65     3.20     8.80    10.50    12.00    20.50

$WAE
       n      NAs  Valid n     Mean St. Dev.     Min.  1st Qu.   Median  3rd Qu.     Max.
  104.00     0.00   104.00    18.45     2.71    11.20    17.00    18.40    20.52    23.10
```

```
$YEP
       n      NAs  Valid n     Mean St. Dev.     Min.  1st Qu.   Median  3rd Qu.     Max.
  146.00     0.00   146.00     6.94     1.05     2.90     6.40     6.90     7.67    10.10
```

4 PSD – Largemouth Bass

4.1 Method I

```
> lmb1 <- lencat(lmb, "inches", w = 1)
> rhead(lmb1)

     species       date     geartype sex inches grams age agestruct LCat
1932     LMB 1999-03-31     FYKE NET       12.2    NA  NA             12
2071     LMB 1999-03-31     FYKE NET       13.6   519  NA             13
1576     LMB 1999-04-13 BOOM SHOCKER       10.2   211  NA             10
1751     LMB 1999-04-15 BOOM SHOCKER       11.1    NA  NA             11
1980     LMB 1999-04-13 BOOM SHOCKER       12.5   458  NA             12
1212     LMB 1999-04-15 BOOM SHOCKER        6.0    NA  NA              6

> lmb.tbl <- table(lmb1$LCat)
> lmb.tbl

  3   4   5   6   7   8   9  10  11  12  13  14  15  17  18  19  20
  5   8  32 125  38  55 114 186 165 129  78  24   8   2   6   3   3

> lmb.rcum <- rcumsum(lmb.tbl)
> lmb.rcum

  3   4   5   6   7   8   9  10  11  12  13  14  15  17  18  19  20
981 976 968 936 811 773 718 604 418 253 124  46  22  14  12   6   3

> RSDval("Largemouth bass", metric = FALSE)

    stock.E   quality.E preferred.E memorable.E    trophy.E
          8          12          15          20          25

> lmb.stock <- lmb.rcum["8"]
> lmb.stock

  8
773

> lmb.qual <- lmb.rcum["12"]
> lmb.qual

 12
253

> lmb.psd <- lmb.qual/lmb.stock
> lmb.psd
```

```
       12
0.3272962
```

```
> bin.ci(lmb.qual, lmb.stock)
```

```
  95% LCI   95% UCI
0.2951430 0.3611575
```

4.2 Method II

```
> lmb.cuts <- RSDval("Largemouth bass", metric = FALSE)
> lmb.cuts
```

```
    stock.E   quality.E preferred.E memorable.E    trophy.E
          8          12          15          20          25
```

```
> lmb2 <- lencat(lmb, "inches", breaks = c(0, lmb.cuts))
> lmb2.tbl <- table(lmb2$LCat)
> lmb2.tbl
```

```
  0   8  12  15  20
208 520 231  19   3
```

```
> lmb2.rcum <- rcumsum(lmb2.tbl)
> lmb2.rcum
```

```
  0   8  12  15  20
981 773 253  22   3
```

```
> lmb.stock <- lmb2.rcum["8"]
> lmb.qual <- lmb2.rcum["12"]
> lmb.psd <- lmb.qual/lmb.stock
> lmb.psd
```

```
       12
0.3272962
```

```
> bin.ci(lmb.qual, lmb.stock)
```

```
  95% LCI   95% UCI
0.2951430 0.3611575
```

5 PSD – Bluegill

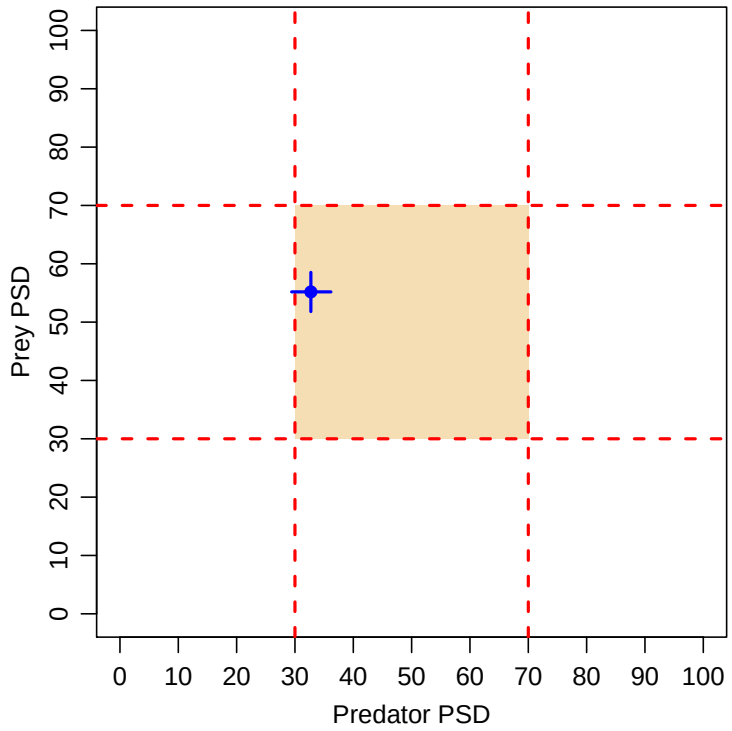
```
> bg.cuts <- RSDval("Bluegill", metric = FALSE)
> bg.cuts
```

```
    stock.E   quality.E preferred.E memorable.E    trophy.E
          3           6           8          10          12
```

```
> bg1 <- lencat(bg, "inches", breaks = c(0, bg.cuts))
> bg.tbl <- table(bg1$LCat)
> bg.rcum <- rcumsum(bg.tbl)
> bg.rcum

   0    3    6    8   10
1160  868  479  156    3

> bg.stock <- bg.rcum["3"]
> bg.qual <- bg.rcum["6"]
> bg.psd <- bg.qual/bg.stock
> bg.psd

        6
0.5518433

> bin.ci(bg.qual, bg.stock)

  95% LCI   95% UCI
0.5186036 0.5846262
```

6 Tic-Tac-Toe Graph – Largemouth Bass and Bluegill

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

Predator PSD was 33 with a 95% CI of (29.4,36.2).
Prey PSD was 55 with a 95% CI of (51.8,58.5).
```



7 PSD – Walleye and Yellow Perch

```
> wae.cuts <- RSDval("Walleye", metric = FALSE)
> wae.cuts

    stock.E   quality.E preferred.E memorable.E    trophy.E
         10          15          20          25          30

> wae1 <- lencat(wae, "inches", breaks = c(0, wae.cuts))
> wae.tbl <- table(wae1$LCat)
> wae.rcum <- rcumsum(wae.tbl)
> wae.stock <- wae.rcum["10"]
> wae.qual <- wae.rcum["15"]
> yep.cuts <- RSDval("Yellow perch", metric = FALSE)
> yep.cuts

    stock.E   quality.E preferred.E memorable.E    trophy.E
          5           8          10          12          15

> yep1 <- lencat(yep, "inches", breaks = c(0, yep.cuts))
> yep.tbl <- table(yep1$LCat)
> yep.rcum <- rcumsum(yep.tbl)
> yep.stock <- yep.rcum["5"]
> yep.qual <- yep.rcum["8"]


> tictactoe.add(c(wae.qual, wae.stock), c(yep.qual, yep.stock), pt.col = "green")


Predator PSD was 91 with a 95% CI of (84.2,96).
Prey PSD was 16 with a 95% CI of (10.3,23.1).
```