Size Structure II

Derek H. Ogle, Northland College

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Preliminaries

```
> library(fishWiDNR)   # for setDBClasses()
> library(FSA)         # for Summarize(), hist(), expandCounts()
> library(magrittr)    # for %<>%
> library(dplyr)       # for %>%, filter(), select(), mutate(), group_by(), summarize()
> library(lubridate)   # for month()

> setwd("C:/aaaWork/Web/fishR/Courses/WiDNR_Statewide_2015/Day1_IntroR_FMData")
> d <- read.csv("SAWYER_fish_raw_data_012915.csv",stringsAsFactors=FALSE,na.strings=c("-","NA","")) %>%
       setDBClasses(type="RDNR") %>%
       expandCounts(~Number.of.Fish,~Length.or.Lower.Length.IN+Length.Upper.IN,new.name="Len") %>%
       mutate(Mon=month(Survey.Begin.Date,label=TRUE),Species1=capFirst(Species)) %>%
       select(Species,Species1,Waterbody.Name,Survey.Year,Mon,Gear,Len)

> Spr <- filterD(d,Survey.Year==2013,Mon %in% c("Apr","May","Jun"))
> BGSpr <- filterD(Spr,Species=="BLUEGILL")
> BGSprLC <- filterD(BGSpr,Waterbody.Name=="LAKE CHETAC",Gear=="BOOM SHOCKER")
> SprLC <- filterD(Spr,Waterbody.Name=="LAKE CHETAC")
```

So ...

- `Spr` has all species sampled from all water bodies in the Spring of 2013.
- `BGSpr` has only Bluegill sampled from all water bodies in the Spring of 2013.
- `BGSprLC` has only Bluegill sampled with boom shockers from Lake Chetac in the Spring of 2013.
- `SprLC` has all species sampled from Lake Chetac (in all gears) in the Spring of 2013.

... and they all look similar to this ...

```
   Species Species1 Waterbody.Name Survey.Year Mon         Gear Len
1 BLUEGILL Bluegill    LAKE CHETAC        2013 May BOOM SHOCKER 4.0
2 BLUEGILL Bluegill    LAKE CHETAC        2013 May BOOM SHOCKER 4.7
3 BLUEGILL Bluegill    LAKE CHETAC        2013 May BOOM SHOCKER 4.7
4 BLUEGILL Bluegill    LAKE CHETAC        2013 May BOOM SHOCKER 7.3
5 BLUEGILL Bluegill    LAKE CHETAC        2013 May BOOM SHOCKER 7.4
6 BLUEGILL Bluegill    LAKE CHETAC        2013 May BOOM SHOCKER 6.6
```

PSDs Single Waterbody and Species

```
> brks <- psdVal("Bluegill",units="in",addLens=7)
> BGSprLC %<>% mutate(lcat=lencat(Len,breaks=brks),
                      lcat1=lencat(Len,breaks=brks,use.names=TRUE),
                      lcat2=lencat(Len,breaks=brks,use.names=TRUE,drop.levels=TRUE))
> head(BGSprLC)
   Species Species1 Waterbody.Name Survey.Year Mon         Gear Len lcat   lcat1   lcat2
1 BLUEGILL Bluegill    LAKE CHETAC        2013 May BOOM SHOCKER 4.0    3   stock   stock
2 BLUEGILL Bluegill    LAKE CHETAC        2013 May BOOM SHOCKER 4.7    3   stock   stock
3 BLUEGILL Bluegill    LAKE CHETAC        2013 May BOOM SHOCKER 4.7    3   stock   stock
4 BLUEGILL Bluegill    LAKE CHETAC        2013 May BOOM SHOCKER 7.3    7       7       7
5 BLUEGILL Bluegill    LAKE CHETAC        2013 May BOOM SHOCKER 7.4    7       7       7
6 BLUEGILL Bluegill    LAKE CHETAC        2013 May BOOM SHOCKER 6.6    6 quality quality

> xtabs(~lcat,data=BGSprLC)
lcat
  3   6   7   8
170 133  90   5

> xtabs(~lcat1,data=BGSprLC)
lcat1
 substock     stock   quality         7 preferred memorable    trophy
        0       170       133        90         5         0         0

> ( freq <- xtabs(~lcat2,data=BGSprLC) )
lcat2
    stock   quality         7 preferred
      170       133        90         5

> ( rcum <- rcumsum(freq) )
    stock   quality         7 preferred
      398       228        95         5

> rcum["stock"]                                          # demo number of stock fish
stock
  398

> rcum/rcum["stock"]*100
     stock    quality          7  preferred
100.000000  57.286432  23.869347   1.256281
```

PSDs for Multiple Waterbodies and Single Species

```
> BGSpr %<>% mutate(lcat2=lencat(Len,breaks=brks,use.names=TRUE,drop.levels=TRUE))
> ( freq <- xtabs(~Waterbody.Name+lcat2,data=BGSpr) )
                  lcat2
Waterbody.Name      substock stock quality   7 preferred
  BLACK DAN LAKE           5   227       7   2         0
  CONNORS LAKE             6    73      28   1         0
  DURPHEE LAKE             1    36     414 123         0
  GREEN LAKE               2    30      49  55         8
  LAKE CHETAC              1   170     133  90         6
  LAKE CHIPPEWA            0   101      44  35         1
  LAKE OF THE PINES        7    66      17   0         0
  LOWER CLAM LAKE          1    30       4   0         0
  MOOSE LAKE               0     0       0   0         0
  ROUND LAKE              13   221      49  20         6
  WHITEFISH LAKE           8    50       4   5         0

> apply(freq,MARGIN=1,FUN=rcumsum)                              # apply result has wrong orientation
          Waterbody.Name
           BLACK DAN LAKE CONNORS LAKE DURPHEE LAKE GREEN LAKE LAKE CHETAC LAKE CHIPPEWA
  substock            241          108          574        144         400           181
  stock               236          102          573        142         399           181
  quality               9           29          537        112         229            80
  7                     2            1          123         63          96            36
  preferred             0            0            0          8           6             1
          Waterbody.Name
           LAKE OF THE PINES LOWER CLAM LAKE MOOSE LAKE ROUND LAKE WHITEFISH LAKE
  substock                90              35          0        309             67
  stock                   83              34          0        296             59
  quality                 17               4          0         75              9
  7                        0               0          0         26              5
  preferred                0               0          0          6              0

> ( rcum <- t(apply(freq,MARGIN=1,FUN=rcumsum)) )

Waterbody.Name      substock stock quality   7 preferred
  BLACK DAN LAKE         241   236       9   2         0
  CONNORS LAKE           108   102      29   1         0
  DURPHEE LAKE           574   573     537 123         0
  GREEN LAKE             144   142     112  63         8
  LAKE CHETAC            400   399     229  96         6
  LAKE CHIPPEWA          181   181      80  36         1
  LAKE OF THE PINES       90    83      17   0         0
  LOWER CLAM LAKE         35    34       4   0         0
  MOOSE LAKE               0     0       0   0         0
  ROUND LAKE             309   296      75  26         6
  WHITEFISH LAKE          67    59       9   5         0

> rcum <- rcum[,-1]                                             # remove "substock" column
> rcum/rcum[,"stock"]*100

Waterbody.Name      stock   quality          7 preferred
  BLACK DAN LAKE      100  3.813559  0.8474576 0.0000000
  CONNORS LAKE        100 28.431373  0.9803922 0.0000000
  DURPHEE LAKE        100 93.717277 21.4659686 0.0000000
  GREEN LAKE          100 78.873239 44.3661972 5.6338028
  LAKE CHETAC         100 57.393484 24.0601504 1.5037594
```

```
  LAKE CHIPPEWA       100 44.198895 19.8895028 0.5524862
  LAKE OF THE PINES   100 20.481928  0.0000000 0.0000000
  LOWER CLAM LAKE     100 11.764706  0.0000000 0.0000000
  MOOSE LAKE          NaN       NaN        NaN       NaN
  ROUND LAKE          100 25.337838  8.7837838 2.0270270
  WHITEFISH LAKE      100 15.254237  8.4745763 0.0000000
```

PSDs for Multiple Species in a Single Waterbody

```
> SprLC %<>% mutate(lcat2=psdAdd(Len,Species1,units="in"))
Warning in max(x, na.rm = TRUE): no non-missing arguments to max; returning -Inf
Warning in min(x, na.rm = TRUE): no non-missing arguments to min; returning Inf
```

```
> head(SprLC)
       Species     Species1 Waterbody.Name Survey.Year Mon     Gear Len    lcat2
1 YELLOW PERCH Yellow Perch    LAKE CHETAC        2013 May FYKE NET 4.7 substock
2 YELLOW PERCH Yellow Perch    LAKE CHETAC        2013 May FYKE NET 5.4    stock
3 YELLOW PERCH Yellow Perch    LAKE CHETAC        2013 May FYKE NET 5.4    stock
4 YELLOW PERCH Yellow Perch    LAKE CHETAC        2013 May FYKE NET 5.2    stock
5 YELLOW PERCH Yellow Perch    LAKE CHETAC        2013 May FYKE NET 4.5 substock
6 YELLOW PERCH Yellow Perch    LAKE CHETAC        2013 May FYKE NET 5.6    stock
```

```
> ( freq <- xtabs(~Species+lcat2,data=SprLC) )
                lcat2
Species          substock stock quality preferred memorable trophy
  BLACK CRAPPIE        28   453      52        14         1      0
  BLUEGILL              1   170     223         6         0      0
  BOWFIN                0     0       0         0         0      0
  LARGEMOUTH BASS      19    81     112        62         0      0
  NORTHERN PIKE         0    20      10         9         1      0
  PUMPKINSEED           0    16      20         0         0      0
  ROCK BASS             0     0       0         0         0      0
  SMALLMOUTH BASS       1     2       5         2         0      0
  WALLEYE               8    17       9        20        17      0
  YELLOW PERCH         34   257      91         3         0      0
```

```
> ( rcum <- t(apply(freq,MARGIN=1,FUN=rcumsum)) )

Species          substock stock quality preferred memorable trophy
  BLACK CRAPPIE       548   520      67        15         1      0
  BLUEGILL            400   399     229         6         0      0
  BOWFIN                0     0       0         0         0      0
  LARGEMOUTH BASS     274   255     174        62         0      0
  NORTHERN PIKE        40    40      20        10         1      0
  PUMPKINSEED          36    36      20         0         0      0
  ROCK BASS             0     0       0         0         0      0
  SMALLMOUTH BASS      10     9       7         2         0      0
  WALLEYE              71    63      46        37        17      0
  YELLOW PERCH        385   351      94         3         0      0
```

```
> rcum <- rcum[,-1]
> rcum/rcum[,"stock"]*100

Species          stock  quality  preferred  memorable trophy
  BLACK CRAPPIE    100 12.88462  2.8846154  0.1923077      0
  BLUEGILL         100 57.39348  1.5037594  0.0000000      0
```

```
BOWFIN            NaN      NaN        NaN        NaN    NaN
LARGEMOUTH BASS   100 68.23529 24.3137255  0.0000000      0
NORTHERN PIKE     100 50.00000 25.0000000  2.5000000      0
PUMPKINSEED       100 55.55556  0.0000000  0.0000000      0
ROCK BASS         NaN      NaN        NaN        NaN    NaN
SMALLMOUTH BASS   100 77.77778 22.2222222  0.0000000      0
WALLEYE           100 73.01587 58.7301587 26.9841270      0
YELLOW PERCH      100 26.78063  0.8547009  0.0000000      0
```

Application Assignment

Create a script that performs the following tasks:

1. Load and prepare your FM data in R (**HINT:** *use all or some of your scripts from previous application assignments*).
2. Compute the PSDs for one species in one waterbody in one year.
3. Compute the PSDs for one species in all waterbodies in one year in your FM data.
4. Compute the PSDs for all species in one waterbody in one year in your FM data.
5. (*Time Permitting*) Repeat any of the above for another year.

Save your script!