

Size Structure II

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Preliminaries

```
> # clears objects in R workspace
> rm(list = ls())

> # load needed packages
> library(fishWiDNR) # for setDBClasses()
> library(FSA)       # for expandCounts(), Summarize(), hist()
> library(magrittr)  # for %<>%
> library(dplyr)     # for %>%, filter(), select(), mutate(), group_by(), summarize()
> # options(dplyr.print_max=1e9)
> library(lubridate) # for month()

> # load FM data, expand lengths, add variables, select pertinent variables
> setwd("C:/aaaWork/Web/fishR/Courses/WiDNR_Statewide_2015/Day1_IntroR_FMDData")
> 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)

> # create some subsets for use below.
> 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")
```

Quick questions

- What variables should be in Spr, BGSpr, BGSprLC, and SprLC.
- What individuals should be in Spr, BGSpr, BGSprLC, and SprLC.

PSDs Single Waterbody and Species

```
> ( brks <- psdVal("Bluegill",units="in",addLens=7) )
substock      stock      quality      7 preferred memorable      trophy
      0          3          6          7          8          10          12

> 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))
> headtail(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
396 BLUEGILL Bluegill    LAKE CHETAC      2013 May BOOM SHOCKER 5.6   3  stock  stock
397 BLUEGILL Bluegill    LAKE CHETAC      2013 May BOOM SHOCKER 6.6   6 quality quality
398 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, only partial results shown
```

```
      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
```

```
> ( 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
```

```
> headtail(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
6872 YELLOW PERCH Yellow Perch LAKE CHETAC 2013 May FYKE NET NA <NA>
6873 YELLOW PERCH Yellow Perch LAKE CHETAC 2013 May FYKE NET NA <NA>
6874 YELLOW PERCH Yellow Perch LAKE CHETAC 2013 May FYKE NET NA <NA>
```

```
> ( 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!