

Size Structure II

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

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 roughly like this ...

	Species	Species1	Waterbody.Name	Survey.Year	Mon	Gear	Len
1	BLUEGILL	Bluegill	LAKE CHETAC	2013	May	BOOM SHOCKER	4.4
2	BLUEGILL	Bluegill	LAKE CHETAC	2013	May	BOOM SHOCKER	8.1
3	BLUEGILL	Bluegill	LAKE CHETAC	2013	May	BOOM SHOCKER	3.9
4	BLUEGILL	Bluegill	LAKE CHETAC	2013	May	BOOM SHOCKER	4.7
5	BLUEGILL	Bluegill	LAKE CHETAC	2013	May	BOOM SHOCKER	4.7
6	BLUEGILL	Bluegill	LAKE CHETAC	2013	May	BOOM SHOCKER	6.7

Single Waterbody and Species PSDs

```
> 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	4.4	3	stock	stock
2	BLUEGILL	Bluegill	LAKE CHETAC	2013	May	BOOM SHOCKER	8.1	8	preferred	preferred
3	BLUEGILL	Bluegill	LAKE CHETAC	2013	May	BOOM SHOCKER	3.9	3	stock	stock
4	BLUEGILL	Bluegill	LAKE CHETAC	2013	May	BOOM SHOCKER	4.7	3	stock	stock
5	BLUEGILL	Bluegill	LAKE CHETAC	2013	May	BOOM SHOCKER	4.7	3	stock	stock
6	BLUEGILL	Bluegill	LAKE CHETAC	2013	May	BOOM SHOCKER	6.7	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
```

Multiple Waterbodies and Single Species PSDs

```
> BGSpr %<>% mutate(lcat2=lencat(Len,breaks=brks,use.names=TRUE,drop.levels=TRUE))
> ( freq <- xtabs(~Waterbody.Name+lcat2,data=BGSpr) )
```

Waterbody.Name	lcat2	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
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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

Multiple Species in a Single Waterbody PSDs

```
> 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	NORTHERN PIKE	Northern Pike	LAKE CHETAC	2013	May	FYKE NET	19.3	stock
2	LARGEMOUTH BASS	Largemouth Bass	LAKE CHETAC	2013	May	FYKE NET	15.5	preferred
3	NORTHERN PIKE	Northern Pike	LAKE CHETAC	2013	May	FYKE NET	18.4	stock
4	NORTHERN PIKE	Northern Pike	LAKE CHETAC	2013	May	FYKE NET	17.8	stock
5	NORTHERN PIKE	Northern Pike	LAKE CHETAC	2013	May	FYKE NET	20.4	stock
6	NORTHERN PIKE	Northern Pike	LAKE CHETAC	2013	May	FYKE NET	30.0	preferred

```
> ( freq <- xtabs(~Species+lcat2,data=SprLC) )
```

Species	lcat2					
	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

Repeat for 2014

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. MORE HERE.

Save your script!