

Size Structure I

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Preliminaries

```
> library(fishWiDNR) # for setDBClasses()
> library(dplyr)      # for filter(), select(), mutate(), group_by(), summarize()
> library(FSA)        # for Summarize(), hist(), expandCounts()
> 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", ""))
> d <- setDBClasses(d, type="RDNR")
> d <- expandCounts(d, ~Number.of.Fish, ~Length.or.Lower.Length.IN+Length.Upper.IN, new.name="Len")
> d <- mutate(d, Mon=month(Survey.Begin.Date, label=TRUE))
> d <- select(d, Species, Waterbody.Name, Survey.Year, Gear, Survey.Begin.Date, Mon, Len)

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

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.

... and they all look roughly like this ...

	Species	Waterbody.Name	Survey.Year	Gear	Survey.Begin.Date	Mon	Len
1	BLUEGILL	LAKE CHETAC	2013	BOOM SHOCKER	2013-05-09	May	4.4
2	BLUEGILL	LAKE CHETAC	2013	BOOM SHOCKER	2013-05-09	May	8.1
3	BLUEGILL	LAKE CHETAC	2013	BOOM SHOCKER	2013-05-09	May	3.9
4	BLUEGILL	LAKE CHETAC	2013	BOOM SHOCKER	2013-05-09	May	4.7
5	BLUEGILL	LAKE CHETAC	2013	BOOM SHOCKER	2013-05-09	May	4.7
6	BLUEGILL	LAKE CHETAC	2013	BOOM SHOCKER	2013-05-09	May	6.7

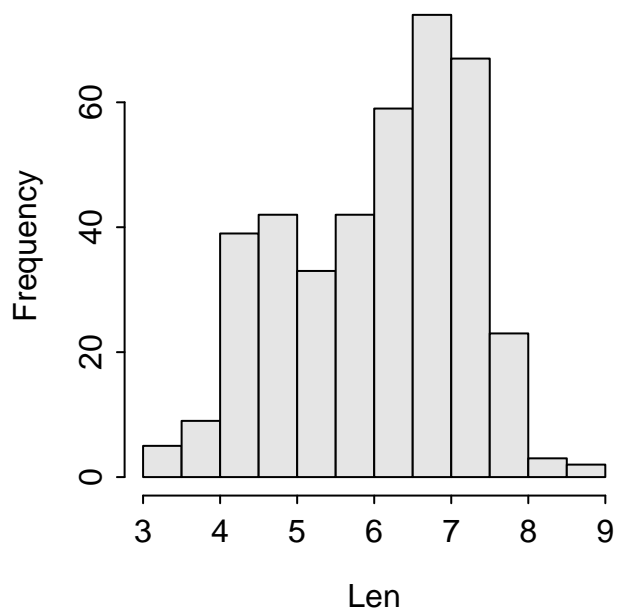
Very Simple Summaries

```
> Summarize(~Len, data=BGSprLC, digits=2)
```

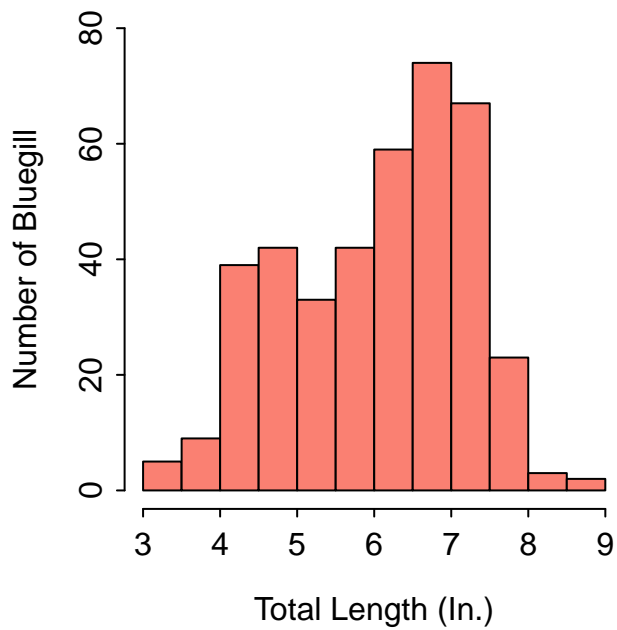
n	mean	sd	min	Q1	median	Q3	max	percZero
398.00	5.98	1.16	3.00	5.00	6.20	6.90	8.90	0.00

Length Frequency Histograms

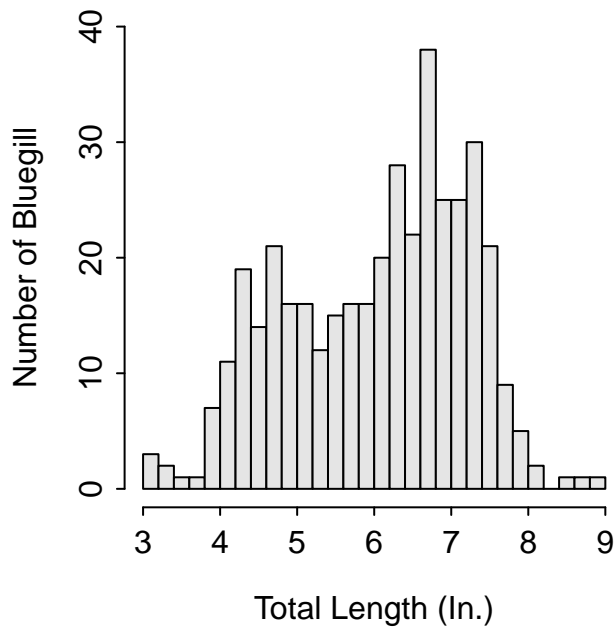
```
> hist(~Len,data=BGSprLC)
```



```
> hist(~Len,data=BGSprLC,xlab="Total Length (In.)",ylab="Number of Bluegill",  
      xlim=c(3,9),ylim=c(0,80),col="salmon")
```



```
> hist(~Len,data=BGSprLC,xlab="Total Length (In.)",ylab="Number of Bluegill",
      xlim=c(3,9),ylim=c(0,40),breaks=seq(3,9,0.2))
```



Multiple Summaries at Once

```
> BGSpr <- group_by(BGSpr,Waterbody.Name)
> summarize(BGSpr,n=n(),meanLen=mean(Len))
```

see use of na.rm=TRUE below

Source: local data frame [11 x 3]

	Waterbody.Name	n	meanLen
1	BLACK DAN LAKE	599	NA
2	CONNORS LAKE	198	NA
3	DURPHEE LAKE	603	NA
4	GREEN LAKE	144	6.567361
5	LAKE CHETAC	589	NA
6	LAKE CHIPPEWA	746	NA
7	LAKE OF THE PINES	303	NA
8	LOWER CLAM LAKE	35	4.554286
9	MOOSE LAKE	1	NA
10	ROUND LAKE	414	NA
11	WHITEFISH LAKE	72	NA

```
> summarize(BGSpr,n=n(),valid_n=sum(!is.na(Len)),
            meanLen=mean(Len,na.rm=TRUE),sdLen=sd(Len,na.rm=TRUE),
            minLen=min(Len,na.rm=TRUE),maxLen=max(Len,na.rm=TRUE) )
```

Source: local data frame [11 x 7]

	Waterbody.Name	n	valid_n	meanLen	sdLen	minLen	maxLen
1	BLACK DAN LAKE	599	241	4.352697	0.9151520	2.1	7.0
2	CONNORS LAKE	198	108	5.155556	1.1018534	1.7	7.0
3	DURPHEE LAKE	603	574	6.603136	0.5071123	1.4	7.9
4	GREEN LAKE	144	144	6.567361	1.1392446	2.8	8.4
5	LAKE CHETAC	589	400	5.979250	1.1819420	2.0	8.9
6	LAKE CHIPPEWA	746	181	5.758011	1.1447001	3.7	8.0
7	LAKE OF THE PINES	303	90	5.000000	1.1646478	1.7	6.8
8	LOWER CLAM LAKE	35	35	4.554286	1.0042096	2.7	6.2
9	MOOSE LAKE	1	0	NaN	NaN	NA	NA
10	ROUND LAKE	414	309	5.070874	1.3018442	1.8	8.7
11	WHITEFISH LAKE	72	67	4.392537	1.3614067	2.1	7.4

```
> BGSpr <- filter(BGSpr,Len>=3)
> summarize(BGSpr,n=n(),valid_n=sum(!is.na(Len)),
            meanLen=round(mean(Len,na.rm=TRUE),2),sdLen=round(sd(Len,na.rm=TRUE),2),
            minLen=min(Len,na.rm=TRUE),maxLen=max(Len,na.rm=TRUE),
            PSDQ=perc(Len,6,digits=0),PSD7=perc(Len,7,digits=0),PSDP=perc(Len,8,digits=0) )
```

Source: local data frame [10 x 10]

	Waterbody.Name	n	valid_n	meanLen	sdLen	minLen	maxLen	PSDQ	PSD7	PSDP
1	BLACK DAN LAKE	236	236	4.39	0.89	3.0	7.0	4	1	0
2	CONNORS LAKE	102	102	5.32	0.89	3.0	7.0	28	1	0
3	DURPHEE LAKE	573	573	6.61	0.46	4.5	7.9	94	21	0
4	GREEN LAKE	142	142	6.62	1.06	3.0	8.4	79	44	6
5	LAKE CHETAC	399	399	5.99	1.17	3.0	8.9	57	24	2
6	LAKE CHIPPEWA	181	181	5.76	1.14	3.7	8.0	44	20	1
7	LAKE OF THE PINES	83	83	5.23	0.87	3.0	6.8	20	0	0
8	LOWER CLAM LAKE	34	34	4.61	0.97	3.0	6.2	12	0	0
9	ROUND LAKE	296	296	5.18	1.21	3.0	8.7	25	9	2
10	WHITEFISH LAKE	59	59	4.65	1.25	3.0	7.4	15	8	0

```
> Spr <- group_by(Spr,Waterbody.Name,Species)
> summarize(Spr,n=n(),valid_n=sum(!is.na(Len)),
            meanLen=round(mean(Len,na.rm=TRUE),2),sdLen=round(sd(Len,na.rm=TRUE),2) )
```

Source: local data frame [122 x 6]

Groups: Waterbody.Name

	Waterbody.Name	Species	n	valid_n	meanLen	sdLen
1	BLACK DAN LAKE	BLACK BULLHEAD	2	0	NaN	NaN
2	BLACK DAN LAKE	BLACK CRAPPIE	402	402	6.89	1.42
3	BLACK DAN LAKE	BLUEGILL	599	241	4.35	0.92
4	BLACK DAN LAKE	LARGEMOUTH BASS	76	76	11.01	3.15
5	BLACK DAN LAKE	MUSKELLUNGE	38	15	34.88	7.35
6	BLACK DAN LAKE	NORTHERN PIKE	8	8	22.91	5.82
7	BLACK DAN LAKE	PUMPKINSEED	43	31	4.61	1.12
8	BLACK DAN LAKE	PUMPKINSEED X BLUEGILL	13	9	5.36	1.01
9	BLACK DAN LAKE	ROCK BASS	4	4	4.40	2.23
10	BLACK DAN LAKE	WALLEYE	180	180	10.74	5.02
..

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. Reduce your data.frame to one year and several (4 or more) fish of interest. Call this the *original data.frame*.
3. Reduce the *original data.frame* to one water body and species of interest.
 - Compute summary statistics for the length variable.
 - Construct a length frequency histogram.
 - Does your description of the length frequency change dramatically with different bin widths?
4. Reduce the *original data.frame* to only one species.
 - Efficiently construct summary statistics for the length variable for each water body. Include PSD values that are of interest to you (**HINT:** *use, for example, `psdVal("Largemouth Bass",units="in")` to find Gabelhouse lengths for a particular species*).
5. (*Time Permitting*) Re-create the summary statistics for one species in each water body but include calculations of the median and first and third quartiles (**HINT:** *use, for example, `quantile(x,0.50,na.rm=TRUE)` to compute the median (i.e., 50% quantile) of the data in x*).
6. (*Time Permitting*) Compute summary statistics of the length variable for each water body AND each of the several species of interest to you. Save the summary statistics to an object and write the results to a CSV file.

Save your script!