FMDB Size Structure Walk-Through

Derek H. Ogle

Packages

Add-on packages are accessed with `library()`. The following packages are required for the analyses demonstrated in this document. Comments following each package are the list of functions used from the package.

```
> library(fishWiDNR)   # for read.FMDB()
> library(FSA)         # for headtail(), filterD(), Summarize(), hist(), lencat(), psdVal(), psdAdd()
> library(dplyr)       # for %>%, select(), mutate(), group_by(), summarize()
> library(magrittr)    # for %<>%
```

Loading CSV File from FM Database

Raw fish data from the FM Database is extracted and saved into a comma-separated values (CSV) file that will have a common format that you are likely familiar with. These files may be read directly into R, but the format of the data in each column and the notation for missing values must be explicitly defined. Additionally, a month field is often needed (but does not exist in the FM Database) and species names must be converted to all lower-case with the exception of the first letter for ease of use with some R functions.

In addition, the FM Database contains some records that reflect counts of fish with a particular length or range of lengths. The analyses demonstrated in this workshop require records of individual fish. Thus, these records need to be expanded (repeated) to represent individual fish. Furthermore, random lengths within length bins can be created so that appropriate summary statistics may be calculated. For example, if five fish were recorded between 8.0 and 8.4 inches, then it is necessary to create five fish that will have random lengths between 8.0 and 8.4 inches.

The `read.FMDB()` function in the `fishWiDNR` package is designed to read the FM Database CSV file, appropriately set the format of the variables, add a month variable (in `Mon`) if `addMonth=TRUE` (the default), and change the species names to the appropriate case (in `Species1`) if `addSpecies=TRUE` (the default). Additionally, the counts of fish will be expanded if `expandCounts=TRUE` (**NOT** the default). By default the expanded lengths will be in inches, but this can be changed to mm with `whichLengths="mm"`.

The example below sets the working directory (with `setwd()`) to where (on my computer) the Sawyer County data is found (you will have to change this to the directory structure for where you saved your FM data), reads the data (and expands the counts) with `read.FMDB()`, and examines the structure (with `str()`) and first and last few rows of the data.frame in R (with `headtail()`).

```
> setwd("C:/aaaWork/Web/GitHub/RcourseWiDNR2016")
> d <- read.FMDB("SAWYER_fish_raw_data_012915.csv",expandCounts=TRUE)
Successfully read SAWYER_fish_raw_data_012915.csv.
Set variable classes.
Created months in 'Mon'.
Renamed species in 'Species1'.
Results messages from expandCounts():
13 rows had zero or no counts in Number.of.Fish.
  38448 rows had an individual measurement.
  10222 rows with multiple measurements were expanded to 94790 rows of individual measurements.
```

```
> str(d)
'data.frame':   133251 obs. of  56 variables:
 $ County                    : Factor w/ 1 level "SAWYER": 1 1 1 1 1 1 1 1 1 1 ...
 $ Waterbody.Name            : Factor w/ 86 levels "ALDER CREEK",..: 73 52 67 85 35 9 35 60 9 9 ...
 $ WBIC                      : Factor w/ 86 levels "99999","1835700",..: 69 77 70 6 54 58 54 53 58 ..
 $ Survey.Year               : int  2010 2010 2011 2012 2012 2012 2012 2012 2012 2012 ...
 $ Station.Name              : Factor w/ 112 levels "ALDER CREEK BELOW BEAVER POND",..: 97 76 89 11..
 $ Swims.Station.Id          : int  10005657 10002492 10005658 10005544 10005605 10005611 10005605 ..
 $ Site.Seq.No               : int  123111 122805 123040 121911 122533 109201 122533 122923 109201 ..
 $ Survey.Seq.No             : int  104342960 104342961 195135342 274195365 274195372 257736123 274..
 $ Survey.Begin.Date         : POSIXct, format: "2010-09-26" "2010-10-18" "2011-10-02" ...
 $ Survey.End.Date           : POSIXct, format: "2010-09-27" "2010-10-20" "2011-10-02" ...
 $ Survey.Status             : Factor w/ 3 levels "DATA ENTRY COMPLETE",..: 2 2 2 2 2 2 2 2 2 2 ...
 $ Data.Entry.Name           : chr  "warwir" "warwir" "warwir" "warwir" ...
 $ Visit.Fish.Seq.No         : int  687017 687020 693862 698904 698912 698213 698931 698908 699165 ..
 $ Visit.Type                : Factor w/ 2 levels "ELECTROFISHING",..: 1 2 1 2 2 2 2 2 2 2 ...
 $ Gear                      : Factor w/ 7 levels "BACKPACK SHOCKER",..: 2 4 2 4 4 3 4 4 3 3 ...
 $ Sample.Date               : POSIXct, format: "2010-09-27" "2010-10-19" "2011-10-02" ...
 $ Substation.Name           : Factor w/ 299 levels " IBI"," STUKY BAY (INDEX)",..: 271 NA 123 NA N..
 $ Target.Species            : Factor w/ 14 levels "ALL SPECIES",..: 14 3 14 6 6 7 6 6 7 7 ...
 $ Fish.Data.Seq.No          : int  9022342 9022358 9343440 9610979 9612673 9553472 9612713 9611371..
 $ Net.Number                : chr  NA "2" NA "3" ...
 $ Species.Code              : Factor w/ 73 levels "A01J","A02","A03",..: 73 73 73 73 73 73 73 73 7..
 $ Species                   : Factor w/ 73 levels "AMERICAN BROOK LAMPREY",..: 43 43 43 43 43 43 4..
 $ Length.or.Lower.Length.IN: num  NA NA NA NA NA NA NA NA NA NA ...
 $ Length.Upper.IN           : num  NA NA NA NA NA NA NA NA NA NA ...
 $ Length.or.Lower.Length.MM: num  NA NA NA NA NA NA NA NA NA NA ...
 $ Length.Upper.MM           : num  NA NA NA NA NA NA NA NA NA NA ...
 $ Weight.Pounds             : num  NA NA NA NA NA NA NA NA NA NA ...
 $ Weight.Grams              : num  NA NA NA NA NA NA NA NA NA NA ...
 $ Gender                    : Factor w/ 3 levels "F","M","U": NA NA NA NA NA NA NA NA NA NA ...
 $ Disease.                  : Factor w/ 0 levels: NA NA NA NA NA NA NA NA NA NA ...
 $ Injury.Type               : Factor w/ 1 level "DEAD": NA NA NA NA NA NA NA NA NA NA ...
 $ Age..observed.annuli.     : int  NA NA NA NA NA NA NA NA NA NA ...
 $ Edge.Counted.Desc         : Factor w/ 1 level "Yes": NA NA NA NA NA NA NA NA NA NA ...
 $ Age.Structure             : Factor w/ 3 levels "OTOLITH","SCALE",..: NA NA NA NA NA NA NA NA NA ..
 $ Mark.Given                : Factor w/ 7 levels "AN","LP","LV",..: NA NA NA NA NA NA NA NA NA ..
 $ Mark.Found                : Factor w/ 9 levels "AN","BC","LP",..: NA NA NA NA NA NA NA NA NA ..
 $ Second.Mark.Found         : Factor w/ 1 level "PIT": NA NA NA NA NA NA NA NA NA NA ...
 $ Tag.Number.Given          : chr  NA NA NA NA ...
 $ Second.Tag.Number.Given   : chr  NA NA NA NA ...
 $ Tag.Number.Found          : chr  NA NA NA NA ...
 $ Second.Tag.Number.Found   : chr  NA NA NA NA ...
 $ YOY                       : Factor w/ 2 levels "N","Y": NA NA NA NA NA NA NA NA NA NA ...
 $ Entry.Date                : POSIXct, format: "2010-12-09" "2010-12-09" "2011-10-06" ...
 $ Last.Update.Date          : POSIXct, format: NA NA NA ...
 $ Data.Ent.Name             : chr  "prattf" "prattf" "prattf" "warwir" ...
 $ Last.Update.Name          : chr  NA NA NA NA ...
 $ Invalid.Species           : chr  NA NA NA NA ...
 $ Non.Standard.Bin          : chr  NA NA NA NA ...
 $ Length.Unit.Error         : chr  NA NA NA NA ...
 $ Length.Outside.Range      : chr  NA NA NA NA ...
 $ Count.Outside.Range       : chr  NA NA NA NA ...
 $ Status.Code               : chr  NA NA NA NA ...
 $ Mon                       : Ord.factor w/ 12 levels "Jan"<"Feb"<"Mar"<..: 9 10 10 4 4 4 4 4 4 4 ..
 $ Species1                  : Factor w/ 73 levels "American Brook Lamprey",..: 43 43 43 43 43 43 4..
 $ Len                       : num  NA NA NA NA NA NA NA NA NA NA ...
 $ lennote                   : chr  "Observed length" "Observed length" "Observed length" "Observe"..
```

```
> headtail(d,n=2)
       County    Waterbody.Name    WBIC Survey.Year                          Station.Name
1      SAWYER TIGER CAT FLOWAGE 2435000        2010 TIGER CAT FLOWAGE_GENERAL LAKE STATION
2      SAWYER       NELSON LAKE 2704200        2010       NELSON LAKE_GENERAL LAKE STATION
133250 SAWYER      WINDIGO LAKE 2046600        2014      WINDIGO LAKE_GENERAL LAKE STATION
133251 SAWYER      WINDIGO LAKE 2046600        2014      WINDIGO LAKE_GENERAL LAKE STATION
       Swims.Station.Id Site.Seq.No Survey.Seq.No Survey.Begin.Date Survey.End.Date
1              10005657      123111     104342960        2010-09-26      2010-09-27
2              10002492      122805     104342961        2010-10-18      2010-10-20
133250         10005544      121911     515077184        2014-10-16      2014-10-17
133251         10005544      121911     515077184        2014-10-16      2014-10-17
                      Survey.Status Data.Entry.Name Visit.Fish.Seq.No     Visit.Type
1      DATA ENTRY COMPLETE AND PROOFED          warwir            687017 ELECTROFISHING
2      DATA ENTRY COMPLETE AND PROOFED          warwir            687020        NETTING
133250 DATA ENTRY COMPLETE AND PROOFED  spooner_treaty            723742 ELECTROFISHING
133251 DATA ENTRY COMPLETE AND PROOFED  spooner_treaty            723742 ELECTROFISHING
              Gear Sample.Date Substation.Name Target.Species Fish.Data.Seq.No Net.Number
1      BOOM SHOCKER  2010-09-27      UPPER TWIN        WALLEYE          9022342       <NA>
2          FYKE NET  2010-10-19            <NA>  BLACK CRAPPIE          9022358          2
133250 BOOM SHOCKER  2014-10-17          GLIFWC        WALLEYE         10711295       <NA>
133251 BOOM SHOCKER  2014-10-17          GLIFWC        WALLEYE         10711295       <NA>
       Species.Code          Species Length.or.Lower.Length.IN Length.Upper.IN
1               Z98 NO FISH CAPTURED                       NA              NA
2               Z98 NO FISH CAPTURED                       NA              NA
133250          X22          WALLEYE                       18            18.4
133251          X22          WALLEYE                       18            18.4
       Length.or.Lower.Length.MM Length.Upper.MM Weight.Pounds Weight.Grams Gender Disease.
1                             NA              NA            NA           NA   <NA>     <NA>
2                             NA              NA            NA           NA   <NA>     <NA>
133250                     457.2          467.36            NA           NA   <NA>     <NA>
133251                     457.2          467.36            NA           NA   <NA>     <NA>
       Injury.Type Age..observed.annuli. Edge.Counted.Desc Age.Structure Mark.Given Mark.Found
1             <NA>                    NA              <NA>          <NA>       <NA>       <NA>
2             <NA>                    NA              <NA>          <NA>       <NA>       <NA>
133250        <NA>                    NA              <NA>          <NA>       <NA>       <NA>
133251        <NA>                    NA              <NA>          <NA>       <NA>       <NA>
       Second.Mark.Found Tag.Number.Given Second.Tag.Number.Given Tag.Number.Found
1                   <NA>             <NA>                    <NA>             <NA>
2                   <NA>             <NA>                    <NA>             <NA>
133250              <NA>             <NA>                    <NA>             <NA>
133251              <NA>             <NA>                    <NA>             <NA>
       Second.Tag.Number.Found  YOY Entry.Date Last.Update.Date  Data.Ent.Name Last.Update.Name
1                         <NA> <NA> 2010-12-09             <NA>         prattf             <NA>
2                         <NA> <NA> 2010-12-09             <NA>         prattf             <NA>
133250                    <NA> <NA> 2015-01-21             <NA> spooner_treaty             <NA>
133251                    <NA> <NA> 2015-01-21             <NA> spooner_treaty             <NA>
       Invalid.Species Non.Standard.Bin Length.Unit.Error Length.Outside.Range Count.Outside.Range
1                 <NA>             <NA>              <NA>                 <NA>                <NA>
2                 <NA>             <NA>              <NA>                 <NA>                <NA>
133250            <NA>             <NA>              <NA>                 <NA>                <NA>
133251            <NA>             <NA>              <NA>                 <NA>                <NA>
       Status.Code Mon          Species1  Len         lennote
1             <NA> Sep No Fish Captured   NA Observed length
2             <NA> Oct No Fish Captured   NA Observed length
133250        <NA> Oct           Walleye 18.0 Expanded length
133251        <NA> Oct           Walleye 18.4 Expanded length
```

Manipulating data.frames for Use

Selecting a Subset of Variables

This data.frame contains a large number of variables, many of which you are likely not interested in for a particular analysis. The data.frame can be reduced to a smaller number of variables with `select()` from the `dplyr` package. This function takes the original data.frame as the first argument followed by the names of the variables that you wish to retain as additional arguments. The code below reduces the original data.frame to only six variables.

```
> d <- select(d,Species1,Waterbody.Name,Gear,Survey.Year,Mon,Len)
```

The `%>%` from the `dplyr` package and `%<>%` from the `magrittr` package can simplify this code. The `%>%` operator "pipes" the data.frame on the left of the operator into the first argument of the function to the right of the operator. For example, the code above could be written as follows.

```
> d <- d %>% select(Species1,Waterbody.Name,Gear,Survey.Year,Mon,Len)
```

The `%<>%` operator also "pipes" the data.frame on the left of the operator into the first argument of the function to the right of the operator, but it **ALSO** assigns the result from the right of the operator to the object on the left of the operator. Thus, the code from above is simplified as follows.

```
> d %<>% select(Species1,Waterbody.Name,Gear,Survey.Year,Mon,Len)
> headtail(d,n=2)
               Species1    Waterbody.Name         Gear Survey.Year Mon  Len
1      No Fish Captured TIGER CAT FLOWAGE BOOM SHOCKER        2010 Sep   NA
2      No Fish Captured       NELSON LAKE     FYKE NET        2010 Oct   NA
133250          Walleye      WINDIGO LAKE BOOM SHOCKER        2014 Oct 18.0
133251          Walleye      WINDIGO LAKE BOOM SHOCKER        2014 Oct 18.4
```

Adding Variables

One often needs to construct a new variable from other variables and add this new variable to the data.frame. A variable can be added to a data.frame with `mutate()` from the `dplyr` package. This function takes the data.frame as the first argument and an argument of the form `newvar=expression`, where `newvar` is the name for the new variable and `expression` describes how the new variable is constructed. For example, the following code adds the natural log of length to the data.frame (note that the `%<>%` was used to pipe `d` into the first argument of `mutate()` so that it appears that `mutate()` only has one argument).

```
> d %<>% mutate(loglen=log(Len))
> headtail(d)
               Species1    Waterbody.Name         Gear Survey.Year Mon  Len   loglen
1      No Fish Captured TIGER CAT FLOWAGE BOOM SHOCKER        2010 Sep   NA       NA
2      No Fish Captured       NELSON LAKE     FYKE NET        2010 Oct   NA       NA
3      No Fish Captured       SPIDER LAKE BOOM SHOCKER        2011 Oct   NA       NA
133249  Largemouth Bass      WINDIGO LAKE BOOM SHOCKER        2014 Oct 12.3 2.509599
133250          Walleye      WINDIGO LAKE BOOM SHOCKER        2014 Oct 18.0 2.890372
133251          Walleye      WINDIGO LAKE BOOM SHOCKER        2014 Oct 18.4 2.912351
```

Adding Length Categories

Length categories are the variable most often added to a data.frame. The `lencat()` function from the `FSA` package provides a flexible mechanism for adding this variable. When used within `mutate()`, `lencat()` takes the name of the variable with the length data as the first argument and the width of the length categories in `w=`. This function will choose "smart" starting values for the categories, but you can also set the starting values with `startcat=` (not demonstrated here). The following code creates a new variable called `Len1` that contains 1-in length categories derived from the `Len` variable.

```
> d %<>% mutate(Len1=lencat(Len,w=1))
> headtail(d)
               Species1    Waterbody.Name         Gear Survey.Year Mon  Len   loglen Len1
1      No Fish Captured TIGER CAT FLOWAGE BOOM SHOCKER        2010 Sep   NA       NA   NA
2      No Fish Captured       NELSON LAKE     FYKE NET        2010 Oct   NA       NA   NA
3      No Fish Captured       SPIDER LAKE BOOM SHOCKER        2011 Oct   NA       NA   NA
133249  Largemouth Bass      WINDIGO LAKE BOOM SHOCKER        2014 Oct 12.3 2.509599   12
133250          Walleye      WINDIGO LAKE BOOM SHOCKER        2014 Oct 18.0 2.890372   18
133251          Walleye      WINDIGO LAKE BOOM SHOCKER        2014 Oct 18.4 2.912351   18
```

Specific length categories ("Stock", "Quality", etc.) have been defined for fisheries management purposes for many game species. These length categories can be viewed for a species with `psdVal()` from the `FSA` package. The first argument to this function is the name of the species. The default is to return the lengths in mm, but lengths in inches may be returned by including `units="in"`. These length categories are shown below for Largemouth Bass and Walleye. [Note that the "substock" value is also returned for completeness.]

```
> psdVal("Largemouth Bass",units="in")
 substock     stock   quality preferred memorable    trophy
        0         8        12        15        20        25

> psdVal("Walleye",units="in")
 substock     stock   quality preferred memorable    trophy
        0        10        15        20        25        30
```

Thus, for example, Largemouth Bass that are 12 inches and longer are considered "quality" fish, whereas Largemouth Bass 20 inches and longer are categorized as "memorable."

A variable that contains these categories for a single species can be added to a data.frame with `lencat()` and the `breaks=` argument (*this is demonstrated below for PSD calculations*). However, it is more efficient to add a variable to a data.frame with these categories for **ALL** species for which the categories have been defined. This is accomplished with `psdAdd()` from the `FSA` package, which when used with `mutate()`, requires the name of the variable with the length measurements as the first argument, the name of the variable with the species names as the second argument, and, if the measurements are in inches, `units="in"`. Note that `psdAdd()` will, by default, return a message for each species for which these length categories have not been defined. The `verbose=FALSE` argument used below will suppress these messages (and is only done here to save space).

```
> d %<>% mutate(Lcat=psdAdd(Len,Species1,units="in",verbose=FALSE))
> headtail(d)
               Species1    Waterbody.Name         Gear Survey.Year Mon  Len   loglen Len1    Lcat
1      No Fish Captured TIGER CAT FLOWAGE BOOM SHOCKER        2010 Sep   NA       NA   NA    <NA>
2      No Fish Captured       NELSON LAKE     FYKE NET        2010 Oct   NA       NA   NA    <NA>
3      No Fish Captured       SPIDER LAKE BOOM SHOCKER        2011 Oct   NA       NA   NA    <NA>
133249  Largemouth Bass      WINDIGO LAKE BOOM SHOCKER        2014 Oct 12.3 2.509599   12 quality
133250          Walleye      WINDIGO LAKE BOOM SHOCKER        2014 Oct 18.0 2.890372   18 quality
133251          Walleye      WINDIGO LAKE BOOM SHOCKER        2014 Oct 18.4 2.912351   18 quality
```

Selecting a Subset of Individuals

The current data.frame contains information from Sawyer County for many years, seasons, species, water bodies, etc. A particular analysis may require you to restrict the data to a species, a water body, a species in a waterbody, a species in a waterbody within a year, etc. Subsets of a data.frame can be constructed with `filterD()` from the `FSA` package (which is simply a modification of `filter()` from the `dplyr` package). This function requires the original data.frame as the first argument followed by expressions that describe the condition for a subset. Multiple conditions (arguments) are joined with an "and" (such that both conditions must be true).

For example, the code below constructs a new data.frame (`Spr`) from `d` that contains only fish that were captured in April, May, or June of 2013. It is generally a good habit to examine the structure of a data.frame following filtering to make sure that it contains the individuals of interest. What evidence is there in this structure that the filtering was successful?

```
> Spr <- filterD(d,Survey.Year==2013,Mon %in% c("Apr","May","Jun"))
> str(Spr)
'data.frame':   18903 obs. of  9 variables:
 $ Species1      : Factor w/ 22 levels "Black Bullhead",..: 3 1 21 1 7 22 21 21 12 14 ...
 $ Waterbody.Name: Factor w/ 14 levels "BLACK DAN LAKE",..: 4 1 1 1 9 9 9 9 9 9 ...
 $ Gear          : Factor w/ 2 levels "BOOM SHOCKER",..: 2 2 2 2 2 2 2 2 2 2 ...
 $ Survey.Year   : int  2013 2013 2013 2013 2013 2013 2013 2013 2013 2013 ...
 $ Mon           : Ord.factor w/ 2 levels "May"<"Jun": 1 1 1 1 1 1 1 1 1 1 ...
 $ Len           : num  NA NA NA NA NA NA NA NA NA NA ...
 $ loglen        : num  NA NA NA NA NA NA NA NA NA NA ...
 $ Len1          : num  NA NA NA NA NA NA NA NA NA NA ...
 $ Lcat          : Factor w/ 6 levels "substock","stock",..: NA NA NA NA NA NA NA NA NA NA ...
```

Three other subsets are created below for later use. Can you describe the data in each of these data.frames?

```
> BGSpr <- filterD(Spr,Species1=="Bluegill")
> BGSprLC <- filterD(BGSpr,Waterbody.Name=="LAKE CHETAC",Gear=="BOOM SHOCKER")
> SprLC <- filterD(Spr,Waterbody.Name=="LAKE CHETAC")
```

Summary Statistics and Graphics

Simple Summaries

Frequencies of individuals are created with `xtabs()` which takes a formula of the form `~rows` or `~rows+cols`, where `rows` and `cols` generically represent the variables to form the rows and columns, respectively, of the frequency table. The data.frame that contains the `rows` and `cols` variables must be given in `data=`.

The following two uses of `xtabs()` produce frequency tables of the number of fish of each type captured from Lake Chetac and the number of Bluegill by month and waterbody in spring samples from 2013.

```
> xtabs(~Species1,data=SprLC)
Species1
  Black Crappie        Bluegill          Bowfin Largemouth Bass   Northern Pike     Pumpkinseed
           3619             589              10             274              40              36
      Rock Bass Smallmouth Bass         Walleye    Yellow Perch
              2              10              72            2222
```

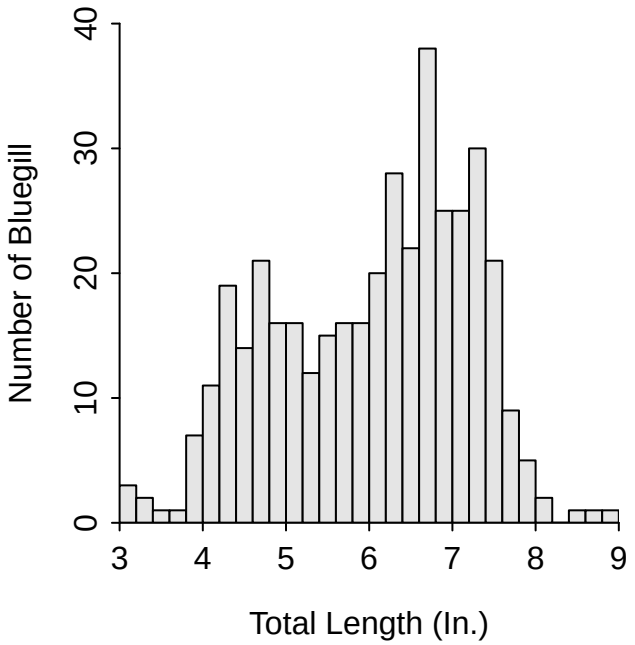
```
> xtabs(~Mon+Waterbody.Name,data=BGSpr)
     Waterbody.Name
Mon   BLACK DAN LAKE CONNORS LAKE DURPHEE LAKE GREEN LAKE LAKE CHETAC LAKE CHIPPEWA
  May            599           90          603           0          589           746
  Jun              0          108            0         144            0             0
     Waterbody.Name
Mon   LAKE OF THE PINES LOWER CLAM LAKE MOOSE LAKE ROUND LAKE WHITEFISH LAKE
  May               213              35          1         414             72
  Jun                90               0          0           0              0
```

Summary statistics for a quantitative variable are efficiently computed with `Summarize()` (note the capital S) from the `FSA` package. This function takes a formula of the form `~quant`, where `quant` generically represents the name of a quantitative variable, as the first argument and the data.frame that contains that variable in `data=`. The number of decimals for the returned statistics is optionally controlled with `digits=`. The code below summarizes the lengths of Bluegill captured in Spring samples from Lake Chetac.

```
> Summarize(~Len,data=BGSprLC,digits=2)
       n   nvalid     mean       sd      min       Q1   median       Q3      max percZero
  398.00   398.00     5.98     1.16     3.00     5.00     6.20     6.90     8.90     0.00
```

A histogram of a quantitative variable is constructed with `hist()` from the `FSA` package. The first two arguments to `hist()` are exactly the same as the first two arguments to `Summarize()`. The cutoffs for the bins used in the histogram may be defined with `breaks=`. For fisheries purposes, the cutoffs are usually evenly spaced and, thus, can be easily constructed as a sequence of values. A simple sequence of values is constructed with `seq()`, which takes the starting value of the sequence as the first argument, the ending value as the last argument, and the step width for the sequence as the last argument. For example, the code in the `breaks=` below constructs a sequence of numbers that starts with 3, ends with 9, and has steps of 0.2 (i.e., 3, 3.2, 3.4, etc.). The x and y axes of the histogram are labeled with a string in `xlab=` and `ylab=`, respectively. The numerical limits of the x and y axes are controlled by including a vector of two values that represent the minimum and maximum values for the axes in `xlim=` and `ylim=`, respectively. The code below constructs the length frequency histogram for Bluegill captured from Lake Chetac in Spring, 2013.

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



Multiple Summaries

Numerical summaries can be efficiently computed for multiple groups using a combination of `group_by()` and `summarize()` (note the lower-case s) from the `dplyr` package. The `group_by` function creates groups for the data.frame given in its first argument based on the groups given in its ensuing arguments. The `group_by()` function below will create groups based on `Waterbody.Name` (i.e., by lakes or rivers) for the `BGSpr` data.frame (which is "piped" into the first argument of `group_by()` with `%>%`). The `summarize()` function then creates summaries defined by the user for each group. A wide variety of summaries can be defined, but the example below uses `n()` to count the number of individuals (i.e., sample size), `mean()` to compute an average, `sd()` to compute a standard deviation, and `min()` and `max()` to compute the minimum and maximum values. The `n()` function does not require any arguments, whereas the other functions require the name of a quantitative variable as the first argument. Also note that these functions use `na.rm=TRUE` to remove missing values from the variable (otherwise, for example, a mean will not be computed). Note that the `sum(!is.na(Len))` code is a "trick" used to count the number of non-missing values in the variable (a "valid" sample size). The result from `summarize()` is "piped" into `as.data.frame()` to remove the grouping structure (which is not needed after the summarization) and other attributes that were added to the result. Thus, the code below computes the sample size, valid sample size, and mean, standard deviation, minimum, and maximum lengths of Bluegill in all water bodies sampled in Spring, 2013.

```
> BGSpr %>%
    group_by(Waterbody.Name) %>%
    summarize(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) ) %>%
    as.data.frame()
      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
```

The code below is similar to that above except that it uses all Spring catches grouped by fish species within water bodies, and the mean and standard deviations were rounded to two decimal places. In addition, the result was "piped" into `write.csv` which will write out the results to the filename given in the first argument (in the current working directory). Note that `row.names=FALSE` was used in `write.csv` to suppress the writing of unneeded row numbers to the file.

```
> Spr %>%
    group_by(Waterbody.Name,Species1) %>%
    summarize(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) ) %>%
    as.data.frame() %>%
    write.csv("LenSum_Sawyer_Spr13.csv",row.names=FALSE)
```

PSD Calculations

Single Waterbody and Species (version 1)

The PSD values are calculated in three steps – (1) find the frequency of individuals between each category with `xtabs()` (as described above), (2) compute a reverse cumulative summary with `rcumsum()` from the `xtabs()` result to find the frequency of individuals in each category (i.e., each category is the number of fish of that size **or greater**), and (3) divide each reverse cumulative frequency by the number of stock-length fish and multiply by 100. These calculations are shown below for the Lake Chetac Bluegill.

```
> ( freq <- xtabs(~Lcat,data=BGSprLC) )
Lcat
    stock   quality preferred
      170       223         5

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

> rcum["stock"]
stock
  398

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

Thus, the PSD-Q for Lake Chetac Bluegill in Spring, 2013 is 57.

Single Waterbody and Species (version 2)

Lengths other than those defined for a species may be of particular interest to the fisheries biologist. For example, one may be interested in PSD-7, which is the percentage of stock-length Bluegill that are 7 inches or longer. To perform this calculation, 7 inches must first be added to the vector of length categories returned by `psdVal()` by including the `addLens=` argument. This vector is then given to `breaks=` in `lencat()` to create a new length category variable that will include a category for 7 inches. In this example, `use.names=TRUE` was used so that category names ("stock","quality", etc.) are used rather than numbers ("3","6", etc.) and `drop.levels=TRUE` was used to drop categories for which no fish were found in the data.frame (for example, "trophy" will be dropped here because no trophy-length fish were captured).

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

> BGSprLC %<>% mutate(Lcat2=lencat(Len,breaks=brks,use.names=TRUE,drop.levels=TRUE))
    Species1 Waterbody.Name         Gear Survey.Year Mon Len   loglen Len1    Lcat   Lcat2
1   Bluegill    LAKE CHETAC BOOM SHOCKER        2013 May 4.0 1.386294    4   stock   stock
2   Bluegill    LAKE CHETAC BOOM SHOCKER        2013 May 4.7 1.547563    4   stock   stock
3   Bluegill    LAKE CHETAC BOOM SHOCKER        2013 May 4.7 1.547563    4   stock   stock
396 Bluegill    LAKE CHETAC BOOM SHOCKER        2013 May 5.6 1.722767    5   stock   stock
397 Bluegill    LAKE CHETAC BOOM SHOCKER        2013 May 6.6 1.887070    6 quality quality
398 Bluegill    LAKE CHETAC BOOM SHOCKER        2013 May 6.6 1.887070    6 quality quality
```

This new variable is then summarized as shown above (code below also demonstrates how to round the final result to one decimal place).

```
> ( 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

> round(rcum/rcum["stock"]*100,1)
    stock   quality         7 preferred
    100.0      57.3      23.9       1.3
```

Thus, the PSD-7 for Lake Chetac Bluegill in Spring, 2013 is 24.

Multiple Waterbodies and Single Species

Frequencies can be computed for multiple water bodies using `xtabs()` as described above (note that a new variable was added to the data.frame of Spring-captured Bluegill from multiple water bodies that included the 7 inch category.)

```
> 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
```

However, it is not as simple to convert these frequencies into PSD values because the reverse cumulative sum must be computed for each **row** of the frequency table. The `apply()` function can be used to "apply" a function to each row or column of a matrix. The `apply()` function takes the matrix (or frequency table, in this case) as the first argument and the function to "apply" is given in `FUN=`. The function will be applied to the rows if `MARGIN=1` and to the columns if `MARGIN=2`. This calculation is demonstrated below.

```
> # apply() result has wrong orientation, only partial results shown
> apply(freq,FUN=rcumsum,MARGIN=1)

           Waterbody.Name
Lcat2       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
```

Unfortunately, the results from `apply()` are not oriented to meet our needs (i.e., water bodies are in columns rather than rows). The orientation of the result can be "transposed" with `t()` as shown below (and note that this result is assigned to the `rcum` object).

```
> ( rcum <- t(apply(freq,FUN=rcumsum,MARGIN=1)) )
                    Lcat2
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
```

Another problem here is that these results contain the substock-length fish. These fish can be removed by eliminating the first column in the `rcum` table.

```
> rcum <- rcum[,-1]
```

The PSD values are then computed as before.

```
> round(rcum/rcum[,"stock"]*100,1)
                    Lcat2
Waterbody.Name       stock quality    7 preferred
  BLACK DAN LAKE       100     3.8  0.8       0.0
  CONNORS LAKE         100    28.4  1.0       0.0
  DURPHEE LAKE         100    93.7 21.5       0.0
  GREEN LAKE           100    78.9 44.4       5.6
  LAKE CHETAC          100    57.4 24.1       1.5
  LAKE CHIPPEWA        100    44.2 19.9       0.6
  LAKE OF THE PINES    100    20.5  0.0       0.0
  LOWER CLAM LAKE      100    11.8  0.0       0.0
  MOOSE LAKE           NaN     NaN  NaN       NaN
  ROUND LAKE           100    25.3  8.8       2.0
  WHITEFISH LAKE       100    15.3  8.5       0.0
```

Multiple Species in a Single Waterbody

Similar code can be used to summarize multiple species in a single waterbody. However, there is no simple way to use "other" lengths for individual species (e.g., it is not simple to include a 7 inch category for Bluegill and a 14 inch category for Largemouth Bass). Thus, this summary can only be computed for the main length categories (which are in the `LCat` variable for the data.frames created further above).

```
> ( freq <- xtabs(~Species1+Lcat,data=SprLC) )
                 Lcat
Species1          substock stock quality preferred memorable
  Black Crappie         28   453      52        14         1
  Bluegill               1   170     223         6         0
  Bowfin                 0     0       0         0         0
  Largemouth Bass       19    81     112        62         0
  Northern Pike          0    20      10         9         1
  Pumpkinseed            0    16      20         0         0
  Rock Bass              0     0       0         0         0
  Smallmouth Bass        1     2       5         2         0
  Walleye                8    17       9        20        17
  Yellow Perch          34   257      91         3         0

> ( rcum <- t(apply(freq,FUN=rcumsum,MARGIN=1)) )
                 Lcat
Species1          substock stock quality preferred memorable
  Black Crappie        548   520      67        15         1
  Bluegill             400   399     229         6         0
  Bowfin                 0     0       0         0         0
  Largemouth Bass      274   255     174        62         0
  Northern Pike         40    40      20        10         1
  Pumpkinseed           36    36      20         0         0
  Rock Bass              0     0       0         0         0
  Smallmouth Bass       10     9       7         2         0
  Walleye               71    63      46        37        17
  Yellow Perch         385   351      94         3         0

> rcum <- rcum[,-1]
> round(rcum/rcum[,"stock"]*100,1)
                 Lcat
Species1          stock quality preferred memorable
  Black Crappie     100    12.9       2.9       0.2
  Bluegill          100    57.4       1.5       0.0
  Bowfin            NaN     NaN       NaN       NaN
  Largemouth Bass   100    68.2      24.3       0.0
  Northern Pike     100    50.0      25.0       2.5
  Pumpkinseed       100    55.6       0.0       0.0
  Rock Bass         NaN     NaN       NaN       NaN
  Smallmouth Bass   100    77.8      22.2       0.0
  Walleye           100    73.0      58.7      27.0
  Yellow Perch      100    26.8       0.9       0.0
```

Reproducibility Information

- **Compiled Date:** Sun Jan 31 2016
- **Compiled Time:** 2:19:39 PM
- **R Version:** R version 3.2.3 (2015-12-10)
- **System:** Windows, i386-w64-mingw32/i386 (32-bit)
- **Base Packages:** base, datasets, graphics, grDevices, methods, stats, utils
- **Required Packages:** knitr, fishWiDNR, FSA, dplyr, magrittr and their dependencies (assertthat, car, DBI, digest, evaluate, formatR, gdata, gplots, graphics, grDevices, highr, Hmisc, lazyeval, lubridate, markdown, methods, plotrix, plyr, R6, Rcpp, sciplot, stats, stringr, tools, utils, yaml)
- **Other Packages:** dplyr_0.4.3, fishWiDNR_0.0.6, FSA_0.8.5, knitr_1.12.3, magrittr_1.5
- **Loaded-Only Packages:** assertthat_0.1, DBI_0.3.1, digest_0.6.9, evaluate_0.8, formatR_1.2.1, gdata_2.17.0, gtools_3.5.0, htmltools_0.3, lazyeval_0.1.10, lubridate_1.5.0, parallel_3.2.3, plyr_1.8.3, R6_2.1.2, Rcpp_0.12.3, rmarkdown_0.9.2, stringi_1.0-1, stringr_1.0.0, tools_3.2.3, yaml_2.1.13
- **Links:** Script / RMarkdown