ParvaPatel_M3_Project3.R

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```r
# 1. Print your name at the top of the script and load these libraries: FSA, FSAdata, magrittr, dplyr,
print(" Myself Parva Patel and NEUID is : 002195186")
```

```
## [1] " Myself Parva Patel and NEUID is : 002195186"
```

```r
#install.packages("plyr")
library(plyr)
```

```r
#install.packages("FSA")
library(FSA)
```

```
## ## FSA v0.9.1. See citation('FSA') if used in publication.
## ## Run fishR() for related website and fishR('IFAR') for related book.
```

```
##
## Attaching package: 'FSA'
```

```
## The following object is masked from 'package:plyr':
##
##     mapvalues
```

```r
#install.packages("FSAdata")
library(FSAdata)
```

```
## ## FSAdata v0.3.8. See ?FSAdata to find data for specific fisheries analyses.
```

```r
#install.packages("magrittr")
library(magrittr)
```

```r
#install.packages("dplyr")
library(dplyr)
```

```
##
## Attaching package: 'dplyr'
```

```
## The following objects are masked from 'package:plyr':
##
##     arrange, count, desc, failwith, id, mutate, rename, summarise,
##     summarize
```

```
## The following objects are masked from 'package:stats':
##
##      filter, lag


## The following objects are masked from 'package:base':
##
##      intersect, setdiff, setequal, union
```

```r
#install.packages("tidyr")
library(tidyr)
```

```
##
## Attaching package: 'tidyr'


## The following object is masked from 'package:magrittr':
##
##      extract
```

```r
#install.packages("tidyverse")
library(tidyverse)
```

```
## -- Attaching packages --------------------------------------- tidyverse 1.3.1 --


## v ggplot2 3.3.5      v purrr   0.3.4
## v tibble  3.1.6      v stringr 1.4.0
## v readr   2.1.1      v forcats 0.5.1


## -- Conflicts ------------------------------------------ tidyverse_conflicts() --
## x dplyr::arrange()   masks plyr::arrange()
## x purrr::compact()   masks plyr::compact()
## x dplyr::count()     masks plyr::count()
## x tidyr::extract()   masks magrittr::extract()
## x dplyr::failwith()  masks plyr::failwith()
## x dplyr::filter()    masks stats::filter()
## x dplyr::id()        masks plyr::id()
## x dplyr::lag()       masks stats::lag()
## x dplyr::mutate()    masks plyr::mutate()
## x dplyr::rename()    masks plyr::rename()
## x purrr::set_names() masks magrittr::set_names()
## x dplyr::summarise() masks plyr::summarise()
## x dplyr::summarize() masks plyr::summarize()
```

```r
# 2. Import the inchBio.csv and name the table <bio>

bio <- read.csv("inchBio.csv")
View(bio)

# 3. Display the head, tail and structure of <bio>

headtail(bio)
```

```
##     netID fishID       species  tl     w  tag scale
## 1      12     16      Bluegill  61   2.9      FALSE
## 2      12     23      Bluegill  66   4.5      FALSE
## 3      12     30      Bluegill  70   5.2      FALSE
## 674   110    863 Black Crappie 307 415.0 1783  TRUE
## 675   129    870 Black Crappie 279 344.0 1789  TRUE
## 676   129    879 Black Crappie 302 397.0 1792  TRUE
```

```
str(bio)
```

```
## 'data.frame':    676 obs. of  7 variables:
##  $ netID  : int  12 12 12 12 12 12 12 13 13 13 ...
##  $ fishID : int  16 23 30 44 50 65 66 68 69 70 ...
##  $ species: chr  "Bluegill" "Bluegill" "Bluegill" "Bluegill" ...
##  $ tl     : int  61 66 70 38 42 54 27 36 59 39 ...
##  $ w      : num  2.9 4.5 5.2 0.5 1 2.1 NA 0.5 2 0.5 ...
##  $ tag    : chr  "" "" "" "" ...
##  $ scale  : logi  FALSE FALSE FALSE FALSE FALSE FALSE ...
```

4. Create an object, <counts>, that counts and lists all the species records

```
counts<- table(bio$species)
counts
```

```
##
##     Black Crappie        Bluegill Bluntnose Minnow     Iowa Darter
##                36             220              103              32
##   Largemouth Bass     Pumpkinseed   Tadpole Madtom    Yellow Perch
##               228              13                6              38
```

5. Display just the 8 levels (names) of the species

```
unique(bio$species)
```

```
## [1] "Bluegill"        "Bluntnose Minnow" "Iowa Darter"      "Largemouth Bass"
## [5] "Pumpkinseed"     "Tadpole Madtom"   "Yellow Perch"     "Black Crappie"
```

#6. Create a <tmp> object that displays the different species and the number of record of each species

```
tmp <- table(bio$species)
tmp
```

```
##
##     Black Crappie        Bluegill Bluntnose Minnow     Iowa Darter
##                36             220              103              32
##   Largemouth Bass     Pumpkinseed   Tadpole Madtom    Yellow Perch
##               228              13                6              38
```

#7. Create a subset, <tmp2>, of just the species variable and display the first five records

```
tmp2 <- subset(bio,select = species)
tmp2
```

```
##           species
## 1        Bluegill
## 2        Bluegill
## 3        Bluegill
## 4        Bluegill
## 5        Bluegill
## 6        Bluegill
## 7        Bluegill
## 8        Bluegill
## 9        Bluegill
## 10       Bluegill
## 11       Bluegill
## 12       Bluegill
## 13       Bluegill
## 14       Bluegill
## 15       Bluegill
## 16       Bluegill
## 17       Bluegill
## 18       Bluegill
## 19       Bluegill
## 20       Bluegill
## 21       Bluegill
## 22       Bluegill
## 23       Bluegill
## 24       Bluegill
## 25       Bluegill
## 26       Bluegill
## 27       Bluegill
## 28       Bluegill
## 29       Bluegill
## 30       Bluegill
## 31       Bluegill
## 32       Bluegill
## 33       Bluegill
## 34       Bluegill
## 35       Bluegill
## 36       Bluegill
## 37       Bluegill
## 38       Bluegill
## 39       Bluegill
## 40       Bluegill
## 41       Bluegill
## 42       Bluegill
## 43       Bluegill
## 44       Bluegill
## 45       Bluegill
## 46       Bluegill
## 47       Bluegill
## 48       Bluegill
## 49       Bluegill
## 50       Bluegill
## 51       Bluegill
## 52       Bluegill
## 53       Bluegill
```

```
## 54          Bluegill
## 55          Bluegill
## 56          Bluegill
## 57          Bluegill
## 58          Bluegill
## 59          Bluegill
## 60          Bluegill
## 61          Bluegill
## 62          Bluegill
## 63          Bluegill
## 64          Bluegill
## 65          Bluegill
## 66          Bluegill
## 67          Bluegill
## 68          Bluegill
## 69          Bluegill
## 70          Bluegill
## 71          Bluegill
## 72          Bluegill
## 73          Bluegill
## 74          Bluegill
## 75          Bluegill
## 76          Bluegill
## 77          Bluegill
## 78          Bluegill
## 79          Bluegill
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## 81          Bluegill
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## 94          Bluegill
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## 96          Bluegill
## 97          Bluegill
## 98          Bluegill
## 99          Bluegill
## 100         Bluegill
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## 106         Bluegill
## 107         Bluegill
```

```
## 108           Bluegill
## 109           Bluegill
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## 116           Bluegill
## 117           Bluegill
## 118           Bluegill
## 119           Bluegill
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## 216          Bluegill
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## 221 Bluntnose Minnow
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## 577   Largemouth Bass
## 578   Largemouth Bass
## 579   Largemouth Bass
## 580   Largemouth Bass
## 581   Largemouth Bass
## 582   Largemouth Bass
## 583   Largemouth Bass
## 584        Pumpkinseed
## 585        Pumpkinseed
## 586        Pumpkinseed
## 587        Pumpkinseed
## 588        Pumpkinseed
## 589        Pumpkinseed
## 590        Pumpkinseed
## 591        Pumpkinseed
## 592        Pumpkinseed
## 593        Pumpkinseed
```

```
## 594       Pumpkinseed
## 595       Pumpkinseed
## 596       Pumpkinseed
## 597    Tadpole Madtom
## 598    Tadpole Madtom
## 599    Tadpole Madtom
## 600    Tadpole Madtom
## 601    Tadpole Madtom
## 602    Tadpole Madtom
## 603      Yellow Perch
## 604      Yellow Perch
## 605      Yellow Perch
## 606      Yellow Perch
## 607      Yellow Perch
## 608      Yellow Perch
## 609      Yellow Perch
## 610      Yellow Perch
## 611      Yellow Perch
## 612      Yellow Perch
## 613      Yellow Perch
## 614      Yellow Perch
## 615      Yellow Perch
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## 619      Yellow Perch
## 620      Yellow Perch
## 621      Yellow Perch
## 622      Yellow Perch
## 623      Yellow Perch
## 624      Yellow Perch
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## 627      Yellow Perch
## 628      Yellow Perch
## 629      Yellow Perch
## 630      Yellow Perch
## 631      Yellow Perch
## 632      Yellow Perch
## 633      Yellow Perch
## 634      Yellow Perch
## 635      Yellow Perch
## 636      Yellow Perch
## 637      Yellow Perch
## 638      Yellow Perch
## 639      Yellow Perch
## 640      Yellow Perch
## 641     Black Crappie
## 642     Black Crappie
## 643     Black Crappie
## 644     Black Crappie
## 645     Black Crappie
## 646     Black Crappie
## 647     Black Crappie
```

```
## 648       Black Crappie
## 649       Black Crappie
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## 672       Black Crappie
## 673       Black Crappie
## 674       Black Crappie
## 675       Black Crappie
## 676       Black Crappie
```

```r
head(tmp2, 5)
```

```
##     species
## 1 Bluegill
## 2 Bluegill
## 3 Bluegill
## 4 Bluegill
## 5 Bluegill
```

```r
#8.Create a table, <w>, of the species variable. Display the class of w
```

```r
w <- table(bio$species)
w
```

```
##
##     Black Crappie         Bluegill Bluntnose Minnow      Iowa Darter
##                36              220              103               32
##   Largemouth Bass      Pumpkinseed   Tadpole Madtom     Yellow Perch
##               228               13                6               38
```

```r
class(w)
```

```
## [1] "table"
```

16

```
#9.Convert <w> to a data frame named <t> and display the results

t <- as.data.frame(w)
t
```

```
##               Var1 Freq
## 1    Black Crappie   36
## 2         Bluegill  220
## 3 Bluntnose Minnow  103
## 4      Iowa Darter   32
## 5  Largemouth Bass  228
## 6      Pumpkinseed   13
## 7   Tadpole Madtom    6
## 8     Yellow Perch   38
```

```
#10. Extract and display the frequency values from the <t> data frame

t$Freq
```

```
## [1]  36 220 103  32 228  13   6  38
```

```
#11.Create a table named <cSpec> from the bio species attribute (variable) and confirm that you created

cSpec <- table(bio$species)*100
cSpec
```

```
## 
##     Black Crappie          Bluegill Bluntnose Minnow      Iowa Darter
##              3600             22000            10300             3200
##   Largemouth Bass       Pumpkinseed    Tadpole Madtom     Yellow Perch
##             22800              1300              600             3800
```

```
class(cSpec)
```

```
## [1] "table"
```

```
#12.Create a table named <cSpecPct> that displays the species and percentage of records for each specie

cSpecPct <-prop.table(cSpec)*100
cSpecPct
```

```
## 
##     Black Crappie          Bluegill Bluntnose Minnow      Iowa Darter
##          5.325444         32.544379        15.236686         4.733728
##   Largemouth Bass       Pumpkinseed    Tadpole Madtom     Yellow Perch
##         33.727811          1.923077         0.887574         5.621302
```

```
class(cSpecPct)
```

```
## [1] "table"
```

```
u <- as.data.frame(cSpecPct)
u
```

```
##              Var1     Freq
## 1    Black Crappie  5.325444
## 2         Bluegill 32.544379
## 3 Bluntnose Minnow 15.236686
## 4      Iowa Darter  4.733728
## 5  Largemouth Bass 33.727811
## 6      Pumpkinseed  1.923077
## 7   Tadpole Madtom  0.887574
## 8     Yellow Perch  5.621302
```
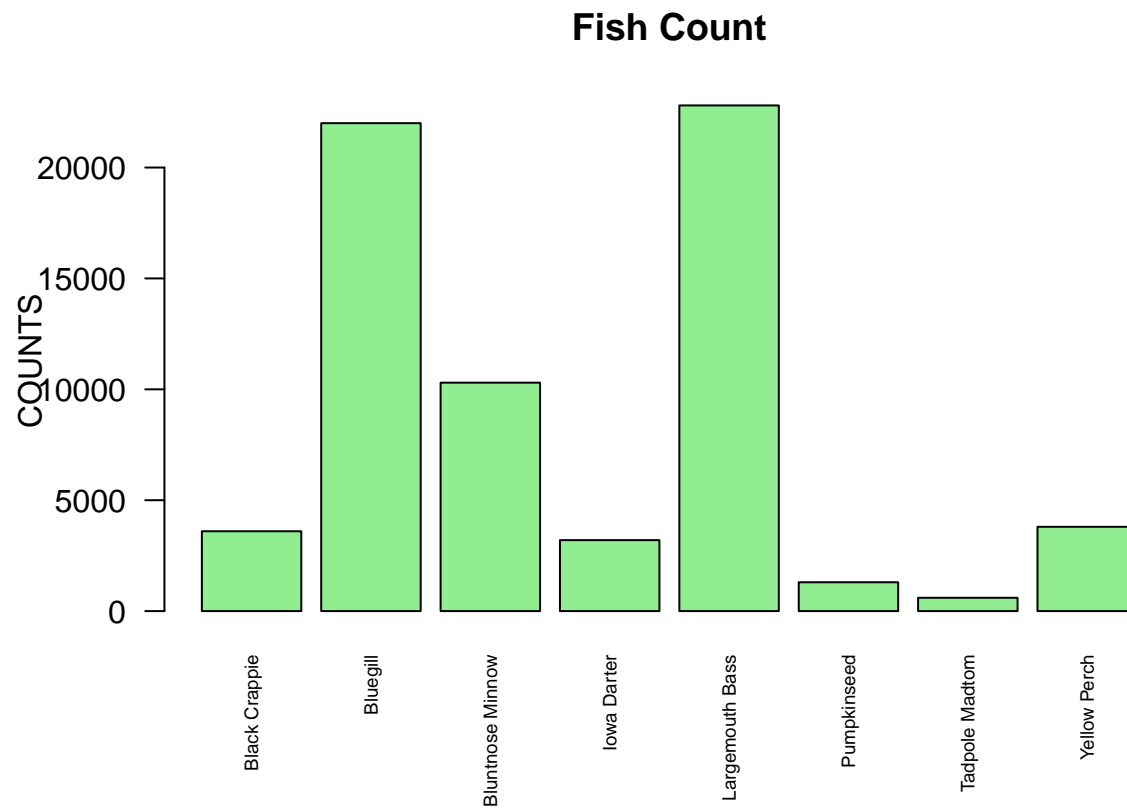
```
class(u)
```

```
## [1] "data.frame"
```

#14.Create a barplot of <cSpec> with the following: titled Fish Count with the following specifications

```
# Title: Fish Count
# Y axis is labeled COUNTS
# Color the bars Light Green
# Rotate Y axis to be horizontal
# Set the X axis font magnification to 60% of nominal
```

```
barplot(cSpec, main="Fish Count", ylab ="COUNTS", col = "lightgreen", cex.names = 0.60, las=2)
```

Fish Count

```
#15.Create a barplot of <cSpecPct>, with the following specifications:

# Y axis limits of 0 to 4
# Y axis label color of Light Blue
# Title of Fish Relative Frequency

barplot(cSpecPct, ylim = c(0,40), main="Fish Relative Frequency", ylab="COUNTS",col.lab="lightblue")
```

Fish Relative Frequency

```
#16.Rearrange the <u> cSpec Pct data frame in descending order of relative frequency. Save the rearrang
```

```
d <- u[order(-u$Freq),]
d
```

```
##                  Var1      Freq
## 5  Largemouth Bass 33.727811
## 2         Bluegill 32.544379
## 3 Bluntnose Minnow 15.236686
## 8     Yellow Perch  5.621302
## 1    Black Crappie  5.325444
## 4      Iowa Darter  4.733728
## 6      Pumpkinseed  1.923077
## 7    Tadpole Madtom  0.887574
```

```
class(d)
```

```
## [1] "data.frame"
```

```
#17.Rename the <d> columns Var 1 to Species, and Freq to RelFreq
```

```
d
```

```
##               Var1      Freq
```

```
## 5   Largemouth Bass 33.727811
## 2           Bluegill 32.544379
## 3 Bluntnose Minnow 15.236686
## 8       Yellow Perch  5.621302
## 1       Black Crappie  5.325444
## 4         Iowa Darter  4.733728
## 6         Pumpkinseed  1.923077
## 7     Tadpole Madtom  0.887574
```

```r
colnames(d) <- c("Species","RelFreq")
d
```

```
##              Species    RelFreq
## 5   Largemouth Bass 33.727811
## 2           Bluegill 32.544379
## 3 Bluntnose Minnow 15.236686
## 8       Yellow Perch  5.621302
## 1       Black Crappie  5.325444
## 4         Iowa Darter  4.733728
## 6         Pumpkinseed  1.923077
## 7     Tadpole Madtom  0.887574
```

#18.Add new variables to <d> and call them cumfreq, counts, and cumcounts

```r
counts
```

```
##
##       Black Crappie          Bluegill Bluntnose Minnow       Iowa Darter
##                  36               220              103                32
##     Largemouth Bass       Pumpkinseed    Tadpole Madtom      Yellow Perch
##                 228                13                6                38
```

```r
t$Freq
```

```
## [1]   36 220 103  32 228  13   6  38
```

```r
tdesc <- t[order(-t$Freq),]
tdesc$Freq
```

```
## [1] 228 220 103  38  36  32  13   6
```

```r
d <- d %>% mutate(cumfreq=cumsum(d$RelFreq), counts=tdesc$Freq, cumcounts=cumsum(tdesc$Freq))
d
```

```
##              Species    RelFreq    cumfreq counts cumcounts
## 5   Largemouth Bass 33.727811  33.72781    228       228
## 2           Bluegill 32.544379  66.27219    220       448
## 3 Bluntnose Minnow 15.236686  81.50888    103       551
## 8       Yellow Perch  5.621302  87.13018     38       589
## 1       Black Crappie  5.325444  92.45562     36       625
## 4         Iowa Darter  4.733728  97.18935     32       657
## 6         Pumpkinseed  1.923077  99.11243     13       670
## 7     Tadpole Madtom  0.887574 100.00000      6       676
```

```
#19.Create a parameter variable <def_par> to store parameter variables

def_par <- par(no.readonly = TRUE)

#20.Create a barplot, <pc>, with the following specifications:

# d$counts of width 1, spacing of .15
# no boarder
# Axes: F
# Yaxis limit 0,3.05*max
# d$counts na.rm is true
# y label is Cummulative Counts
# scale x axis to 70%
# names.arg: d$Species
# Title of the barplot is Species Pareto
# las: 2)

pc <- barplot(d$counts, width = 1, space = 0.15,border = NA, axes = F,
              ylim = c(0,3.05*228), ylab = "Cummulative Counts",
              names.arg = d$Species, las=2, cex.names = 0.70,
              main = "Species Pareto",d$counts,na.rm = TRUE)
```
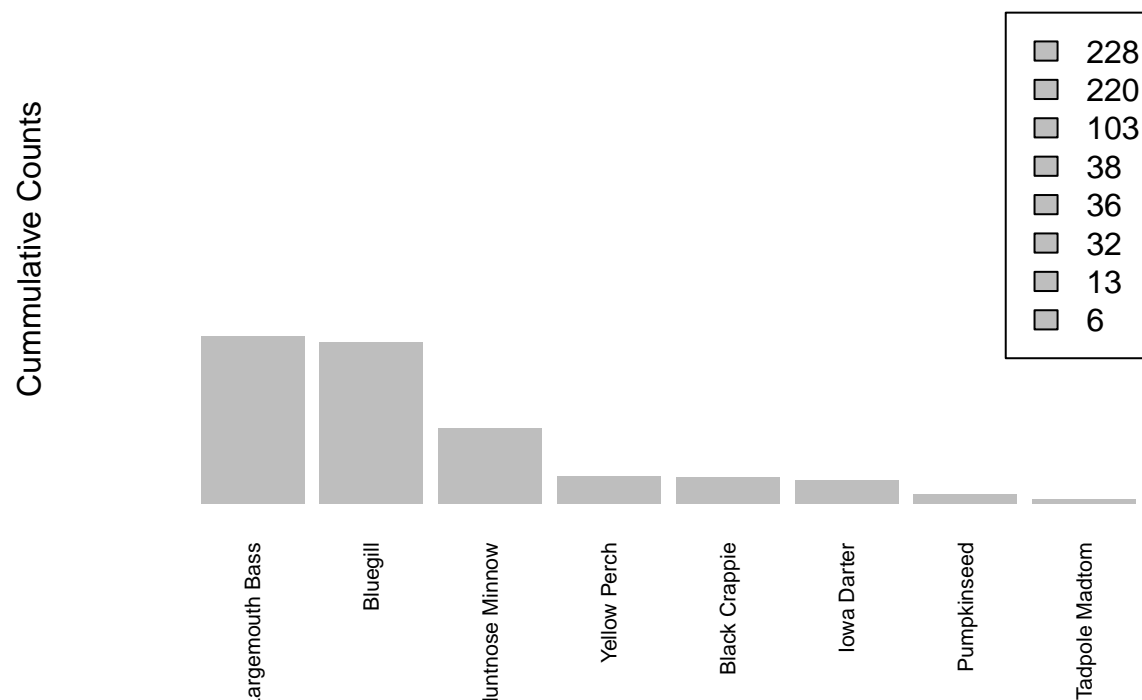
```
## Warning in plot.window(xlim, ylim, log = log, ...): "na.rm" is not a graphical
## parameter

## Warning in axis(if (horiz) 2 else 1, at = at.l, labels = names.arg, lty =
## axis.lty, : "na.rm" is not a graphical parameter

## Warning in title(main = main, sub = sub, xlab = xlab, ylab = ylab, ...): "na.rm"
## is not a graphical parameter
```
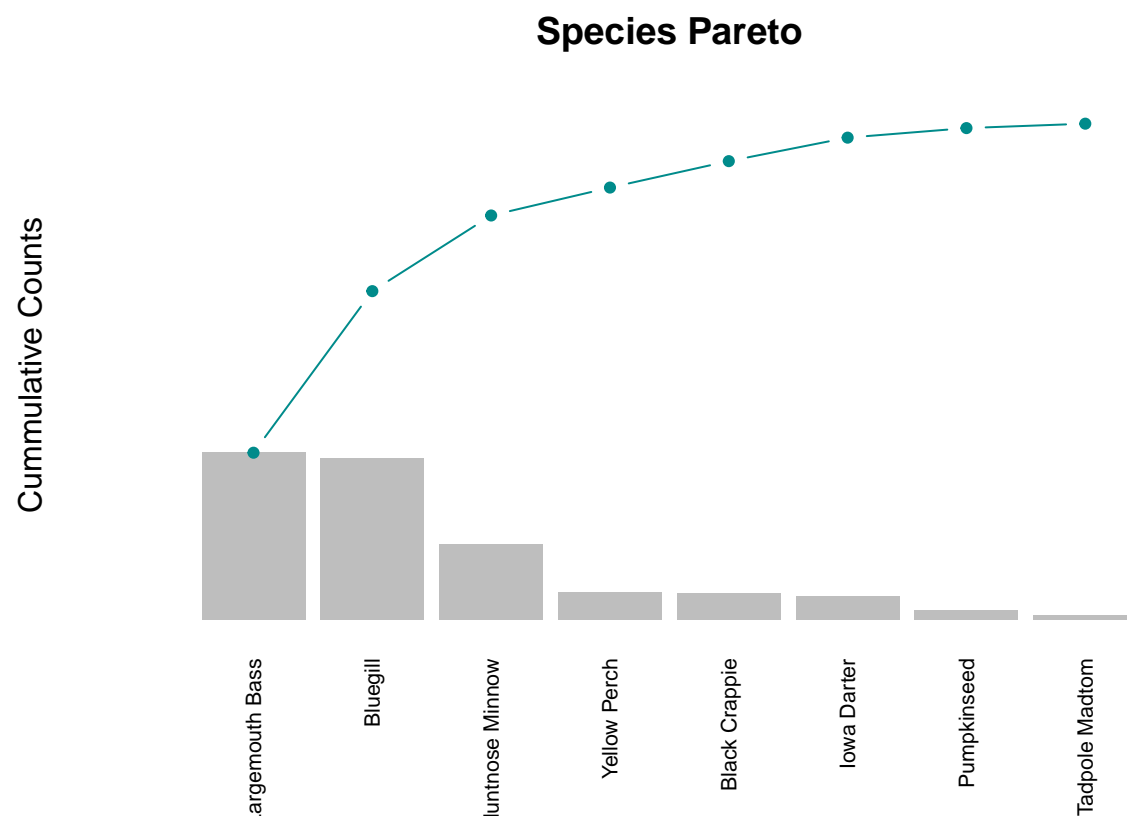
Species Pareto

Cummulative Counts

☐	228
☐	220
☐	103
☐	38
☐	36
☐	32
☐	13
☐	6

argemouth Bass Bluegill luntnose Minnow Yellow Perch Black Crappie Iowa Darter Pumpkinseed Tadpole Madtom

```
#21.Add a cumulative counts line to the <pc> plot with the following:
# Spec line type is b
# Scale plotting text at 70%
# Data values are solid circles with color cyan4

pc <- barplot(d$counts, width = 1, space = 0.15,border = NA, axes = F, ylim = c(0,3.05*228), ylab = "Cu
lines(pc, d$cumcounts, type = "b", cex = 0.7, pch = 19, col="cyan4")
```
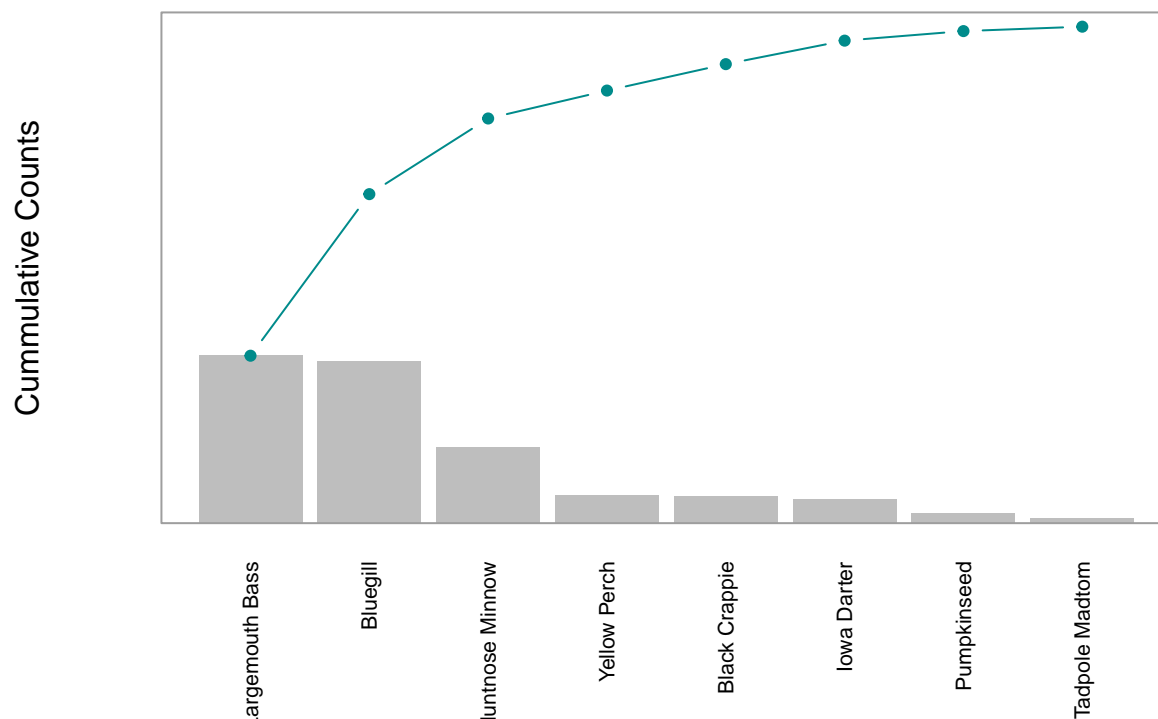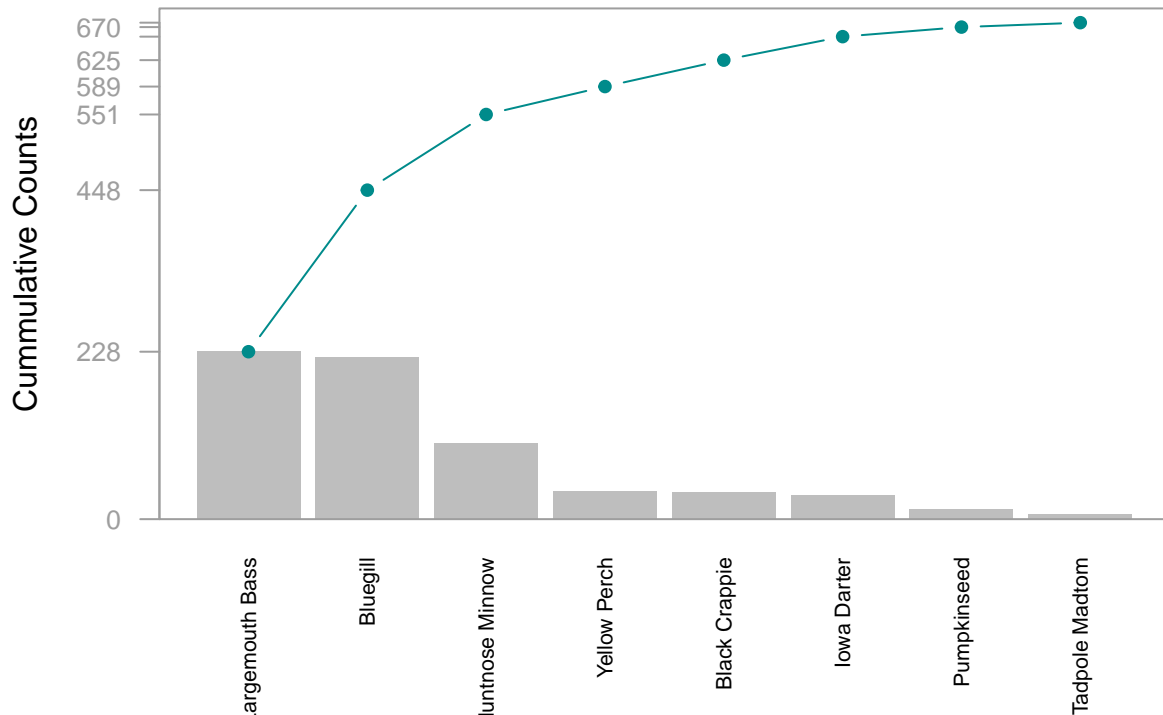
Species Pareto

Species Pareto


```
#22.Place a grey box around the pareto plot.

pc <- barplot(d$counts, width = 1, space = 0.15,border = NA, axes = F, ylim = c(0,3.05*228), ylab = "Cu
lines(pc, d$cumcounts, type = "b", cex = 0.7, pch = 19, col="cyan4")
box(col = "grey62")
```

Species Pareto

Cummulative Counts (y-axis label)

Bar categories (x-axis): argemouth Bass, Bluegill, luntnose Minnow, Yellow Perch, Black Crappie, Iowa Darter, Pumpkinseed, Tadpole Madtom

```
#23.Add a left side axis with the following specifications
# Horizontal values at tick marks at cumcounts on side 2
# Tickmark color of grey62
# Color of axis is grey62
# Axis scaled to 80% of normal

pc <- barplot(d$counts, width = 1, space = 0.15,border = NA, axes = F, ylim = c(0,3.05*228), ylab = "Cu
lines(pc, d$cumcounts, type = "b", cex = 0.8, pch = 19, col="cyan4")
box(col = "grey62")
axis(side = 2, at = c(0, d$cumcounts), las = 1, col.axis = "grey62", col = "grey62", cex.axis = 0.8)
```

Species Pareto
Parva Patel

```
pc <- barplot(d$counts, width = 1, space = 0.15,border = NA, axes = F, ylim = c(0,3.05*228), ylab = "Cum
lines(pc, d$cumcounts, type = "b", cex = 0.8, pch = 19, col="cyan4")
box(col = "grey62")
axis(side = 2, at = c(0, d$cumcounts), las = 1, col.axis = "grey62", col = "grey62", cex.axis = 0.8)
axis(side = 4, at = c(0, d$cumcounts), labels = paste(c(0, round(d$cumfreq)) ,"%",sep=""),
     las = 1, col.axis = "cyan4", col = "cyan4", cex.axis = 0.8)
```

Species Pareto
Parva Patel