

ALY 6000: Introduction to Analytics

Module 3 - Project Assignment

Executive Summary Report 3

Devi Somalinga Bhuvanesh

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Key Findings

The inchBio dataset has information about distinct types of fish and its characteristics in terms of Net ID, Fish ID, type of species, length, width, and presence of scale.

1. Descriptive Analysis

Statistical analysis for entire dataset of inchBio data:

```
> summary(bio)
  netID      fishID      species      tl
Min.   : 1.00   Min.   : 7.0   Length:676   Min.   : 27.0
1st Qu.: 13.00  1st Qu.:175.8   Class :character 1st Qu.: 66.0
Median : 37.00  Median :345.5   Mode  :character Median :189.5
Mean   : 67.65  Mean   :434.2      Mean :186.5
3rd Qu.:109.00 3rd Qu.:695.5      3rd Qu.:295.0
Max.   :206.00 Max.   :915.0      Max.   :429.0

  w      tag      scale
Length:676   Length:676   Mode :logical
Class :character Class :character FALSE:213
Mode  :character Mode  :character TRUE :463

> str(bio) #to check structure of 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      : chr "2.9" "4.5" "5.2" "0.5" ...
 $ tag    : chr "" "" "" "" "" ...
 $ scale  : logi FALSE FALSE FALSE FALSE FALSE FALSE ...
```

Species	RelFreq	CumFreq	Counts	Cumcounts
Largemouth Bass	33.73	33.73	228	228
Bluegill	32.54	66.27	220	448
Bluntnose Minnow	15.24	81.51	103	551
Yellow Perch	5.62	87.13	38	589
Black Crappie	5.33	92.46	36	625
Iowa Darter	4.73	97.19	32	657
Pumpkinseed	1.92	99.11	13	670
Tadpole Madtom	0.89	100.00	6	676

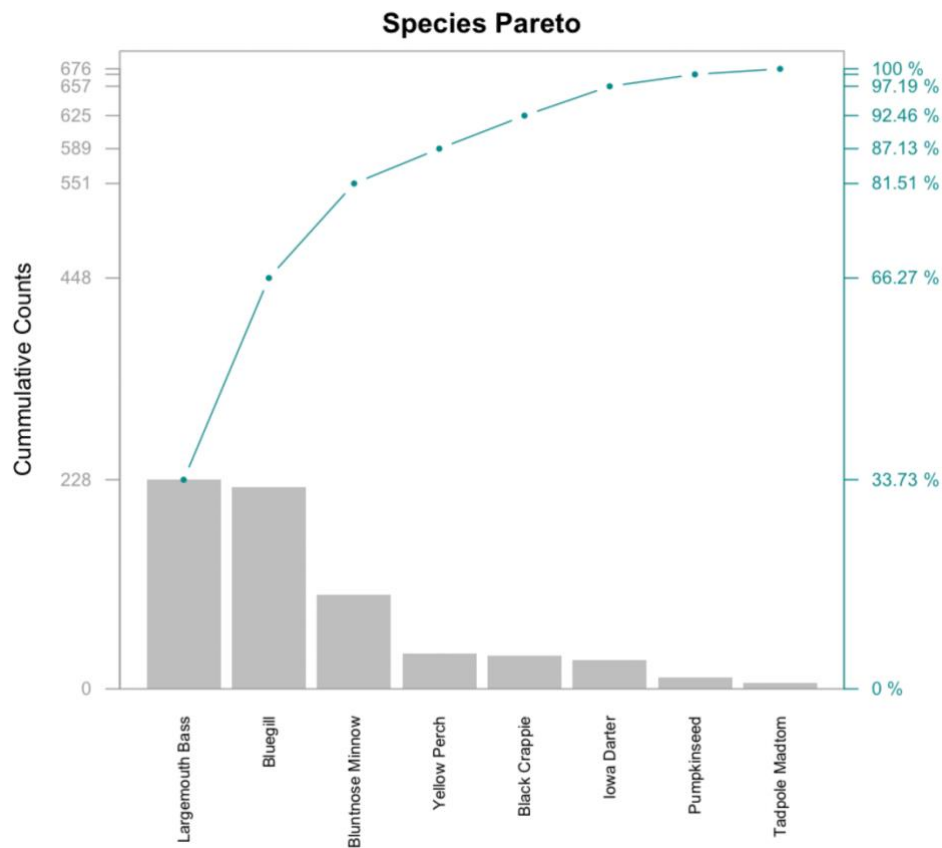
Overall, there are 676 fish of 8 distinct species. The total length of the fish starts from 27 reaching the maximum length of 429. The average fish size is 186.5. Scales in fish act as a layer of protection as well as helping to determine the age of the fish. Out of 676 fish, 68.49% (463) of the fish have scales.

More than two-thirds (66.27%) of the species of fish belong to Largemouth Bass and Bluegill species which dominate the fish population in this dataset. Whereas Tadpole Madtom and Pumpkinseed species together makeup for only 2.81% of the population. Almost equal number of fish are from Yellow Perch (38), Black Crappie (36), and Iowa Darter (32) species.

2. Visualization

In the Visualization section, distinct types of species of fish and their characteristics are studied. This analysis focuses on the fish scale and its total length.

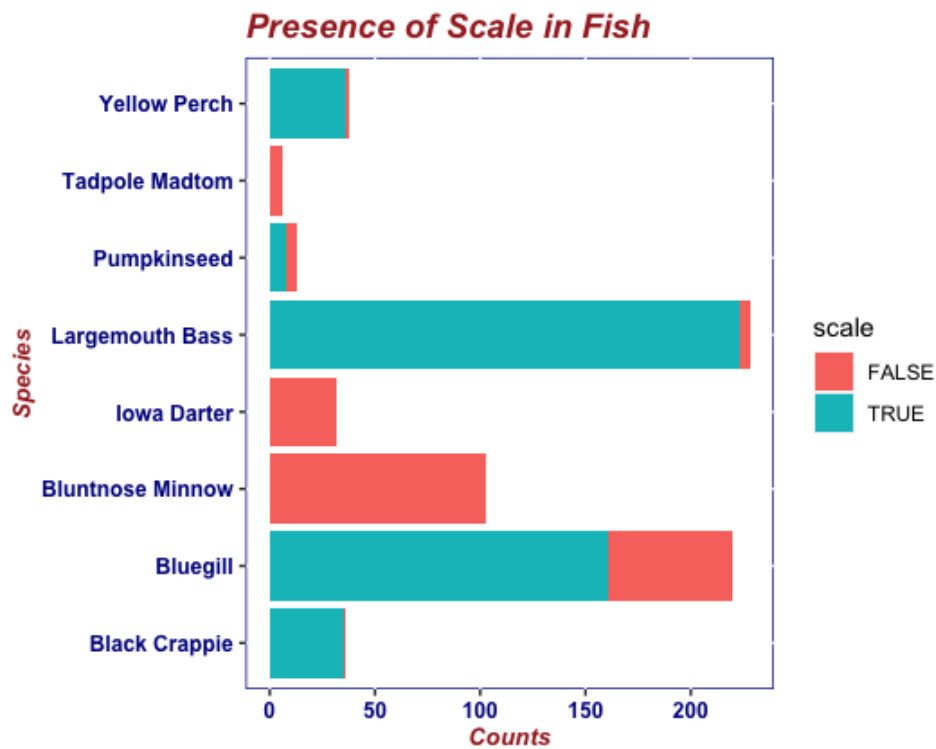
Plot1: Type of Species



The above graph shows the number of fish present in each species. The Y-axis indicates the cumulative frequency and cumulative percentage of fish.

There are 8 distinct species of fish, i.e., Black Crappie, Bluegill, Bluntnose Minnow, Iowa Darter, Largemouth Bass, Pumpkinseed, Tadpole Madtom, and Yellow Perch. Out of 676 fish, 33.73% of them, the maximum number, belong to Largemouth Bass species (228) followed by Bluegill (220) with 32.54% and Bluntnose Minnow (103) with 15.24%. Yellow Perch (38), Black Crappie (36), and Iowa Darter (32) have almost equal number of fish. On the other hand, the least number of fish are Tadpole Madtom (6) with 0.89% and Pumpkinseed (13) with 1.92%.

Plot 2: Presence of Scale in Fish



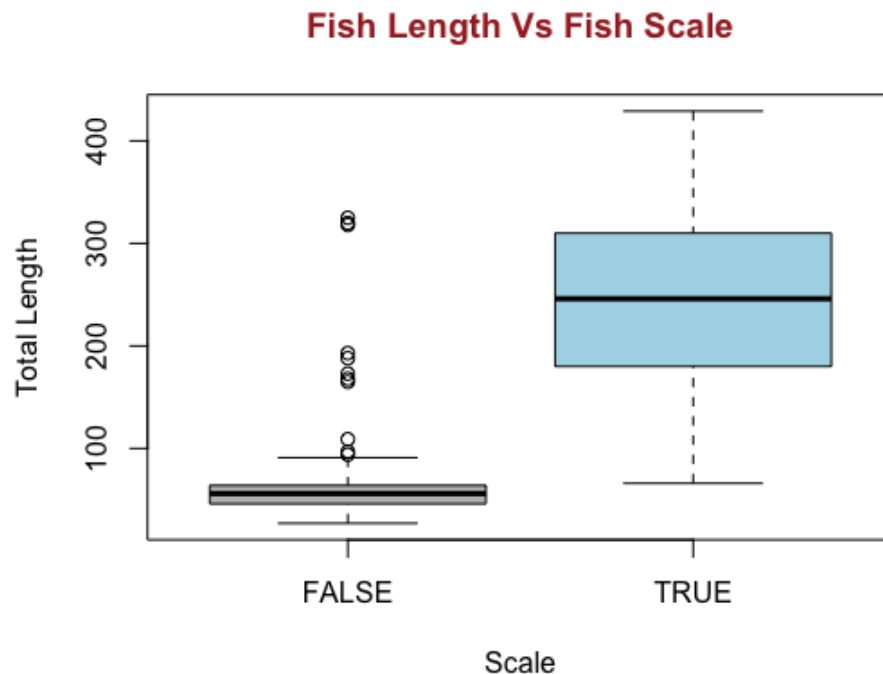
The above stacked bar graph shows whether the fish have scales or not in each type of species present in the database.

Overall, out of 676 fish, 68.49% (463) of the fish have scales which act as a layer of protection to the fish. Most of the fish of Largemouth Bass (98%), Black Crappie (97%), Yellow Perch (95%), and Bluegill species (73%) have scales on their skin. Pumpkinseed fish type has almost equal number of fish with (8) and without scales (5). On the other hand, there are no scales present in Tadpole Madtom, Iowa Darter, and Bluntnose Minnow fish species.

Through this analysis, it can be noted that 31.51% (213) of the fish does not have scale. Except 3 species, each type of species has fish both with scales and without scales.

To understand the impact of growth/age on the development of scales, total length of the fish and its scales are compared in the section below.

Plot 3: Fish Length vs Fish Scale



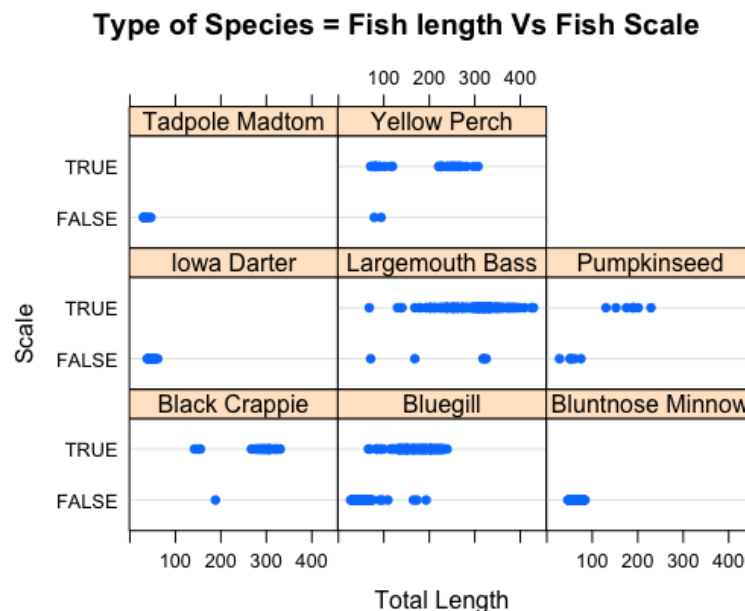
The boxplot depicts the comparison between the total length of fish with and without scales.

Out of 676, 463 fish (68.49%) with scales seems to be bigger in size having total length ranging from 66 to 429 with a median approximately 250. Meanwhile, out of 213 fish without scales, 96% (204) have comparatively lesser total length (less than 100) which indicates that they are smaller in size. Also, the remaining 9 fish (which act as outliers) are bigger with total length ranging from 109 to 325 yet do not have scales in their skin.

Therefore, it is evident that in general fish having scales are bigger in size compared to fish which does not have scales. However, there are certain fish bigger in size yet lack scales.

To understand if missing scales are a characteristic of a species, fish total length versus scale analysis of each type of species has been examined below.

Plot 4: Type of Species – Fish Length vs Fish Scale



To analyze the total length with its scale type, the above graph depicts the comparison in 8 distinct species present in the database.

Out of 8 species, it can be noted that 463 fish with scales are present in 5 species, i.e., Black Crappie, Bluegill, Largemouth Bass, Pumpkinseed, and Yellow Perch. The minimum total length for each of these species is 65.

Alternatively, 213 fish without scales are present in all 8 types of species. Especially, all the fish in Tadpole Madtom (6), Iowa Darter (32), and Bluntnose Minnow (103) species do not have scales and are also smaller in size with a maximum total length of 85. Similarly, 55 Bluegill, 5 Pumpkinseed, 2 Yellow Perch, 1 and 1 Largemouth Bass species of fish do not have scales and are smaller in size (total length less than 100). However, 9 fish, i.e., 1 Black Crappie, 4 Largemouth Bass, and 4 Bluegill species are bigger in size (total length more than 100) yet do not have scales.

Hence, out of 8 species, fish in 5 species have fish both with and without scales and 3 species do not have any scales. Overall, 33.14% fish (224) are smaller in size (total length less than 100) and of these, 91% (204) of the fish do not have scales. This could also indicate that around 30% of the fish are young when compared to other fish.

Summary

Overall, the study examines 676 fish of 8 distinct species. Out of 68.49% (463) of the fish having scales which act as a layer of protection to the fish, 95.68% (443) are bigger in size (length more than 100). Similarly, out of 213 fish which do not have scales, 95.77% (204) fish are smaller in size. Fish in 3 species (Tadpole Madtom, Iowa Darter, Bluntnose Minnow) have no scales and are smaller. Therefore, it is evident that most of the fish that have scales are bigger in size compared to fish which do not have scales. This could also help to determine the age of fish, i.e., around 30% (204) of the fish are young when compared to other fish as they have no scales and are smaller in size. However, there are 9 fish who are bigger in size yet do not have scales.

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Discussed with Ms. Anisha, a student of MPS Project Management regarding Q19 and Q25 on 6th February 2023 over phone-call.

Appendix

#Q1 Print your name at the top of the script

#load these libraries: FSA, FSAdat, magrittr, dplyr, tidyr, plyr, tidyverse

```
> print("Devi Somalinga Bhuvanesh") #To print the name
```

```
[1] "Devi Somalinga Bhuvanesh"
```

```
> install.packages("FSA") #to install the package
```

```
Error in install.packages : Updating loaded packages
```

Restarting R session...

```
> install.packages("FSA")
```

```
trying URL 'https://cran.rstudio.com/bin/macosx/contrib/4.2/FSA_0.9.4.tgz'
```

```
Content type 'application/x-gzip' length 1130850 bytes (1.1 MB)
```

```
=====
```

```
downloaded 1.1 MB
```

The downloaded binary packages are in

```
/var/folders/1y/qwg6z9nj78nfkv1gf3qrgts40000gp/T//RtmpNbQBHh/downloaded_packages
```

```
> library(FSA) #to import the package in the library
```

```
## FSA v0.9.4. See citation('FSA') if used in publication.
```

```
## Run fishR() for related website and fishR('IFAR') for related book.
```

```
> install.packages("FSAdat")
```

```
trying URL 'https://cran.rstudio.com/bin/macosx/contrib/4.2/FSAdat_0.4.0.tgz'
```

```
Content type 'application/x-gzip' length 957828 bytes (935 KB)
```

```
=====
```

```
downloaded 935 KB
```

The downloaded binary packages are in

/var/folders/1y/qwg6z9nj78nfkv1gf3qrgts40000gp/T//RtmpNbQBHh/downloaded_packages

```
> library(FSadata)
```

FSadata v0.4.0. See ?FSadata to find data for specific fisheries analyses.

```
> install.packages("magrittr")
```

trying URL 'https://cran.rstudio.com/bin/macosx/contrib/4.2/magrittr_2.0.3.tgz'

Content type 'application/x-gzip' length 227506 bytes (222 KB)

=====

downloaded 222 KB

The downloaded binary packages are in

/var/folders/1y/qwg6z9nj78nfkv1gf3qrgts40000gp/T//RtmpNbQBHh/downloaded_packages

```
> library(magrittr)
```

```
> install.packages("dplyr")
```

trying URL 'https://cran.rstudio.com/bin/macosx/contrib/4.2/dplyr_1.1.0.tgz'

Content type 'application/x-gzip' length 1554483 bytes (1.5 MB)

=====

downloaded 1.5 MB

The downloaded binary packages are in

/var/folders/1y/qwg6z9nj78nfkv1gf3qrgts40000gp/T//RtmpNbQBHh/downloaded_packages

```
> library(dplyr)
```

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':

filter, lag

The following objects are masked from 'package:base':

intersect, setdiff, setequal, union

```
> install.packages("tidyr")
trying URL 'https://cran.rstudio.com/bin/macosx/contrib/4.2/tidyr_1.3.0.tgz'
Content type 'application/x-gzip' length 1324272 bytes (1.3 MB)
=====
downloaded 1.3 MB
```

The downloaded binary packages are in

/var/folders/1y/qwg6z9nj78nfkv1gf3qrgts40000gp/T//RtmpNbQBHh/downloaded_packages

```
> library(tidyr)
```

Attaching package: 'tidyr'

The following object is masked from 'package:magrittr':

extract

```
> install.packages("plyr")
trying URL 'https://cran.rstudio.com/bin/macosx/contrib/4.2/plyr_1.8.8.tgz'
Content type 'application/x-gzip' length 1015309 bytes (991 KB)
=====
downloaded 991 KB
```

The downloaded binary packages are in

/var/folders/1y/qwg6z9nj78nfkv1gf3qrgts40000gp/T//RtmpNbQBHh/downloaded_packages

```
> library(plyr)
```

You have loaded plyr after dplyr - this is likely to cause problems.

If you need functions from both plyr and dplyr, please load plyr first, then dplyr:

```
library(plyr); library(dplyr)
```

Attaching package: 'plyr'

The following objects are masked from 'package:dplyr':

arrange, count, desc, failwith, id, mutate, rename, summarise,
summarize

The following object is masked from 'package:FSA':

mapvalues

```
> install.packages("tidyverse")
```

trying URL 'https://cran.rstudio.com/bin/macosx/contrib/4.2/tidyverse_1.3.2.tgz'

Content type 'application/x-gzip' length 420896 bytes (411 KB)

=====

downloaded 411 KB

The downloaded binary packages are in

/var/folders/1y/qwg6z9nj78nfkv1gf3qrgts40000gp/T//RtmpNbQBHh/downloaded_packages

```
> library(tidyverse)
```

— Attaching packages — tidyverse 1.3.2 —

✓ ggplot2 3.4.0 ✓ purrr 1.0.1

✓ tibble 3.1.8 ✓ stringr 1.5.0

✓ readr 2.1.3 ✓ forcats 0.5.2

— Conflicts — tidyverse_conflicts() —

✗ plyr::arrange() masks dplyr::arrange()

✗ purrr::compact() masks plyr::compact()

✗ plyr::count() masks dplyr::count()

✗ plyr::desc() masks dplyr::desc()

✗ tidyr::extract() masks magrittr::extract()

✗ plyr::failwith() masks dplyr::failwith()

✗ dplyr::filter() masks stats::filter()

✗ plyr::id() masks dplyr::id()

✗ dplyr::lag() masks stats::lag()

✗ plyr::mutate() masks dplyr::mutate()

✗ plyr::rename() masks dplyr::rename()

✗ purrr::set_names() masks magrittr::set_names()

✗ plyr::summarise() masks dplyr::summarise()

✗ plyr::summarize() masks dplyr::summarize()

> #Q2 Import inchBio.csv and name the table bio

```
> bio <- read.csv2("/Users/devi/Documents/Devi/MPS Analytics/Introduction to Analytics/Module 3/inchBio.csv", sep=",") #to read the database in R
```

```
> bio #to view the database
```

```
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
4	12	44 Bluegill	38	0.5	FALSE
5	12	50 Bluegill	42	1	FALSE
6	12	65 Bluegill	54	2.1	FALSE
7	12	66 Bluegill	27		FALSE
8	13	68 Bluegill	36	0.5	FALSE
9	13	69 Bluegill	59	2	FALSE
10	13	70 Bluegill	39	0.5	FALSE
11	13	71 Bluegill	34	0.5	FALSE
12	13	73 Bluegill	40	1	FALSE
13	13	74 Bluegill	35	0.5	FALSE
14	13	75 Bluegill	32	1	FALSE
15	13	76 Bluegill	37	0.5	FALSE
16	13	77 Bluegill	38	1	FALSE
17	13	78 Bluegill	69	7	FALSE
18	13	80 Bluegill	39	1	FALSE
19	13	81 Bluegill	37	0.5	FALSE
20	13	82 Bluegill	38	1	FALSE
21	13	83 Bluegill	47		FALSE
22	14	86 Bluegill	33	0.5	FALSE
23	14	87 Bluegill	31	1.5	FALSE
24	14	88 Bluegill	36	1.5	FALSE
25	4	118 Bluegill	150	60	TRUE
26	4	119 Bluegill	193	145	TRUE
27	4	120 Bluegill	185	123	TRUE
28	4	121 Bluegill	152	67	TRUE
29	4	122 Bluegill	160	75	TRUE

30	4	123 Bluegill	185 118	TRUE
31	4	124 Bluegill	170 100	TRUE
32	4	125 Bluegill	135 35	TRUE
33	4	126 Bluegill	183 120	TRUE
34	4	127 Bluegill	168 90	TRUE
35	4	128 Bluegill	165 85	TRUE
36	4	129 Bluegill	178 100	TRUE
37	4	130 Bluegill	193 155	TRUE
38	4	131 Bluegill	193 140	TRUE
39	4	132 Bluegill	201 180	TRUE
40	4	133 Bluegill	203 185	TRUE
41	4	134 Bluegill	99 15	TRUE
42	5	138 Bluegill	135 42	TRUE
43	5	139 Bluegill	38 2	FALSE
44	5	140 Bluegill	41	FALSE
45	5	141 Bluegill	41	FALSE
46	5	142 Bluegill	46	FALSE
47	5	143 Bluegill	165 68	TRUE
48	5	144 Bluegill	43	FALSE
49	5	145 Bluegill	51 4	FALSE
50	5	146 Bluegill	203 184	TRUE
51	5	147 Bluegill	168 98	TRUE
52	5	148 Bluegill	152 62	TRUE
53	5	149 Bluegill	64	FALSE
54	5	150 Bluegill	157 76	TRUE
55	10	151 Bluegill	173 100	TRUE
56	10	152 Bluegill	173 95	TRUE
57	10	153 Bluegill	185 130	TRUE
58	10	154 Bluegill	218 250	TRUE

59	10	155 Bluegill	206 197	TRUE
60	10	156 Bluegill	165 78	TRUE
61	10	157 Bluegill	152 72	TRUE
62	10	158 Bluegill	170 98	TRUE
63	9	161 Bluegill	206 175	TRUE
64	9	162 Bluegill	191 144	TRUE
65	9	163 Bluegill	193 148	TRUE
66	9	164 Bluegill	183 130	TRUE
67	9	165 Bluegill	201 185	TRUE
68	9	166 Bluegill	221 225	TRUE
69	9	167 Bluegill	165 80	FALSE
70	9	168 Bluegill	206 180	TRUE
71	9	169 Bluegill	203 175	TRUE
72	9	170 Bluegill	165	TRUE
73	9	171 Bluegill	193 160	FALSE
74	9	172 Bluegill	173	FALSE
75	6	176 Bluegill	213 200	TRUE
76	6	177 Bluegill	155 74	TRUE
77	6	178 Bluegill	157 62	TRUE
78	6	179 Bluegill	211 220	TRUE
79	6	180 Bluegill	188 149	TRUE
80	6	181 Bluegill	188 139	TRUE
81	6	182 Bluegill	196 132	TRUE
82	6	183 Bluegill	188 139	TRUE
83	6	184 Bluegill	160 73	TRUE
84	6	185 Bluegill	196 120	TRUE
85	6	186 Bluegill	221 242	TRUE
86	6	187 Bluegill	180 130	TRUE
87	6	188 Bluegill	152 70	TRUE

88	6	189 Bluegill	140	40	TRUE
89	6	190 Bluegill	203	170	TRUE
90	6	191 Bluegill	145	52	TRUE
91	6	192 Bluegill	147	32	TRUE
92	11	193 Bluegill	211	218	TRUE
93	11	194 Bluegill	147	60	TRUE
94	11	195 Bluegill	152	70	TRUE
95	17	196 Bluegill	203	192	TRUE
96	17	197 Bluegill	132	31	TRUE
97	17	199 Bluegill	142	59	TRUE
98	20	201 Bluegill	140	54	TRUE
99	15	203 Bluegill	142	40	TRUE
100	15	206 Bluegill	147	30	TRUE
101	15	207 Bluegill	119	20	TRUE
102	16	210 Bluegill	229	280	TRUE
103	16	211 Bluegill	224	260	TRUE
104	16	212 Bluegill	224	260	TRUE
105	16	213 Bluegill	224	240	TRUE
106	16	214 Bluegill	150	60	TRUE
107	16	215 Bluegill	137	60	TRUE
108	21	217 Bluegill	94	14	TRUE
109	21	219 Bluegill	130	38	TRUE
110	26	220 Bluegill	132	49	TRUE
111	26	221 Bluegill	137	41	TRUE
112	23	224 Bluegill	114	20	TRUE
113	27	226 Bluegill	127	20	TRUE
114	27	228 Bluegill	122	20	TRUE
115	28	230 Bluegill	137	50	TRUE
116	28	231 Bluegill	234	280	TRUE

```

117 37 322 Bluegill 152 TRUE
118 37 356 Bluegill 201 TRUE
119 206 501 Bluegill 38 0.7 FALSE
120 205 502 Bluegill 43 1.4 FALSE
121 205 503 Bluegill 56 1.5 FALSE
122 205 504 Bluegill 53 1.4 FALSE
123 205 505 Bluegill 38 1 FALSE
124 205 506 Bluegill 48 1.8 FALSE
125 205 507 Bluegill 48 1.4 FALSE
126 205 508 Bluegill 36 0.6 FALSE
127 205 509 Bluegill 30 0.3 FALSE
128 205 510 Bluegill 36 0.8 FALSE
129 205 511 Bluegill 51 1.3 FALSE
130 205 512 Bluegill 58 2.4 FALSE
131 205 513 Bluegill 33 0.7 FALSE
132 205 514 Bluegill 38 1 FALSE
133 205 515 Bluegill 33 0.6 FALSE
134 205 516 Bluegill 56 2.8 FALSE
135 205 517 Bluegill 33 1.1 FALSE
136 205 518 Bluegill 53 2 FALSE
137 205 519 Bluegill 66 4.5 FALSE
138 205 520 Bluegill 71 4.9 FALSE
139 101 533 Bluegill 213 190 TRUE
140 101 538 Bluegill 216 198 1021 TRUE
141 101 539 Bluegill 216 210 1022 TRUE
142 101 540 Bluegill 231 258 1023 TRUE
[ reached 'max' / getOption("max.print") -- omitted 534 rows ]

```

> #Q3 Display head, tail and structure of bio

```
> head(bio) #to check default top few rows and columns of bio database
```

```
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
4 12 44 Bluegill 38 0.5 FALSE
5 12 50 Bluegill 42 1 FALSE
6 12 65 Bluegill 54 2.1 FALSE
```

```
> tail(bio) #to check default last few rows and columns of bio database
```

```
netID fishID species tl w tag scale
671 121 808 Black Crappie 323 509 1050 TRUE
672 121 809 Black Crappie 282 352 1700 TRUE
673 121 812 Black Crappie 142 37 TRUE
674 110 863 Black Crappie 307 415 1783 TRUE
675 129 870 Black Crappie 279 344 1789 TRUE
676 129 879 Black Crappie 302 397 1792 TRUE
```

```
> str(bio) #to check structure of bio
```

```
'data.frame': 676 obs. of 7 variables:
 $ netID : int 12 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 : chr "2.9" "4.5" "5.2" "0.5" ...
 $ tag : chr "" "" "" "" ...
 $ scale : logi FALSE FALSE FALSE FALSE FALSE FALSE ...
```

```
> #Q4 Create an object, <counts>, that counts and lists all the species records
```

```
> counts <- bio[3] #to retrieve the list of species name with the row numbers
```

```
> counts #to view the count and list of all species records
```

	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
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213 Bluegill

214 Bluegill

215 Bluegill

216 Bluegill

217 Bluegill

218 Bluegill

219 Bluegill

220 Bluegill

221 Bluntnose Minnow

222 Bluntnose Minnow

223 Bluntnose Minnow

224 Bluntnose Minnow

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324 Iowa Darter

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327 Iowa Darter

328 Iowa Darter

329 Iowa Darter

330 Iowa Darter

331 Iowa Darter

332 Iowa Darter

333 Iowa Darter

334 Iowa Darter

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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
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603 Yellow Perch
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641 Black Crappie
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674 Black Crappie
675 Black Crappie
676 Black Crappie
```

> #Q5 Display just the 8 levels (names) of the species

```
> unique(bio[3]) #to view the unique names
```

```
species
1      Bluegill
221 Bluntnose Minnow
324 Iowa Darter
356 Largemouth Bass
584 Pumpkinseed
597 Tadpole Madtom
603 Yellow Perch
641 Black Crappie
```

> #Q6 Create a <tmp> object that displays the different species and the number of record in each species in the dataset.

```
> tmp <- table(bio[3]) #to create a table of different species and its frequency
```

```
> tmp #to view the different species and its frequency which is horizontally placed
```

```
species
```

```
Black Crappie    Bluegill Bluntnose Minnow    Iowa Darter
```

36	220	103	32
Largemouth Bass	Pumpkinseed	Tadpole Madtom	Yellow Perch
228	13	6	38

```
> tmp <- as.data.frame(tmp) #convert tmp to data frame
```

```
> tmp          #to view the different species and its frequency in a table/list format
```

```
species 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
```

> #Q7 Create a subset, <tmp2>, of just the species variable and display the first five records

> #Option 1 - To view the first five value under each Species

```
> tmp2 <- ddply(bio, .(species), function(x) head(x, n=5) [3]) #Using ddply function, displayed the first five records of each species in the dataset
```

```
> tmp2 #to view the output of tmp2
```

```
species
```

```
1 Black Crappie
2 Black Crappie
3 Black Crappie
4 Black Crappie
5 Black Crappie
6   Bluegill
7   Bluegill
```

- 8 Bluegill
- 9 Bluegill
- 10 Bluegill
- 11 Bluntnose Minnow
- 12 Bluntnose Minnow
- 13 Bluntnose Minnow
- 14 Bluntnose Minnow
- 15 Bluntnose Minnow
- 16 Iowa Darter
- 17 Iowa Darter
- 18 Iowa Darter
- 19 Iowa Darter
- 20 Iowa Darter
- 21 Largemouth Bass
- 22 Largemouth Bass
- 23 Largemouth Bass
- 24 Largemouth Bass
- 25 Largemouth Bass
- 26 Pumpkinseed
- 27 Pumpkinseed
- 28 Pumpkinseed
- 29 Pumpkinseed
- 30 Pumpkinseed
- 31 Tadpole Madtom
- 32 Tadpole Madtom
- 33 Tadpole Madtom
- 34 Tadpole Madtom
- 35 Tadpole Madtom
- 36 Yellow Perch

37 Yellow Perch
38 Yellow Perch
39 Yellow Perch
40 Yellow Perch

> #Option 2 - To view the subset of bio and the first five records

> tmp2 <- subset(bio[3]) #to extract the subset values under bio species column

> tmp2 #to view the subset of bio

	species
1	Bluegill
2	Bluegill
3	Bluegill
4	Bluegill
5	Bluegill
6	Bluegill
7	Bluegill
8	Bluegill
9	Bluegill
10	Bluegill
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311 Bluntnose Minnow

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315 Bluntnose Minnow

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318 Bluntnose Minnow

319 Bluntnose Minnow

320 Bluntnose Minnow

321 Bluntnose Minnow

322 Bluntnose Minnow

323 Bluntnose Minnow

324 Iowa Darter

325 Iowa Darter

326 Iowa Darter

327 Iowa Darter

328 Iowa Darter

329 Iowa Darter

330 Iowa Darter

331 Iowa Darter

332 Iowa Darter

333 Iowa Darter

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596 Pumpkinseed
597 Tadpole Madtom
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599 Tadpole Madtom
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601 Tadpole Madtom

602 Tadpole Madtom

603 Yellow Perch

604 Yellow Perch

605 Yellow Perch

606 Yellow Perch

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611 Yellow Perch

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613 Yellow Perch

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619 Yellow Perch

620 Yellow Perch

621 Yellow Perch

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627 Yellow Perch

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629 Yellow Perch

630 Yellow Perch

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637	Yellow Perch
638	Yellow Perch
639	Yellow Perch
640	Yellow Perch
641	Black Crappie
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676 Black Crappie
```

```
> head(tmp2,n=5)    #to view the first five records
```

```
species
```

```
1 Bluegill
```

```
2 Bluegill
```

```
3 Bluegill
```

```
4 Bluegill
```

```
5 Bluegill
```

```
>
```

```
> #Q8 Create a table, <w>, of the species variable. Display the class of w
```

```
> w <- table(bio[3]) #table created for displaying species variable and its frequency
```

```
> w          #to view the species and its frequency
```

```
species
```

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

```
> class(w)    #to view the type of class of w
```

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

> #Q9 Convert <w> to a data frame named <t> and display the results

```
> t <- as.data.frame(w)  # to convert w from table format to a dataframe
```

```
> class(t)          # to view the type of class of t
```

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

```
> t                # to view the output of t in table formatt
```

```
species 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

> #Q10 Extract and display the frequency values from the <t> data frame

```
> t[2]          #extract the second column of t which has the frequency values
```

```
Freq
```

```
1 36
```

```
2 220
```

3 103

4 32

5 228

6 13

7 6

8 38

>

> **#Q11 Create a table named <cSpec> from the bio species attribute (variable)**

> **#confirm that it displays the number of species in the dataset <bio>**

> cSpec <- table(bio[3]) #to create a table cSpec of bio species with frequency

> cSpec #to view the output of cSpec

species

Black Crappie	Bluegill	Bluntnose Minnow	Iowa Darter
---------------	----------	------------------	-------------

36	220	103	32
----	-----	-----	----

Largemouth Bass	Pumpkinseed	Tadpole Madtom	Yellow Perch
-----------------	-------------	----------------	--------------

228	13	6	38
-----	----	---	----

> class(cSpec) #to view the class of cSpec

[1] "table"

> totalcSpec <- sum(cSpec) #to add all the values in cSpec

> totalcSpec #to view total values in cSpec

[1] 676

> totaldataset <- nrow(bio) #to check number of values in dataset bio

> totaldataset #to view total values in dataset bio

[1] 676

> totalcSpec == totaldataset #to verify whether the total values in cSpec and in dataset are same

[1] TRUE

> #Q12 Create a table named <cSpecPct> that displays the species and percentage of records for each species. Confirm you created a table class.

```
> cSpec          #to view the cSpec data stored in R
```

```
species
```

Black Crappie	Bluegill	Bluntnose Minnow	Iowa Darter
---------------	----------	------------------	-------------

36	220	103	32
----	-----	-----	----

Largemouth Bass	Pumpkinseed	Tadpole Madtom	Yellow Perch
-----------------	-------------	----------------	--------------

228	13	6	38
-----	----	---	----

```
> nrow(cSpec)      #to check number of rows in cSpec
```

```
[1] 8
```

```
> cSpecPct <- round(prop.table(cSpec)*100, 2) #to calculate percentage of frequency of each species
```

```
> cSpecPct          #to view the output of cSpecPct which has the percentages of frequency of each species
```

```
species
```

Black Crappie	Bluegill	Bluntnose Minnow	Iowa Darter
---------------	----------	------------------	-------------

5.33	32.54	15.24	4.73
------	-------	-------	------

Largemouth Bass	Pumpkinseed	Tadpole Madtom	Yellow Perch
-----------------	-------------	----------------	--------------

33.73	1.92	0.89	5.62
-------	------	------	------

```
> class(cSpecPct)   #to check the class of cSpecPct
```

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

> #Q13 Convert the table, <cSpecPct>, to a data frame named <u> and confirm that <u> is a data frame

```
> u <- as.data.frame(cSpecPct) #convert cSpecPct from table to dataframe and store in u
```

```
> u              # to view the output of u
```

```
  species Freq
```

```
1 Black Crappie 5.33
```

```
2   Bluegill 32.54
```

```
3 Bluntnose Minnow 15.24
```



```

4 Iowa Darter 4.73
5 Largemouth Bass 33.73
6 Pumpkinseed 1.92
7 Tadpole Madtom 0.89
8 Yellow Perch 5.62
> class(u)          #to view the class of u
[1] "data.frame"
>

```

#Q14 Create a barplot of <cSpec> with the following:

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

```

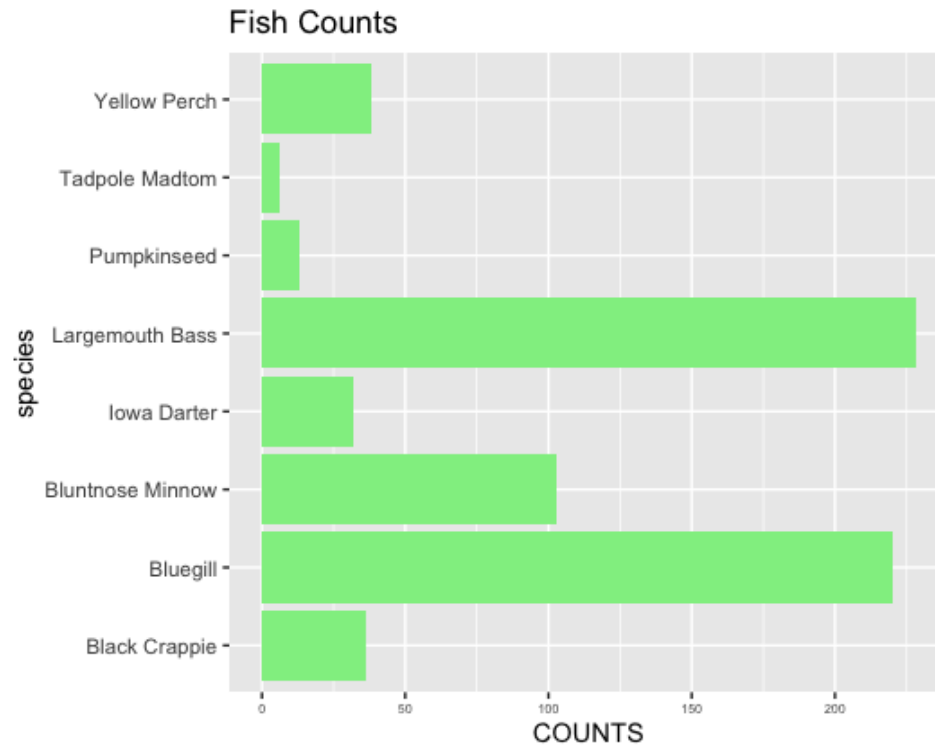
> cSpec <- as.data.frame(cSpec)  #convert cSpec from table to data frame format
> cSpec                          # to view cSpec
  species Freq
1 Black Crappie 36
2 Bluegill 220
3 Bluntnose Minnow 103
4 Iowa Darter 32
5 Largemouth Bass 228
6 Pumpkinseed 13
7 Tadpole Madtom 6
8 Yellow Perch 38
> ggplot(data=cSpec) +          #Using ggplot, ggtitle, geom_bar, to provide the features
+ ggtitle("Fish Counts") +
+ geom_bar(stat = "identity", aes(x=species, y=Freq),fill="lightgreen") +

```

```

+ labs(y="COUNTS")+
+ theme(axis.text.x = element_text(size = rel(0.60))) + #to set x axis to 60% of nominal
+ coord_flip()      #to rotate Y axis to the horizontal
>

```



#Q15 Create a barplot of <cSpecPct>, with the following specifications:

Y axis limits of 0 to 40

Y axis label color of Light Blue

Title of "Fish Relative Frequency"

```
> cSpecPct <- as.data.frame(cSpecPct) #to convert cSpecPct to data frame format to make the bar chart
```

```
> cSpecPct #to view the output of cSpecPct
```

```
species Freq
```

```
1 Black Crappie 5.33
```

```
2 Bluegill 32.54
```

```
3 Bluntnose Minnow 15.24
```

```
4 Iowa Darter 4.73
```

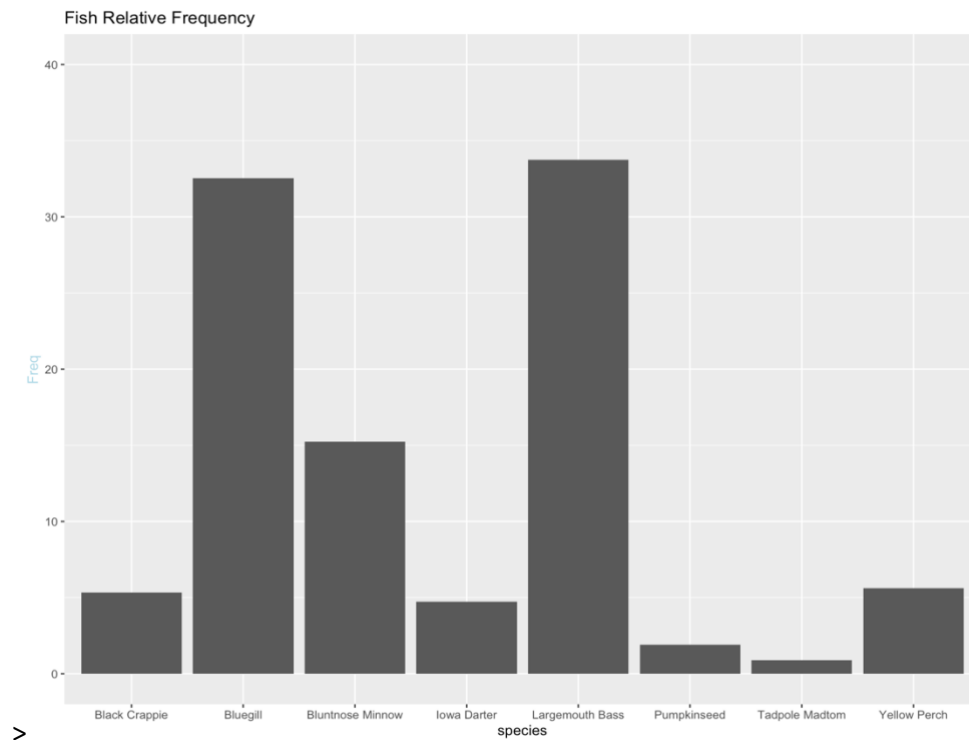
5 Largemouth Bass 33.73

6 Pumpkinseed 1.92

7 Tadpole Madtom 0.89

8 Yellow Perch 5.62

```
> ggplot(data=cSpecPct) +          #Using ggplot function to make the barchart
+ ggtitle("Fish Relative Frequency") +
+ geom_bar(stat = "identity",aes(x=species, y=Freq)) +
+ coord_cartesian(ylim = c(0,40))+
+ theme(axis.title.y = element_text(colour="lightblue"))
```



> **#Q16 Rearrange the <u> cSpecPct data frame in descending order of relative frequency.**

> **#Save the rearranged data frame as the object <d>**

> u #to view cSpecPct data stored in u

species Freq

1 Black Crappie 5.33

2 Bluegill 32.54

3 Bluntnose Minnow 15.24

4 Iowa Darter 4.73

5 Largemouth Bass 33.73

6 Pumpkinseed 1.92

7 Tadpole Madtom 0.89

8 Yellow Perch 5.62

```
> class(u)      #to know the type of class
```

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

```
> d <- u[order(-u$Freq), ]  #to order the frequency in descending order
```

```
> d              #to view the values stored in d
```

```
species Freq
```

5 Largemouth Bass 33.73

2 Bluegill 32.54

3 Bluntnose Minnow 15.24

8 Yellow Perch 5.62

1 Black Crappie 5.33

4 Iowa Darter 4.73

6 Pumpkinseed 1.92

7 Tadpole Madtom 0.89

```
> #Q17 Rename the <d> columns Var 1 to Species, and Freq to RelFreq
```

```
> colnames(d) <- c("Species", "RelFreq") #to change the column names
```

```
> d              #to view the output of d with names changed
```

```
Species RelFreq
```

5 Largemouth Bass 33.73

2 Bluegill 32.54

3 Bluntnose Minnow 15.24

8 Yellow Perch 5.62

1 Black Crappie 5.33

```

4 Iowa Darter 4.73
6 Pumpkinseed 1.92
7 Tadpole Madtom 0.89
> class(d) #to view the class of d
[1] "data.frame"

```

#Q18 Add new variables to <d> and call them cumfreq, counts, and cumcounts

> #to calculate Cumulative Frequency from d database

```

> d #to view the values stored in d
  Species RelFreq
5 Largemouth Bass 33.73
2 Bluegill 32.54
3 Bluntnose Minnow 15.24
8 Yellow Perch 5.62
1 Black Crappie 5.33
4 Iowa Darter 4.73
6 Pumpkinseed 1.92
7 Tadpole Madtom 0.89
> cumfreq <- cumsum(d$RelFreq) #to calculate cumulative frequency
> cumfreq #to view cumulative frequency
[1] 33.73 66.27 81.51 87.13 92.46 97.19 99.11 100.00

```

> #to calculate counts from bio database

```

> cSpec #to view the values stored in cSpec
  species 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
> class(cSpec)          #to view class of cSpec
[1] "data.frame"
> counts <- cSpec[order(-cSpec$Freq), ] #descending order of cSpec
> counts                #value of counts
      species Freq
5 Largemouth Bass 228
2   Bluegill  220
3 Bluntnose Minnow 103
8   Yellow Perch  38
1  Black Crappie  36
4   Iowa Darter  32
6   Pumpkinseed  13
7  Tadpole Madtom  6
> #to calculate cumulative counts
> cumcounts <- cumsum(counts$Freq)  #to calculate cumulative counts
> cumcounts                #to view cumulative counts
[1] 228 448 551 589 625 657 670 676
> #to add new columns with its values in the table
> d <- cbind(d,cumfreq,counts$Freq,cumcounts)  #to bind values of each column
> colnames(d) <- c("Species", "RelFreq", "CumFreq", "Counts", "Cumcounts") #Column names
> d #to view output of d
      Species RelFreq CumFreq Counts Cumcounts
5 Largemouth Bass 33.73  33.73   228     228
2   Bluegill  32.54  66.27   220     448
3 Bluntnose Minnow 15.24  81.51   103     551
8   Yellow Perch  5.62  87.13    38     589

```

1	Black Crappie	5.33	92.46	36	625
4	Iowa Darter	4.73	97.19	32	657
6	Pumpkinseed	1.92	99.11	13	670
7	Tadpole Madtom	0.89	100.00	6	676

> #Q19 Create a parameter variable <def_par> to store parameter variables

```
> def_par <- list(cex.axis = 0.7, mar = c(10, 5, 2, 4), yaxs = "i", las = 2 ) #listed to set parameter variables of
font axis, margin of plot, set y limits within internal axis, set label of axis
```

```
> par(def_par) #to store listed parameter variables
```

```
> def_par #to view the default parameter
```

```
$cex.axis
```

```
[1] 0.7
```

```
$mar
```

```
[1] 10 5 2 4
```

```
$yaxs
```

```
[1] "i"
```

```
$las
```

```
[1] 2
```

```
>
```

#Q20 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 Cumulative Counts

scale x axis to 70%

names.arg: d\$Species

Title of the barplot is "Species Pareto"

las: 2

> dev.new(width=7, height=7) #to open the plot in new window and set the size

NULL

> par(mar=c(10, 5, 2, 4)) #default margin in parameter

> pc <- barplot(d\$Counts, width = 1, space = 0.15, border = NA, axes = F,

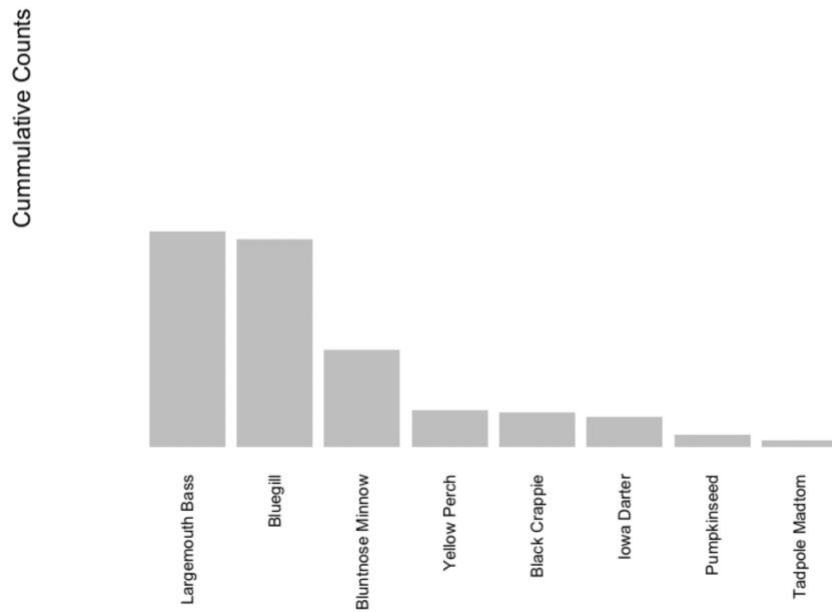
+ ylim = c(0, 3.05 * max(d\$Counts, na.rm = TRUE)),

+ ylab = "Cumulative Counts" , cex.names = 0.70,

+ names.arg = d\$Species,

+ main = "Species Pareto", las=2) #create barplot as per instruction

Species Pareto



> #Q21. Add a cumulative counts line to the <pc> plot with the following:

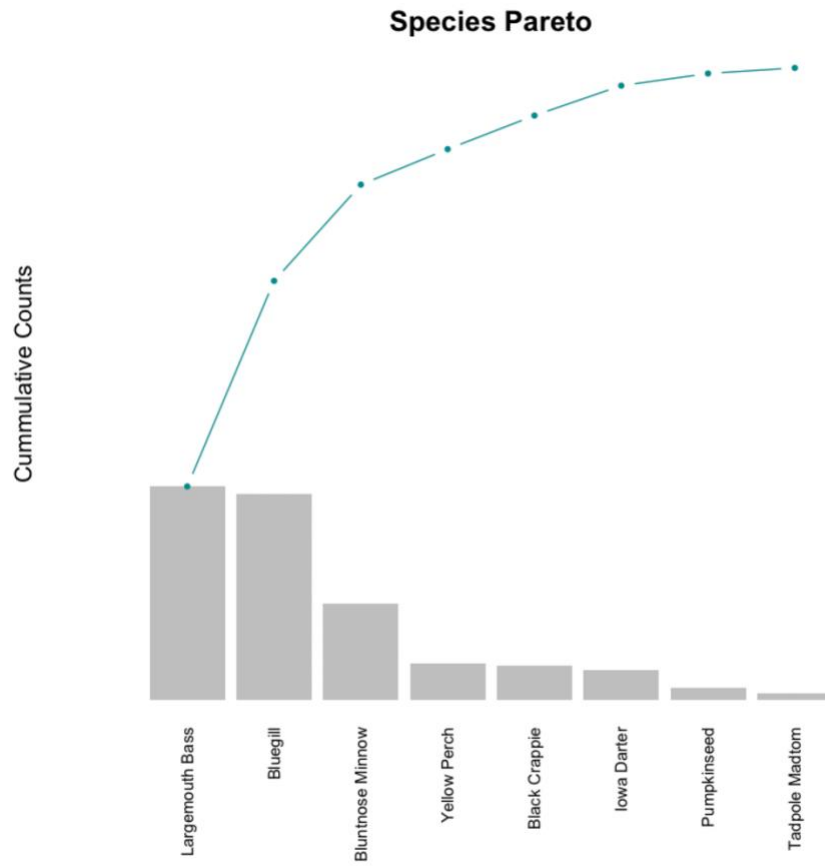
> # Spec line type is b

> # Scale plotting text at 70%

> # Data values are solid circles with color cyan4

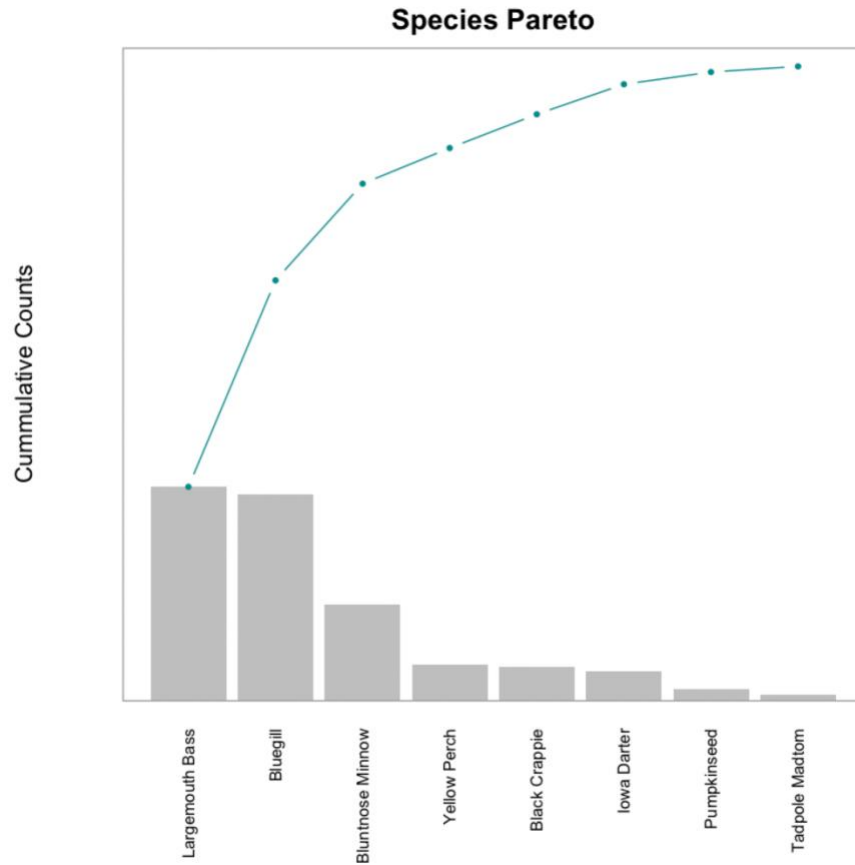
> lines(pc, d\$Cumcounts, type = "b", cex = 0.7, pch = 20, col="cyan4") #draw line with values as per instruction

>



#Q22 Place a grey box around the pareto plot

```
> box(col="grey62") #draw box for plot
```



> #Q23 Add a left side axis with the following specifications

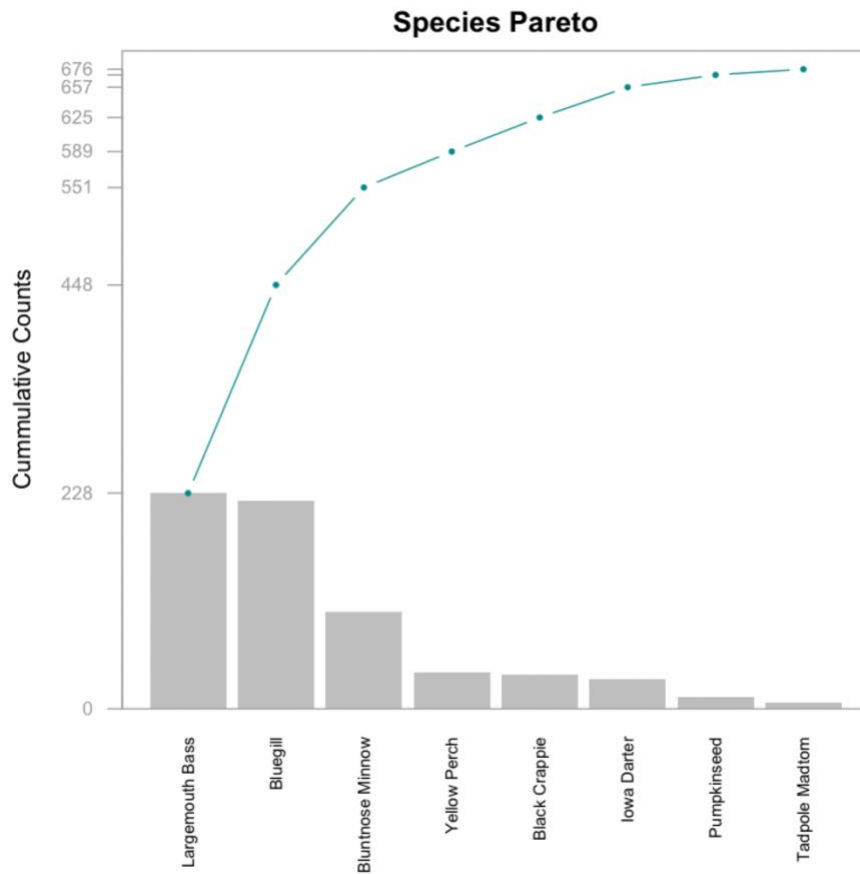
> #Horizontal values at tick marks at cumcounts on side 2

> #Tickmark color of grey62

> #Color of axis is grey62

> #Axis scaled to 80% of normal

```
> axis(side = 2, at = c(0, d$Cumcounts), las = 1, col.axis = "grey62", col = "grey62", cex.axis = 0.8) #add
features to axis as mentioned
```



> #Q24 Add axis details on right side of box with the specifications:

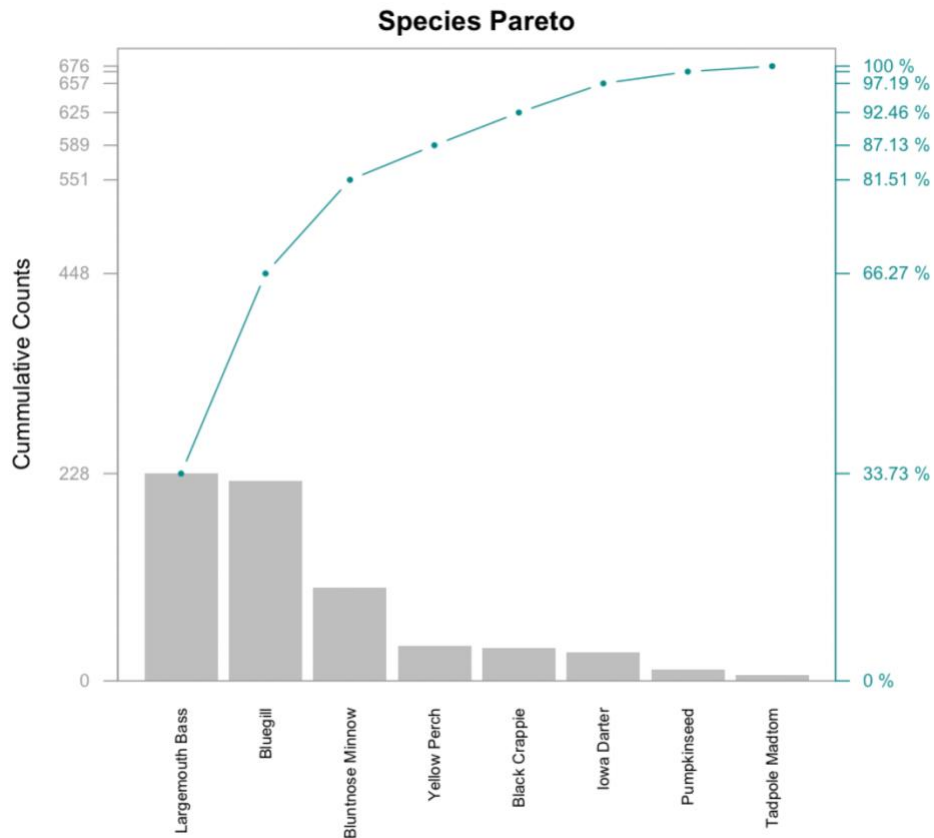
> # Spec: Side 4

> # Tickmarks at cumcounts with labels from 0 to cumfreq with %,

> # Axis color of cyan5 and label color of cyan4

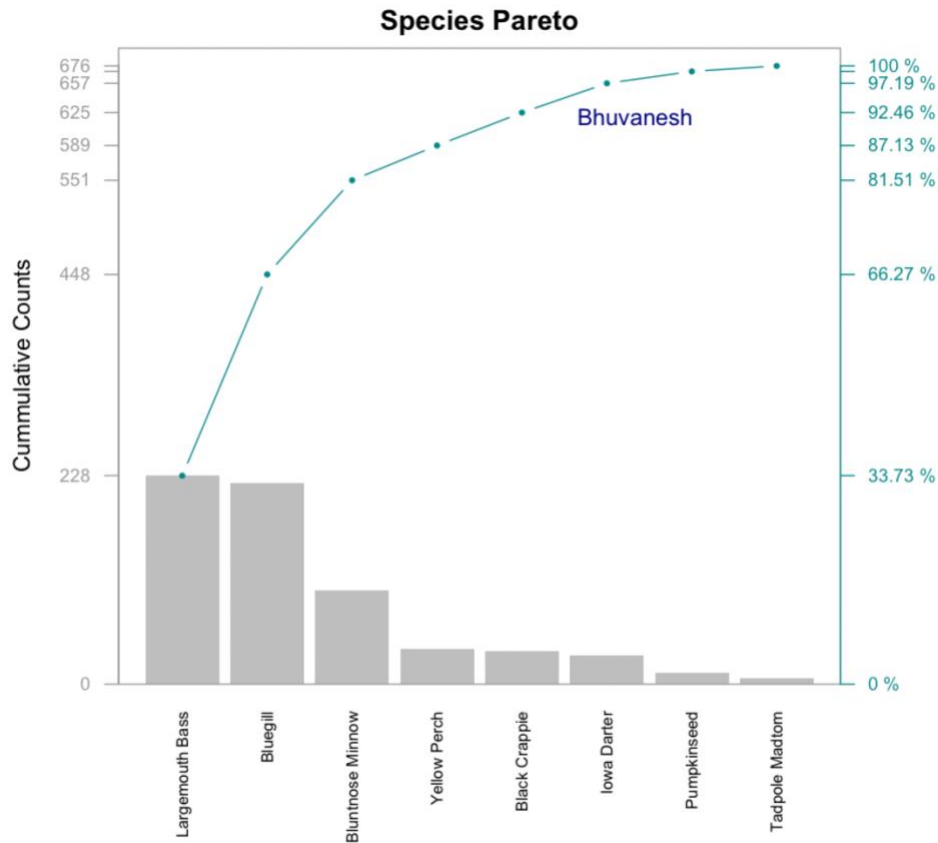
> # Axis font scaled to 80% of nominal

```
> axis(side = 4, at=c(0,d$Cumcounts), labels=paste(c(0,d$CumFreq),"%"),las = 1, col.axis = "cyan4", col = "cyan4", cex.axis=0.8) #add features to axis as mentioned
```



> #Q25 Display the finished Species Pareto Plot (without the star watermarks). Have your last name on the plot

```
> mtext("Bhuvanesh", las=1,
+       at=6,
+       adj = 0,
+       side=3, line=-3, col="navyblue") #to add text inside pareto plot
```



> #Report

> #Descriptive Analysis

> summary(bio)

netID	fishID	species	tl
Min. : 1.00	Min. : 7.0	Length:676	Min. : 27.0
1st Qu.: 13.00	1st Qu.:175.8	Class :character	1st Qu.: 66.0
Median : 37.00	Median :345.5	Mode :character	Median :189.5
Mean : 67.65	Mean :434.2		Mean :186.5
3rd Qu.:109.00	3rd Qu.:695.5		3rd Qu.:295.0
Max. :206.00	Max. :915.0		Max. :429.0
w	tag	scale	
Length:676	Length:676	Mode :logical	
Class :character	Class :character	FALSE:213	

Mode :character Mode :character TRUE :463

> 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 : chr "2.9" "4.5" "5.2" "0.5" ...

\$ tag : chr "" "" "" "" ...

\$ scale : logi FALSE FALSE FALSE FALSE FALSE FALSE ...

> d

Species RelFreq CumFreq Counts Cumcounts

5 Largemouth Bass 33.73 33.73 228 228

2 Bluegill 32.54 66.27 220 448

3 Bluntnose Minnow 15.24 81.51 103 551

8 Yellow Perch 5.62 87.13 38 589

1 Black Crappie 5.33 92.46 36 625

4 Iowa Darter 4.73 97.19 32 657

6 Pumpkinseed 1.92 99.11 13 670

7 Tadpole Madtom 0.89 100.00 6 676

>

> #1. Stacked Bar Chart - Species vs Scale type

> install.packages("ggplot2")

Error in install.packages : Updating loaded packages

> install.packages("ggplot2")

trying URL 'https://cran.rstudio.com/bin/macosx/contrib/4.2/ggplot2_3.4.0.tgz'

Content type 'application/x-gzip' length 4211307 bytes (4.0 MB)

=====

downloaded 4.0 MB

The downloaded binary packages are in

/var/folders/1y/qwg6z9nj78nfkv1gf3qrgts40000gp/T//RtmpnHas9A/downloaded_packages

```
> library(ggplot2)
```

```
> bio <- read.csv2("/Users/devi/Documents/Devi/MPS Analytics/Introduction to Analytics/Module 3/inchBio.csv", sep=",") #to read the database in R
```

```
> 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
4	12	44	Bluegill	38	0.5		FALSE
5	12	50	Bluegill	42	1		FALSE
6	12	65	Bluegill	54	2.1		FALSE
7	12	66	Bluegill	27			FALSE
8	13	68	Bluegill	36	0.5		FALSE
9	13	69	Bluegill	59	2		FALSE
10	13	70	Bluegill	39	0.5		FALSE
11	13	71	Bluegill	34	0.5		FALSE
12	13	73	Bluegill	40	1		FALSE
13	13	74	Bluegill	35	0.5		FALSE
14	13	75	Bluegill	32	1		FALSE
15	13	76	Bluegill	37	0.5		FALSE
16	13	77	Bluegill	38	1		FALSE
17	13	78	Bluegill	69	7		FALSE
18	13	80	Bluegill	39	1		FALSE

19	13	81 Bluegill	37	0.5	FALSE
20	13	82 Bluegill	38	1	FALSE
21	13	83 Bluegill	47		FALSE
22	14	86 Bluegill	33	0.5	FALSE
23	14	87 Bluegill	31	1.5	FALSE
24	14	88 Bluegill	36	1.5	FALSE
25	4	118 Bluegill	150	60	TRUE
26	4	119 Bluegill	193	145	TRUE
27	4	120 Bluegill	185	123	TRUE
28	4	121 Bluegill	152	67	TRUE
29	4	122 Bluegill	160	75	TRUE
30	4	123 Bluegill	185	118	TRUE
31	4	124 Bluegill	170	100	TRUE
32	4	125 Bluegill	135	35	TRUE
33	4	126 Bluegill	183	120	TRUE
34	4	127 Bluegill	168	90	TRUE
35	4	128 Bluegill	165	85	TRUE
36	4	129 Bluegill	178	100	TRUE
37	4	130 Bluegill	193	155	TRUE
38	4	131 Bluegill	193	140	TRUE
39	4	132 Bluegill	201	180	TRUE
40	4	133 Bluegill	203	185	TRUE
41	4	134 Bluegill	99	15	TRUE
42	5	138 Bluegill	135	42	TRUE
43	5	139 Bluegill	38	2	FALSE
44	5	140 Bluegill	41		FALSE
45	5	141 Bluegill	41		FALSE
46	5	142 Bluegill	46		FALSE
47	5	143 Bluegill	165	68	TRUE

48	5	144 Bluegill	43	FALSE
49	5	145 Bluegill	51 4	FALSE
50	5	146 Bluegill	203 184	TRUE
51	5	147 Bluegill	168 98	TRUE
52	5	148 Bluegill	152 62	TRUE
53	5	149 Bluegill	64	FALSE
54	5	150 Bluegill	157 76	TRUE
55	10	151 Bluegill	173 100	TRUE
56	10	152 Bluegill	173 95	TRUE
57	10	153 Bluegill	185 130	TRUE
58	10	154 Bluegill	218 250	TRUE
59	10	155 Bluegill	206 197	TRUE
60	10	156 Bluegill	165 78	TRUE
61	10	157 Bluegill	152 72	TRUE
62	10	158 Bluegill	170 98	TRUE
63	9	161 Bluegill	206 175	TRUE
64	9	162 Bluegill	191 144	TRUE
65	9	163 Bluegill	193 148	TRUE
66	9	164 Bluegill	183 130	TRUE
67	9	165 Bluegill	201 185	TRUE
68	9	166 Bluegill	221 225	TRUE
69	9	167 Bluegill	165 80	FALSE
70	9	168 Bluegill	206 180	TRUE
71	9	169 Bluegill	203 175	TRUE
72	9	170 Bluegill	165	TRUE
73	9	171 Bluegill	193 160	FALSE
74	9	172 Bluegill	173	FALSE
75	6	176 Bluegill	213 200	TRUE
76	6	177 Bluegill	155 74	TRUE

77	6	178 Bluegill	157 62	TRUE
78	6	179 Bluegill	211 220	TRUE
79	6	180 Bluegill	188 149	TRUE
80	6	181 Bluegill	188 139	TRUE
81	6	182 Bluegill	196 132	TRUE
82	6	183 Bluegill	188 139	TRUE
83	6	184 Bluegill	160 73	TRUE
84	6	185 Bluegill	196 120	TRUE
85	6	186 Bluegill	221 242	TRUE
86	6	187 Bluegill	180 130	TRUE
87	6	188 Bluegill	152 70	TRUE
88	6	189 Bluegill	140 40	TRUE
89	6	190 Bluegill	203 170	TRUE
90	6	191 Bluegill	145 52	TRUE
91	6	192 Bluegill	147 32	TRUE
92	11	193 Bluegill	211 218	TRUE
93	11	194 Bluegill	147 60	TRUE
94	11	195 Bluegill	152 70	TRUE
95	17	196 Bluegill	203 192	TRUE
96	17	197 Bluegill	132 31	TRUE
97	17	199 Bluegill	142 59	TRUE
98	20	201 Bluegill	140 54	TRUE
99	15	203 Bluegill	142 40	TRUE
100	15	206 Bluegill	147 30	TRUE
101	15	207 Bluegill	119 20	TRUE
102	16	210 Bluegill	229 280	TRUE
103	16	211 Bluegill	224 260	TRUE
104	16	212 Bluegill	224 260	TRUE
105	16	213 Bluegill	224 240	TRUE

106	16	214 Bluegill	150	60	TRUE
107	16	215 Bluegill	137	60	TRUE
108	21	217 Bluegill	94	14	TRUE
109	21	219 Bluegill	130	38	TRUE
110	26	220 Bluegill	132	49	TRUE
111	26	221 Bluegill	137	41	TRUE
112	23	224 Bluegill	114	20	TRUE
113	27	226 Bluegill	127	20	TRUE
114	27	228 Bluegill	122	20	TRUE
115	28	230 Bluegill	137	50	TRUE
116	28	231 Bluegill	234	280	TRUE
117	37	322 Bluegill	152		TRUE
118	37	356 Bluegill	201		TRUE
119	206	501 Bluegill	38	0.7	FALSE
120	205	502 Bluegill	43	1.4	FALSE
121	205	503 Bluegill	56	1.5	FALSE
122	205	504 Bluegill	53	1.4	FALSE
123	205	505 Bluegill	38	1	FALSE
124	205	506 Bluegill	48	1.8	FALSE
125	205	507 Bluegill	48	1.4	FALSE
126	205	508 Bluegill	36	0.6	FALSE
127	205	509 Bluegill	30	0.3	FALSE
128	205	510 Bluegill	36	0.8	FALSE
129	205	511 Bluegill	51	1.3	FALSE
130	205	512 Bluegill	58	2.4	FALSE
131	205	513 Bluegill	33	0.7	FALSE
132	205	514 Bluegill	38	1	FALSE
133	205	515 Bluegill	33	0.6	FALSE
134	205	516 Bluegill	56	2.8	FALSE

```

135 205 517 Bluegill 33 1.1 FALSE
136 205 518 Bluegill 53 2 FALSE
137 205 519 Bluegill 66 4.5 FALSE
138 205 520 Bluegill 71 4.9 FALSE
139 101 533 Bluegill 213 190 TRUE
140 101 538 Bluegill 216 198 1021 TRUE
141 101 539 Bluegill 216 210 1022 TRUE
142 101 540 Bluegill 231 258 1023 TRUE

```

```
[ reached 'max' / getOption("max.print") -- omitted 534 rows ]
```

```
> par(ask=TRUE)
```

```
> bio$species
```

```

[1] "Bluegill" "Bluegill" "Bluegill" "Bluegill"
[5] "Bluegill" "Bluegill" "Bluegill" "Bluegill"
[9] "Bluegill" "Bluegill" "Bluegill" "Bluegill"
[13] "Bluegill" "Bluegill" "Bluegill" "Bluegill"
[17] "Bluegill" "Bluegill" "Bluegill" "Bluegill"
[21] "Bluegill" "Bluegill" "Bluegill" "Bluegill"
[25] "Bluegill" "Bluegill" "Bluegill" "Bluegill"
[29] "Bluegill" "Bluegill" "Bluegill" "Bluegill"
[33] "Bluegill" "Bluegill" "Bluegill" "Bluegill"
[37] "Bluegill" "Bluegill" "Bluegill" "Bluegill"
[41] "Bluegill" "Bluegill" "Bluegill" "Bluegill"
[45] "Bluegill" "Bluegill" "Bluegill" "Bluegill"
[49] "Bluegill" "Bluegill" "Bluegill" "Bluegill"
[53] "Bluegill" "Bluegill" "Bluegill" "Bluegill"
[57] "Bluegill" "Bluegill" "Bluegill" "Bluegill"
[61] "Bluegill" "Bluegill" "Bluegill" "Bluegill"
[65] "Bluegill" "Bluegill" "Bluegill" "Bluegill"
[69] "Bluegill" "Bluegill" "Bluegill" "Bluegill"

```

[73]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[77]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[81]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[85]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[89]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[93]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[97]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[101]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[105]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[109]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[113]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[117]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[121]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[125]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[129]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[133]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[137]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[141]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[145]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[149]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[153]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[157]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[161]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[165]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[169]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[173]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[177]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[181]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"
[185]	"Bluegill"	"Bluegill"	"Bluegill"	"Bluegill"

[217] "Bluegill" "Bluegill" "Bluegill" "Bluegill"

[301] "Bluntnose Minnow" "Bluntnose Minnow" "Bluntnose Minnow" "Bluntnose Minnow"

[305] "Bluntnose Minnow" "Bluntnose Minnow" "Bluntnose Minnow" "Bluntnose Minnow"

[309] "Bluntnose Minnow" "Bluntnose Minnow" "Bluntnose Minnow" "Bluntnose Minnow"

[313] "Bluntnose Minnow" "Bluntnose Minnow" "Bluntnose Minnow" "Bluntnose Minnow"

[317] "Bluntnose Minnow" "Bluntnose Minnow" "Bluntnose Minnow" "Bluntnose Minnow"

[321] "Bluntnose Minnow" "Bluntnose Minnow" "Bluntnose Minnow" "Iowa Darter"

[325] "Iowa Darter" "Iowa Darter" "Iowa Darter" "Iowa Darter"

[329] "Iowa Darter" "Iowa Darter" "Iowa Darter" "Iowa Darter"

[333] "Iowa Darter" "Iowa Darter" "Iowa Darter" "Iowa Darter"

[337] "Iowa Darter" "Iowa Darter" "Iowa Darter" "Iowa Darter"

[341] "Iowa Darter" "Iowa Darter" "Iowa Darter" "Iowa Darter"

[345] "Iowa Darter" "Iowa Darter" "Iowa Darter" "Iowa Darter"

[349] "Iowa Darter" "Iowa Darter" "Iowa Darter" "Iowa Darter"

[353] "Iowa Darter" "Iowa Darter" "Iowa Darter" "Largemouth Bass"

[357] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"

[361] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"

[365] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"

[369] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"

[373] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"

[377] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"

[381] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"

[385] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"

[389] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"

[393] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"

[397] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"

[401] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"

[405] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"

[409] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"

[413] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"

[417] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"

[illegible]

[537] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"
[541] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"
[545] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"
[549] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"
[553] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"
[557] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"
[561] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"
[565] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"
[569] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"
[573] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"
[577] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Largemouth Bass"
[581] "Largemouth Bass" "Largemouth Bass" "Largemouth Bass" "Pumpkinseed"
[585] "Pumpkinseed" "Pumpkinseed" "Pumpkinseed" "Pumpkinseed"
[589] "Pumpkinseed" "Pumpkinseed" "Pumpkinseed" "Pumpkinseed"
[593] "Pumpkinseed" "Pumpkinseed" "Pumpkinseed" "Pumpkinseed"
[597] "Tadpole Madtom" "Tadpole Madtom" "Tadpole Madtom" "Tadpole Madtom"
[601] "Tadpole Madtom" "Tadpole Madtom" "Yellow Perch" "Yellow Perch"
[605] "Yellow Perch" "Yellow Perch" "Yellow Perch" "Yellow Perch"
[609] "Yellow Perch" "Yellow Perch" "Yellow Perch" "Yellow Perch"
[613] "Yellow Perch" "Yellow Perch" "Yellow Perch" "Yellow Perch"
[617] "Yellow Perch" "Yellow Perch" "Yellow Perch" "Yellow Perch"
[621] "Yellow Perch" "Yellow Perch" "Yellow Perch" "Yellow Perch"
[625] "Yellow Perch" "Yellow Perch" "Yellow Perch" "Yellow Perch"
[629] "Yellow Perch" "Yellow Perch" "Yellow Perch" "Yellow Perch"
[633] "Yellow Perch" "Yellow Perch" "Yellow Perch" "Yellow Perch"
[637] "Yellow Perch" "Yellow Perch" "Yellow Perch" "Yellow Perch"
[641] "Black Crappie" "Black Crappie" "Black Crappie" "Black Crappie"
[645] "Black Crappie" "Black Crappie" "Black Crappie" "Black Crappie"
[649] "Black Crappie" "Black Crappie" "Black Crappie" "Black Crappie"

```

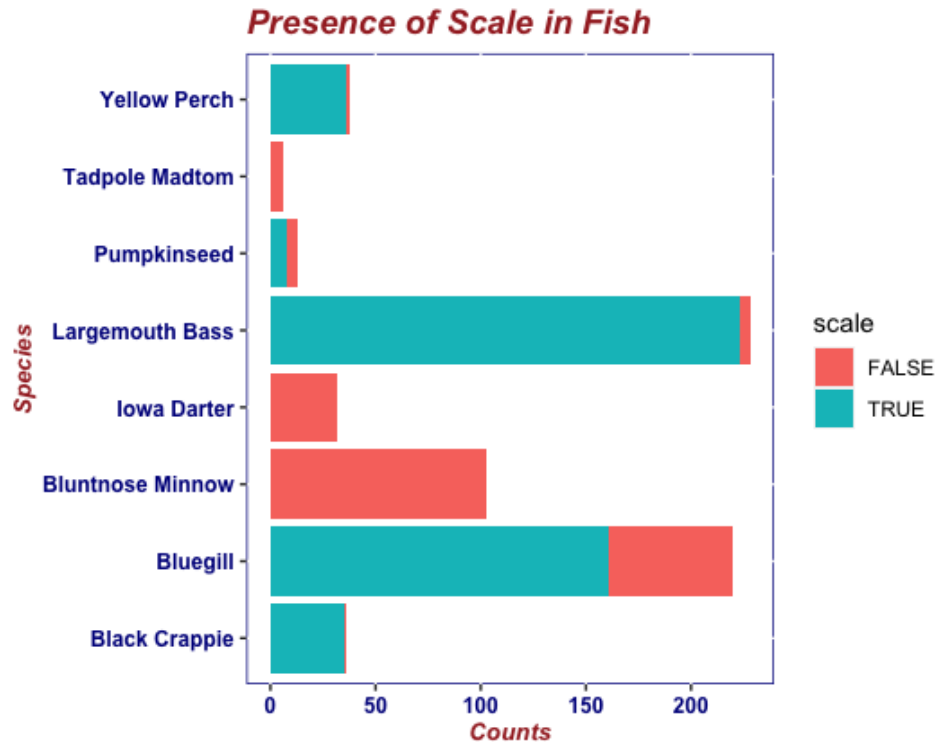
[653] "Black Crappie" "Black Crappie" "Black Crappie" "Black Crappie"
[657] "Black Crappie" "Black Crappie" "Black Crappie" "Black Crappie"
[661] "Black Crappie" "Black Crappie" "Black Crappie" "Black Crappie"
[665] "Black Crappie" "Black Crappie" "Black Crappie" "Black Crappie"
[669] "Black Crappie" "Black Crappie" "Black Crappie" "Black Crappie"
[673] "Black Crappie" "Black Crappie" "Black Crappie" "Black Crappie"

```

```

> ggplot(data = bio, aes(x = species, fill = scale))+
+ geom_bar() +
+ ggtitle("Presence of Scale in Fish") +
+ labs(x="Species",y="Counts") +
+ theme(plot.title=element_text(face="bold.italic",
+                               size="14", color="brown"),
+       axis.title=element_text(face="bold.italic",
+                               size=10, color="brown"),
+       axis.text=element_text(face="bold", size=9,
+                               color="darkblue"),
+       panel.background=element_rect(fill="white",
+                                       color="darkblue"),
+       panel.grid.minor.x=element_blank(),
+       legend.position="right") +
+ coord_flip()

```



> #2:Length vs Scale

```
> bio$scale <- as.factor(bio$scale)
```

```
> bio$scale
```

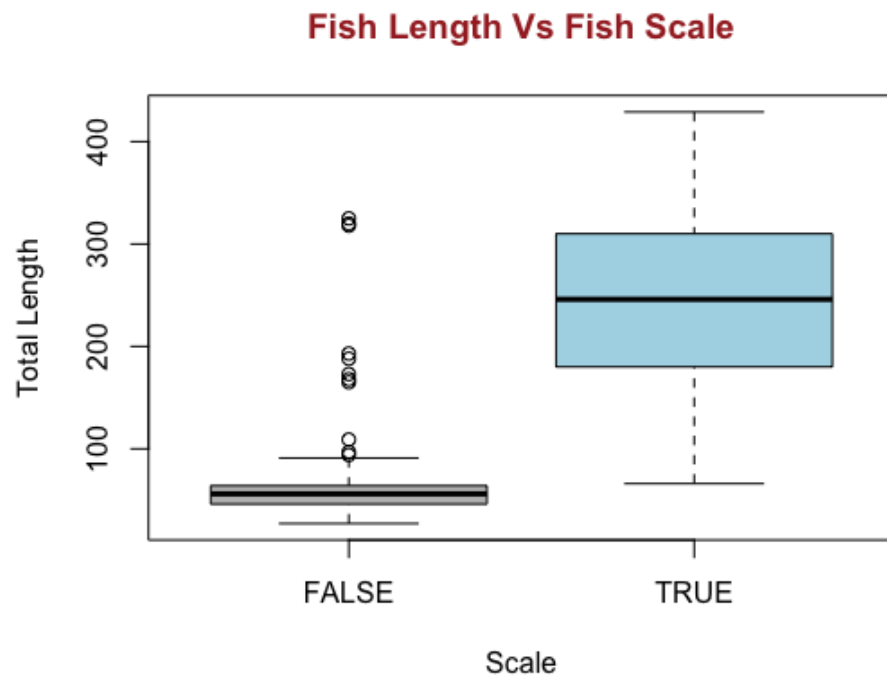
```
[1] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[13] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[25] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[37] TRUE TRUE TRUE TRUE TRUE TRUE FALSE FALSE FALSE FALSE TRUE FALSE
[49] FALSE TRUE TRUE TRUE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[61] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE FALSE TRUE TRUE TRUE
[73] FALSE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[85] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[97] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[109] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE FALSE FALSE
[121] FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE FALSE
[133] FALSE FALSE FALSE FALSE FALSE FALSE TRUE TRUE TRUE TRUE TRUE TRUE
```

[illegible]

[493] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[505] FALSE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[517] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[529] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[541] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[553] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[565] TRUE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[577] TRUE TRUE TRUE TRUE TRUE TRUE FALSE FALSE FALSE FALSE FALSE FALSE
[589] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE FALSE FALSE FALSE FALSE
[601] FALSE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[613] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[625] TRUE TRUE FALSE FALSE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[637] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[649] TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE TRUE
[661] TRUE TRUE TRUE TRUE TRUE TRUE TRUE FALSE TRUE TRUE TRUE TRUE TRUE
[673] TRUE TRUE TRUE TRUE

Levels: FALSE TRUE

```
> plot(bio$scale,bio$tl,  
+   main="Fish Length Vs Fish Scale",  
+   col.main="brown",  
+   ylab="Total Length", xlab="Scale", col=c("gray", "lightblue"))
```



> #3 Scale vs Length of each species

```
> library(lattice) #to split and plot the data based on each species
```

```
> dotplot(bio$scale~bio$tl | bio$species,
```

```
+   main="Type of Species = Fish length Vs Fish Scale",
```

```
+   xlab="Total Length", ylab="Scale")
```

Type of Species = Fish length Vs Fish Scale

