

My Report

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9/17/24

Table of contents

```
library(Hmisc)
```

Warning: package 'Hmisc' was built under R version 4.2.3

Attaching package: 'Hmisc'

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

```
format.pval, units
```

```
library(palmerpenguins)
```

Warning: package 'palmerpenguins' was built under R version 4.2.3

```
library(ggplot2)
```

Warning: package 'ggplot2' was built under R version 4.2.3

```
head(penguins_raw)
```

```
# A tibble: 6 x 17
  studyName `Sample Number` Species      Region Island Stage `Individual ID`
  <chr>          <dbl> <chr>          <chr> <chr> <chr> <chr>
1 PAL0708          1 Adelie Penguin ~ Anvers Torge~ Adul~ N1A1
2 PAL0708          2 Adelie Penguin ~ Anvers Torge~ Adul~ N1A2
3 PAL0708          3 Adelie Penguin ~ Anvers Torge~ Adul~ N2A1
4 PAL0708          4 Adelie Penguin ~ Anvers Torge~ Adul~ N2A2
5 PAL0708          5 Adelie Penguin ~ Anvers Torge~ Adul~ N3A1
6 PAL0708          6 Adelie Penguin ~ Anvers Torge~ Adul~ N3A2
# i 10 more variables: `Clutch Completion` <chr>, `Date Egg` <date>,
#   `Culmen Length (mm)` <dbl>, `Culmen Depth (mm)` <dbl>,
#   `Flipper Length (mm)` <dbl>, `Body Mass (g)` <dbl>, Sex <chr>,
#   `Delta 15 N (o/oo)` <dbl>, `Delta 13 C (o/oo)` <dbl>, Comments <chr>
```

```
summary(penguins_raw)
```

studyName	Sample Number	Species	Region
Length:344	Min. : 1.00	Length:344	Length:344
Class :character	1st Qu.: 29.00	Class :character	Class :character
Mode :character	Median : 58.00	Mode :character	Mode :character
	Mean : 63.15		
	3rd Qu.: 95.25		
	Max. :152.00		

Island	Stage	Individual ID	Clutch Completion
Length:344	Length:344	Length:344	Length:344
Class :character	Class :character	Class :character	Class :character
Mode :character	Mode :character	Mode :character	Mode :character

Date Egg	Culmen Length (mm)	Culmen Depth (mm)	Flipper Length (mm)
Min. :2007-11-09	Min. :32.10	Min. :13.10	Min. :172.0
1st Qu.:2007-11-28	1st Qu.:39.23	1st Qu.:15.60	1st Qu.:190.0
Median :2008-11-09	Median :44.45	Median :17.30	Median :197.0
Mean :2008-11-27	Mean :43.92	Mean :17.15	Mean :200.9
3rd Qu.:2009-11-16	3rd Qu.:48.50	3rd Qu.:18.70	3rd Qu.:213.0
Max. :2009-12-01	Max. :59.60	Max. :21.50	Max. :231.0
	NA's :2	NA's :2	NA's :2
Body Mass (g)	Sex	Delta 15 N (o/oo)	Delta 13 C (o/oo)

Min. :2700	Length:344	Min. : 7.632	Min. : -27.02
1st Qu.:3550	Class :character	1st Qu.: 8.300	1st Qu.: -26.32
Median :4050	Mode :character	Median : 8.652	Median : -25.83
Mean :4202		Mean : 8.733	Mean : -25.69
3rd Qu.:4750		3rd Qu.: 9.172	3rd Qu.: -25.06
Max. :6300		Max. :10.025	Max. : -23.79
NA's :2		NA's :14	NA's :13

Comments
 Length:344
 Class :character
 Mode :character

```
str(penguins_raw)
```

```

tibble [344 x 17] (S3: tbl_df/tbl/data.frame)
 $ studyName      : chr [1:344] "PAL0708" "PAL0708" "PAL0708" "PAL0708" ...
 $ Sample Number  : num [1:344] 1 2 3 4 5 6 7 8 9 10 ...
 $ Species        : chr [1:344] "Adelie Penguin (Pygoscelis adeliae)" "Adelie Penguin (Pygoscelis adeliae)" ...
 $ Region         : chr [1:344] "Anvers" "Anvers" "Anvers" "Anvers" ...
 $ Island         : chr [1:344] "Torgersen" "Torgersen" "Torgersen" "Torgersen" ...
 $ Stage          : chr [1:344] "Adult, 1 Egg Stage" "Adult, 1 Egg Stage" "Adult, 1 Egg Stage" ...
 $ Individual ID   : chr [1:344] "N1A1" "N1A2" "N2A1" "N2A2" ...
 $ Clutch Completion : chr [1:344] "Yes" "Yes" "Yes" "Yes" ...
 $ Date Egg       : Date[1:344], format: "2007-11-11" "2007-11-11" ...
 $ Culmen Length (mm) : num [1:344] 39.1 39.5 40.3 NA 36.7 39.3 38.9 39.2 34.1 42 ...
 $ Culmen Depth (mm) : num [1:344] 18.7 17.4 18 NA 19.3 20.6 17.8 19.6 18.1 20.2 ...
 $ Flipper Length (mm): num [1:344] 181 186 195 NA 193 190 181 195 193 190 ...
 $ Body Mass (g)     : num [1:344] 3750 3800 3250 NA 3450 ...
 $ Sex             : chr [1:344] "MALE" "FEMALE" "FEMALE" NA ...
 $ Delta 15 N (o/oo) : num [1:344] NA 8.95 8.37 NA 8.77 ...
 $ Delta 13 C (o/oo) : num [1:344] NA -24.7 -25.3 NA -25.3 ...
 $ Comments         : chr [1:344] "Not enough blood for isotopes." NA NA "Adult not sampled" ...
- attr(*, "spec")=List of 3
 ..$ cols      :List of 17
 .. ..$ studyName      : list()
 .. ..$- attr(*, "class")= chr [1:2] "collector_character" "collector"
 .. ..$ Sample Number  : list()
  
```

```

.. .. .- attr(*, "class")= chr [1:2] "collector_double" "collector"
.. ..$ Species           : list()
.. .. .- attr(*, "class")= chr [1:2] "collector_character" "collector"
.. ..$ Region            : list()
.. .. .- attr(*, "class")= chr [1:2] "collector_character" "collector"
.. ..$ Island             : list()
.. .. .- attr(*, "class")= chr [1:2] "collector_character" "collector"
.. ..$ Stage              : list()
.. .. .- attr(*, "class")= chr [1:2] "collector_character" "collector"
.. ..$ Individual ID      : list()
.. .. .- attr(*, "class")= chr [1:2] "collector_character" "collector"
.. ..$ Clutch Completion  : list()
.. .. .- attr(*, "class")= chr [1:2] "collector_character" "collector"
.. ..$ Date Egg           :List of 1
.. .. .- attr(*, "class")= chr [1:2] "collector_double" "collector"
.. ..$ Culmen Length (mm) : list()
.. .. .- attr(*, "class")= chr [1:2] "collector_double" "collector"
.. ..$ Culmen Depth (mm)  : list()
.. .. .- attr(*, "class")= chr [1:2] "collector_double" "collector"
.. ..$ Flipper Length (mm): list()
.. .. .- attr(*, "class")= chr [1:2] "collector_double" "collector"
.. ..$ Body Mass (g)       : list()
.. .. .- attr(*, "class")= chr [1:2] "collector_double" "collector"
.. ..$ Sex                 : list()
.. .. .- attr(*, "class")= chr [1:2] "collector_character" "collector"
.. ..$ Delta 15 N (o/oo)   : list()
.. .. .- attr(*, "class")= chr [1:2] "collector_double" "collector"
.. ..$ Delta 13 C (o/oo)   : list()
.. .. .- attr(*, "class")= chr [1:2] "collector_double" "collector"
.. ..$ Comments            : list()
.. .. .- attr(*, "class")= chr [1:2] "collector_character" "collector"
..$ default: list()
.. ..- attr(*, "class")= chr [1:2] "collector_guess" "collector"
..$ skip      : num 1
..- attr(*, "class")= chr "col_spec"

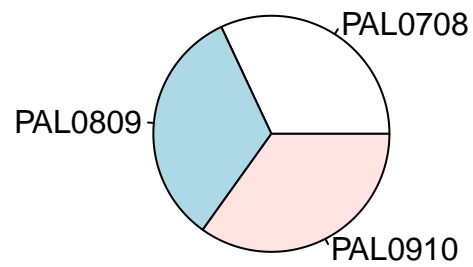
```

```

pie(table(c(penguins_raw$studyName)), main = "StudyName Pie Chart")

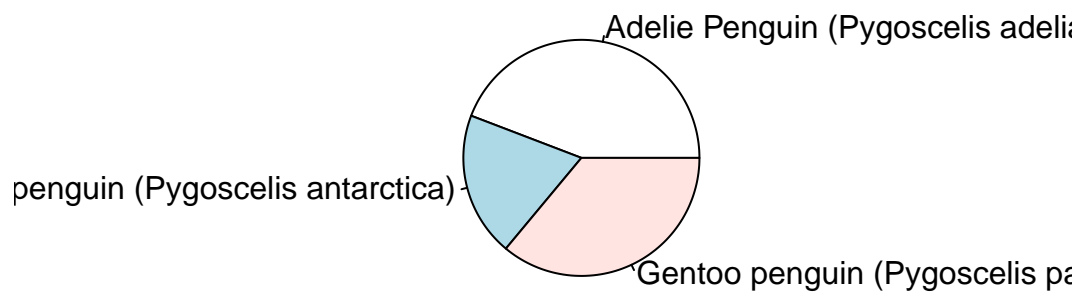
```

StudyName Pie Chart



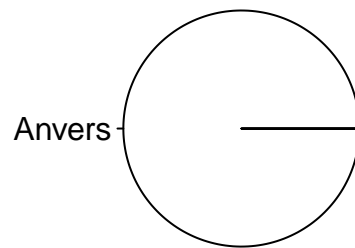
```
pie(table(c(penguins_raw$Species)), main = "Species Pie Chart")
```

Species Pie Chart



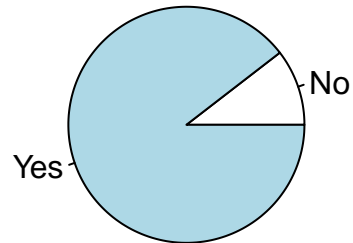
```
pie(table(c(penguins_raw$Region)), main = "Region Pie Chart")
```

Region Pie Chart



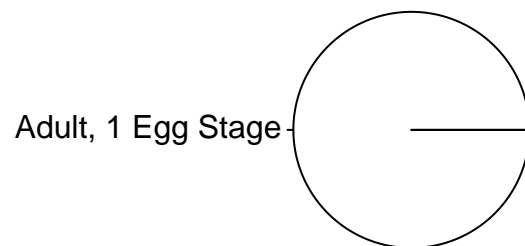
```
pie(table(c(penguins_raw$`Clutch Completion`)), main = "Clutch Completion Pie Chart")
```

Clutch Completion Pie Chart

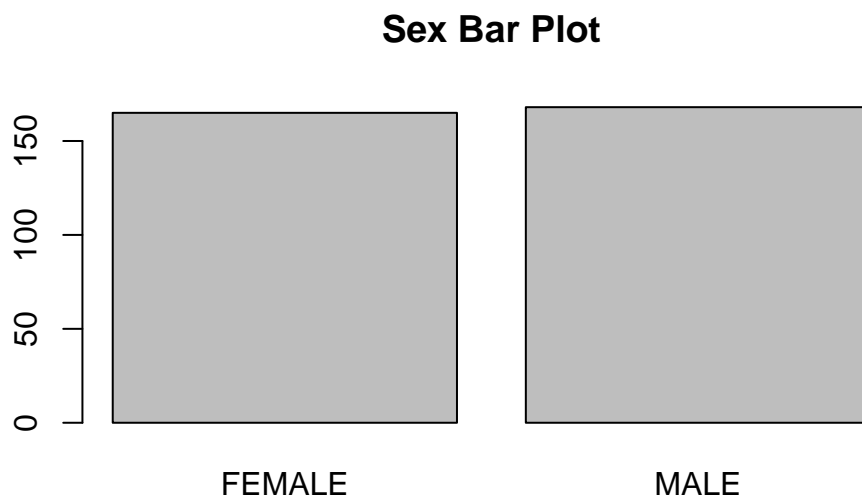


```
pie(table(c(penguins_raw$Stage)), main = "Stage Pie Chart")
```

Stage Pie Chart

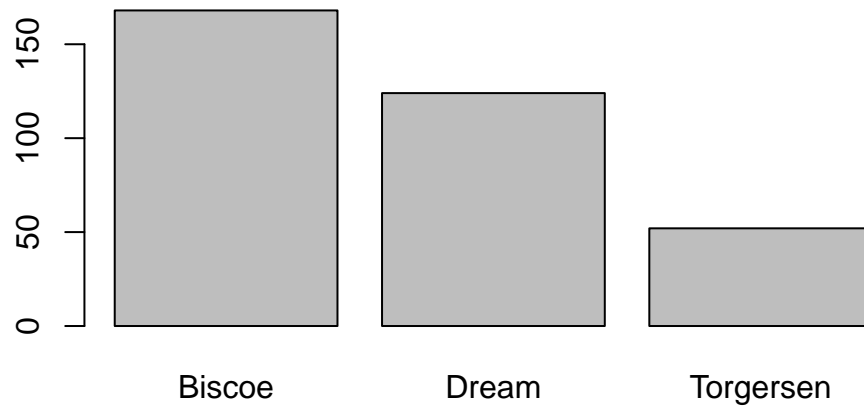


```
barplot(table(c(penguins_raw$Sex)), main = "Sex Bar Plot")
```



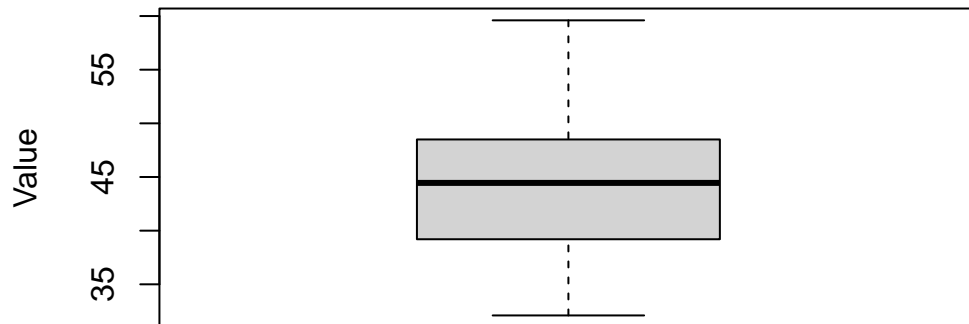
```
barplot(table(c(penguins_raw$Island)), main = "Island Bar Plot")
```


Island Bar Plot



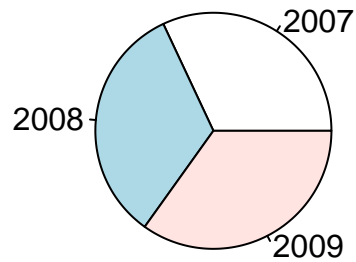
```
boxplot(penguins_raw$`Culmen Length (mm)`, main = "Culmen Length of Boxplot", ylab = "Value")
```

Culmen Length of Boxplot



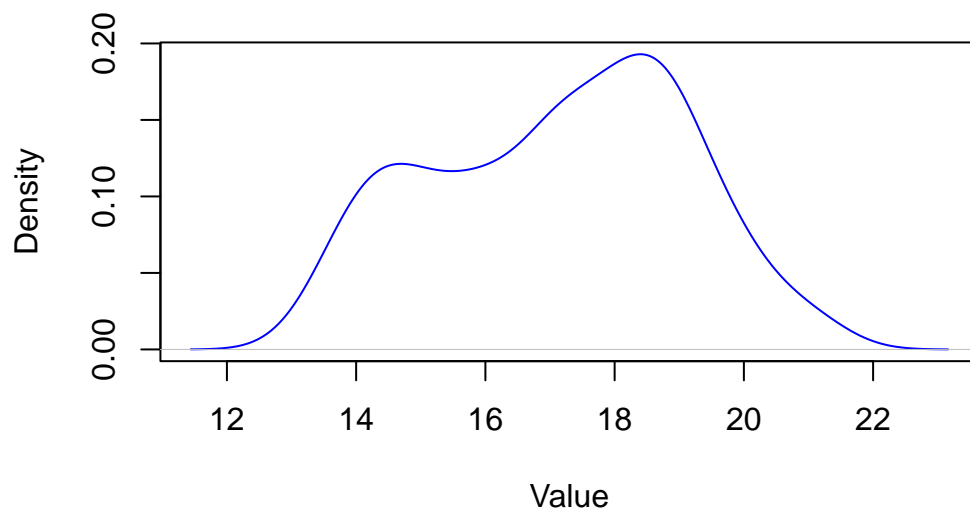
```
x <- penguins_raw$`Date Egg`  
y <- format(x, "%Y")  
pie(table(c(as.numeric(y)))), main = "Year of Date Egg Pie Chart")
```

Year of Date Egg Pie Chart



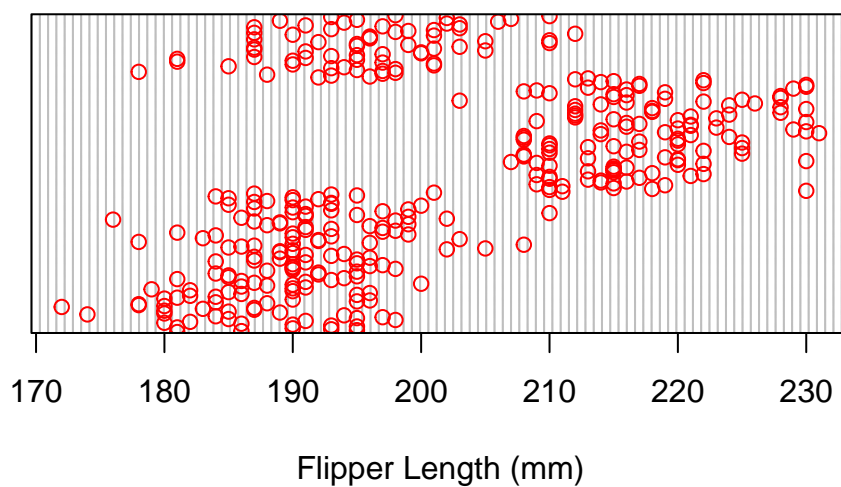
```
nona <- na.omit(penguins_raw$`Culmen Depth (mm)`)  
plot(density(nona), main = "Culmen Depth of Density Plot", xlab = "Value", col = "blue")
```

Culmen Depth of Density Plot



```
nona1 <- na.omit(penguins_raw$`Flipper Length (mm)`)  
dotchart(x=as.numeric(nona1), col = "red", xlab = "Flipper Length (mm)", main = "Flipper L
```

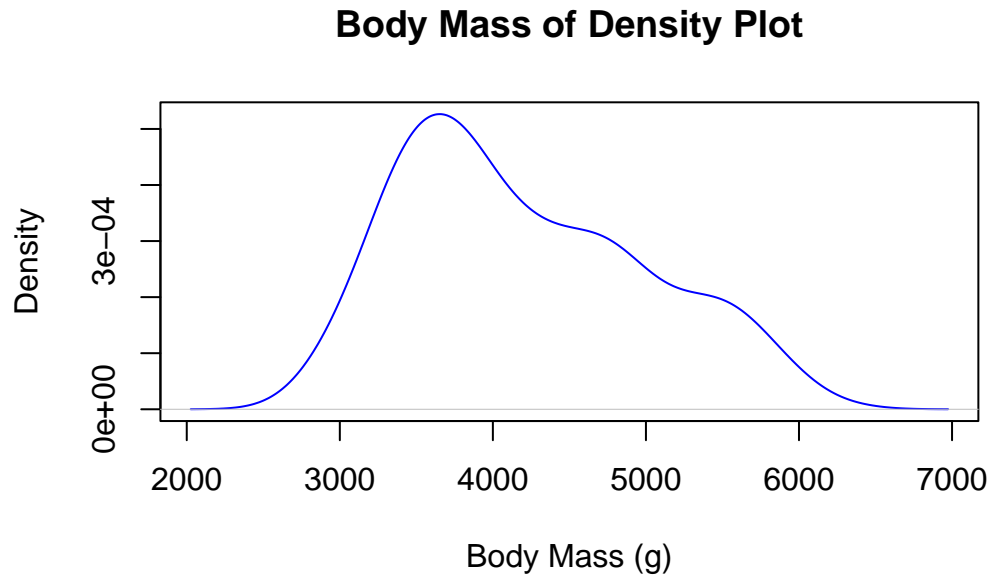
Flipper Length of Dot Chart



```

nona2 <- na.omit(penguins_raw$`Body Mass (g)`)
plot(density(nona2), main = "Body Mass of Density Plot", xlab = "Body Mass (g)", col = "blue")

```

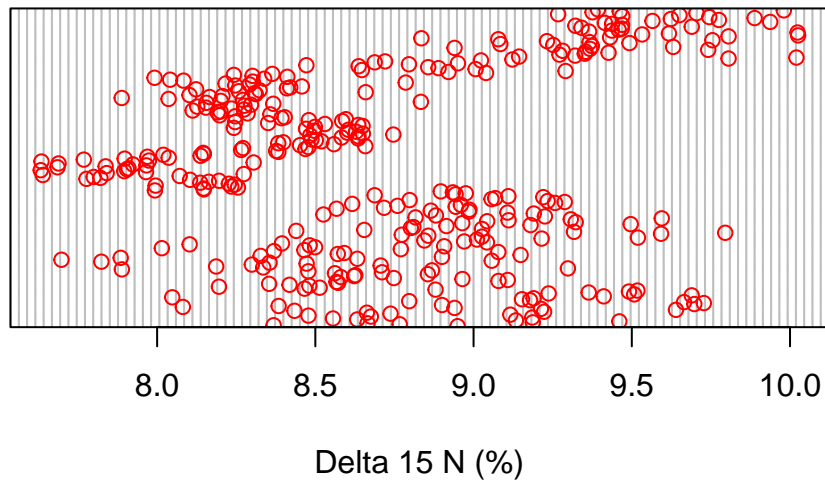


```

nona3 <- na.omit(penguins_raw$`Delta 15 N (o/oo)`)
dotchart(x=as.numeric(nona3), col = "red", xlab = "Delta 15 N (%)", main = "Delta 15 N of")

```

Delta 15 N of Dot Chart



```
nona4 <- na.omit(penguins_raw$`Delta 13 C (o/oo)`)  
dotchart(x=as.numeric(nona4), col = "red", xlab = "Delta 13 C (%)", main = "Delta 13 C of
```

Delta 13 C of Dot Chart

