

Summary report for the penguins_raw dataset

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2024-09-15

Table of contents

Statistical Thinking	1
Summary Staistic	1
Data Structure	5
Missing Values	6
Descriptive Statistics	7
Data Visualization	10

Statistical Thinking

Reference: <https://www.fharrell.com/post/rflow/>

Summary Staistic

```
library(Hmisc)
```

Warning: 'Hmisc' R 4.3.3

```
'Hmisc'
```

```
'package:base':
```

```
format.pval, units
```

```
library(palmerpenguins)
latex(describe(penguins_raw), file = "", caption.placement = "top")
```

penguins_raw
17 Variables 344 Observations

studyName

n	missing	distinct
344	0	3

Value	PAL0708	PAL0809	PAL0910
Frequency	110	114	120
Proportion	0.320	0.331	0.349

Sample Number

n	missing	distinct	Info	Mean	Gmd	.05	.10	.25	.50	.75	.90	.95
344	0	152	1	63.15	46.35	6.15	12.00	29.00	58.00	95.25	121.00	134.85

lowest : 1 2 3 4 5, highest: 148 149 150 151 152

Species

n	missing	distinct
344	0	3

Value	Adelie Penguin (Pygoscelis adeliae)	Chinstrap penguin (Pygoscelis antarctica)
Frequency	152	68
Proportion	0.442	0.198

Value	Gentoo penguin (Pygoscelis papua)
Frequency	124
Proportion	0.360

Region

n	missing	distinct	value
344	0	1	Anvers

Value	Anvers
Frequency	344
Proportion	1

Island

n missing distinct
344 0 3

Value	Biscoe	Dream	Torgersen
Frequency	168	124	52
Proportion	0.488	0.360	0.151

Stage

n missing distinct value
344 0 1 Adult, 1 Egg Stage

Value	Adult, 1 Egg Stage
Frequency	344
Proportion	1

Individual ID

n missing distinct
344 0 190

lowest : N100A1 N100A2 N10A1 N10A2 N11A1 , highest: N98A2 N99A1 N99A2 N9A1 N9A2

Clutch Completion

n missing distinct
344 0 2

Value	No	Yes
Frequency	36	308
Proportion	0.105	0.895

Date Egg

.....

n	missing	distinct	Info	Mean	Gmd	.05	.10
344	0	50	0.999	2008-11-27	328	2007-11-12	2007-11-16
.25	.50	.75	.90	.95			
2007-11-28	2008-11-09	2009-11-16	2009-11-22	2009-11-26			

lowest : 2007-11-09 2007-11-10 2007-11-11 2007-11-12 2007-11-13
highest: 2009-11-22 2009-11-23 2009-11-25 2009-11-27 2009-12-01

Culmen Length (mm)

.....

n	missing	distinct	Info	Mean	Gmd	.05	.10	.25	.50	.75	.90	.95
342	2	164	1	43.92	6.274	35.70	36.60	39.23	44.45	48.50	50.80	51.99

lowest : 32.1 33.1 33.5 34 34.1, highest: 55.1 55.8 55.9 58 59.6

Culmen Depth (mm)

n	missing	distinct	Info	Mean	Gmd	.05	.10	.25	.50	.75	.90	.95
342	2	80	1	17.15	2.267	13.9	14.3	15.6	17.3	18.7	19.5	20.0

lowest : 13.1 13.2 13.3 13.4 13.5, highest: 20.7 20.8 21.1 21.2 21.5

Flipper Length (mm)

n	missing	distinct	Info	Mean	Gmd	.05	.10	.25	.50	.75	.90	.95
342	2	55	0.999	200.9	16.03	181.0	185.0	190.0	197.0	213.0	220.9	225.0

lowest : 172 174 176 178 179, highest: 226 228 229 230 231

Body Mass (g)

n	missing	distinct	Info	Mean	Gmd	.05	.10	.25	.50	.75	.90	.95
342	2	94	1	4202	911.8	3150	3300	3550	4050	4750	5400	5650

lowest : 2700 2850 2900 2925 2975, highest: 5850 5950 6000 6050 6300

Sex

n	missing	distinct
333	11	2

Value	FEMALE	MALE
Frequency	165	168
Proportion	0.495	0.505

Δ 15 N (o/oo):

n	missing	distinct	Info	Mean	Gmd	.05	.10	.25	.50	.75	.90	.95
330	14	330	1	8.733	0.6323	7.897	8.047	8.300	8.652	9.172	9.491	9.689

lowest : 7.6322 7.63452 7.63884 7.68528 7.6887 , highest: 9.93727 9.98044 10.0202 10.0237 10.0254

Δ 13 C (o/oo):

n	missing	distinct	Info	Mean	Gmd	.05	.10	.25	.50	.75	.90	.95
331	13	331	1	-25.69	0.9093	-26.79	-26.69	-26.32	-25.83	-25.06	-24.53	-24.36

lowest : -27.0185 -26.9547 -26.8964 -26.8648 -26.8635, highest: -24.1657 -24.1026 -23.9031 -23.8902 -23.7877

Comments

n	missing	distinct
54	290	10

lowest : Adult not sampled.
highest: No blood sample obtained.

Adult not sampled. Nest never observed with ful
No delta15N data received from lab.

Data Structure

```
library(table1)
library(palmerpenguins)
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
.. ..$ format: chr ""
.. .. - attr(*, "class")= chr [1:2] "collector_date" "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"

```

Missing Values

```

library(Hmisc)
library(DataExplorer)

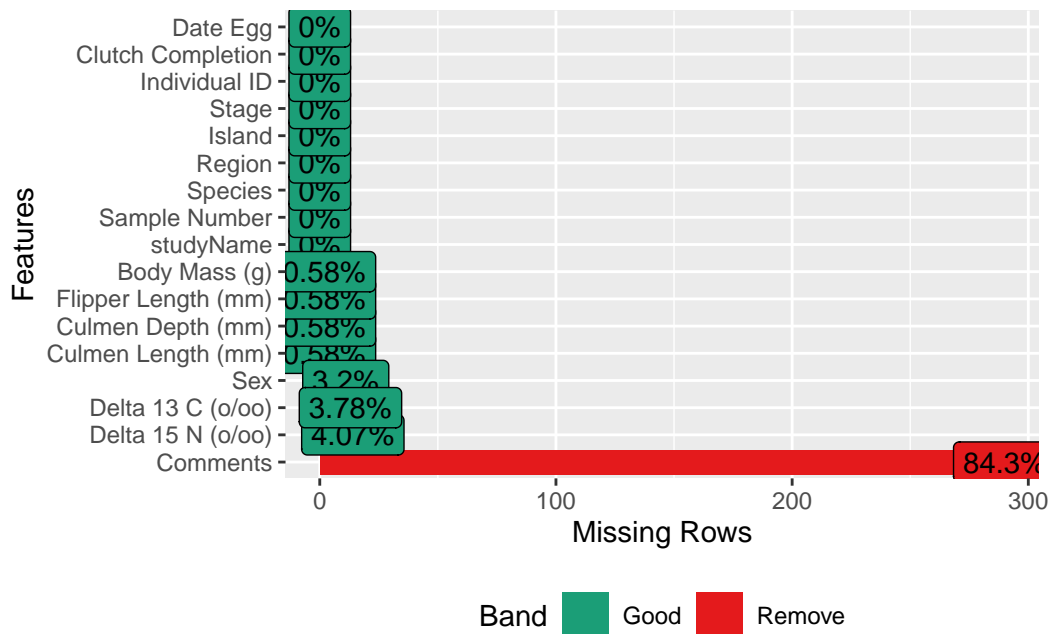
```

Warning: 'DataExplorer' R 4.3.2

```

plot_missing(penguins_raw)

```



Descriptive Statistics

Summary Statistics for Numeric Variables

```
library(dplyr)
```

```
'dplyr'
```

```
'package:Hmisc':
```

```
src, summarize
```

```
'package:stats':
```

```
filter, lag
```

```
'package:base':
```

```
intersect, setdiff, setequal, union
```

```

numeric_vars <- data.frame(Variable_Name = character(), stringsAsFactors = FALSE)

for (i in 1:ncol(penguins_raw)) {
  if (is.numeric(penguins_raw[[i]])) {
    numeric_vars <- rbind(numeric_vars,
                          data.frame(Variable_Name = colnames(penguins_raw)[i],
                                    stringsAsFactors = FALSE))
  }
}

print(numeric_vars)

```

```

      Variable_Name
1      Sample Number
2 Culmen Length (mm)
3 Culmen Depth (mm)
4 Flipper Length (mm)
5      Body Mass (g)
6 Delta 15 N (o/oo)
7 Delta 13 C (o/oo)

```

```

library(dplyr)
library(knitr)

calculate_stats <- function(x) {
  data.frame(
    Mean = mean(x, na.rm = TRUE),
    Median = median(x, na.rm = TRUE),
    SD = sd(x, na.rm = TRUE),
    Min = min(x, na.rm = TRUE),
    Max = max(x, na.rm = TRUE)
  )
}

all_stats <- data.frame(Variable = character(),
                        Mean = numeric(),
                        Median = numeric(),
                        SD = numeric(),
                        Min = numeric(),
                        Max = numeric(),
                        stringsAsFactors = FALSE)

```



```

for (var in numeric_vars$Variable_Name) {
  stats <- calculate_stats(penguins_raw[[var]])
  stats <- cbind(Variable = var, stats)
  all_stats <- rbind(all_stats, stats)
}

print(kable(all_stats, caption = "Summary Statistics for Numeric Variables"))

```

Table: Summary Statistics for Numeric Variables

Variable	Mean	Median	SD	Min	Max
Sample Number	63.151163	58.000000	40.4301990	1.00000	152.00000
Culmen Length (mm)	43.921930	44.450000	5.4595837	32.10000	59.60000
Culmen Depth (mm)	17.151170	17.300000	1.9747932	13.10000	21.50000
Flipper Length (mm)	200.915205	197.000000	14.0617137	172.00000	231.00000
Body Mass (g)	4201.754386	4050.000000	801.9545357	2700.00000	6300.00000
Delta 15 N (o/oo)	8.733382	8.652405	0.5517703	7.63220	10.02544
Delta 13 C (o/oo)	-25.686291	-25.833520	0.7939612	-27.01854	-23.78767

```

calculate_stats <- function(x) {
  data.frame(
    Q25 = quantile(x, 0.25, na.rm = TRUE),
    Q50 = quantile(x, 0.50, na.rm = TRUE),
    Q75 = quantile(x, 0.75, na.rm = TRUE),
    IQR = IQR(x, na.rm = TRUE)
  )
}

all_stats <- data.frame(Variable = character(),
  Q25 = numeric(),
  Q50 = numeric(),
  Q75 = numeric(),
  IQR = numeric(),
  stringsAsFactors = FALSE)

for (var in numeric_vars$Variable_Name) {
  stats <- calculate_stats(penguins_raw[[var]])
  stats <- cbind(Variable = var, stats)
  all_stats <- rbind(all_stats, stats)
}

```

```
}
```

```
print(all_stats)
```

	Variable	Q25	Q50	Q75	IQR
25%	Sample Number	29.00000	58.000000	95.250000	66.2500000
25%1	Culmen Length (mm)	39.22500	44.450000	48.500000	9.2750000
25%2	Culmen Depth (mm)	15.60000	17.300000	18.700000	3.1000000
25%3	Flipper Length (mm)	190.00000	197.000000	213.000000	23.0000000
25%4	Body Mass (g)	3550.00000	4050.000000	4750.000000	1200.0000000
25%5	Delta 15 N (o/oo)	8.29989	8.652405	9.172123	0.8722325
25%6	Delta 13 C (o/oo)	-26.32030	-25.833520	-25.062050	1.2582550

Data Visualization

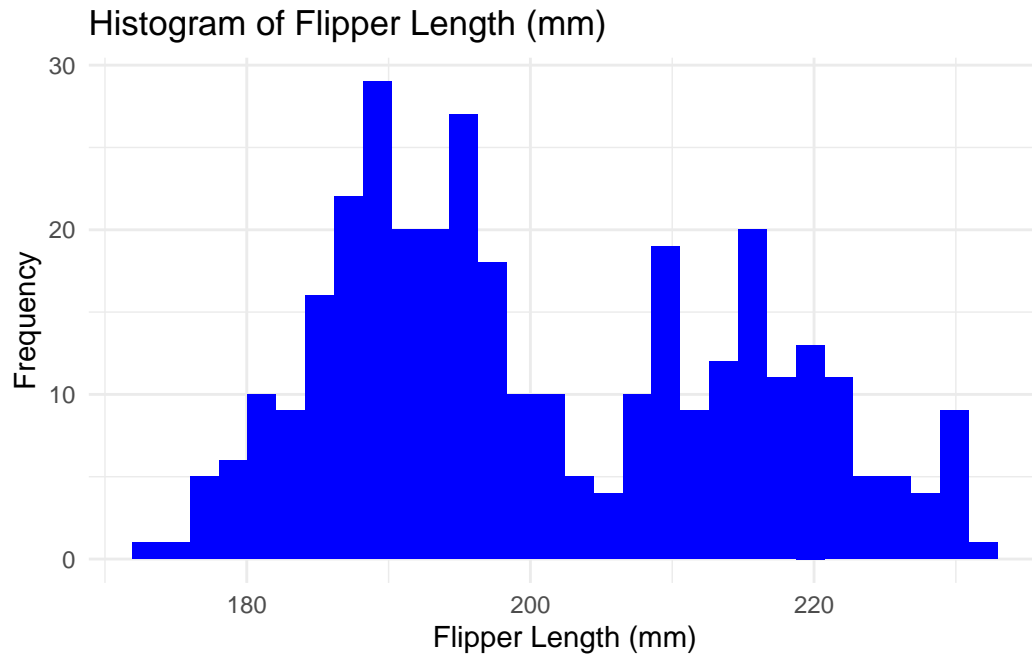
1.Histograms

```
library(ggplot2)

ggplot(penguins_raw, aes(x = `Flipper Length (mm)`) +
  geom_histogram(fill = "blue") +
  labs(title = "Histogram of Flipper Length (mm)",
        x = "Flipper Length (mm)", y = "Frequency") +
  theme_minimal()
```

``stat_bin()`` using ``bins = 30``. Pick better value with ``binwidth``.

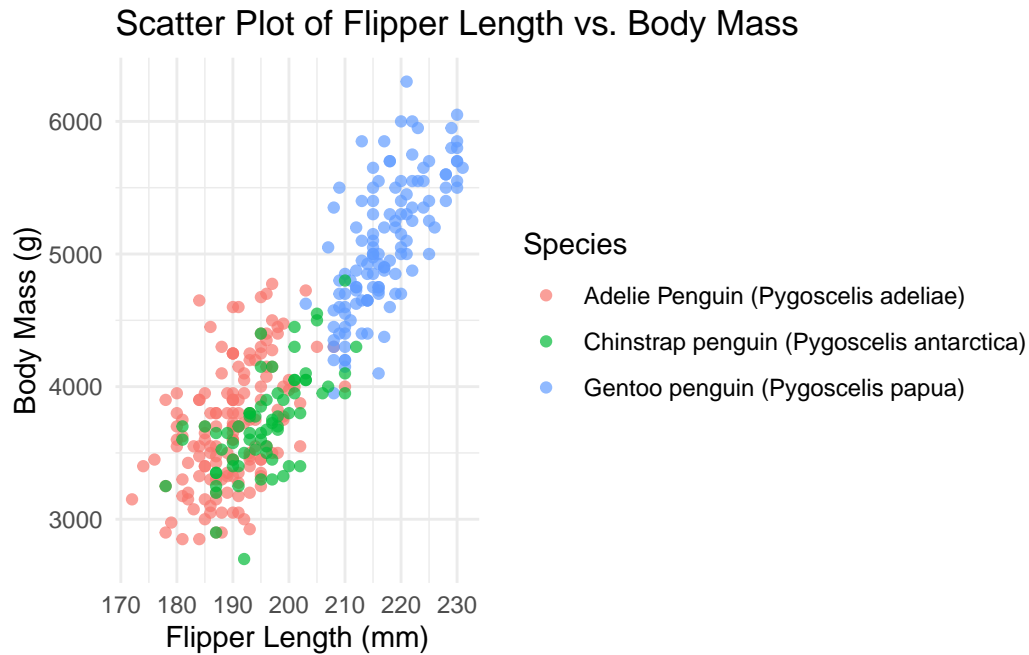
Warning: Removed 2 rows containing non-finite values (``stat_bin()``).



2.Scatter Plots

```
ggplot(penguins_raw, aes(x = `Flipper Length (mm)`, y = `Body Mass (g)`) +  
  geom_point(aes(color = Species), alpha = 0.7) +  
  labs(title = "Scatter Plot of Flipper Length vs. Body Mass", x = "Flipper Length (mm)", y =  
  theme_minimal()
```

Warning: Removed 2 rows containing missing values (`geom_point()`).



3. Violin Plots

```
ggplot(penguins_raw, aes(x = Species, y = `Flipper Length (mm)`, fill = Species)) +
  geom_violin() +
  labs(title = "Violin Plot of Flipper Length by Species",
       x = "Species",
       y = "Flipper Length (mm)") +
  scale_x_discrete(labels = c("Adelie Penguin (Pygoscelis adeliae)" = "Adelie", "Chinstrap penguin (Pygoscelis antarctica)" = "Chinstrap", "Gentoo penguin (Pygoscelis papua)" = "Gentoo")) +
  theme_minimal()
```

Warning: Removed 2 rows containing non-finite values (`stat_ydensity()`).

Violin Plot of Flipper Length by Species

