HW1

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2024-09-17

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<pre>library(palmerpenguins) library(dplyr) library(ggplot2) library(Hmisc) theme_set(theme_minimal())</pre>	

Summary Staistic

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

penguins_raw 17 Variables 344 Observations

study Namedistinct 3 missing 0 344
 Value
 PAL0708
 PAL0809
 PAL0910

 Frequency
 110
 114
 120

 Proportion
 0.320
 0.331
 0.349
 Sample Number Info 1 .05 6.15 missing 0 distinct Mean 63.15 Gmd .10 12.00 .25 29.00 .50 58.00 .75 95.25 .90 121.00 n 344 152 46.35 lowest: 1 2 3 4 5, highest: 148 149 150 151 152 Species distinct 3 n 344 missing 0 Adelie Penguin (Pygoscelis adeliae) Chinstrap penguin (Pygoscelis antarctica) \$152\$Value Frequency Proportion 0.442 0.198 Value Gentoo penguin (Pygoscelis papua) Frequency 0.360 Proportion Region missing 0 distinct value 344 Anvers Value Frequency Proportion Island 1 n 344 missing n distinct Value Biscoe Dream Torgersen Frequency 168 124 52 0.488 0.360 0.151 Proportion Stage missing 0 distinct value 344 Adult, 1 Egg Stage Value Adult, 1 Egg Stage Frequency Proportion

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

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

randarahimitatahannaanitainir

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
```

distinct missing 333

Value FEMALE MALE Frequency 165 168 Proportion 0.495 0.505

Δ 15 N (o/oo):

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

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):

.

distinct 331 Gmd 0.9093 .05 -26.79 .10 -26.69 Info Mean -25.69 .75 -25.06

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

Comments

missing 290 n 54 distinct

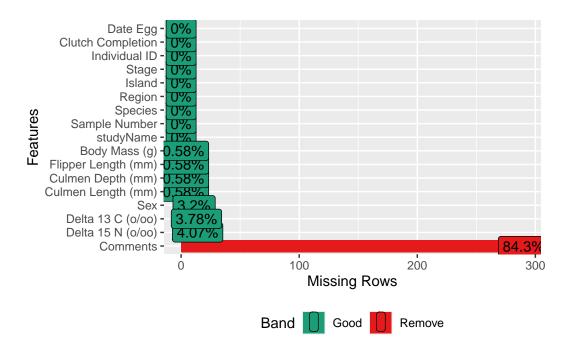
lowest : Adult not sampled.

highest: No blood sample obtained.

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

Missing Values

library(Hmisc) library(DataExplorer) plot_missing(penguins_raw)



Note that the variable "Comment" is additional information for certain situations causing the missing values, we can just ignore it.

We also notice that missing values can be roughly categorized into three situations as follows:

- 1. Missing body measurements: includes culmen length, culmen depth, flipper length and body mass.
- 2. Missing blood isotope measurement: missing delta 15 N or both delta 15 N and delta 13 C.
- 3. Missing gender info.

When situation 1 occurs, situation 2 and 3 will also occur. (Comment: Adult not sampled.)

```
mypenguins <- penguins_raw[,-17]</pre>
```

Male v.s.Female: Body Measurement

Table1

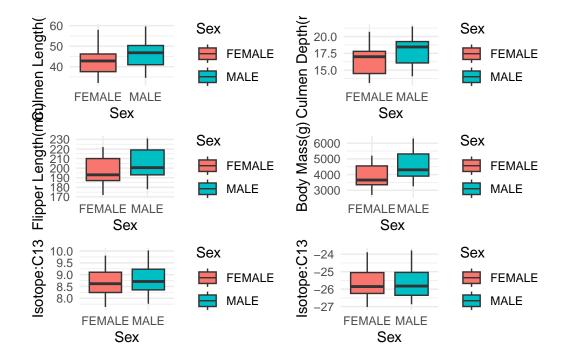
	FEMALE	MALE	Overall
	(N=165)	(N=168)	(N=333)
Culmen_Length			
Mean (SD)	42.1 (4.90)	45.9 (5.37)	44.0 (5.47)
Median [Min,	42.8 [32.1, 58.0]	46.8 [34.6, 59.6]	44.5 [32.1, 59.6]
Max]			
Culmen_Depth			
Mean (SD)	16.4 (1.80)	17.9 (1.86)	17.2 (1.97)
Median [Min,	17.0 [13.1, 20.7]	18.5 [14.1, 21.5]	17.3 [13.1, 21.5]
Max]			
Flipper_Length			
Mean (SD)	197 (12.5)	205 (14.5)	201 (14.0)
Median [Min,	193 [172, 222]	201 [178, 231]	197 [172, 231]
Max]			
Body_Mass			
Mean (SD)	3860 (666)	4550 (788)	4210 (805)
Median [Min,	3650 [2700, 5200]	4300 [3250, 6300]	4050 [2700, 6300]
Max]			
Delta_15_N			
Mean (SD)	8.68 (0.552)	8.81 (0.546)	8.74 (0.552)
Median [Min,	8.62 [7.63, 9.81]	8.71 [7.77, 10.0]	8.66 [7.63, 10.0]
Max]			
Missing	2 (1.2%)	7 (4.2%)	9 (2.7%)
Delta_13_C			

	FEMALE	MALE	Overall
Mean (SD) Median [Min,	-25.7 (0.798) -25.9 [-27.0, -23.9]	-25.7 (0.798) -25.8 [-26.9, -23.8]	-25.7 (0.797) -25.8 [-27.0, -23.8]
Max] Missing	2 (1.2%)	6 (3.6%)	8 (2.4%)

Graph

```
library(ggplot2)
library(gridExtra)
library(gapminder)
library(dplyr)
p1 <- ggplot(pen_table,aes(x = Sex,</pre>
                           y = Culmen_Length, fill = Sex)) +
      geom_boxplot() +
      scale_y_continuous(name = "Culmen Length(mm)") +
      scale_x_discrete( name = "Sex")
p2 <- ggplot(pen_table,aes(x = Sex,
                           y = Culmen_Depth, fill = Sex)) +
      geom_boxplot() +
      scale_y_continuous(name = "Culmen Depth(mm)") +
      scale_x_discrete( name = "Sex")
p3 <- ggplot(pen_table,aes(x = Sex,
                           y = Flipper_Length, fill = Sex)) +
      geom_boxplot() +
      scale_y_continuous(name = "Flipper Length(mm)") +
      scale_x_discrete( name = "Sex")
p4 <- ggplot(pen_table,aes(x = Sex,
                           y = Body_Mass,fill = Sex)) +
      geom_boxplot() +
      scale_y_continuous(name = "Body Mass(g)") +
      scale_x_discrete( name = "Sex")
p5 <- ggplot(pen_table,aes(x = Sex,
                           y = Delta_15_N,fill = Sex)) +
      geom_boxplot() +
      scale_y_continuous(name = "Isotope:C13") +
      scale_x_discrete( name = "Sex")
p6 <- ggplot(pen_table,aes(x = Sex,
                           y = Delta_13_C,fill = Sex)) +
```

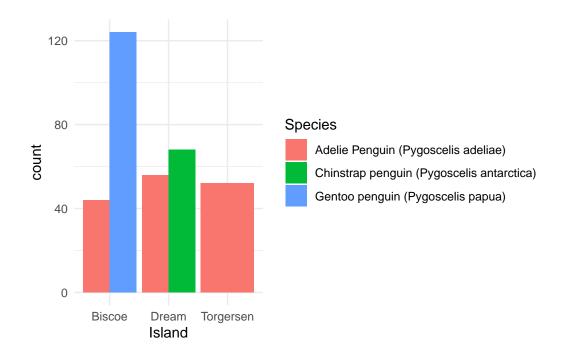
```
geom_boxplot() +
    scale_y_continuous(name = "Isotope:C13") +
    scale_x_discrete( name = "Sex")
grid.arrange(p1,p2,p3,p4,p5,p6,
    ncol = 2, nrow = 3)
```



We can see that the body measurements of male penguins appear to be larger than those of female penguins.

Species v.s. Island

```
p <- ggplot(data = mypenguins) +
   geom_bar(mapping = aes(x = Island,fill = Species),position = "dodge")
p</pre>
```



Of the three species, only the Adelie Penguin (Pygoscelis adeliae) has been observed on all three islands.