

My Report

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9/12/24

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Summary Staistic

```
library(palmerpenguins)
```

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

```
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

```
sum(is.na(penguins_raw))
```

```
[1] 336
```

Columns introduction

```
colnames(penguins_raw)
```

[1]	"studyName"	"Sample Number"	"Species"
[4]	"Region"	"Island"	"Stage"
[7]	"Individual ID"	"Clutch Completion"	"Date Egg"
[10]	"Culmen Length (mm)"	"Culmen Depth (mm)"	"Flipper Length (mm)"
[13]	"Body Mass (g)"	"Sex"	"Delta 15 N (o/oo)"
[16]	"Delta 13 C (o/oo)"	"Comments"	

連續變數 (數值) :

Culmen Length (mm) : 企鵝鳥喙長度

Culmen Depth (mm) : 企鵝鳥喙寬度

Flipper Length (mm) : 企鵝腳蹼長度

Body Mass (g) : 企鵝體重

Delta 15 N (o/oo) - The ratio of isotope $\delta^{15}\text{N}$

Delta 13 C (o/oo) - The ratio of isotope $\delta^{13}\text{C}$

類別變數 (分類) :

studyName : 研究名稱

Sample Number : 編號

Species : 物種 , 有Chinstrap、Adélie、Gentoo三種

Region : 地區

Island : 島嶼 , 有Dream、Torgersen、Biscoe三個

Stage : 狀態階段

Individual ID : 各企鵝的個人ID

Clutch Completion : 卵窩完整

Sex : 性別 , 男女

Comments : 評論

Continuous variables

```
#
continuous_vars <- c('Culmen Length (mm)', 'Culmen Depth (mm)',
                     'Flipper Length (mm)', 'Body Mass (g)',
                     'Delta 15 N (o/oo)', 'Delta 13 C (o/oo)')

# Step 1: Summary
summary_stats <- lapply(penguins_raw[continuous_vars], summary)
print("Summary statistics for continuous variables:")
```

```
[1] "Summary statistics for continuous variables:"
```

```
print(summary_stats)
```

```
$`Culmen Length (mm)`
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 32.10  39.23  44.45  43.92  48.50  59.60     2

$`Culmen Depth (mm)`
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 13.10  15.60  17.30  17.15  18.70  21.50     2

$`Flipper Length (mm)`
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 172.0  190.0  197.0  200.9  213.0  231.0     2

$`Body Mass (g)`
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 2700   3550   4050   4202   4750   6300     2

$`Delta 15 N (o/oo)`
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
  7.632   8.300   8.652   8.733   9.172  10.025    14

$`Delta 13 C (o/oo)`
  Min. 1st Qu.  Median    Mean 3rd Qu.    Max.   NA's
 -27.02 -26.32 -25.83 -25.69 -25.06  -23.79    13
```

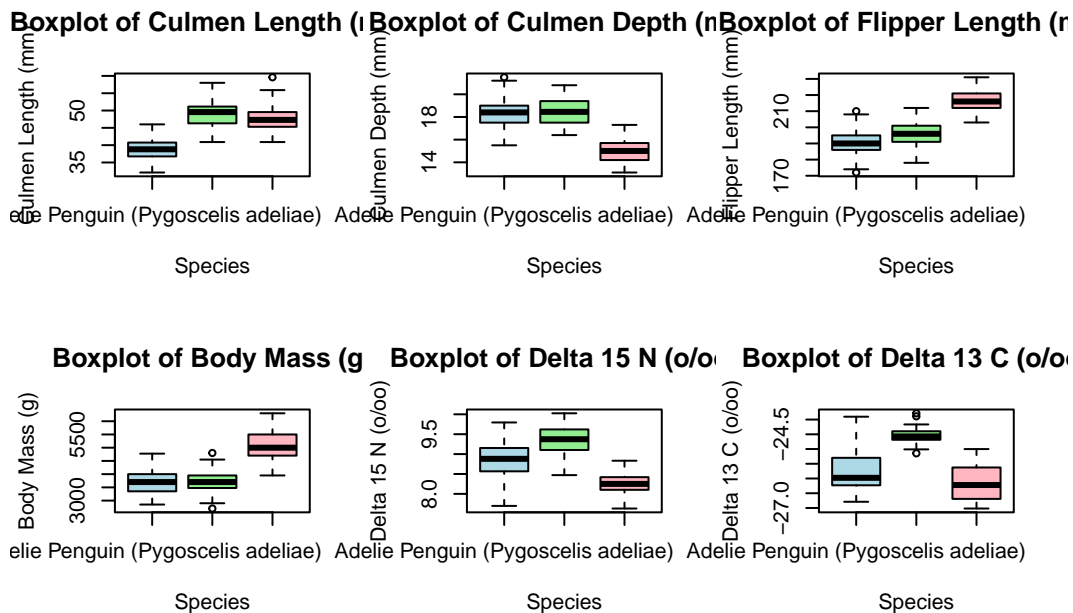
Step 2:繪製每個連續變數的 boxplot · 並根據 Species 分組

```

par(mfrow = c(2, 3)) #

for (var in continuous_vars) {
  boxplot(penguins_raw[[var]] ~ penguins_raw$Species,
          main = paste("Boxplot of", var),
          xlab = "Species",
          ylab = var,
          col = c("lightblue", "lightgreen", "lightpink"))
}

```



Categorical variables

次數分配表

```

categorical_columns1 <- c("studyName", 'Species', "Island", 'Region', 'Stage',
                          "Sex", 'Clutch Completion')

#
for (col in categorical_columns1) {
  print(paste("Category Distribution for", col, ":"))
}

```

```

#
value_counts <- table(penguins_raw[[col]])

#
percentage <- (value_counts / nrow(penguins_raw)) * 100

#
result <- data.frame(Count = value_counts, `Percentage (%)` = percentage)

print(result)
cat("\n")
}

```

[1] "Category Distribution for studyName :"

	Count.Var1	Count.Freq	Percentage.....Var1	Percentage.....Freq
1	PAL0708	110	PAL0708	31.97674
2	PAL0809	114	PAL0809	33.13953
3	PAL0910	120	PAL0910	34.88372

[1] "Category Distribution for Species :"

	Count.Var1	Count.Freq		
1	Adelie Penguin (Pygoscelis adeliae)	152		
2	Chinstrap penguin (Pygoscelis antarctica)	68		
3	Gentoo penguin (Pygoscelis papua)	124		
	Percentage.....Var1	Percentage.....Freq		
1	Adelie Penguin (Pygoscelis adeliae)	44.18605		
2	Chinstrap penguin (Pygoscelis antarctica)	19.76744		
3	Gentoo penguin (Pygoscelis papua)	36.04651		

[1] "Category Distribution for Island :"

	Count.Var1	Count.Freq	Percentage.....Var1	Percentage.....Freq
1	Biscoe	168	Biscoe	48.83721
2	Dream	124	Dream	36.04651
3	Torgersen	52	Torgersen	15.11628

[1] "Category Distribution for Region :"

	Count.Var1	Count.Freq	Percentage.....Var1	Percentage.....Freq
1	Anvers	344	Anvers	100

[1] "Category Distribution for Stage :"

	Count.Var1	Count.Freq	Percentage.....Var1	Percentage.....Freq
1	Adult, 1 Egg Stage	344	Adult, 1 Egg Stage	100

```
[1] "Category Distribution for Sex :"
```

	Count.Var1	Count.Freq	Percentage.....Var1	Percentage.....Freq
1	FEMALE	165	FEMALE	47.96512
2	MALE	168	MALE	48.83721

```
[1] "Category Distribution for Clutch Completion :"
```

	Count.Var1	Count.Freq	Percentage.....Var1	Percentage.....Freq
1	No	36	No	10.46512
2	Yes	308	Yes	89.53488

```
table(penguins_raw$`Individual ID`)#
```

N100A1	N100A2	N10A1	N10A2	N11A1	N11A2	N12A1	N12A2	N13A1	N13A2	N14A1
1	1	1	1	2	2	2	2	3	3	2
N14A2	N15A1	N15A2	N16A1	N16A2	N17A1	N17A2	N18A1	N18A2	N19A1	N19A2
2	2	2	1	1	2	2	3	3	2	2
N1A1	N1A2	N20A1	N20A2	N21A1	N21A2	N22A1	N22A2	N23A1	N23A2	N24A1
2	2	2	2	3	3	3	3	3	3	3
N24A2	N25A1	N25A2	N26A1	N26A2	N27A1	N27A2	N28A1	N28A2	N29A1	N29A2
3	2	2	1	1	2	2	3	3	3	3
N2A1	N2A2	N30A1	N30A2	N31A1	N31A2	N32A1	N32A2	N33A1	N33A2	N34A1
2	2	2	2	1	1	3	3	1	1	3
N34A2	N35A1	N35A2	N36A1	N36A2	N37A1	N37A2	N38A1	N38A2	N39A1	N39A2
3	3	3	3	3	2	2	3	3	3	3
N3A1	N3A2	N40A1	N40A2	N41A1	N41A2	N42A1	N42A2	N43A1	N43A2	N44A1
1	1	2	2	2	2	2	2	1	1	2
N44A2	N45A1	N45A2	N46A1	N46A2	N47A1	N47A2	N48A1	N48A2	N49A1	N49A2
2	1	1	2	2	2	2	1	1	2	2
N4A1	N4A2	N50A1	N50A2	N51A1	N51A2	N53A1	N53A2	N54A1	N54A2	N55A1
2	2	2	2	2	2	2	2	1	1	2
N55A2	N56A1	N56A2	N58A1	N58A2	N5A1	N5A2	N60A1	N60A2	N61A1	N61A2
2	2	2	2	2	2	2	2	2	3	3
N62A1	N62A2	N63A1	N63A2	N64A1	N64A2	N65A1	N65A2	N66A1	N66A2	N67A1
2	2	2	2	2	2	1	1	2	2	3
N67A2	N68A1	N68A2	N69A1	N69A2	N6A1	N6A2	N70A1	N70A2	N71A1	N71A2
3	1	1	3	3	3	3	1	1	2	2
N72A1	N72A2	N73A1	N73A2	N74A1	N74A2	N75A1	N75A2	N76A1	N76A2	N77A1
3	3	2	2	1	1	1	1	1	1	1
N77A2	N78A1	N78A2	N79A1	N79A2	N7A1	N7A2	N80A1	N80A2	N81A1	N81A2
1	1	1	1	1	2	2	1	1	1	1

N82A1	N82A2	N83A1	N83A2	N84A1	N84A2	N85A1	N85A2	N86A1	N86A2	N87A1
1	1	1	1	1	1	2	2	1	1	1
N87A2	N88A1	N88A2	N89A1	N89A2	N8A1	N8A2	N90A1	N90A2	N92A1	N92A2
1	1	1	1	1	3	3	1	1	1	1
N93A1	N93A2	N94A1	N94A2	N95A1	N95A2	N96A1	N96A2	N98A1	N98A2	N99A1
1	1	1	1	1	1	1	1	1	1	1
N99A2	N9A1	N9A2								
1	1	1								

```
table(penguins_raw$Comments)#
```

```

Adult not sampled.
1
Adult not sampled. Nest never observed with full clutch.
1
Nest never observed with full clutch.
34
Nest never observed with full clutch. Not enough blood for isotopes.
1
No blood sample obtained for sexing.
2
No blood sample obtained.
2
No delta15N data received from lab.
1
Not enough blood for isotopes.
7
Sexing primers did not amplify.
4
Sexing primers did not amplify. Not enough blood for isotopes.
1

```

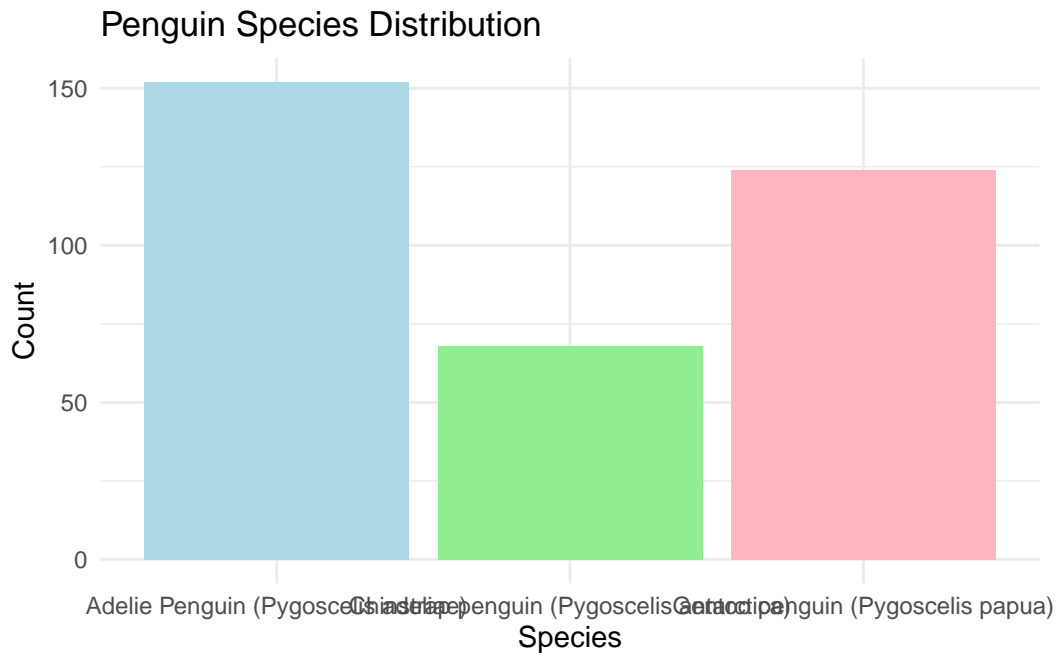
繪畫長條圖，以Species做分類

```
library(ggplot2)
```

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

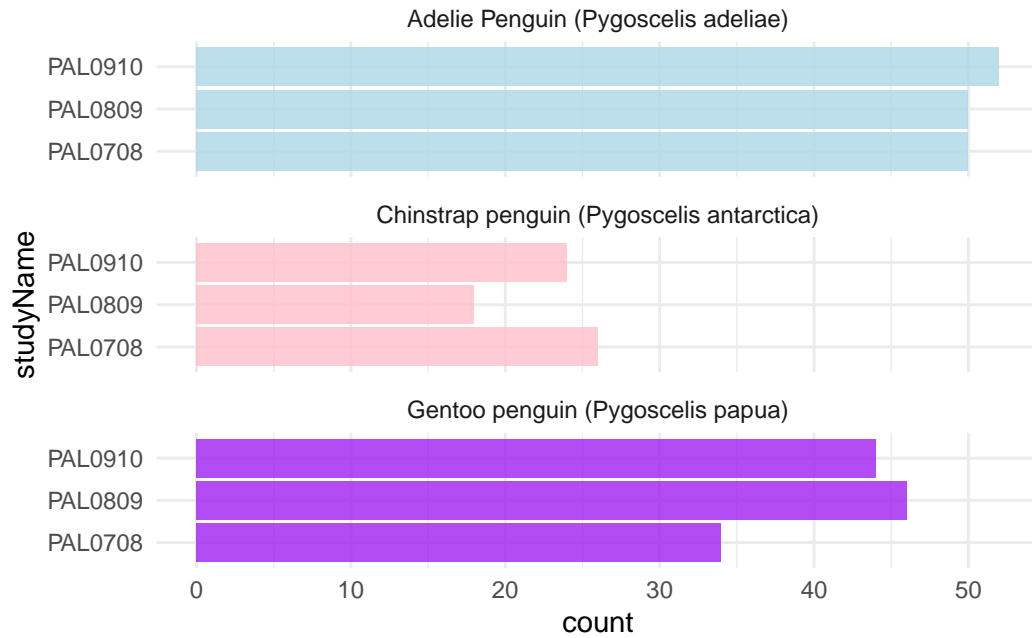


```
#Species bar chart
ggplot(penguins_raw, aes(x = Species)) +
  geom_bar(fill = c("lightblue", "lightgreen", "lightpink")) +
  labs(title = "Penguin Species Distribution", x = "Species", y = "Count") +
  theme_minimal()
```

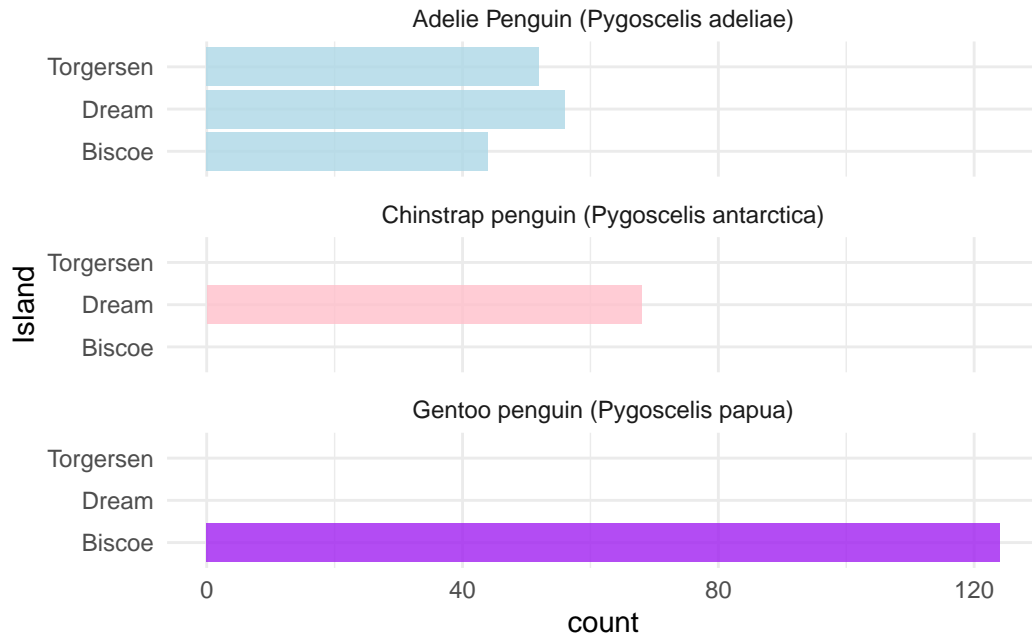


```
#studyName
ggplot(penguins_raw, aes(x = studyName, fill = Species)) +
  geom_bar(alpha = 0.8) +
  scale_fill_manual(values = c("lightblue", "pink", "purple"),
                    guide = FALSE) +
  theme_minimal() +
  facet_wrap(~Species, ncol = 1) +
  coord_flip()
```

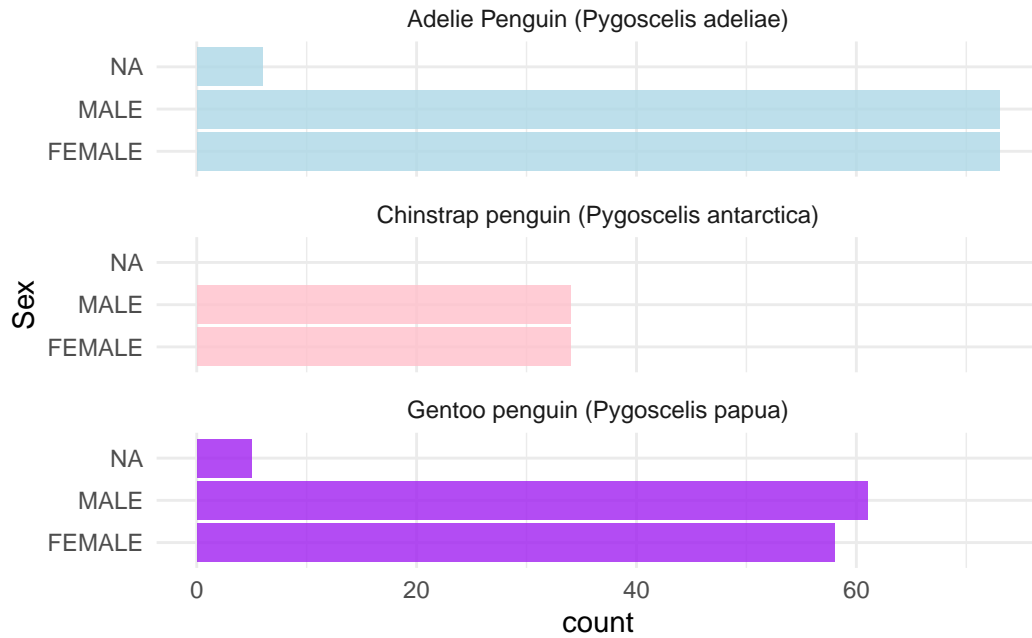
Warning: The `guide` argument in `scale_*()` cannot be `FALSE`. This was deprecated in ggplot2 3.3.4.
i Please use "none" instead.



```
#Island
ggplot(penguins_raw, aes(x = Island, fill = Species)) +
  geom_bar(alpha = 0.8) +
  scale_fill_manual(values = c("lightblue", "pink", "purple"),
                    guide = FALSE) +
  theme_minimal() +
  facet_wrap(~Species, ncol = 1) +
  coord_flip()
```



```
#Sex
ggplot(penguins_raw, aes(x = Sex, fill = Species)) +
  geom_bar(alpha = 0.8) +
  scale_fill_manual(values = c("lightblue", "pink", "purple"),
                    guide = FALSE) +
  theme_minimal() +
  facet_wrap(~Species, ncol = 1) +
  coord_flip()
```



```
#Clutch Completion
ggplot(penguins_raw, aes(x = `Clutch Completion`, fill = Species)) +
  geom_bar(alpha = 0.8) +
  scale_fill_manual(values = c("lightblue", "pink", "purple"),
                    guide = FALSE) +
  theme_minimal() +
  facet_wrap(~Species, ncol = 1) +
  coord_flip()
```

