Kelompok 1

Hans Rhesa Andersen (2502032346)
Ilham Hadi Shahputra (2502042164)
Elvano Jethro Mogi Pardede (250202543)
Liecardo Antonio (2502027876)

PALMER PENGUINS DATASET

Dataset

https://www.kaggle.com/datasets/larsen0966/penguins

| Adelie	Gentoo	Chinstrap
181	211	192
186	230	196
195	210	193
193	218	188
190	215	197
181	210	198
195	211	178
193	219	197
190	209	195
186	215	198
180	214	193
182	216	194
191	214	185
198	213	201
185	210	190
195	217	201
197	210	197
184	221	181
194	209	190
174	222	195
180	218	181
189	215	191
185	213	187
180	215	193
⋮	⋮	⋮
n=151	n=123	n=68

flipper length in mm

Goals

We are interested to find if there exists a significant difference between the flipper length of penguins based on the observed species (Adelie, Gentoo, Chinstrap)
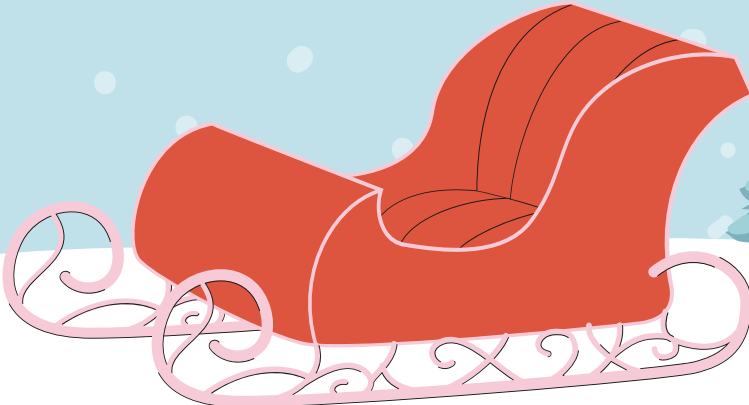
ANOVA

Hypothesis

$H_0 : \mu_1 = \mu_2 = \mu_3$

$H_1 : \mu_i \neq \mu_j \text{ for i, j} \in \{1,2,3\}$

Significance Level

$\alpha = 0.05$

ANOVA

```
                Df Sum Sq Mean Sq F value Pr(>F)
species          2  52473   26237   594.8 <2e-16 ***
Residuals      339  14953      44
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

ANOVA

Source of Var.	SS	df	MS	F	P-value	F crit
Treatment	52473.3	2	26236.6	594.8	1.4E-111	3.0
Within Groups	14953.3	339	44.1			
Total	67426.5	341				

Rejection Region

$$p\text{-value} \leq \alpha$$

We reject the null hypothesis if p-value is less than or equal to α.

ANOVA

Conclusion

$$1.4 \times 10^{-111} \leq 0.05$$

Since the acquired p-value is less than α (0.05), we reject the null hypothesis. It can be concluded that there exists a difference in the mean of **flipper length** on at least one penguin species.

Chinstrap

Gentoo

Adelie

Distributed Normally

Hypothesis

- **H0: The residuals are normally distributed**
- **H1: The residuals are not normally distributed**
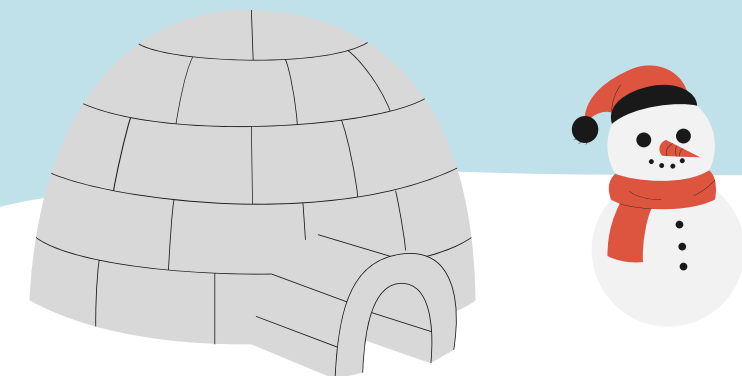
Significance Level

$\alpha = 0.05$

P-value*

Shapiro-Wilk normality test

data: resid(anova)
W = 0.99452, p-value = 0.2609

*From output in R using Shapiro Test

Distributed Normally

Reject H_0 if p-value $\leq \alpha$

P-value vs Significance Level
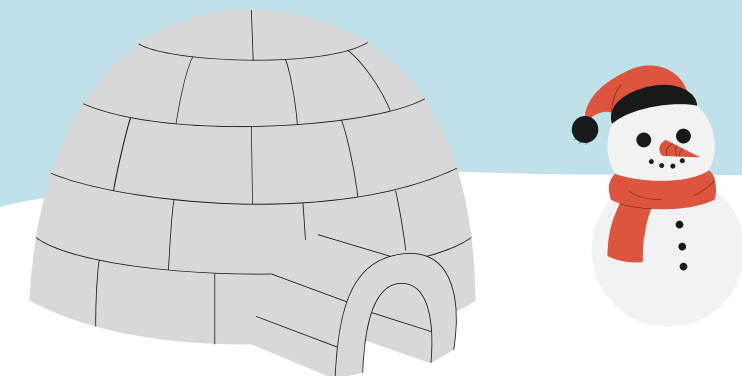
$0.2609 \nleq 0.05$

$\therefore$ Fail to reject H_0

Conclution

We do not have enough evidence to conclude that the residuals are not distributed normally. In other words, the residuals are distributed normally

Homoskedasticity Checking

Hypothesis

- **H0: There is homoskedasticity, meaning, the variance of error is constant.**
- **H1: There is heteroskedasticity, meaning, the variance of error is not constant.**

Output in R using Levene Test

```
Levene's Test for Homogeneity of Variance (center = median)
          Df  F value  Pr(>F)
group     2   0.3306   0.7188
          339
```

Rejection Region

We reject H0 if p-value is smaller than our significance level (α), and otherwise, we fail to reject H0.

Conclusion

At the significance level of 5% (α=0.05), we failed to reject H0, which means there is Homoskedasticity, meaning the variance of error is proven to be constant

Independent Assumption

Hypothesis

- H0: The observation residuals are not autocorrelated (independent).
- H1: The observation residuals are autocorrelated (dependent).

Output in R using DW-Test

```
Durbin-Watson test

DW = 2.2662, p-value = 0.9909
```

Rejection Region

$$\alpha = 0.05$$

We reject H0 if p-value is smaller than our significance level (α), and otherwise, we fail to reject H0.
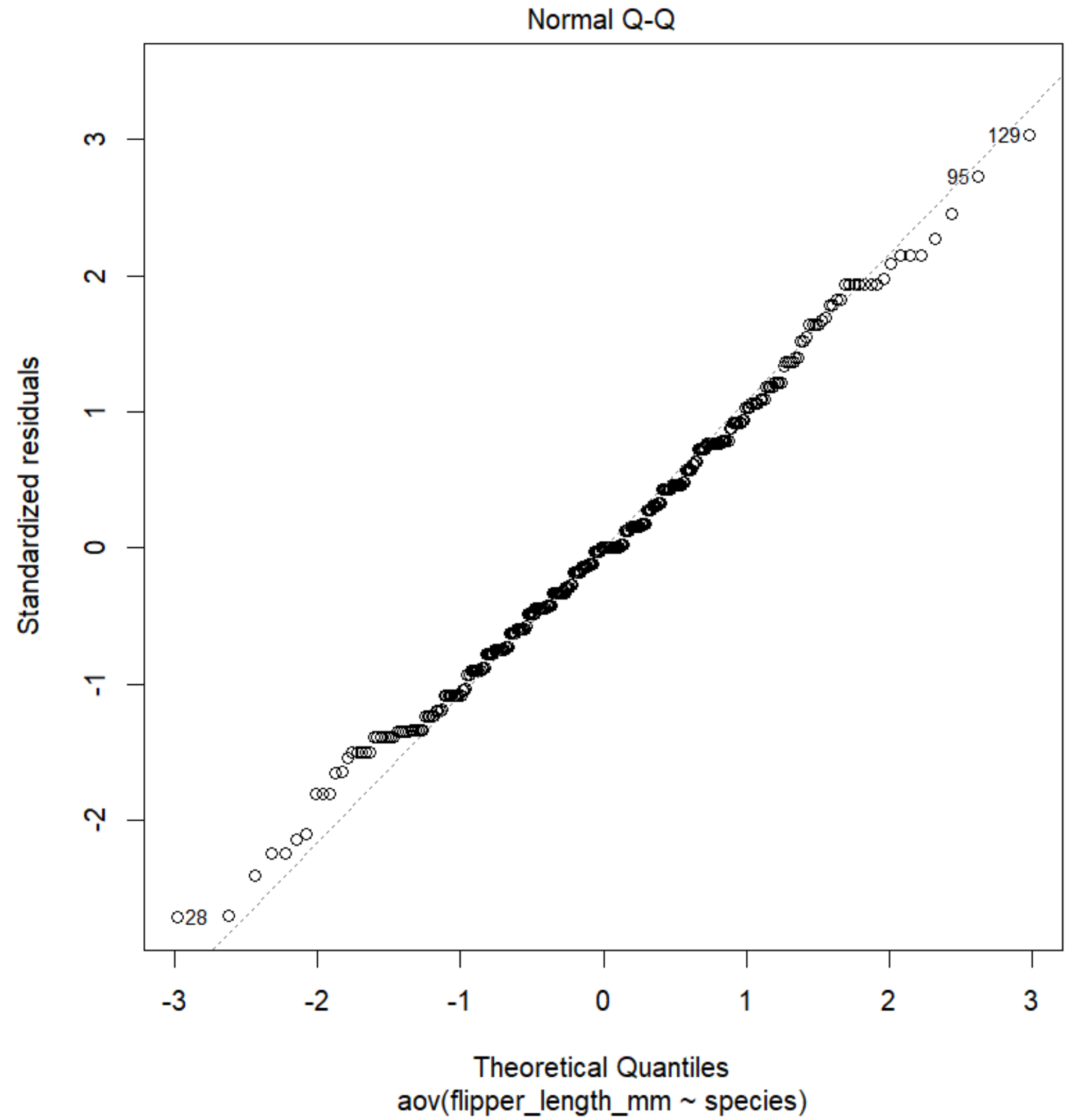
Conclusion

At the significance level of 5% (α=0.05), we fail to reject H0, and we can conclude that our observations are independently distributed.
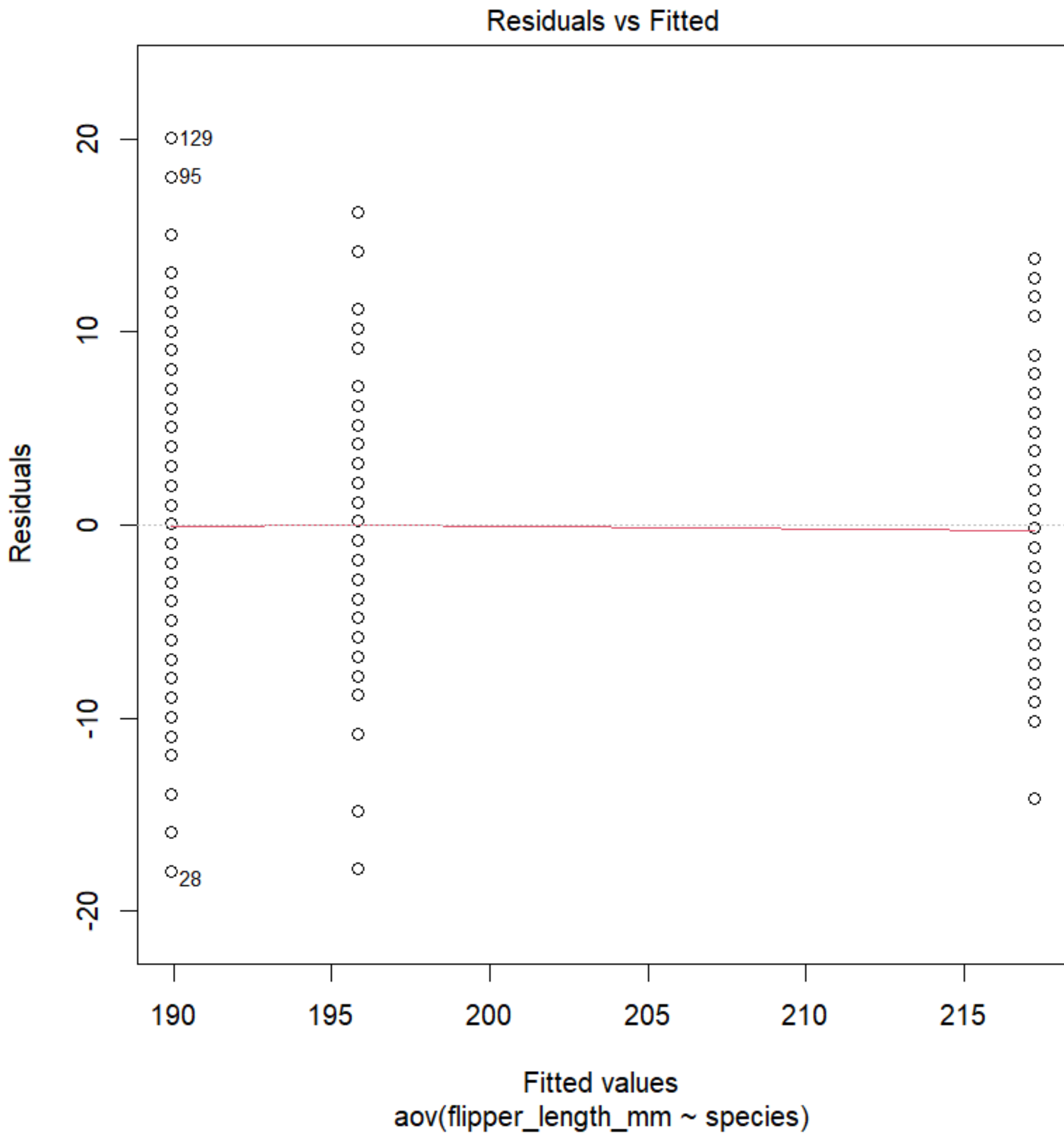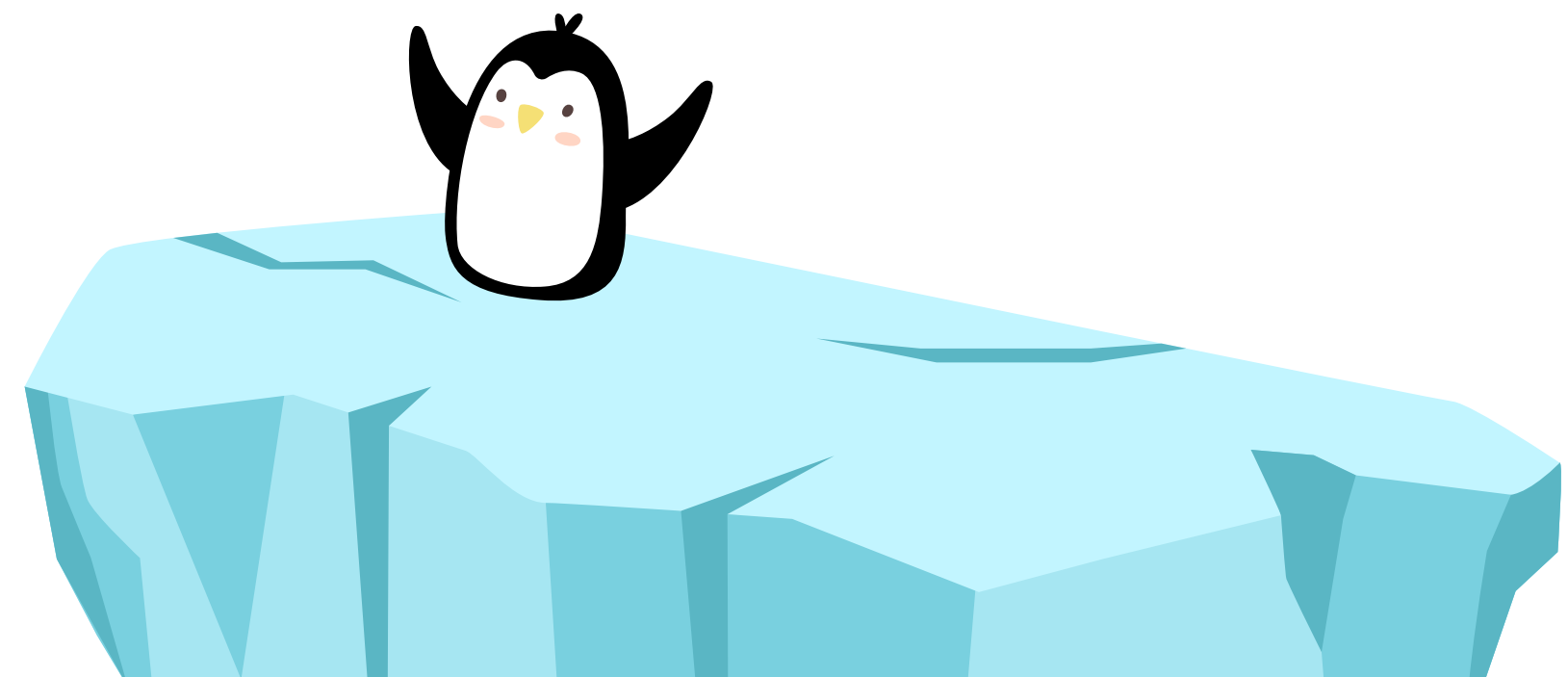
Model Adequacy Checking
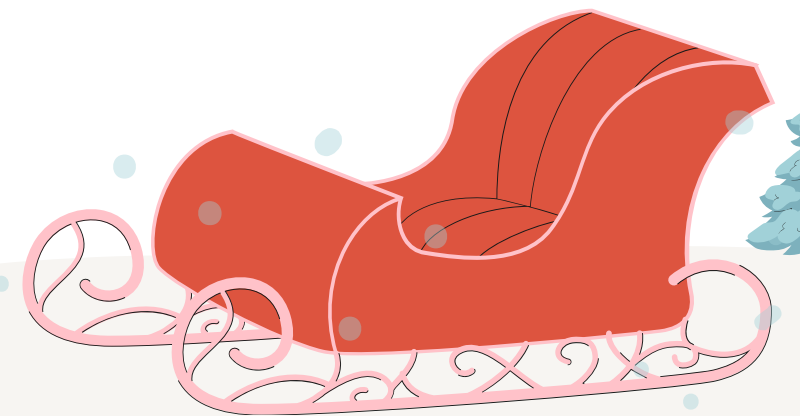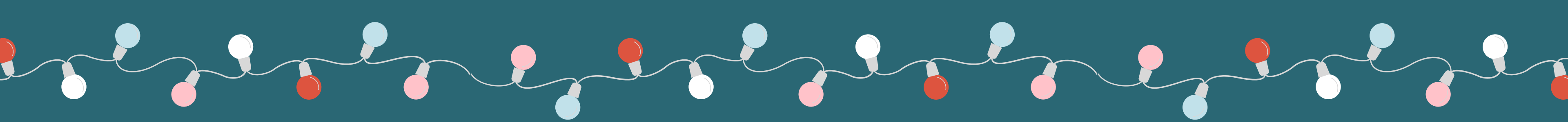
Plot

Residuals vs Fitted

Post-Hoc

Tukey HSD (Honestly Significant Difference)

Recall: ANOVA

F-Test (R)

```
            Df  Sum Sq  Mean Sq  F value  Pr(>F)
species      2   52473    26237    594.8  <2e-16  ***
Residuals  339   14953       44
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

F-Test (Excel)

Source of Var.	SS	df	MS	F	P-value	F crit
Treatment	52473.3	2	26236.6	594.8	1.4E-111	3.0
Within Groups	14953.3	339	44.1			
Total	67426.5	341				

Tukey HSD

```
Tukey multiple comparisons of means
  95% family-wise confidence level

Fit: aov(formula = flipper_length_mm ~ species, data = data)


$species

                      diff       lwr       upr p adj
Chinstrap-Adelie  5.869887  3.586583  8.153191     0
Gentoo-Adelie    27.233349 25.334376 29.132323     0
Gentoo-Chinstrap 21.363462 19.000841 23.726084     0
```
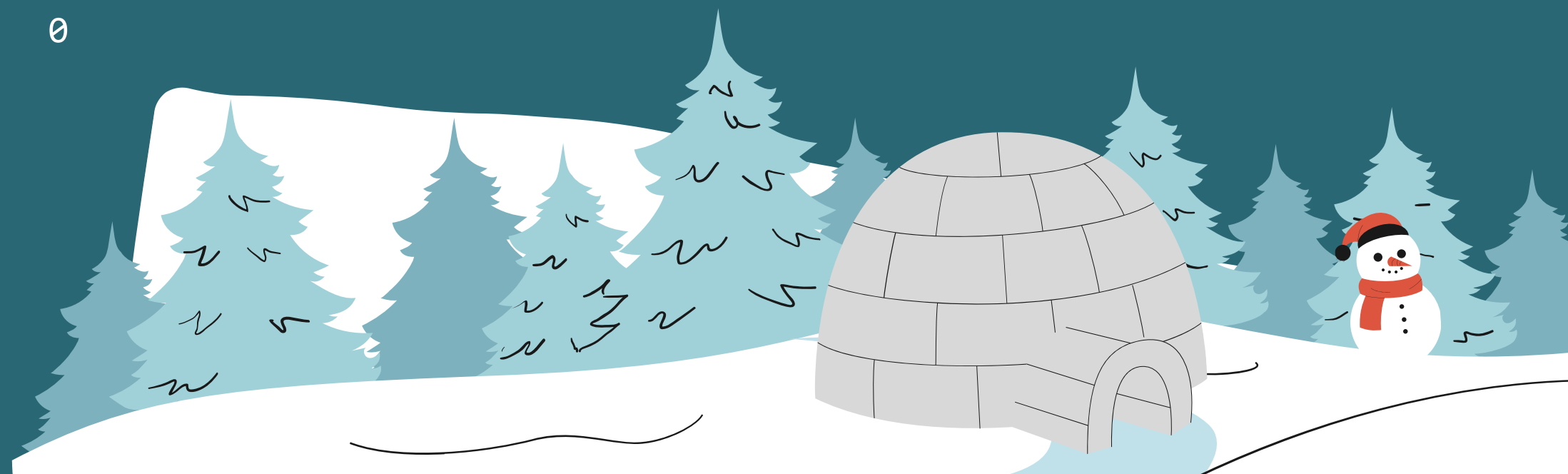
Conclusion

We can see that the p-value is less than our significance level of 0.05 (p-value < 0.0....) for all combinations. From that we can conclude that all combinations of mean are significant.

Thank you