

A Report on Antarctic Penguins

A mock article for a Quarto course

Tiny van Boekel Jos Hageman

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Abstract

This mock paper is based upon the open access paper by Gorman, Williams, and Fraser (2014). It is meant as an exercise to write scientific papers in Quarto. The setup of the paper is in the common traditional way. The data are freely available in the R Package `palmerpenguins`.

27 This mock paper contains some of these data in the form of Tables and Figures and performs
28 some data analysis using linear regression and ANOVA.

29 Introduction

30 Ecological sexual dimorphism was examined among adult *Pygoscelis* penguins nesting within
31 the northwestern AP, along the Palmer Archipelago located near Anvers Island. Specifically,
32 variation in ^{13}C and ^{15}N SI signatures of blood tissue was investigated, obtained during egg
33 laying, as abiogeochemical proxy of pre-breeding trophic foraging given that these isotopes are
34 known to reliably reflect trophic position by integrating dietary information over approximately
35 the previous 30 to 60 days given allometric turn-over rates for the cellular fraction of blood.
36 We predicted that males and females of all three species investigated should show sex-specific
37 foraging given that male and female gentoo penguins nesting at Bird Island, South Georgia,
38 have been shown to differ in their breeding foraging niche and hold generally similar, moderate
39 levels of SSD as Adélie and chinstrap penguins.

40 Materials and Methods

41 *Ethics statement*

42 Research was conducted in accordance with an Antarctic Conservation Act permit to WRF
43 (2008-020), in addition to Canadian Committee on Animal Care guidelines (Simon Fraser Uni-
44 versity, SFU, Animal Care Permit 890B-08 to KBG and TDW).

45 *Field methods*

46 Field research was conducted on *Pygoscelis* penguins nesting on several islands within the
47 Palmer Archipelago west of the AP near Anvers Island (64° , $64'$, during the austral summers
48 of 2007/08, 2008/09, and 2009/10. Specifically, study nests were located on Biscoe (64° , $63'$),
49 Torgersen (64° , $64'$), and Dream (64° , $64'$) Islands. Each study season, Adélie penguin study
50 nests ($n=30$) were distributed equally between the three study islands, with 10 nests located
51 on each island. Gentoo penguin study nests ($n=30$) were all located on Biscoe Island, while
52 chinstrap penguin study nests ($n=15$) were all located on Dream Island. The reduced sample
53 size for chinstraps was due to the overall smaller number of individuals breeding at rookeries
54 on Dream Island.

55 *Statistical methods*

56 Least-squares general linear models (LM) were used to examine continuous variation in ^{13}C
57 and ^{15}N SI signatures of adult penguin RBCs in relation to three parameters treated as main-
58 effects including 1-sex, as determined by molecular data and treated categorically, 2-overall size
59 using a principal component score (PC1) based on culmen depth and length, and flipper length-
60 hand treated continuously, and 3-year, treated categorically. Individual scores for PC1 were
61 calculated using the `prcomp` function in R for datasets consisting of both males and females, but

62 calculated separately for each species. A prior set of eight candidate models consisted of an
63 equal-means model, each predictor variable as a main effect (three models), additive models
64 for sex or size with year, defined so that sex and size were never included in the same model
65 (two models), and interaction models for these same additive models where an interaction was
66 included for each parameter considered as a main effect in the model (two models). This same
67 candidate model set was evaluated for each isotope separately using datasets for each species
68 (Adelie n= 127 for ^{13}C and n= 128 for ^{15}N due to the exclusion of one datapoint as a ^{13}C
69 outlier based on residual plots for normality, chinstrap n= 53, gentoo n= 115).

70 *Data*

71 The data were obtained from the R package `palmerpenguins` (Horst, Presmanes Hill, and
72 Gorman 2020). Incomplete data reported as ‘NA’ were removed before analysis.

73 *Data management*¹

74 Data reported here are publicly available within the PAL-LTER data system (datasets#219,
75 220, and 221): <http://oceaninformatics.ucsd.edu/datazoo/data/pallter/datasets>. These data
76 are additionally archived within the United States (US) LTER Network’s Information System
77 Data Portal: <https://portal.lternet.edu/>. Individuals interested in using these data are there-
78 fore expected to follow the US LTER Network’s Data Access Policy, Requirements and Use
79 Agreement <http://www.lternet.edu/policies/data-access>

80 *Penguin body parts*

81 Figure 1 explains the terminology used in the measurements.

82 *Software*

83 This paper was written in `Quarto` to contribute to open science (Perkel 2022). Graphs were
84 made with the R package `ggplot` (Wickham 2016), tables with `kable` from the R package
85 `knitr`.

86 **Results and discussion**

87 *Exploratory Data Analysis*

88 A first overview is a summary report about the data. There are 3 penguin species in the data
89 and 3 islands. The names of the type of penguins are Adelie, Gentoo, Chinstrap, respectively,
90 while the names of the islands are Torgersen, Biscoe, Dream. The average bill length is 43.99
91 mm and the average bill depth is 17.16 mm. The data per species (pooled over years and
92 islands) are summarized in Table 1, while Table 2 shows that the number of individuals per
93 species is rather different.

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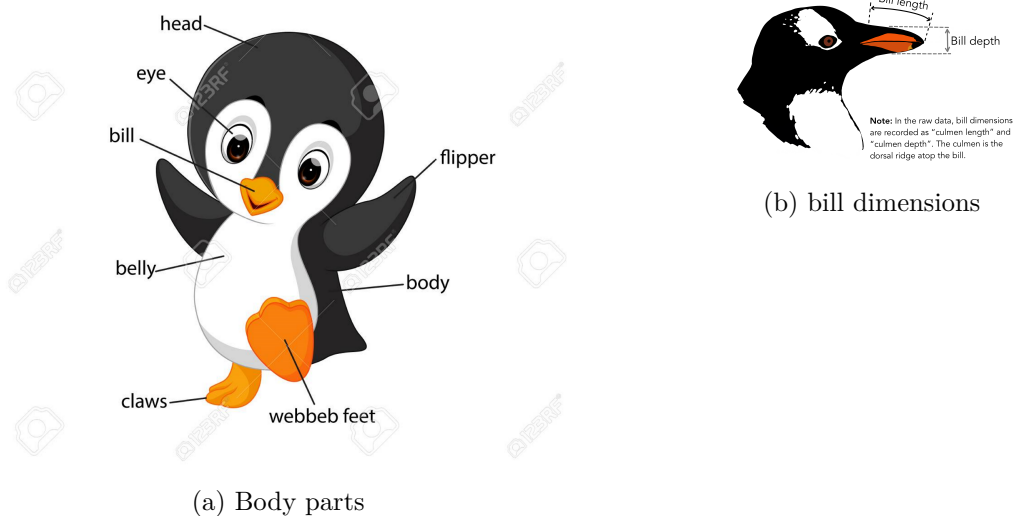


Figure 1: Body and bill parts of penguins

Table 1: Summary of the pooled palmer penguin dataset

Species	bill length (mm)	bill depth (mm)	flipper length (mm)	body mass (g)
Adelie	38.82	18.35	190.10	3706.16
Chinstrap	48.83	18.42	195.82	3733.09
Gentoo	47.57	15.00	217.24	5092.44

Table 2: Number n of individuals per species

species	n
Adelie	146
Chinstrap	68
Gentoo	119

94 A graphic way of data exploration is via boxplots and violin plots: see Figure 2. It gives an
 95 idea about the variation in the data.

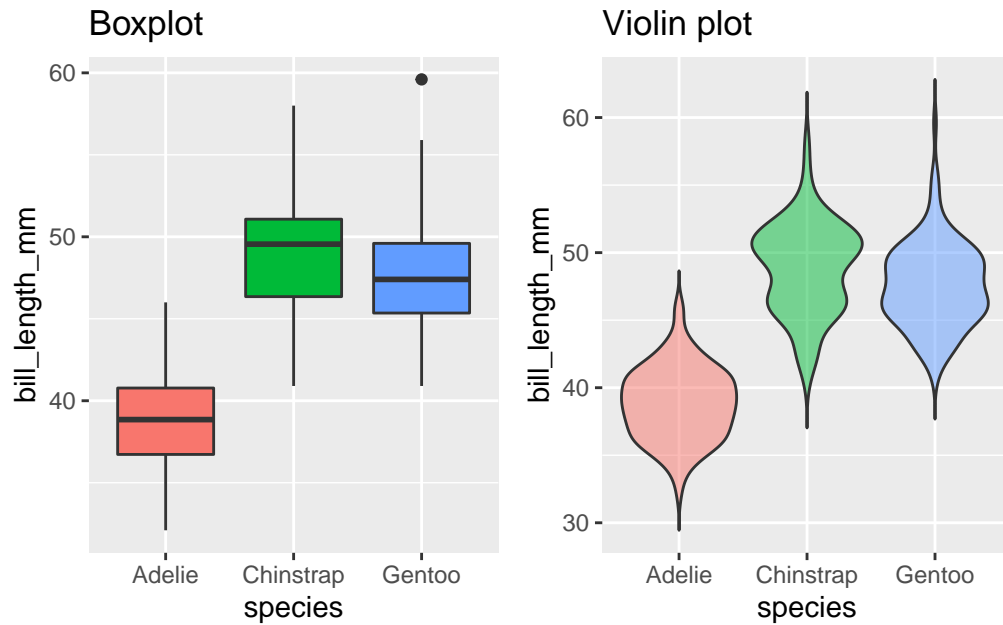


Figure 2: Boxplot and violin plot of bill length for three penguin species

96 All kinds of scatterplots can be made. For instance, Figure 3 shows a scatterplot of body
 97 mass versus flipper length for all species pooled (A) and per species (B). The plot suggests a
 98 positive, more or less linear relation between the two variables: increase in flipper length goes
 99 along with increase in body mass. The quantitative relation appears to depend on sex: see
 100 Figure 4.

101 Yet another way of data exploration is to show a plot where species is separated (Figure 5),
 102 showing the relation between bill length and flipper length, which appears to be different for
 103 the species. Data can be shown in many more ways, for instance, by splitting them up in year
 104 and species as in Figure 6. Figure 3, Figure 4 and Figure 5 show that there are considerable
 105 differences visible when clusters in the data are recognized. Of course, it is also possible to
 106 show numerical summaries of data. Table 3 shows a numerical summary of the mean body
 107 mass per year and per island, for instance, pooled for species.

108 Analysis of the data: regression

109 A first analysis of the data is to investigate whether quantitative relations between variables
 110 can be detected. Figure 7 shows the result of linear regression of bill depth versus bill length.
 111 The regression equation is depicted in Equation 1

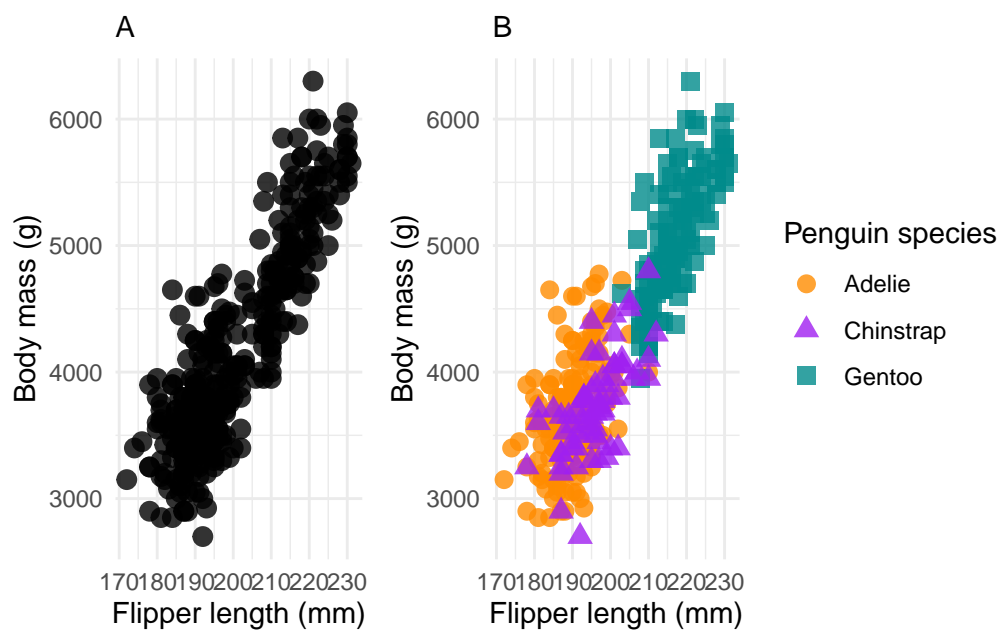


Figure 3: Penguin flipper length and body mass, pooled (A) and separate by species (B)

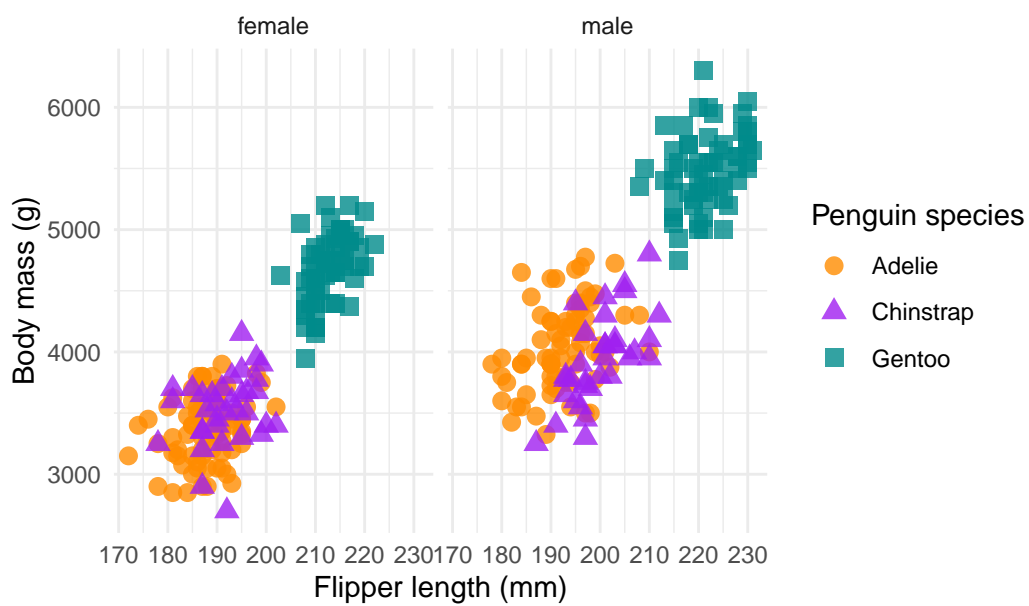


Figure 4: Penguin flipper length and body mass per species and per sex

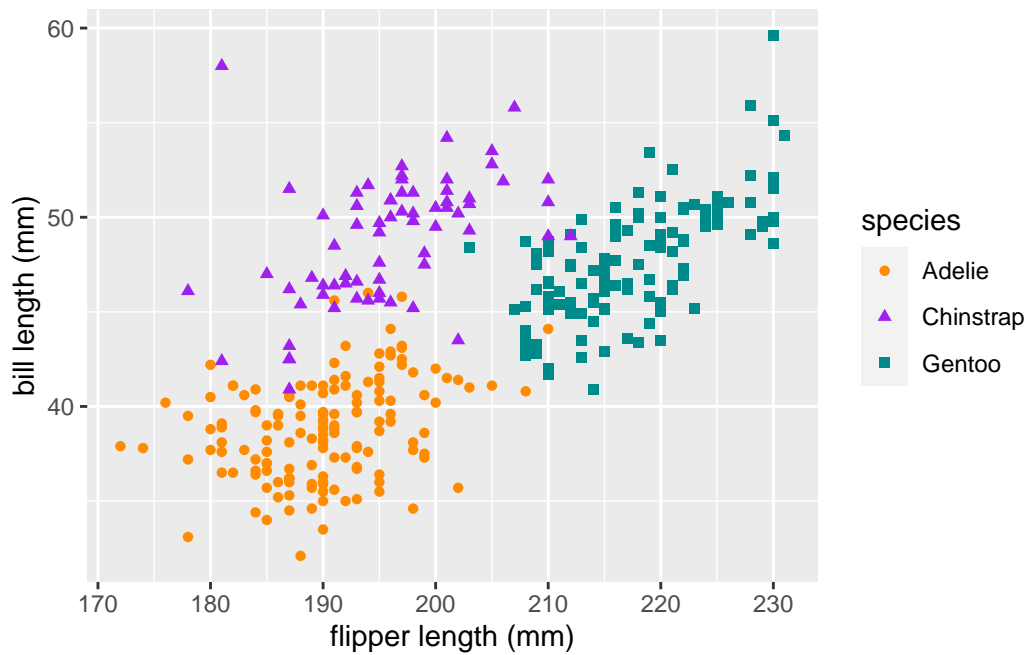


Figure 5: Relation between bill length and flipper length for three penguin species

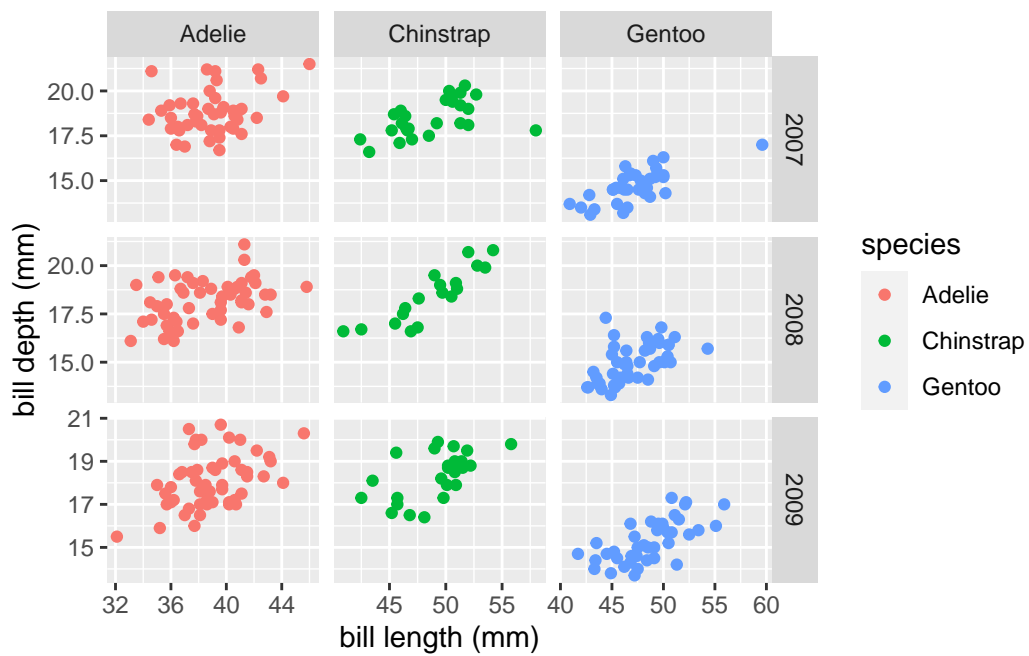


Figure 6: Bill depth as a function of bill length per year and per species

Table 3: Mean body mass of penguins on different islands over time

Island	Year	Mean Body Mass (g)
Biscoe	2007	4756
Biscoe	2008	4628
Biscoe	2009	4793
Dream	2007	3700
Dream	2008	3779
Dream	2009	3691
Torgersen	2007	3785
Torgersen	2008	3856
Torgersen	2009	3489

Table 4: numerical results of regression of bill depth versus bill length

term	estimate	std.error	statistic	p.value
Intercept	20.79	0.85	24.34	0.0e+00
Slope	-0.08	0.02	-4.27	2.5e-05

$$y = a + bx + \epsilon \quad (1)$$

where a represents the intercept, b the slope and ϵ the residual error. The dependent variable y represents in this case bill depth and x the independent variable bill length (this is not necessarily a causal relation!). The result in Figure 7 suggests a negative correlation between bill depth and bill length when all data are pooled: the slope = -0.08 and the intercept 20.79. However, this is deceptive. It is a nice example of Simpson's paradox what may happen if clusters in data are neglected. As Figure 5 and Figure 4 show, clusters can indeed be detected in the data. Figure 8 shows the regression lines resulting from analysis per species: all of a sudden, the correlation between bill depth and bill length is now positive! These data lend themselves well to multilevel modeling, for instance by using the R package `lme4`. A blog where this is done using the penguins data is [multilevel models](#) This will not further pursued here.

ANOVA and post-hoc tests

A research question is in how far flipper length is different between the three penguin species. With ANOVA it can be tested whether or not differences between groups are significant (not, however, which groups are different; if one wants to know that post-hoc tests are needed). A blog that gives a nice overview, also using the penguin data set, is [ANOVA in R](#). A Student

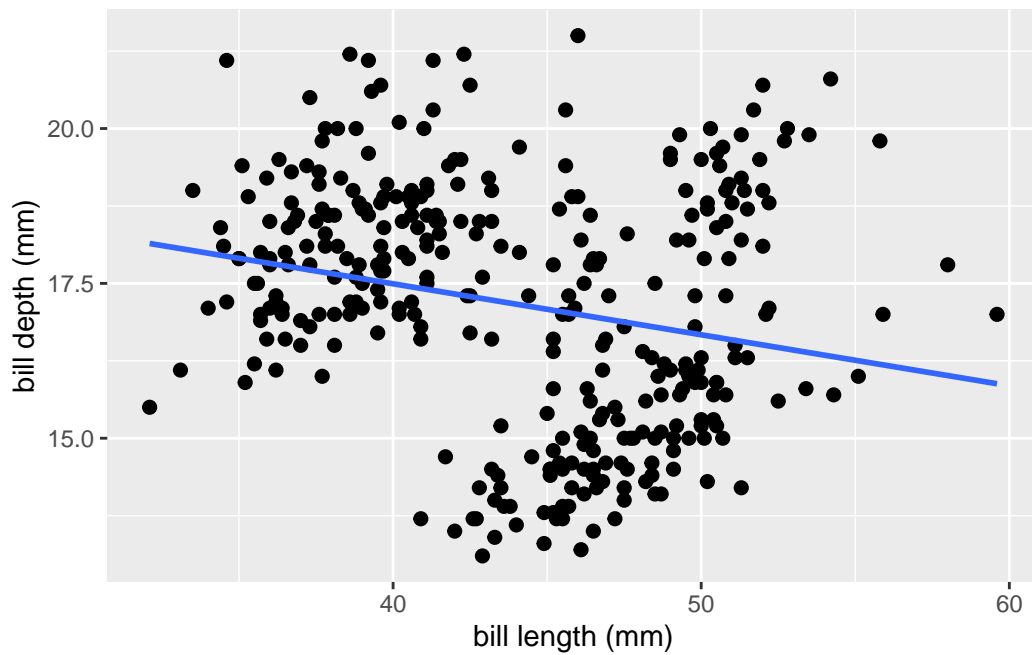


Figure 7: Regression line following from linear regression of bill depth versus bill length

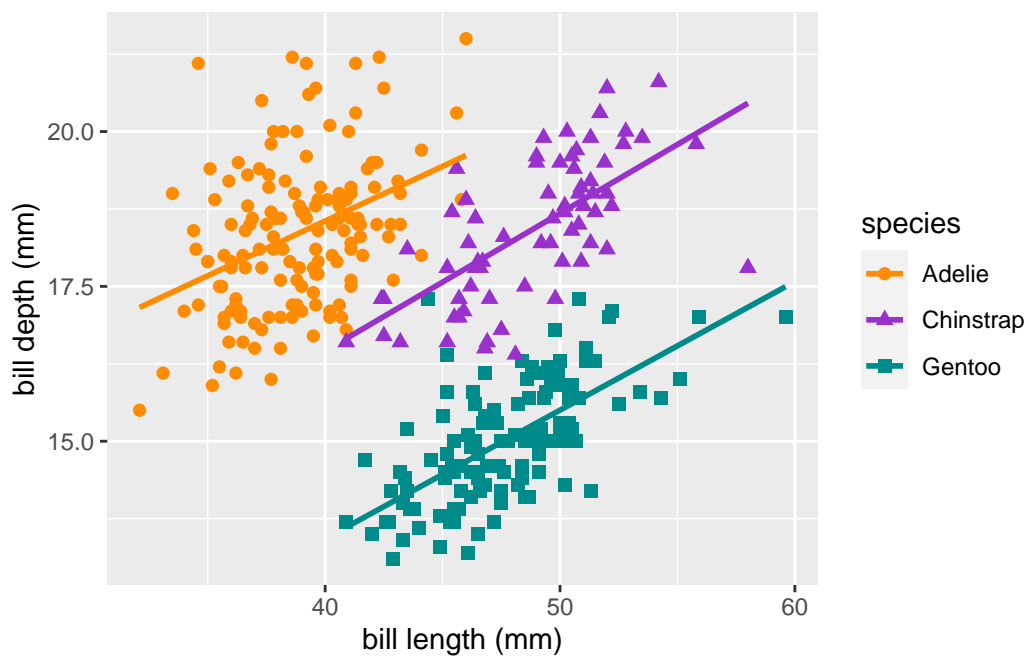


Figure 8: Regression lines obtained when clustered data are analyzed separately

Table 5: ANOVA of flipper length per species

term	df	sumsq	meansq	statistic	p.value
species	2	50526	25263	567.41	0
Residuals	330	14693	45	NA	NA

Table 6: Post-hoc result using Tukey’s HSD test for differences in flipper length between species

term	contrast	null.value	estimate	conf.low	conf.high	adj.p.value
species	Chinstrap-Adelie	0	5.72	3.41	8.03	0
species	Gentoo-Adelie	0	27.13	25.19	29.07	0
species	Gentoo-Chinstrap	0	21.41	19.02	23.80	0

t-test can be used to compare two groups, ANOVA for three or more groups. See also [R Pubs](#)
- [Gentle guide to Tidy Statistics in R](#)

Figure 2 showed that variances are roughly equal, an important assumption for ANOVA. Table 5 gives the result of the ANOVA analysis and shows that there are indeed significant differences; however, it does not tell which differences, only that at least one species is different. To get to know that, a post-hoc analysis is needed where the groups are compared two-by-two. This could be done by a Student t-test but more common is to do multiple testing, which can be done in various ways. A Tukey HSD test is used to compare all groups: see Table 6. It turns out that the differences between all species are significant.

Figure 9 visualizes ANOVA and post-hoc results in one plot (using the R Package `ggstatsplot` and shows similarly that there are significant differences between the species in terms of flipper length.

Conclusion

This mock paper has shown how to report data in a scientific paper using Quarto illustrated by the freely available data set about Palmer penguins. Because data exploration, analysis, summaries and graphics are all combined in one file, this appears to be an excellent tool to perform open science, i.e., to make the whole scientific process transparent and reproducible.

Acknowledgements

The authors would like to thank the authors of the original paper for making their data publicly available as well as Alison Horst for producing the R package `palmerpenguins`.

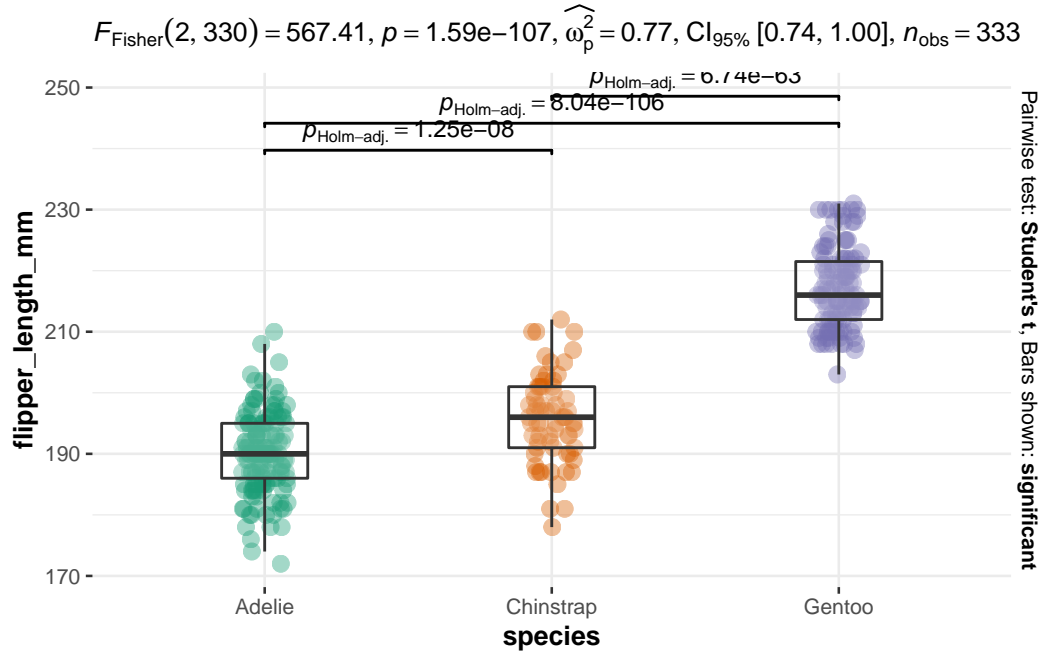


Figure 9: Boxplots of flipper length combined with ANOVA results

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