My title*

My subtitle if needed

First author Another author

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First sentence. Second sentence. Third sentence. Fourth sentence.

1 Introduction

You can and should cross-reference sections and sub-sections.

The remainder of this paper is structured as follows. Section 2….

2 Data

col.names = c("Year of Death", "Cause of Death", "Age Group", "Gender", "Count", "Cause Group"), Some of our data is of penguins (**?@fig-bills**), from Horst, Hill, and Gorman (2020).

```
file_path <- "../../inputs/data/raw_data.csv"
toronto_homeless_death <- read.csv(file_path)
sample_data <- head(toronto_homeless_death, 6)
table_output <- kable(sample_data,

                      caption = "Sample Table for Causes of Death")
# Print the table
cat(table_output)
```

```
Table: Sample Table for Causes of Death  | X_id| Year.of.death|Cause_of_death |Age_group |Ge
```

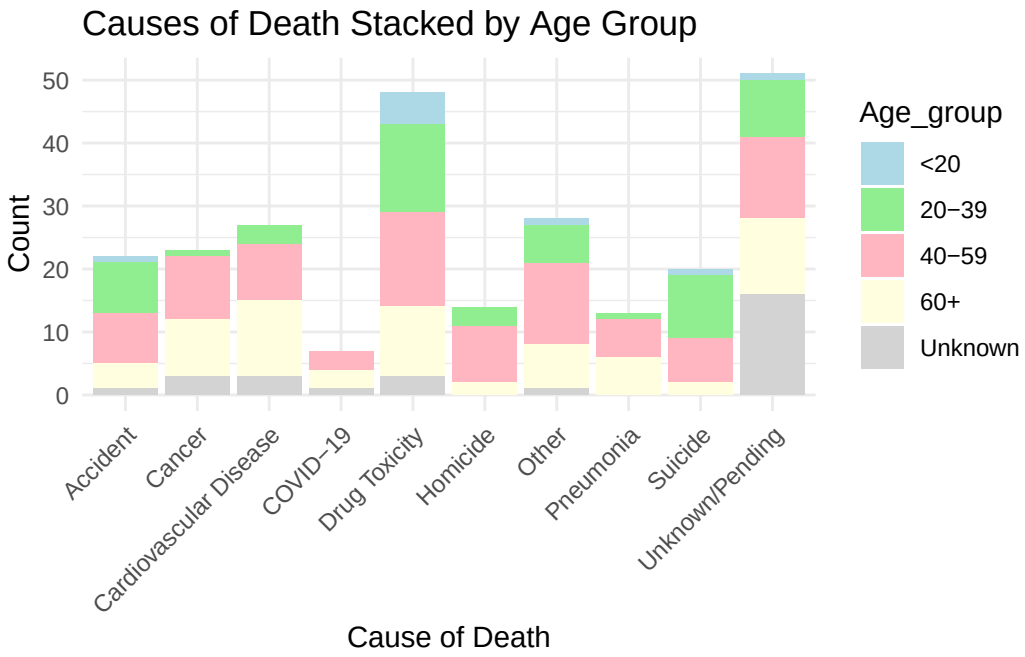

Figure 1: Causes of death analysis

Talk more about it.

And also planes (**?@fig-planes**). (You can change the height and width, but don't worry about doing that until you have finished every other aspect of the paper - Quarto will try to make it look nice and the defaults usually work well once you have enough text.)

#| label: fig-planes #| fig-cap: Relationship between wing length and width #| echo: false #| warning: false #| message: false

analysis_data <- read_csv(here::here("outputs/data/analysis_data.csv"))

analysis_data |> ggplot(aes(x = width, y = length)) + geom_point(alpha = 0.8) + theme_minimal() + labs(x = "Wing width (mm)", y = "Wing length (mm)")

Talk way more about it.

3 Model

The goal of our modelling strategy is twofold. Firstly,...

*Code and data are available at: LINK.

Here we briefly describe the Bayesian analysis model used to investigate… Background details and diagnostics are included in Appendix B.

3.1 Model set-up

Define y_i as the number of seconds that the plane remained aloft. Then β_i is the wing width and γ_i is the wing length, both measured in millimeters.

$$y_i|\mu_i, \sigma \sim \text{Normal}(\mu_i, \sigma) \tag{1}$$
$$\mu_i = \alpha + \beta_i + \gamma_i \tag{2}$$
$$\alpha \sim \text{Normal}(0, 2.5) \tag{3}$$
$$\beta \sim \text{Normal}(0, 2.5) \tag{4}$$
$$\gamma \sim \text{Normal}(0, 2.5) \tag{5}$$
$$\sigma \sim \text{Exponential}(1) \tag{6}$$

We run the model in R (R Core Team 2022) using the `rstanarm` package of Goodrich et al. (2022). We use the default priors from `rstanarm`.

3.1.1 Model justification

We expect a positive relationship between the size of the wings and time spent aloft. In particular…

We can use maths by including latex between dollar signs, for instance θ.

4 Results

Our results are summarized in **?@tbl-modelresults**. #| echo: false #| eval: true #| warning: false #| message: false

library(rstanarm)

first_model <- readRDS(file = here::here("outputs/models/first_model.rds"))

#| echo: false #| eval: true #| label: tbl-modelresults #| tbl-cap: "Explanatory models of flight time based on wing width and wing length" #| warning: false

modelsummary::modelsummary(list("First model" = first_model), statistic = "mad", fmt = 2)

5 Discussion

5.1 First discussion point

If my paper were 10 pages, then should be be at least 2.5 pages. The discussion is a chance to show off what you know and what you learnt from all this.

5.2 Second discussion point

5.3 Third discussion point

5.4 Weaknesses and next steps

Weaknesses and next steps should also be included.

Appendix

A Additional data details

B Model details

B.1 Posterior predictive check

In **?@fig-ppcheckandposteriorvsprior-1** we implement a posterior predictive check. This shows…

In **?@fig-ppcheckandposteriorvsprior-2** we compare the posterior with the prior. This shows… #| eval: true #| echo: false #| message: false #| warning: false #| label: fig-ppcheckandposteriorvsprior #| layout-ncol: 2 #| fig-cap: "Examining how the model fits, and is affected by, the data" #| fig-subcap: ["Posterior prediction check", "Comparing the posterior with the prior"]

pp_check(first_model) + theme_classic() + theme(legend.position = "bottom")

posterior_vs_prior(first_model) + theme_minimal() + scale_color_brewer(palette = "Set1") + theme(legend.position = "bottom") + coord_flip()

B.2 Diagnostics

?@fig-stanareyouokay-1 is a trace plot. It shows… This suggests…

?@fig-stanareyouokay-2 is a Rhat plot. It shows… This suggests… #| echo: false #| eval: true #| message: false #| warning: false #| label: fig-stanareyouokay #| fig-cap: "Checking the convergence of the MCMC algorithm" #| fig-subcap: ["Trace plot", "Rhat plot"] #| layout-ncol: 2

plot(first_model, "trace")

plot(first_model, "rhat")

References

Goodrich, Ben, Jonah Gabry, Imad Ali, and Sam Brilleman. 2022. "Rstanarm: Bayesian Applied Regression Modeling via Stan." https://mc-stan.org/rstanarm/.

Horst, Allison Marie, Alison Presmanes Hill, and Kristen B Gorman. 2020. *Palmerpenguins: Palmer Archipelago (Antarctica) Penguin Data*. https://doi.org/10.5281/zenodo.3960218.

R Core Team. 2022. *R: A Language and Environment for Statistical Computing*. Vienna, Austria: R Foundation for Statistical Computing. https://www.R-project.org/.