

Research Methods and Data Analysis (IAWEL)

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1 Research Methods and Data Analysis (IAWEL)

Preface

This book accompanies the Research Methods and Data Analysis course on the International Animal Welfare Ethics and Law MSc at the Royal (Dick) School of Veterinary Studies.

It is a companion document to the course, and not core to the materials.

Throughout the RMDA Lectures, you will see a number of statistical tests, data visualisations, data manipulation, text mining, and simple calculations. Almost inevitably, each one of these steps will have been performed in R.

Your R textbook is [R@R\(D\)SVS](#), and that textbook will explain [how to download and install R](#), [how to run simple commands in R](#), and more. This RMDA textbook is like an accompanying document to your lecture materials, and is a place to help you move your R and statistical knowledge along.

Packages in this textbook

There are a range of packages used in this book, including Tidyverse (Wickham et al. 2019), effsize (Torchiano 2020), ggstatsplot (Patil 2021), vcd (Zeileis, Meyer, and Hornik 2007), wordcloud (Fellows 2018), easystats (Lüdecke et al. 2022), rstan (Stan Development Team 2023), rstanarm (Brilleman et al. 2018)

You may need to [download and install a package](#) or [load a package](#) for some of these commands to work.

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2 Week 1: The Philosophy of Science

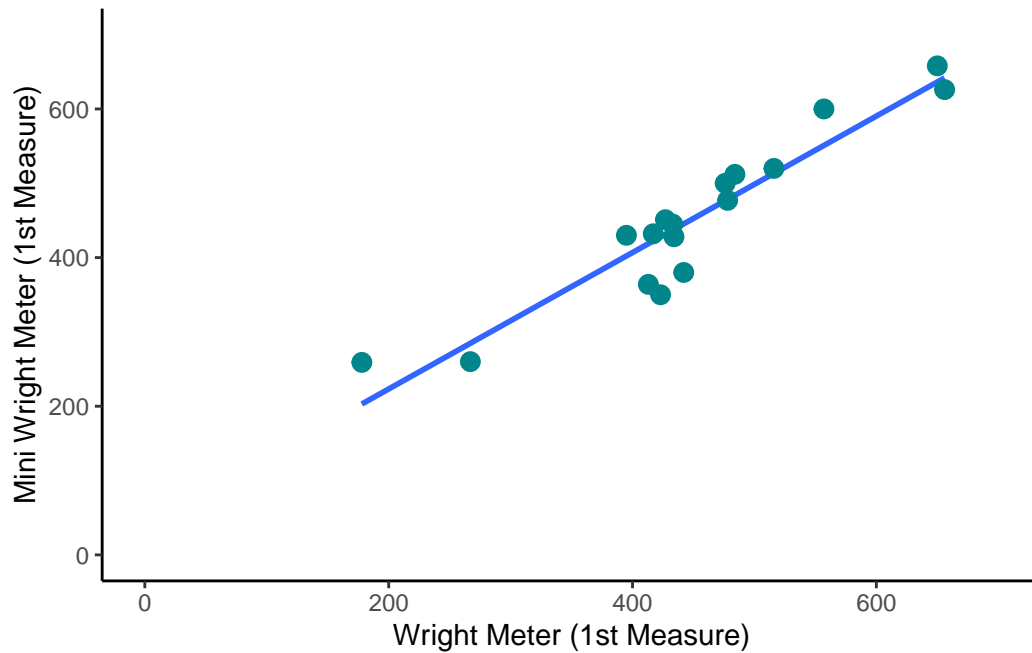
Lecture 3: The Replication Crisis

Bland-Altman Plots are generated with the following code.

```
library(tidyverse)

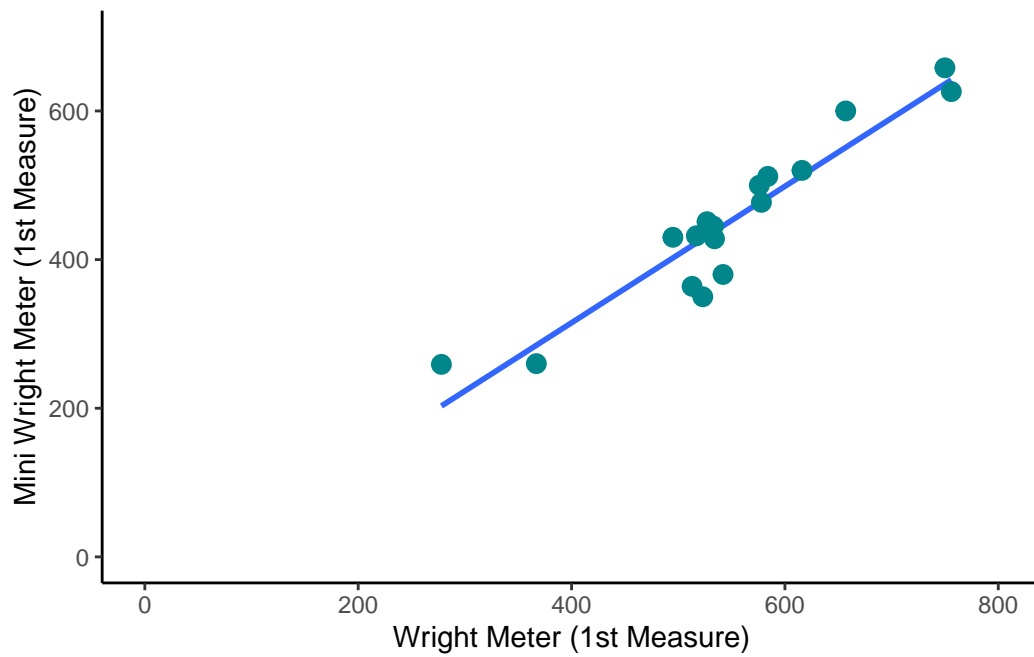
bland <- tibble(
  subject = c(1:17),
  Wright1 = c(484,395,516,434,476,557,413,442,650,433,417,656,267,478,178,423,427),
  Wright2 = c(490,397,512,401,470,611,415,431,638,429,420,633,275,492,165,372,421),
  Mini1 = c(512,430,520,428,500,600,364,380,658,445,432,626,260,477,259,350,451),
  Mini2 = c(525,415,508,444,500,625,460,390,642,432,420,605,227,467,268,370,443)
)

bland |>
  ggplot(aes(x = Wright1, y = Mini1)) +
  stat_smooth(method="lm", se=FALSE) +
  geom_point(colour = "turquoise4", size = 3) +
  scale_x_continuous(limits = c(0,700)) +
  scale_y_continuous(limits = c(0,700)) +
  theme_classic() +
  labs(x = "Wright Meter (1st Measure)", y = "Mini Wright Meter (1st Measure)")
```



And then if we add 100 to each measure, we see a very similar plot:

```
bland |>
  mutate (Wright1 = (Wright1+100)) %>%
  ggplot(aes(x = Wright1, y = Mini1)) +
  stat_smooth(method="lm", se=FALSE) +
  geom_point(colour = "turquoise4", size = 3) +
  scale_x_continuous(limits = c(0,800)) +
  scale_y_continuous(limits = c(0,700)) +
  theme_classic() +
  labs(x = "Wright Meter (1st Measure)", y = "Mini Wright Meter (1st Measure)")
```



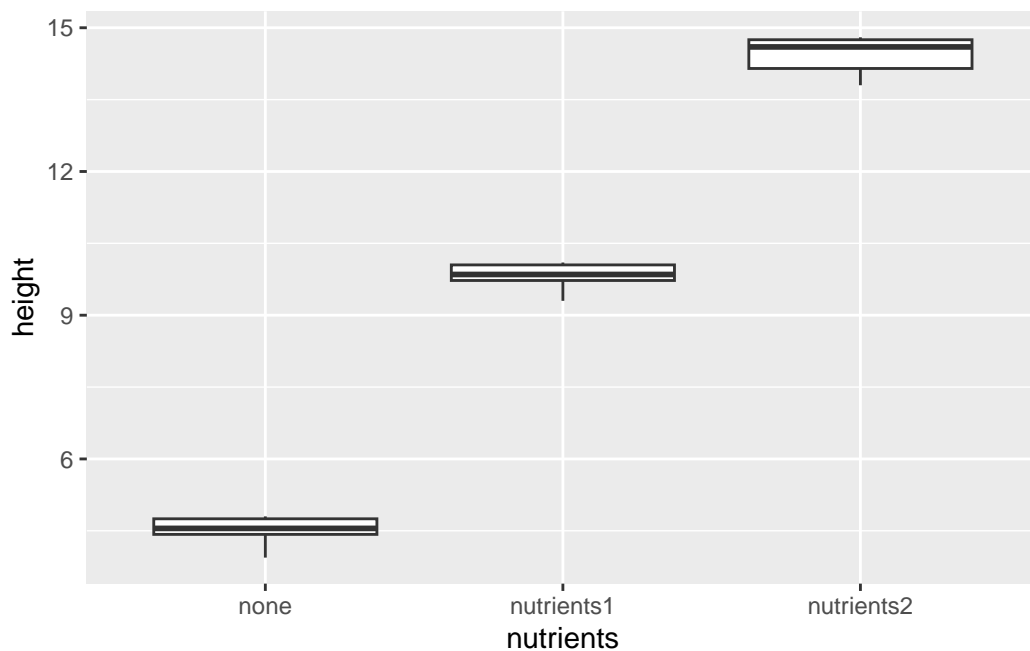
Lecture 5: Introduction to Research Methods

2.1 Create data and plot

```
library(tidyverse)

plants <- tibble(none = c(4.8, 4.8, 3.94, 4.4,4.5,4.6),
                 nutrients1 = c( 10.1, 9.7, 9.8, 9.9, 9.3, 10.1),
                 nutrients2 = c(14.8, 14.6, 14.8, 14, 13.8, 14.6))

plants |>
  pivot_longer(cols = c(none, nutrients1,nutrients2),
               names_to = "nutrients",
               values_to = "height") |>
  ggplot(aes(x = nutrients, y = height)) +
  geom_boxplot()
```



2.2 Run an ANOVA on Plant data

```
longplants <- plants |>
  pivot_longer(cols = c(none, nutrients1, nutrients2),
               names_to = "nutrients",
               values_to = "height")

plant_model <- aov(height ~ nutrients, data = longplants)

summary(plant_model)
```

```
              Df Sum Sq Mean Sq F value Pr(>F)
nutrients      2  296.10   148.05    1184 <2e-16 ***
Residuals     15    1.88    0.13
---
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

2.3 Read and Run Crude Chicken Correlations

```
crudechicks <- tibble(year = c("2000", "2001", "2002", "2003",
                               "2004", "2005", "2006", "2007",
                               "2008", "2009"),
                      chicken = c(54.2, 54, 56.8, 57.5, 59.3, 60.5, 60.9,
                                   59.9, 58.7, 56),
                      crude = c(3311, 3405, 3336, 3521, 3674, 3670, 3685,
                                 3656, 3571, 3307))

cor.test(crudechicks$chicken, crudechicks$crude, method = "spearman")
```

Spearman's rank correlation rho

```
data: crudechicks$chicken and crudechicks$crude
S = 20, p-value = 0.001977
alternative hypothesis: true rho is not equal to 0
sample estimates:
      rho
0.8787879
```

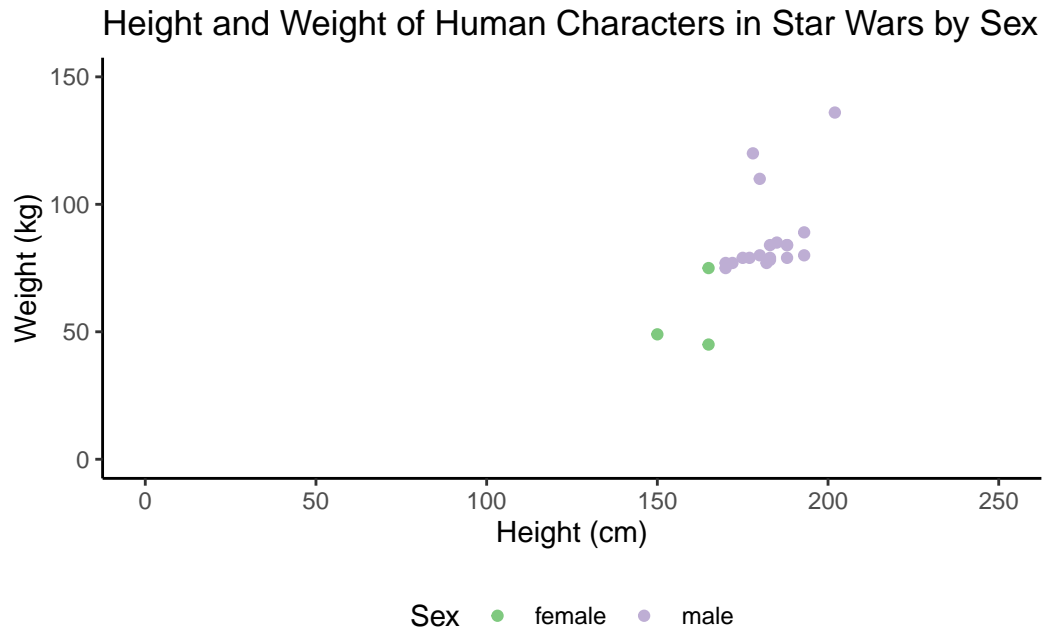
3 Week 2: The Use and Abuse of Data

Lecture 2: Data Visualisation

This code will help you replicate the charts in Lecture 2

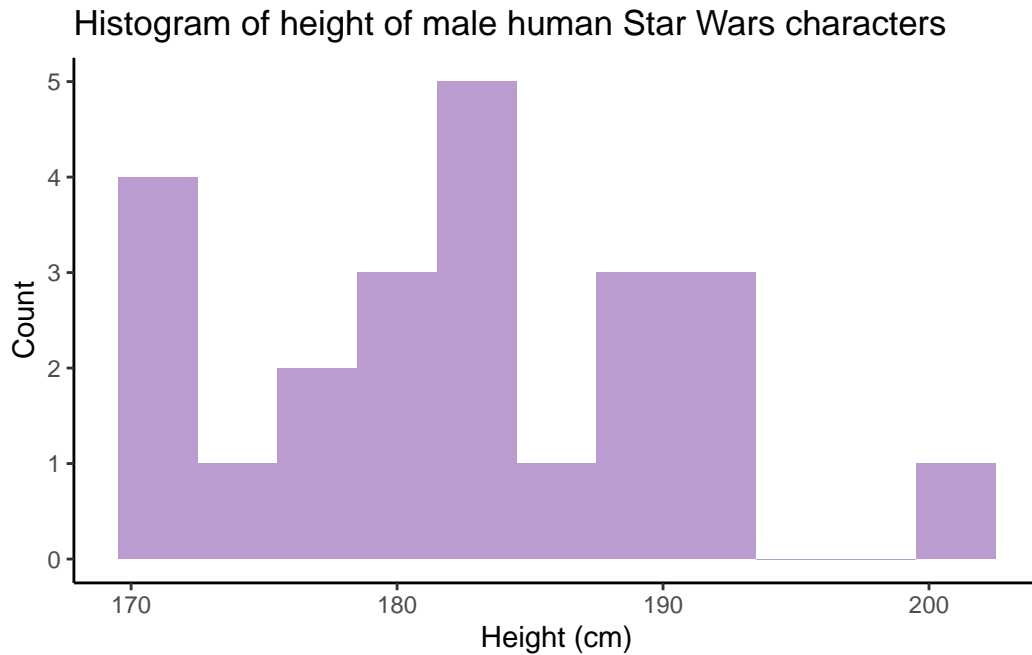
Height vs Weight by Sex

```
starwars |>
  filter(species == "Human") |>
  ggplot(aes(x = height, y = mass, colour = sex)) +
  geom_point() +
  theme_classic() +
  scale_x_continuous(limits = c(0,250)) +
  scale_y_continuous(limits = c(0,150)) +
  scale_colour_brewer(palette = "Accent", name = "Sex") +
  theme(legend.position = "bottom") +
  labs(x = "Height (cm)",
       y = "Weight (kg)",
       title = "Height and Weight of Human Characters in Star Wars by Sex")
```



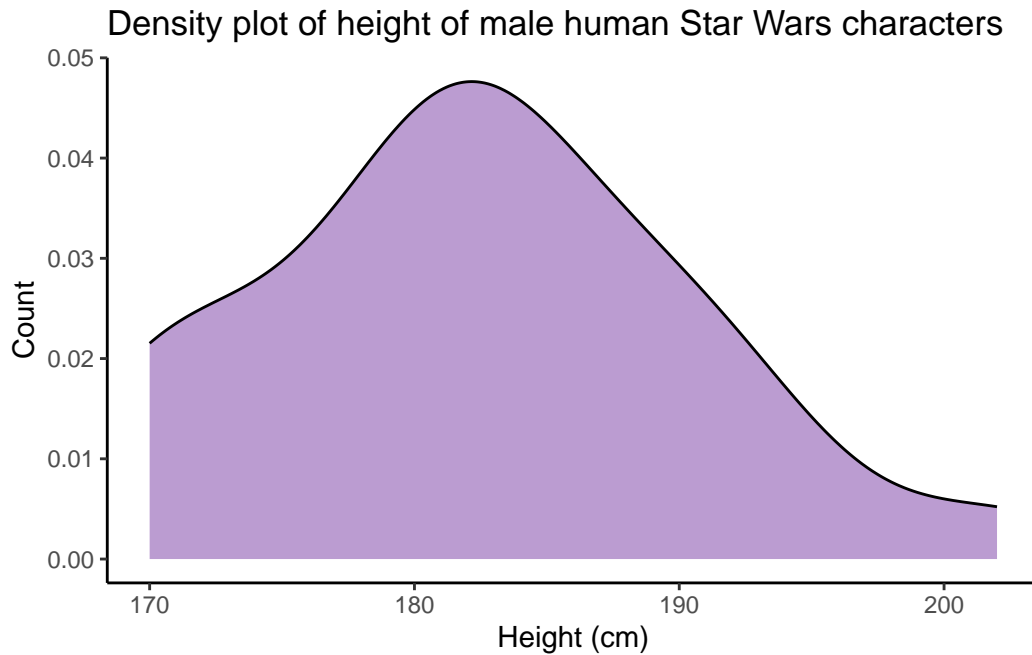
Histogram of male height

```
starwars |>
  filter(species == "Human",
         sex == "male") |>
  ggplot(aes(x = height)) +
  geom_histogram(binwidth = 3, fill = "#bb9cd1") +
  theme_classic() +
  labs(x = "Height (cm)",
       y = "Count",
       title = "Histogram of height of male human Star Wars characters")
```

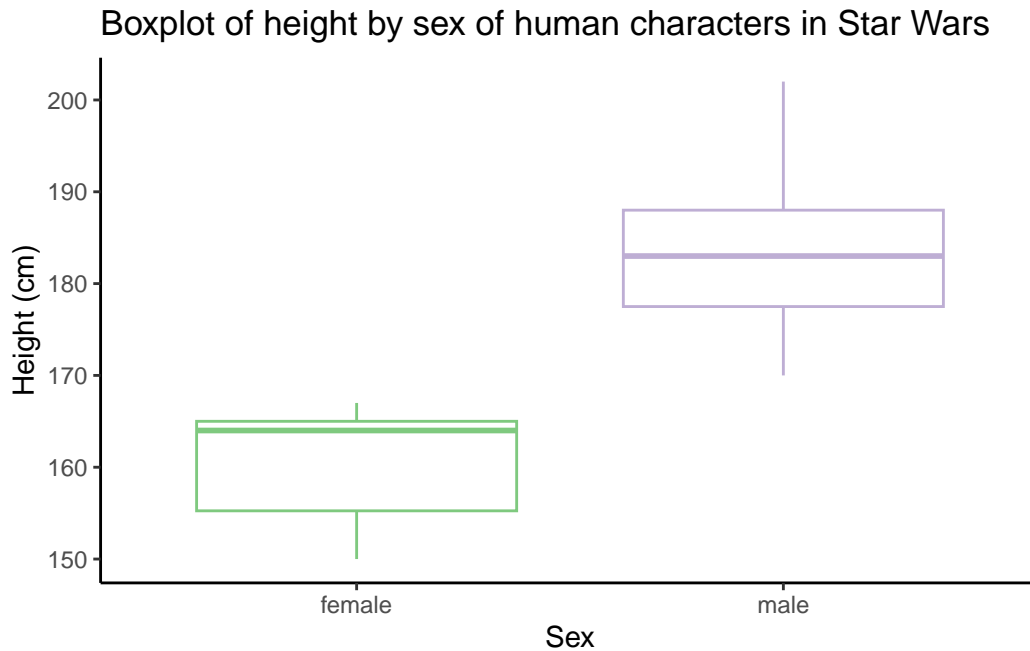
Density plot of male height

```
starwars |>
  filter(species == "Human",
         sex == "male") |>
  ggplot(aes(x = height)) +
  geom_density(fill = "#bb9cd1") +
  theme_classic() +
  labs(x = "Height (cm)",
       y = "Count",
       title = "Density plot of height of male human Star Wars characters")
```



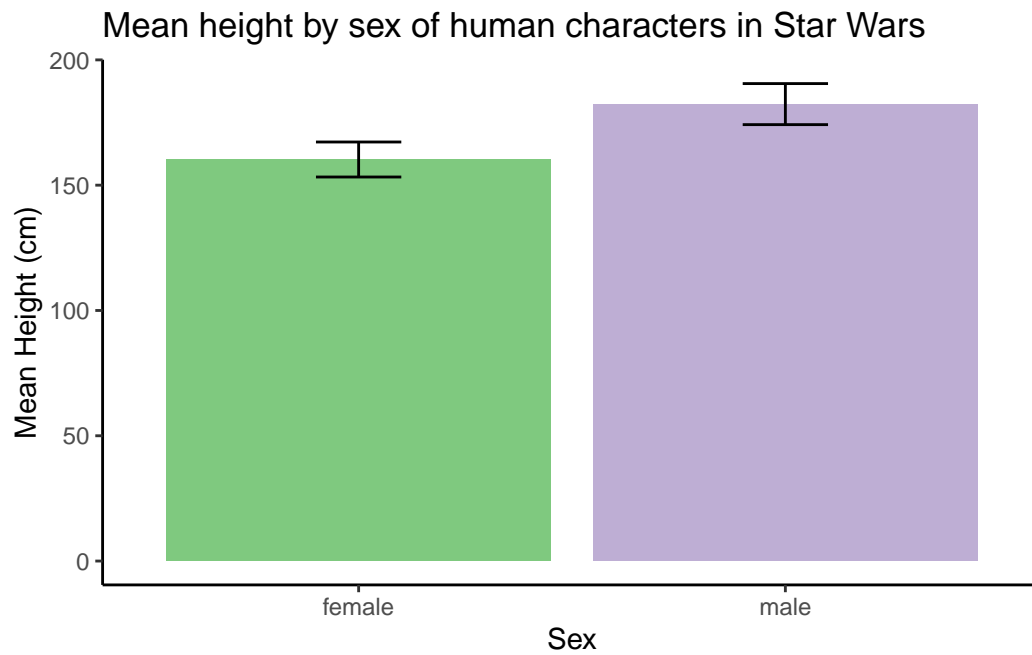
Boxplot of height

```
starwars |>
  filter(species == "Human") |>
  ggplot(aes(y = height, x = sex, colour = sex)) +
  geom_boxplot() +
  theme_classic() +
  scale_colour_brewer(palette = "Accent", name = "Sex") +
  labs(y = "Height (cm)",
       x = "Sex",
       title = "Boxplot of height by sex of human characters in Star Wars") +
  theme(legend.position = "none")
```



Mean height (bar chart)

```
starwars |>
  filter(species == "Human") |>
  group_by(sex) |>
  summarise(ht = mean(height, na.rm = TRUE),
            sd = sd(height, na.rm = TRUE)) |>
  ggplot(aes(x = sex, y = ht, fill = sex)) +
  geom_bar(stat = "identity") +
  geom_errorbar(aes(ymin = ht-sd, ymax = ht+sd), width = 0.2)+
  scale_fill_brewer(palette = "Accent") +
  labs(y = "Mean Height (cm)",
       x = "Sex",
       title = "Mean height by sex of human characters in Star Wars") +
  theme_classic() +
  theme(legend.position = "none")
```

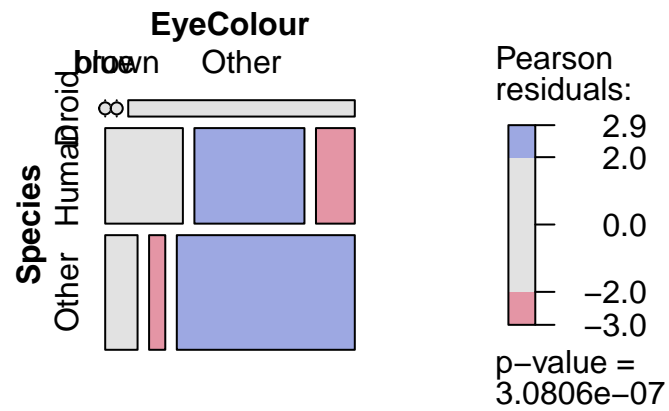


Mosaic Plot

```
library(vcd)

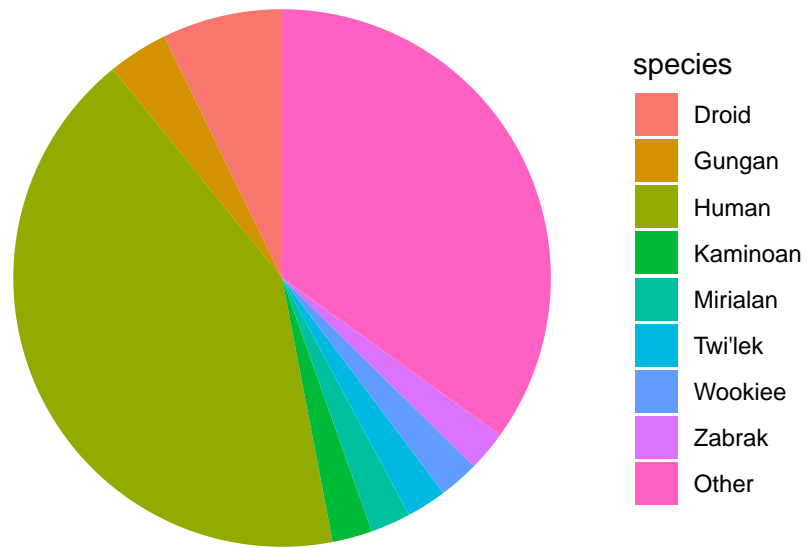
startbl <- starwars |>
  mutate(Species = fct_lump_n(species, 2),
         EyeColour = fct_lump_n(eye_color, 2))

mosaic(~ Species + EyeColour, data = startbl, shade = TRUE, legend = TRUE)
```

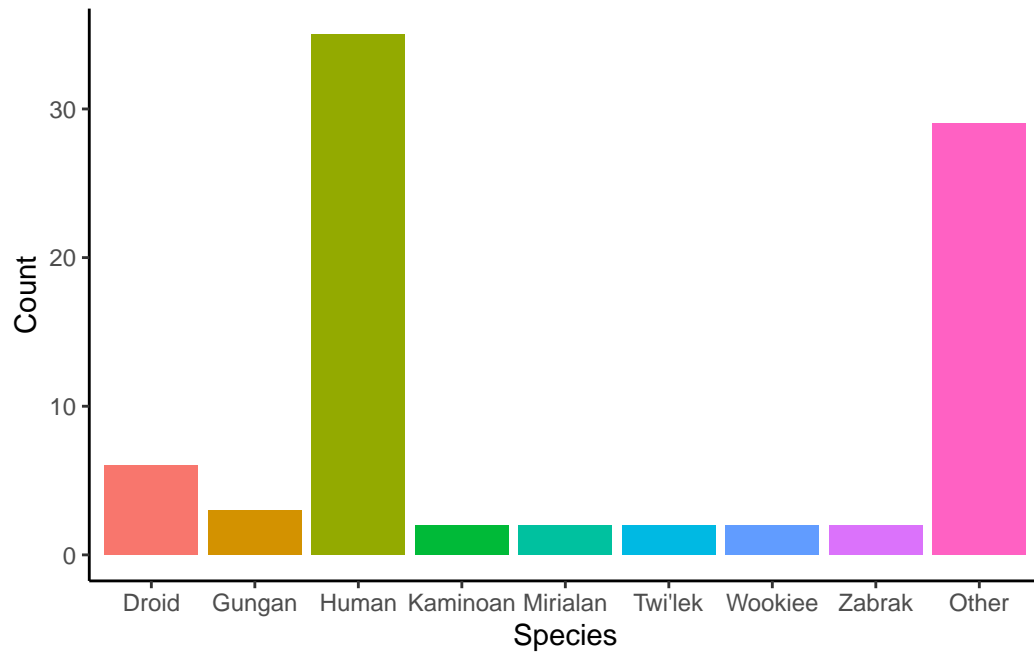


Pie Charts are Just Bad Bar Charts

```
starwars |>
  mutate(species = fct_lump_n(species, 4)) |>
  group_by(species) |>
  filter(!is.na(species)) |>
  tally() |>
  ggplot(aes(x = "", fill = species, y = n)) +
  geom_bar(stat = "identity", width = 1) +
  theme_void() +
  coord_polar("y", start = 0)
```



```
starwars |>
  mutate(species = fct_lump_n(species, 4)) |>
  group_by(species) |>
  filter(!is.na(species)) |>
  tally() |>
  ggplot(aes(x = species, fill = species, y = n)) +
  geom_bar(stat = "identity") +
  theme_classic() +
  labs(x = "Species", y = "Count") +
  theme(legend.position = "none")
```



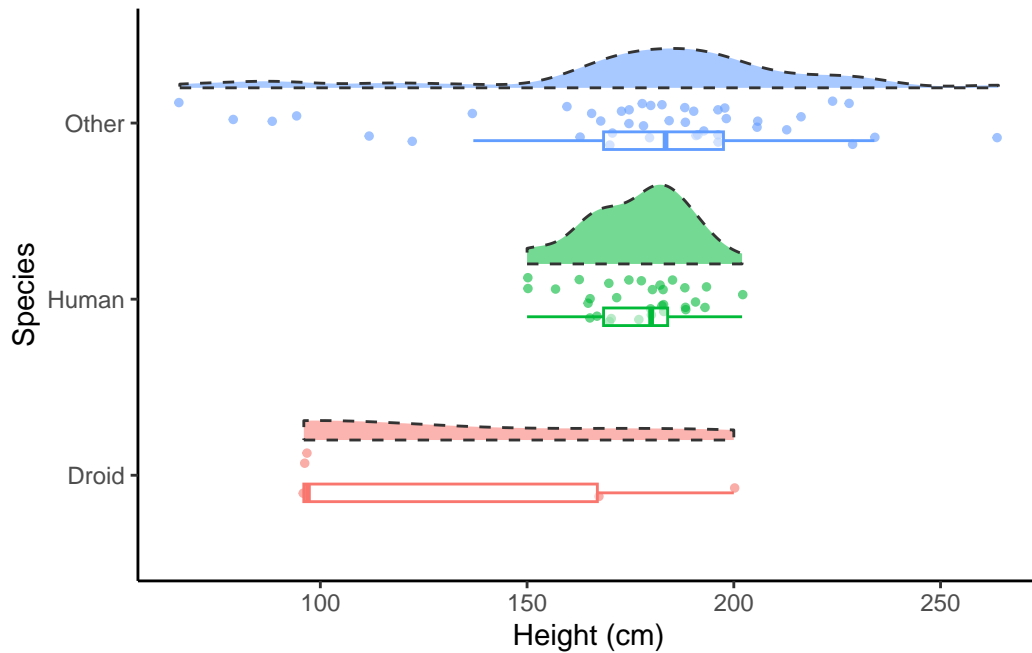
Wordclouds

```
library(wordcloud)
starwars |>
  count(homeworld) |>
  with(wordcloud(words = homeworld, freq = n, min.freq=1, random.order = FALSE, rot.per =
    colors = brewer.pal(6, "Accent"), use.r.layout = FALSE))
```



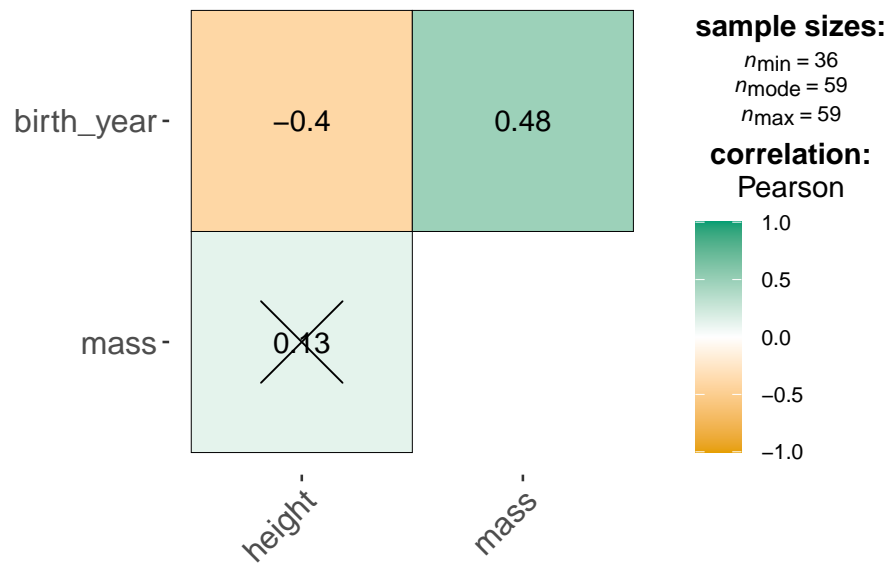
Raincloud Plots

```
starwars |>
  mutate(species = fct_lump_n(species,2)) |>
  filter(!is.na(species)) |>
  ggplot(aes(x = species)) +
  geom_point(aes(y = height, colour = species), position = position_jitter(width = .13), s
  see::geom_violinhalf(aes(y = height, alpha= 0.3, fill = species), linetype = "dashed", p
  geom_boxplot(aes(y = height, alpha = 0.3, colour = species), position = position_nudge(x
  theme_classic() +
  labs(x = "Species", y = "Height (cm)") +
  theme(legend.position = "none") +
  coord_flip()
```

Bubble plots

```
starwars |>
  mutate(col = fct_lump_n(species, 2)) |>
  ggplot(aes(x = birth_year, y = mass, size = height, colour = col)) +
  geom_point() +
  scale_size(range = c(.1, 24), name="Height") +
  theme_classic() +
  scale_x_continuous(limits = c(0,250)) +
  scale_y_continuous(limits = c(0,300)) +
  scale_colour_brewer(palette = "Accent", name = "Species") +
  theme(legend.position = "bottom") +
  labs(x = "Birth Year (Before Battle of Yavin)",
       y = "Weight (kg)",
       title = "Weight by Age of Characters in Star Wars")
```

X = non-significant at $p < 0.05$ (Adjustment: Holm)

Lecture 3: The Mean as a Basic Model

Data and custom function for this lecture

```
library(tidyverse)

heifers <- tibble(heifers = c(211.3, 200.4, 220.1, 200.8, 222.0, 209.3,
                             195.8, 220.4, 226.2, 218.7, 193.7, 209.7))

wage <- readxl::read_excel("assets/UKWageData2023ONS.xlsx",
                           skip = 5)

find_mode <- function(x) {
  ux <- unique(x)
  tab <- tabulate(match(x, ux))
  ux[tab == max(tab)]
}
```

Finding central tendency

```
heifers |>
  summarise(mean = mean(heifers),
            median = median(heifers),
            min = min(heifers),
            max = max(heifers),
            mode = find_mode(round(heifers, 0)))
```

A tibble: 1 x 5

	mean	median	min	max	mode
	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	211.	210.	194.	226.	220

```
wage |>
  summarise(mean = mean(Median),
            median = median(Median),
            min = min(Median),
            max = max(Median),
            mode = find_mode(round(Median,0)))
```

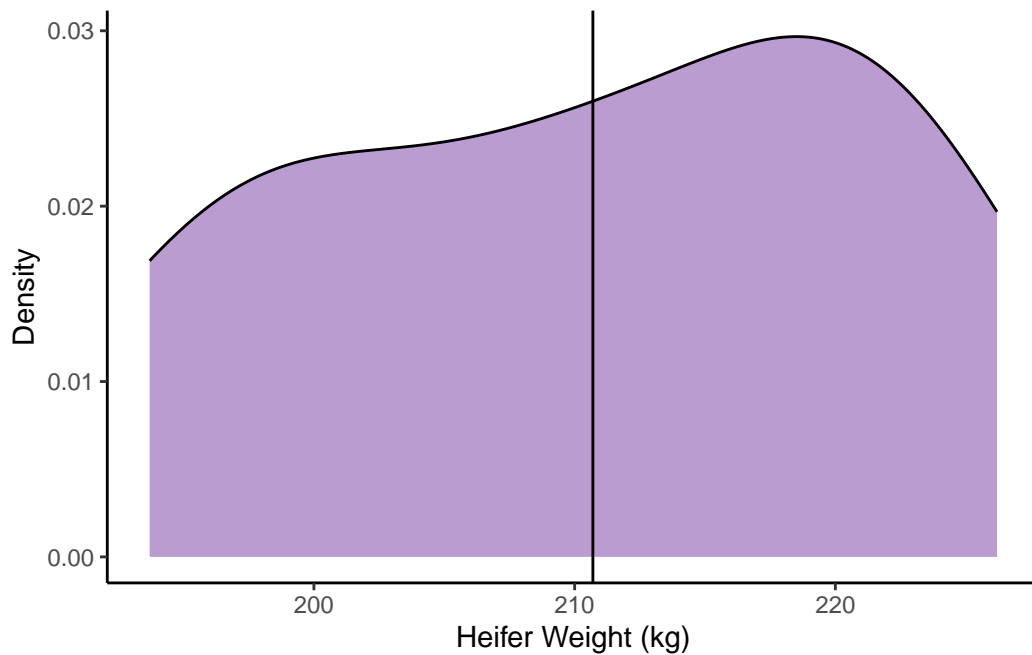
```
# A tibble: 4 x 5
   mean median   min   max  mode
  <dbl>  <dbl> <dbl> <dbl> <dbl>
1 34475.   31988 17859 84131 28216
2 34475.   31988 17859 84131 35248
3 34475.   31988 17859 84131 26000
4 34475.   31988 17859 84131 25000
```

The Mean and Outliers

```
heifers |>
  ggplot(aes(x = heifers)) +
  geom_density(fill = "#bb9cd1") +
  theme_classic() +
  labs(x = "Heifer Weight (kg)",
       y = "Density")
```

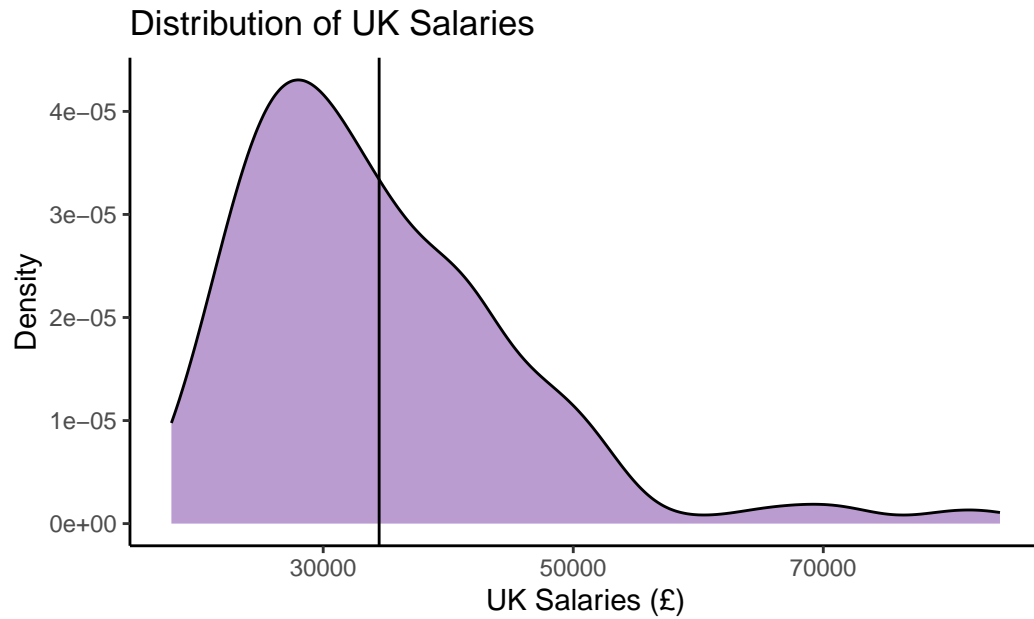


```
heifers |>
  ggplot(aes(x = heifers)) +
  geom_density(fill = "#bb9cd1") +
  geom_vline(aes(xintercept = 210.7)) +
  theme_classic() +
  labs(x = "Heifer Weight (kg)",
       y = "Density")
```



Mean UK Salary

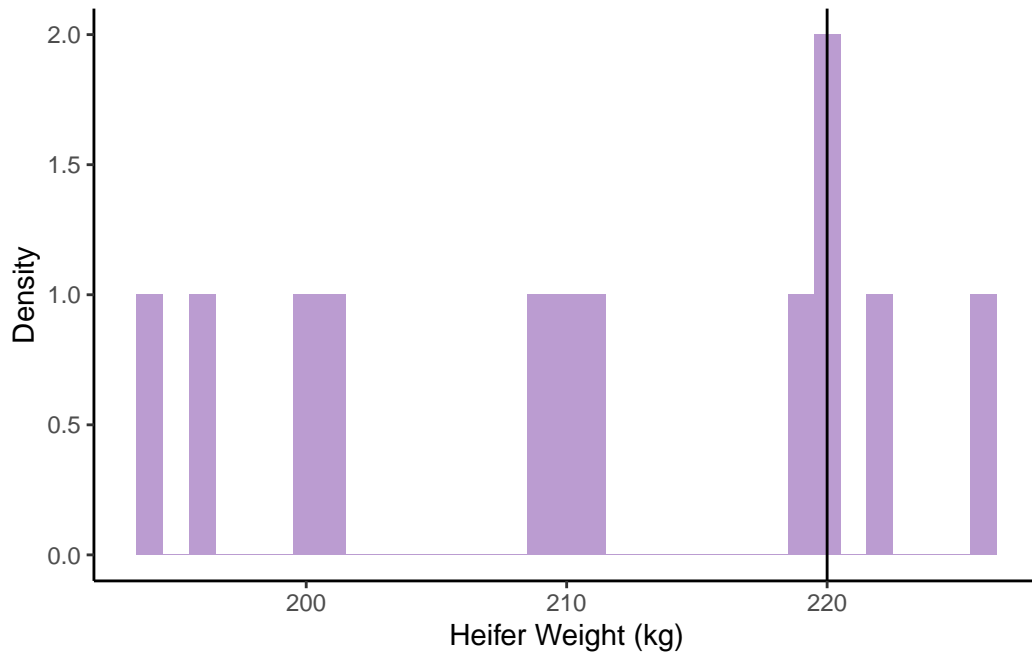
```
wage |>
  ggplot(aes(x = Median)) +
  geom_density(fill = "#bb9cd1") +
  theme_classic() +
  geom_vline(aes(xintercept = 34475)) +
  labs(x = "UK Salaries (£)",
       y = "Density",
       title = "Distribution of UK Salaries",
       caption = "Data taken from ONS 2023 Median Salaries by Field, n = 329 fields")
```



Data taken from ONS 2023 Median Salaries by Field, n = 329 fields

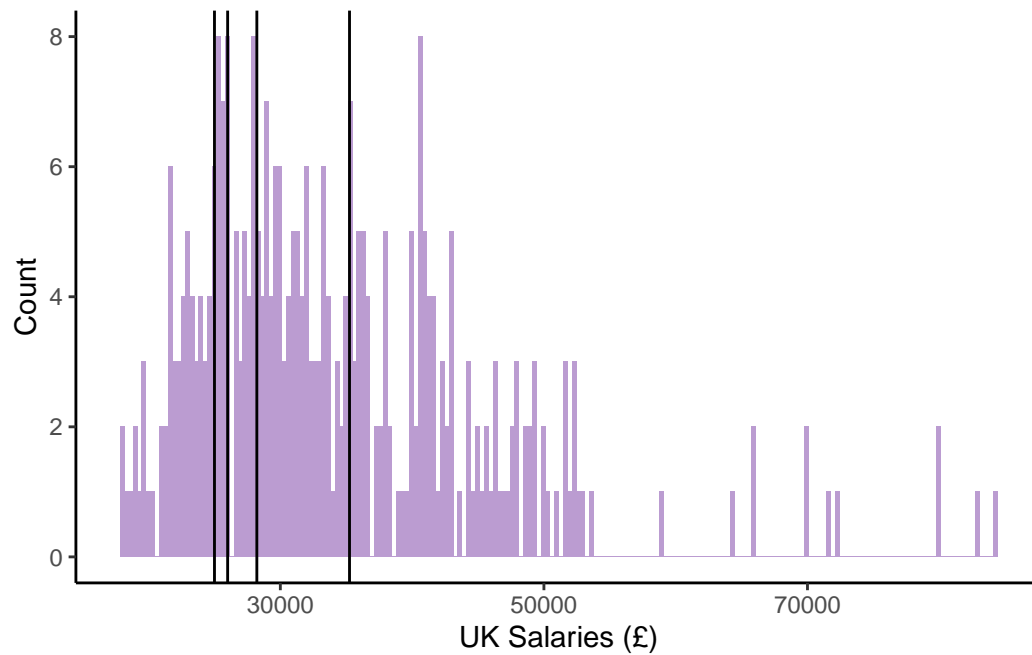
The Mode

```
heifers |>
  ggplot(aes(x = heifers)) +
  geom_histogram(fill = "#bb9cd1", binwidth = 1) +
  geom_vline(aes(xintercept = 220)) +
  theme_classic() +
  labs(x = "Heifer Weight (kg)",
       y = "Density")
```

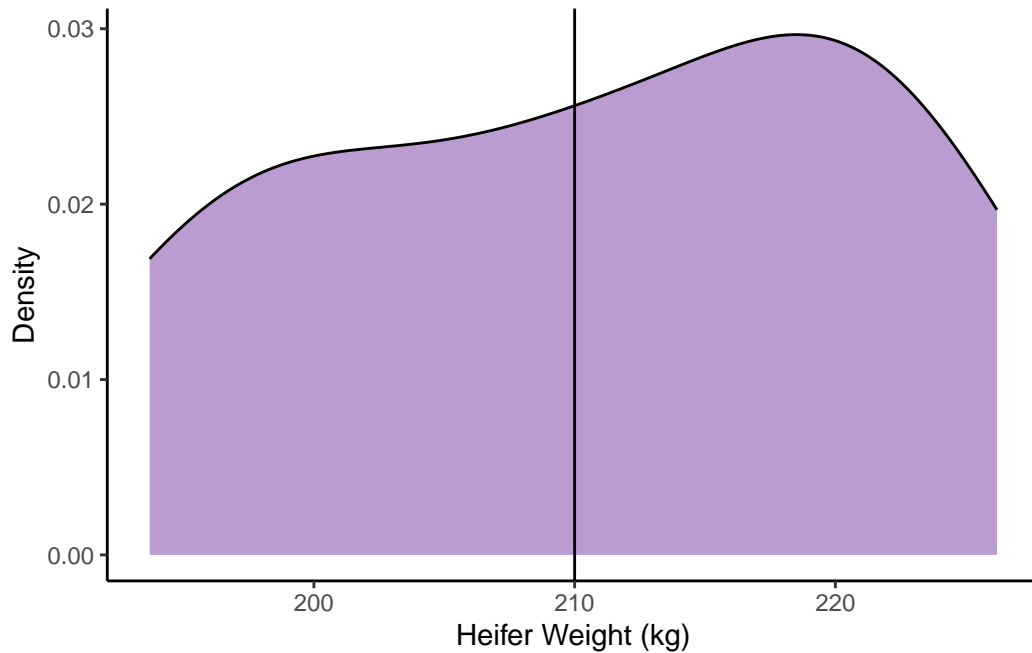
Multiple Modes

```
wage |>
  ggplot(aes(x = Median)) +
  geom_histogram(fill = "#bb9cd1", bins = 200) +
  geom_vline(aes(xintercept = 25000)) +
  geom_vline(aes(xintercept = 26000)) +
  geom_vline(aes(xintercept = 28216)) +
  geom_vline(aes(xintercept = 35248)) +
  theme_classic() +
  labs(x = "UK Salaries (£)",
       y = "Count")
```



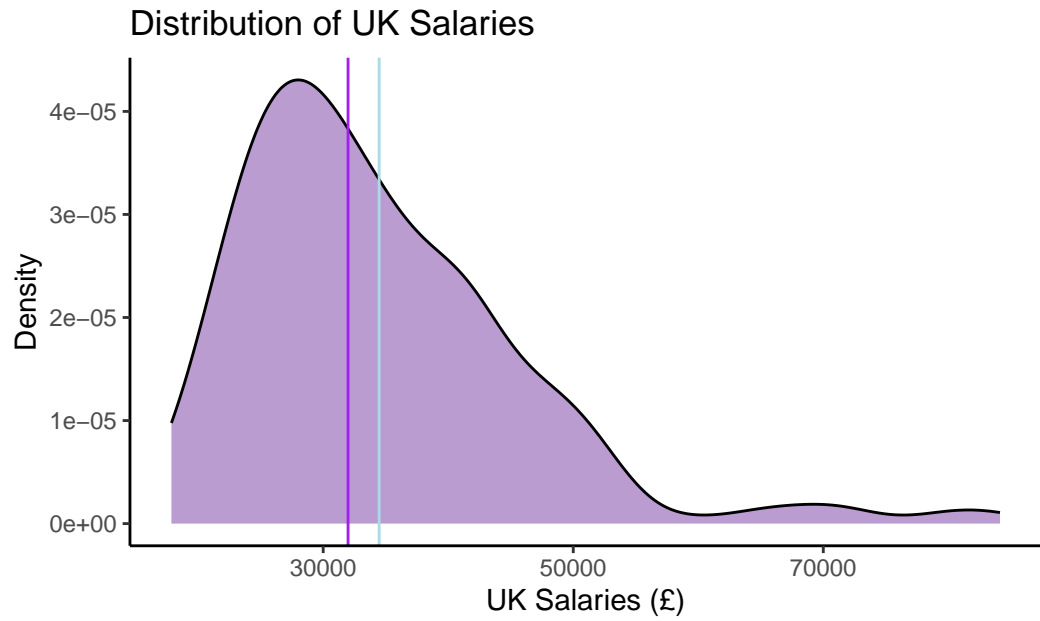
The Median

```
heifers |>
  ggplot(aes(x = heifers)) +
  geom_density(fill = "#bb9cd1") +
  geom_vline(aes(xintercept = 210)) +
  theme_classic() +
  labs(x = "Heifer Weight (kg)",
       y = "Density")
```



Median UK Salary

```
wage |>
  ggplot(aes(x = Median)) +
  geom_density(fill = "#bb9cd1") +
  theme_classic() +
  geom_vline(aes(xintercept = 34475), colour = "lightblue") +
  geom_vline(aes(xintercept = 31988), colour = "purple") +
  labs(x = "UK Salaries (£)",
       y = "Density",
       title = "Distribution of UK Salaries",
       caption = "Data taken from ONS 2023 Median Salaries by Field, n = 329 fields")
```



Data taken from ONS 2023 Median Salaries by Field, n = 329 fields

4 Week 3: Introduction to Analyses

Lecture 2: Introduction to statistics

Set up your environment and packages

```
library(tidyverse)
library(easystats)
library(rstan)
library(rstanarm)

cat_weights <- tibble(avg_daily_snacks = c(3, 2, 4, 2, 3, 1, 1, 0, 1, 0, 2, 3, 1, 2, 1, 3),
  weight = c(3.8, 3.9, 5, 3.7, 4.1, 3.6, 3.7, 3.6, 3.8, 4.1, 4.3, 3.9, 3.7, 3.8, 3.9),
  environ = c("Indoor", "Indoor", "Outdoor", "Indoor",
    "Outdoor", "Indoor", "Outdoor", "Indoor",
    "Indoor", "Indoor", "Outdoor", "Indoor",
    "Outdoor", "Indoor", "Indoor", "Outdoor"))
```

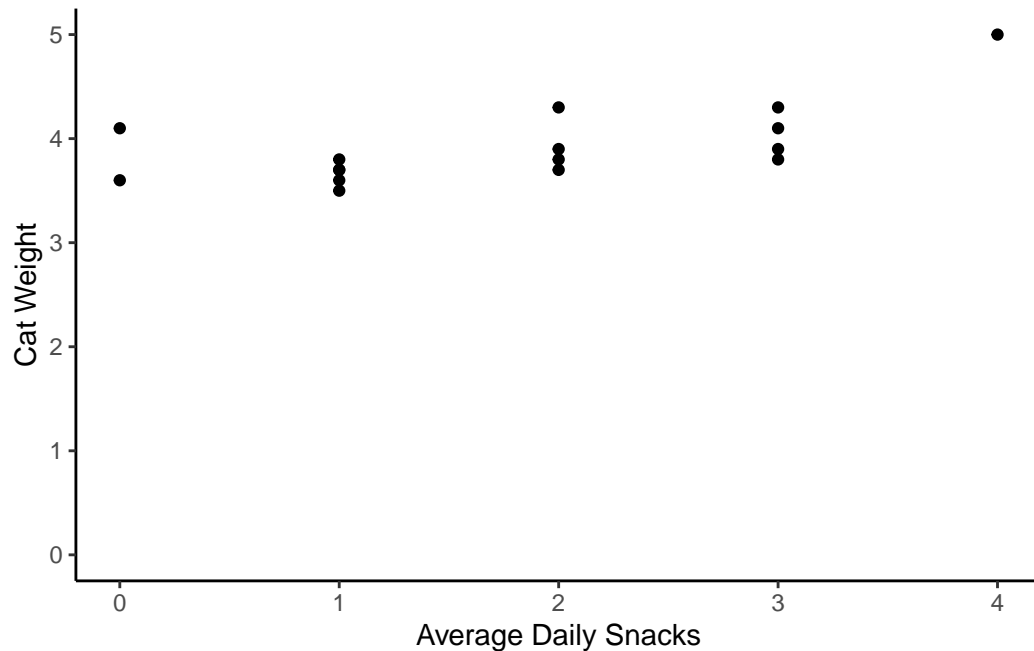
Summarise example data

```
cat_weights |>
  summarise("Mean Weight (kg)" = mean(weight),
            "SD Weight (kg)" = sd(weight),
            "Mean Daily Snacks" = mean (avg_daily_snacks),
            )
```

```
# A tibble: 1 x 3
  `Mean Weight (kg)` `SD Weight (kg)` `Mean Daily Snacks`
      <dbl>          <dbl>          <dbl>
1      3.92         0.373          1.81
```

Visualise example data

```
cat_weights |>
  ggplot(aes(x = avg_daily_snacks, y = weight)) +
  geom_point() +
  labs(x = "Average Daily Snacks", y = "Cat Weight") +
  theme_classic() +
  scale_y_continuous(limits = c(0,5))
```



A Linear Model

```
model_fcat <- lm(weight ~ avg_daily_snacks, data = cat_weights)
summary(model_fcat)
```

Call:

```
lm(formula = weight ~ avg_daily_snacks, data = cat_weights)
```

Residuals:

Min	1Q	Median	3Q	Max
-----	----	--------	----	-----

```
-0.36758 -0.18723 -0.06116 0.06705 0.62813
```

Coefficients:

```
              Estimate Std. Error t value Pr(>|t|)
(Intercept)    3.55474    0.14045  25.309 4.33e-13 ***
avg_daily_snacks 0.20428    0.06576   3.107 0.00773 **
---
```

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.2973 on 14 degrees of freedom

Multiple R-squared: 0.4081, Adjusted R-squared: 0.3658

F-statistic: 9.652 on 1 and 14 DF, p-value: 0.007729

```
report::report(model_fcat)
```

We fitted a linear model (estimated using OLS) to predict weight with avg_daily_snacks (formula: weight ~ avg_daily_snacks). The model explains a statistically significant and substantial proportion of variance ($R^2 = 0.41$, $F(1, 14) = 9.65$, $p = 0.008$, adj. $R^2 = 0.37$). The model's intercept, corresponding to avg_daily_snacks = 0, is at 3.55 (95% CI [3.25, 3.86], $t(14) = 25.31$, $p < .001$). Within this model:

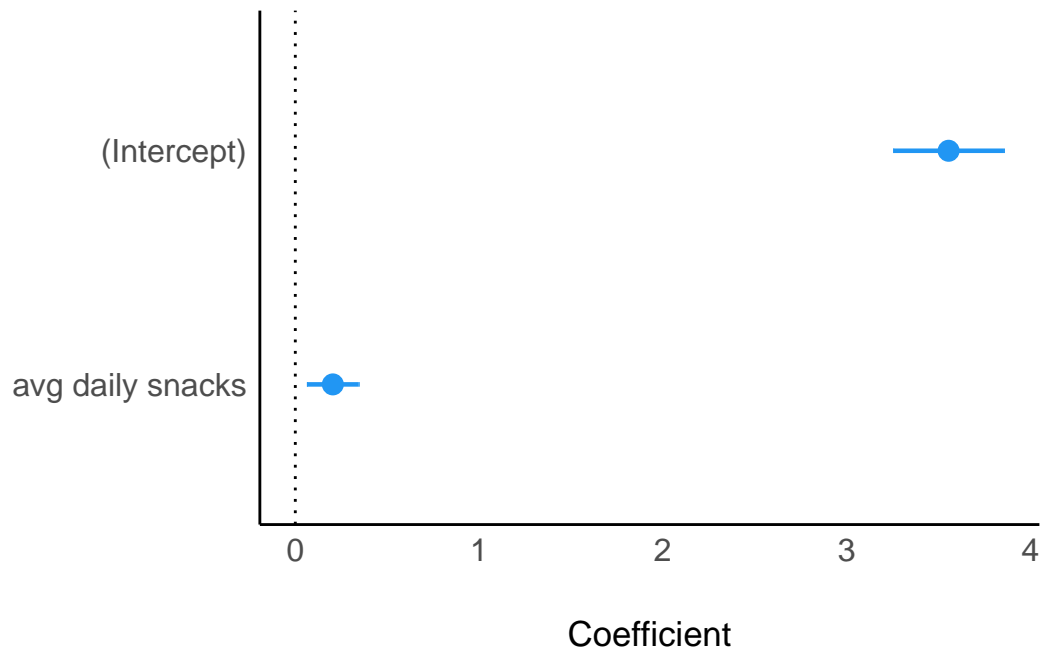
- The effect of avg daily snacks is statistically significant and positive (beta = 0.20, 95% CI [0.06, 0.35], $t(14) = 3.11$, $p = 0.008$; Std. beta = 0.64, 95% CI [0.20, 1.08])

Standardized parameters were obtained by fitting the model on a standardized version of the dataset. 95% Confidence Intervals (CIs) and p-values were computed using a Wald t-distribution approximation.

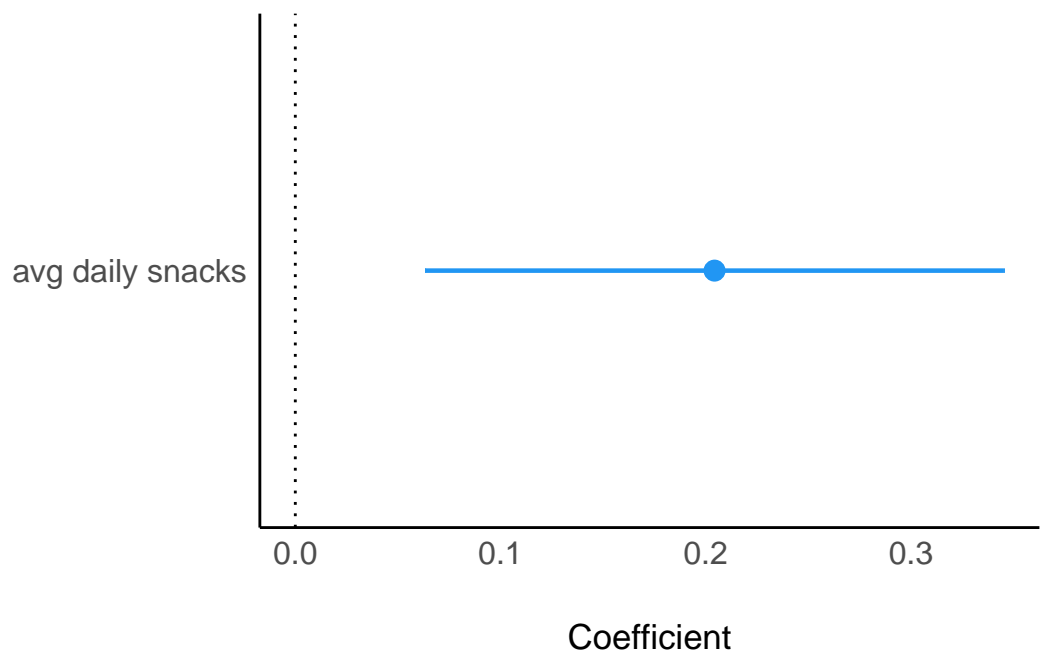
```
parameters(model_fcat)
```

Parameter	Coefficient	SE	95% CI	t(14)	p
(Intercept)	3.55	0.14	[3.25, 3.86]	25.31	< .001
avg daily snacks	0.20	0.07	[0.06, 0.35]	3.11	0.008

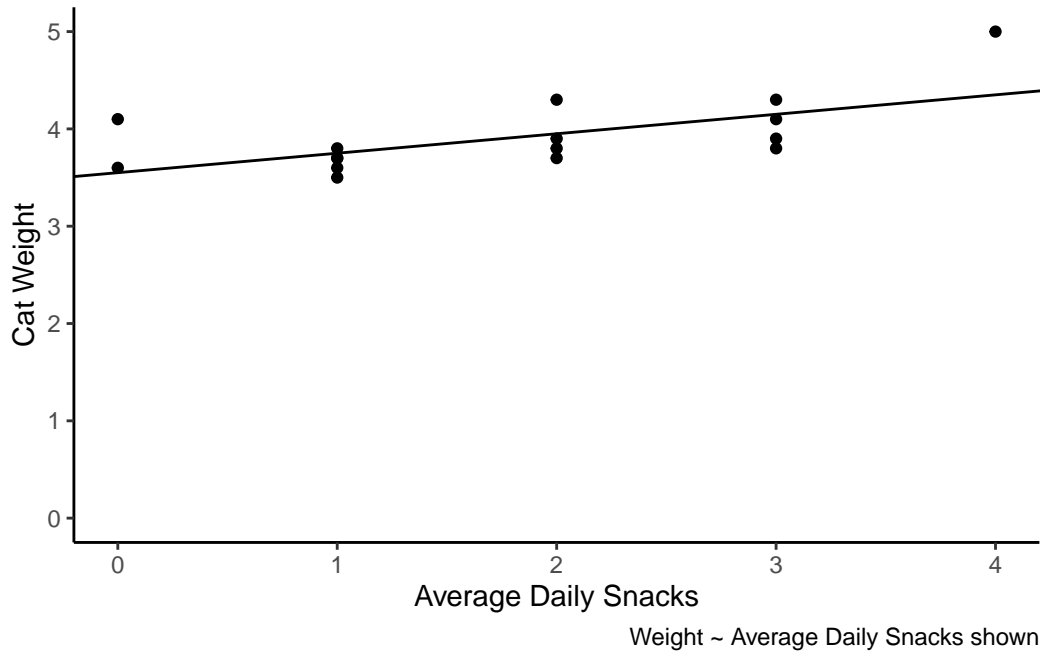
```
plot(model_parameters(model_fcat), show_intercept = TRUE)
```

```
plot(model_parameters(model_fcat))
```



```
cat_weights |>
  ggplot(aes(x = avg_daily_snacks, y = weight)) +
  geom_point() +
  labs(x = "Average Daily Snacks", y = "Cat Weight",
       caption = "Weight ~ Average Daily Snacks shown") +
  theme_classic() +
  scale_y_continuous(limits = c(0,5)) +
  geom_abline(slope = 0.20, intercept = 3.55)
```



A Bayesian Model

```
set.seed(10)

model_bcat <- stan_glm(weight ~ avg_daily_snacks, data = cat_weights)
```

SAMPLING FOR MODEL 'continuous' NOW (CHAIN 1).

Chain 1:

Chain 1: Gradient evaluation took 0.002048 seconds

Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 20.48 seconds.

Chain 1: Adjust your expectations accordingly!

Chain 1:

Chain 1:

Chain 1: Iteration: 1 / 2000 [0%] (Warmup)

Chain 1: Iteration: 200 / 2000 [10%] (Warmup)

Chain 1: Iteration: 400 / 2000 [20%] (Warmup)

Chain 1: Iteration: 600 / 2000 [30%] (Warmup)

Chain 1: Iteration: 800 / 2000 [40%] (Warmup)

Chain 1: Iteration: 1000 / 2000 [50%] (Warmup)

Chain 1: Iteration: 1001 / 2000 [50%] (Sampling)

Chain 1: Iteration: 1200 / 2000 [60%] (Sampling)

Chain 1: Iteration: 1400 / 2000 [70%] (Sampling)

Chain 1: Iteration: 1600 / 2000 [80%] (Sampling)

Chain 1: Iteration: 1800 / 2000 [90%] (Sampling)

Chain 1: Iteration: 2000 / 2000 [100%] (Sampling)

Chain 1:

Chain 1: Elapsed Time: 0.053 seconds (Warm-up)

Chain 1: 0.04 seconds (Sampling)

Chain 1: 0.093 seconds (Total)

Chain 1:

SAMPLING FOR MODEL 'continuous' NOW (CHAIN 2).

Chain 2:

Chain 2: Gradient evaluation took 1.4e-05 seconds

Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 0.14 seconds.

Chain 2: Adjust your expectations accordingly!

Chain 2:

Chain 2:

Chain 2: Iteration: 1 / 2000 [0%] (Warmup)

Chain 2: Iteration: 200 / 2000 [10%] (Warmup)

Chain 2: Iteration: 400 / 2000 [20%] (Warmup)

Chain 2: Iteration: 600 / 2000 [30%] (Warmup)

Chain 2: Iteration: 800 / 2000 [40%] (Warmup)

Chain 2: Iteration: 1000 / 2000 [50%] (Warmup)

Chain 2: Iteration: 1001 / 2000 [50%] (Sampling)

Chain 2: Iteration: 1200 / 2000 [60%] (Sampling)

Chain 2: Iteration: 1400 / 2000 [70%] (Sampling)

Chain 2: Iteration: 1600 / 2000 [80%] (Sampling)

Chain 2: Iteration: 1800 / 2000 [90%] (Sampling)

Chain 2: Iteration: 2000 / 2000 [100%] (Sampling)

Chain 2:

Chain 2: Elapsed Time: 0.037 seconds (Warm-up)

Chain 2: 0.042 seconds (Sampling)

Chain 2: 0.079 seconds (Total)

Chain 2:

SAMPLING FOR MODEL 'continuous' NOW (CHAIN 3).

Chain 3:

Chain 3: Gradient evaluation took 1.4e-05 seconds

Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 0.14 seconds.

Chain 3: Adjust your expectations accordingly!

Chain 3:

Chain 3:

Chain 3: Iteration: 1 / 2000 [0%] (Warmup)

Chain 3: Iteration: 200 / 2000 [10%] (Warmup)

Chain 3: Iteration: 400 / 2000 [20%] (Warmup)

Chain 3: Iteration: 600 / 2000 [30%] (Warmup)

Chain 3: Iteration: 800 / 2000 [40%] (Warmup)

Chain 3: Iteration: 1000 / 2000 [50%] (Warmup)

Chain 3: Iteration: 1001 / 2000 [50%] (Sampling)

Chain 3: Iteration: 1200 / 2000 [60%] (Sampling)

Chain 3: Iteration: 1400 / 2000 [70%] (Sampling)

Chain 3: Iteration: 1600 / 2000 [80%] (Sampling)

Chain 3: Iteration: 1800 / 2000 [90%] (Sampling)

Chain 3: Iteration: 2000 / 2000 [100%] (Sampling)

Chain 3:

Chain 3: Elapsed Time: 0.038 seconds (Warm-up)

Chain 3: 0.038 seconds (Sampling)

Chain 3: 0.076 seconds (Total)

Chain 3:

SAMPLING FOR MODEL 'continuous' NOW (CHAIN 4).

Chain 4:

Chain 4: Gradient evaluation took 1.1e-05 seconds

Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 0.11 seconds.

Chain 4: Adjust your expectations accordingly!

Chain 4:

Chain 4:

Chain 4: Iteration: 1 / 2000 [0%] (Warmup)

Chain 4: Iteration: 200 / 2000 [10%] (Warmup)

Chain 4: Iteration: 400 / 2000 [20%] (Warmup)

Chain 4: Iteration: 600 / 2000 [30%] (Warmup)

Chain 4: Iteration: 800 / 2000 [40%] (Warmup)

Chain 4: Iteration: 1000 / 2000 [50%] (Warmup)

Chain 4: Iteration: 1001 / 2000 [50%] (Sampling)

Chain 4: Iteration: 1200 / 2000 [60%] (Sampling)

```
Chain 4: Iteration: 1400 / 2000 [ 70%] (Sampling)
Chain 4: Iteration: 1600 / 2000 [ 80%] (Sampling)
Chain 4: Iteration: 1800 / 2000 [ 90%] (Sampling)
Chain 4: Iteration: 2000 / 2000 [100%] (Sampling)
Chain 4:
Chain 4: Elapsed Time: 0.039 seconds (Warm-up)
Chain 4:           0.039 seconds (Sampling)
Chain 4:           0.078 seconds (Total)
Chain 4:
```

```
summary(model_bcat)
```

Model Info:

```
function:      stan_glm
family:        gaussian [identity]
formula:       weight ~ avg_daily_snacks
algorithm:     sampling
sample:        4000 (posterior sample size)
priors:        see help('prior_summary')
observations:  16
predictors:    2
```

Estimates:

	mean	sd	10%	50%	90%
(Intercept)	3.6	0.2	3.4	3.6	3.7
avg_daily_snacks	0.2	0.1	0.1	0.2	0.3
sigma	0.3	0.1	0.2	0.3	0.4

Fit Diagnostics:

	mean	sd	10%	50%	90%
mean_PPD	3.9	0.1	3.8	3.9	4.1

The mean_ppd is the sample average posterior predictive distribution of the outcome variable

MCMC diagnostics

	mcse	Rhat	n_eff
(Intercept)	0.0	1.0	3066
avg_daily_snacks	0.0	1.0	2981
sigma	0.0	1.0	2539
mean_PPD	0.0	1.0	3573

```
log-posterior    0.0  1.0  1450
```

For each parameter, mcse is Monte Carlo standard error, n_eff is a crude measure of effective

```
describe_posterior(model_bcat)
```

Summary of Posterior Distribution

Parameter	Median	95% CI	pd	ROPE	% in ROPE	Rhat	
(Intercept)	3.55	[3.26, 3.86]	100%	[-0.04, 0.04]	0%	1.001	3066
avg_daily_snacks	0.20	[0.06, 0.35]	99.62%	[-0.04, 0.04]	0%	1.000	2981

```
report::report(model_bcat)
```

SAMPLING FOR MODEL 'continuous' NOW (CHAIN 1).

Chain 1:

Chain 1: Gradient evaluation took 1.4e-05 seconds

Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 0.14 seconds.

Chain 1: Adjust your expectations accordingly!

Chain 1:

Chain 1:

Chain 1: Iteration: 1 / 2000 [0%] (Warmup)

Chain 1: Iteration: 200 / 2000 [10%] (Warmup)

Chain 1: Iteration: 400 / 2000 [20%] (Warmup)

Chain 1: Iteration: 600 / 2000 [30%] (Warmup)

Chain 1: Iteration: 800 / 2000 [40%] (Warmup)

Chain 1: Iteration: 1000 / 2000 [50%] (Warmup)

Chain 1: Iteration: 1001 / 2000 [50%] (Sampling)

Chain 1: Iteration: 1200 / 2000 [60%] (Sampling)

Chain 1: Iteration: 1400 / 2000 [70%] (Sampling)

Chain 1: Iteration: 1600 / 2000 [80%] (Sampling)

Chain 1: Iteration: 1800 / 2000 [90%] (Sampling)

Chain 1: Iteration: 2000 / 2000 [100%] (Sampling)

Chain 1:

Chain 1: Elapsed Time: 0.039 seconds (Warm-up)

Chain 1: 0.051 seconds (Sampling)

Chain 1: 0.09 seconds (Total)

Chain 1:

SAMPLING FOR MODEL 'continuous' NOW (CHAIN 2).

Chain 2:

Chain 2: Gradient evaluation took 1.2e-05 seconds

Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 0.12 seconds.

Chain 2: Adjust your expectations accordingly!

Chain 2:

Chain 2:

Chain 2: Iteration: 1 / 2000 [0%] (Warmup)

Chain 2: Iteration: 200 / 2000 [10%] (Warmup)

Chain 2: Iteration: 400 / 2000 [20%] (Warmup)

Chain 2: Iteration: 600 / 2000 [30%] (Warmup)

Chain 2: Iteration: 800 / 2000 [40%] (Warmup)

Chain 2: Iteration: 1000 / 2000 [50%] (Warmup)

Chain 2: Iteration: 1001 / 2000 [50%] (Sampling)

Chain 2: Iteration: 1200 / 2000 [60%] (Sampling)

Chain 2: Iteration: 1400 / 2000 [70%] (Sampling)

Chain 2: Iteration: 1600 / 2000 [80%] (Sampling)

Chain 2: Iteration: 1800 / 2000 [90%] (Sampling)

Chain 2: Iteration: 2000 / 2000 [100%] (Sampling)

Chain 2:

Chain 2: Elapsed Time: 0.037 seconds (Warm-up)

Chain 2: 0.047 seconds (Sampling)

Chain 2: 0.084 seconds (Total)

Chain 2:

SAMPLING FOR MODEL 'continuous' NOW (CHAIN 3).

Chain 3:

Chain 3: Gradient evaluation took 9e-06 seconds

Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 0.09 seconds.

Chain 3: Adjust your expectations accordingly!

Chain 3:

Chain 3:

Chain 3: Iteration: 1 / 2000 [0%] (Warmup)

Chain 3: Iteration: 200 / 2000 [10%] (Warmup)

Chain 3: Iteration: 400 / 2000 [20%] (Warmup)

Chain 3: Iteration: 600 / 2000 [30%] (Warmup)

Chain 3: Iteration: 800 / 2000 [40%] (Warmup)

Chain 3: Iteration: 1000 / 2000 [50%] (Warmup)

Chain 3: Iteration: 1001 / 2000 [50%] (Sampling)

Chain 3: Iteration: 1200 / 2000 [60%] (Sampling)

Chain 3: Iteration: 1400 / 2000 [70%] (Sampling)

Chain 3: Iteration: 1600 / 2000 [80%] (Sampling)

```
Chain 3: Iteration: 1800 / 2000 [ 90%] (Sampling)
Chain 3: Iteration: 2000 / 2000 [100%] (Sampling)
Chain 3:
Chain 3: Elapsed Time: 0.039 seconds (Warm-up)
Chain 3:           0.05 seconds (Sampling)
Chain 3:           0.089 seconds (Total)
Chain 3:
```

SAMPLING FOR MODEL 'continuous' NOW (CHAIN 4).

```
Chain 4:
Chain 4: Gradient evaluation took 1.2e-05 seconds
Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 0.12 seconds.
Chain 4: Adjust your expectations accordingly!
Chain 4:
Chain 4:
Chain 4: Iteration:    1 / 2000 [  0%] (Warmup)
Chain 4: Iteration:   200 / 2000 [ 10%] (Warmup)
Chain 4: Iteration:   400 / 2000 [ 20%] (Warmup)
Chain 4: Iteration:   600 / 2000 [ 30%] (Warmup)
Chain 4: Iteration:   800 / 2000 [ 40%] (Warmup)
Chain 4: Iteration:  1000 / 2000 [ 50%] (Warmup)
Chain 4: Iteration: 1001 / 2000 [ 50%] (Sampling)
Chain 4: Iteration: 1200 / 2000 [ 60%] (Sampling)
Chain 4: Iteration: 1400 / 2000 [ 70%] (Sampling)
Chain 4: Iteration: 1600 / 2000 [ 80%] (Sampling)
Chain 4: Iteration: 1800 / 2000 [ 90%] (Sampling)
Chain 4: Iteration: 2000 / 2000 [100%] (Sampling)
Chain 4:
Chain 4: Elapsed Time: 0.039 seconds (Warm-up)
Chain 4:           0.058 seconds (Sampling)
Chain 4:           0.097 seconds (Total)
Chain 4:
```

We fitted a Bayesian linear model (estimated using MCMC sampling with 4 chains of 2000 iterations and a warmup of 1000) to predict weight with avg_daily_snacks (formula: weight ~ avg_daily_snacks). Priors over parameters were set as normal (mean = 0.00, SD = 0.80) distributions. The model's explanatory power is substantial ($R^2 = 0.38$, 95% CI [6.54e-06, 0.62], adj. $R^2 = 0.15$). The model's intercept, corresponding to avg_daily_snacks = 0, is at 3.55 (95% CI [3.26, 3.86]). Within this model:

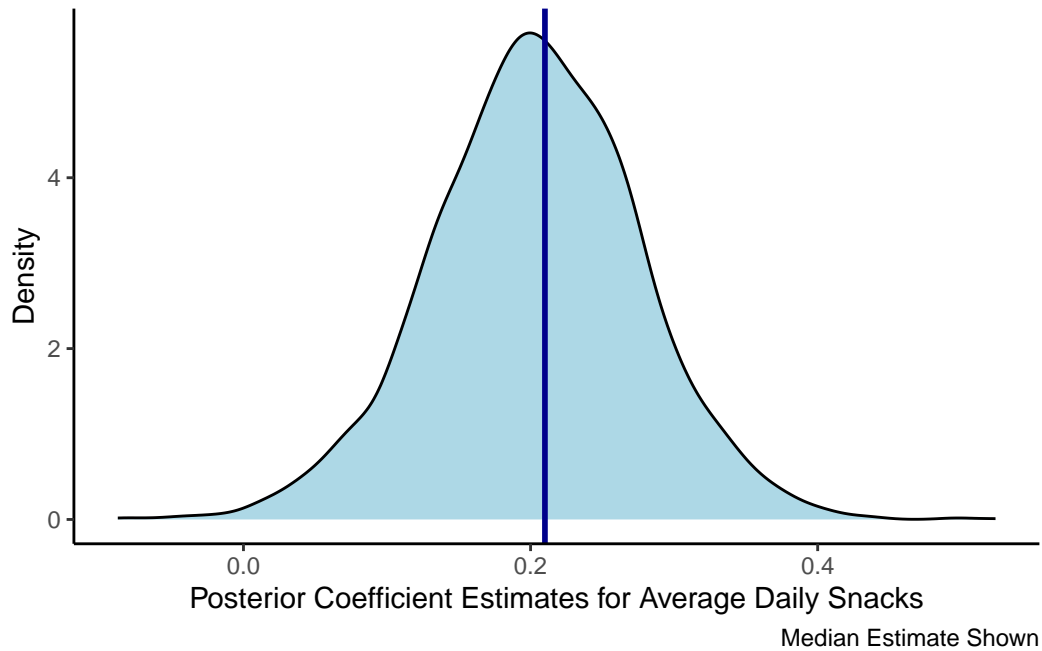
- The effect of avg daily snacks (Median = 0.20, 95% CI [0.06, 0.35]) has a

99.62% probability of being positive (> 0), 99.30% of being significant (> 0.02), and 90.10% of being large (> 0.11). The estimation successfully converged ($R_{\text{hat}} = 1.000$) and the indices are reliable ($\text{ESS} = 2981$)

Following the Sequential Effect eXistence and sIgnificance Testing (SEXIT) framework, we report the median of the posterior distribution and its 95% CI (Highest Density Interval), along the probability of direction (pd), the probability of significance and the probability of being large. The thresholds beyond which the effect is considered as significant (i.e., non-negligible) and large are $|0.02|$ and $|0.11|$ (corresponding respectively to 0.05 and 0.30 of the outcome's SD). Convergence and stability of the Bayesian sampling has been assessed using R_{hat} , which should be below 1.01 (Vehtari et al., 2019), and Effective Sample Size (ESS), which should be greater than 1000 (Burkner, 2017).

```
posteriors <- get_parameters(model_bcat)

posteriors |>
  ggplot(aes(x = avg_daily_snacks)) +
  geom_density(fill = "lightblue") +
  theme_classic() +
  labs(x = "Posterior Coefficient Estimates for Average Daily Snacks",
       y = "Density",
       caption = "Median Estimate Shown") +
  geom_vline(xintercept = 0.21, color = "darkblue", linewidth = 1)
```



A Linear model with a factor

```
model_fcat2 <- lm(weight ~ avg_daily_snacks + environ, data = cat_weights)
summary(model_fcat2)
```

Call:

```
lm(formula = weight ~ avg_daily_snacks + environ, data = cat_weights)
```

Residuals:

Min	1Q	Median	3Q	Max
-0.2678	-0.1897	-0.0700	0.0821	0.5725

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	3.52748	0.13078	26.972	8.49e-13 ***
avg_daily_snacks	0.16168	0.06512	2.483	0.0275 *
environOutdoor	0.27860	0.15203	1.833	0.0899 .

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 0.275 on 13 degrees of freedom
 Multiple R-squared: 0.5296, Adjusted R-squared: 0.4572
 F-statistic: 7.318 on 2 and 13 DF, p-value: 0.007431

```
report::report(model_fcat2)
```

We fitted a linear model (estimated using OLS) to predict weight with avg_daily_snacks and environ (formula: weight ~ avg_daily_snacks + environ). The model explains a statistically significant and substantial proportion of variance ($R^2 = 0.53$, $F(2, 13) = 7.32$, $p = 0.007$, adj. $R^2 = 0.46$). The model's intercept, corresponding to avg_daily_snacks = 0 and environ = Indoor, is at 3.53 (95% CI [3.24, 3.81], $t(13) = 26.97$, $p < .001$). Within this model:

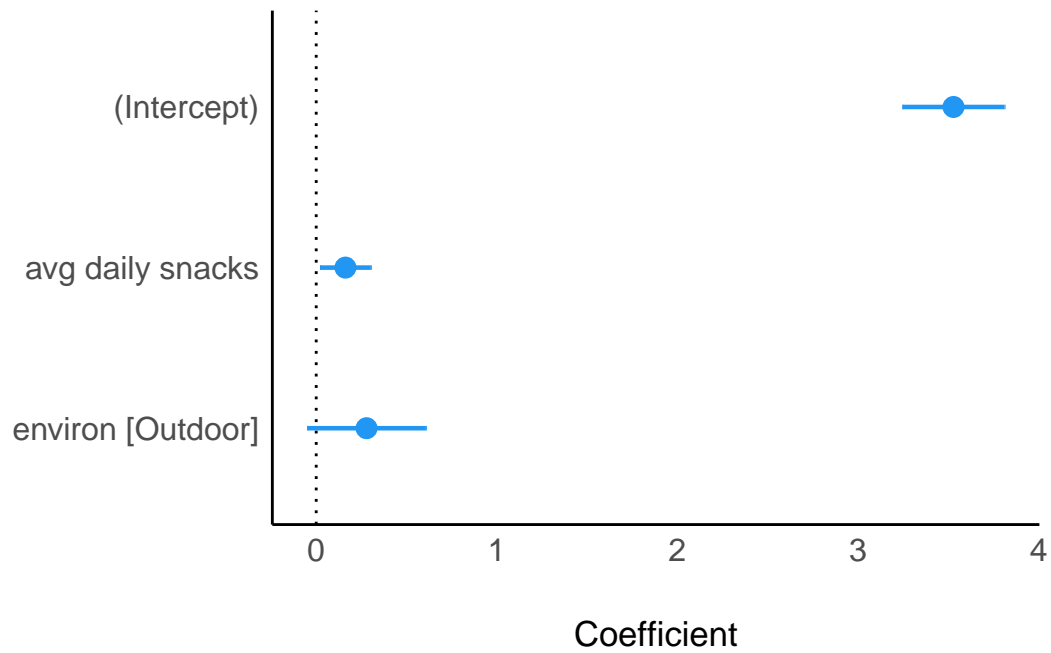
- The effect of avg daily snacks is statistically significant and positive (beta = 0.16, 95% CI [0.02, 0.30], $t(13) = 2.48$, $p = 0.027$; Std. beta = 0.51, 95% CI [0.07, 0.95])
- The effect of environ [Outdoor] is statistically non-significant and positive (beta = 0.28, 95% CI [-0.05, 0.61], $t(13) = 1.83$, $p = 0.090$; Std. beta = 0.75, 95% CI [-0.13, 1.63])

Standardized parameters were obtained by fitting the model on a standardized version of the dataset. 95% Confidence Intervals (CIs) and p-values were computed using a Wald t-distribution approximation.

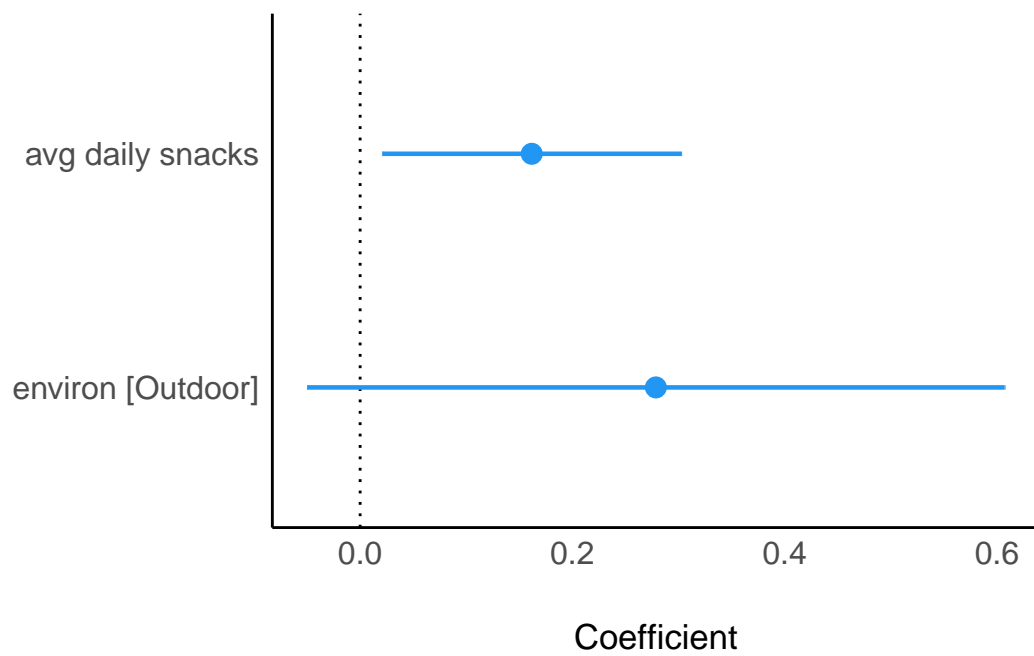
```
parameters(model_fcat2)
```

Parameter	Coefficient	SE	95% CI	t(13)	p
(Intercept)	3.53	0.13	[3.24, 3.81]	26.97	< .001
avg daily snacks	0.16	0.07	[0.02, 0.30]	2.48	0.027
environ [Outdoor]	0.28	0.15	[-0.05, 0.61]	1.83	0.090

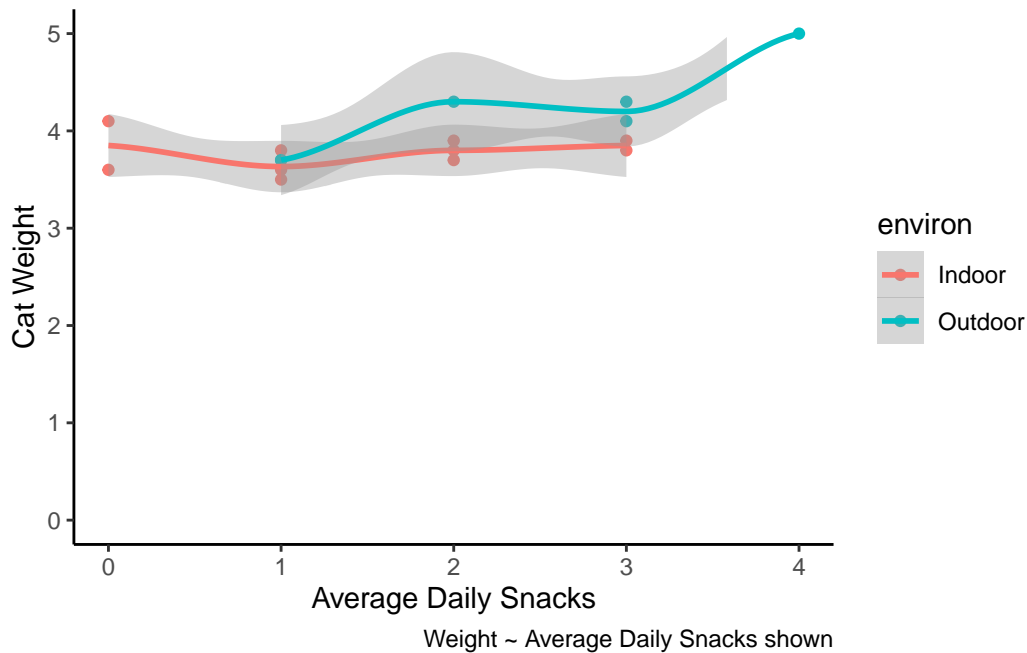
```
plot(model_parameters(model_fcat2), show_intercept = TRUE)
```



```
plot(model_parameters(model_fcat2))
```



```
cat_weights |>
  ggplot(aes(x = avg_daily_snacks, y = weight, colour = environ)) +
  geom_point() +
  labs(x = "Average Daily Snacks", y = "Cat Weight",
       caption = "Weight ~ Average Daily Snacks shown") +
  theme_classic() +
  scale_y_continuous(limits = c(0,5)) +
  geom_smooth()
```



Bayesian Framework

```
model_bcat2 <- stan_glm(weight ~ avg_daily_snacks + environ, data = cat_weights)
```

SAMPLING FOR MODEL 'continuous' NOW (CHAIN 1).

Chain 1:

Chain 1: Gradient evaluation took 1.8e-05 seconds

Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 0.18 seconds.

Chain 1: Adjust your expectations accordingly!

Chain 1:

```

Chain 1:
Chain 1: Iteration:    1 / 2000 [  0%] (Warmup)
Chain 1: Iteration:   200 / 2000 [ 10%] (Warmup)
Chain 1: Iteration:   400 / 2000 [ 20%] (Warmup)
Chain 1: Iteration:   600 / 2000 [ 30%] (Warmup)
Chain 1: Iteration:   800 / 2000 [ 40%] (Warmup)
Chain 1: Iteration:  1000 / 2000 [ 50%] (Warmup)
Chain 1: Iteration:  1001 / 2000 [ 50%] (Sampling)
Chain 1: Iteration:  1200 / 2000 [ 60%] (Sampling)
Chain 1: Iteration:  1400 / 2000 [ 70%] (Sampling)
Chain 1: Iteration:  1600 / 2000 [ 80%] (Sampling)
Chain 1: Iteration:  1800 / 2000 [ 90%] (Sampling)
Chain 1: Iteration:  2000 / 2000 [100%] (Sampling)
Chain 1:
Chain 1: Elapsed Time: 0.059 seconds (Warm-up)
Chain 1:                  0.065 seconds (Sampling)
Chain 1:                  0.124 seconds (Total)
Chain 1:

```

SAMPLING FOR MODEL 'continuous' NOW (CHAIN 2).

```

Chain 2:
Chain 2: Gradient evaluation took 1.3e-05 seconds
Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 0.13 seconds.
Chain 2: Adjust your expectations accordingly!
Chain 2:
Chain 2:
Chain 2: Iteration:    1 / 2000 [  0%] (Warmup)
Chain 2: Iteration:   200 / 2000 [ 10%] (Warmup)
Chain 2: Iteration:   400 / 2000 [ 20%] (Warmup)
Chain 2: Iteration:   600 / 2000 [ 30%] (Warmup)
Chain 2: Iteration:   800 / 2000 [ 40%] (Warmup)
Chain 2: Iteration:  1000 / 2000 [ 50%] (Warmup)
Chain 2: Iteration:  1001 / 2000 [ 50%] (Sampling)
Chain 2: Iteration:  1200 / 2000 [ 60%] (Sampling)
Chain 2: Iteration:  1400 / 2000 [ 70%] (Sampling)
Chain 2: Iteration:  1600 / 2000 [ 80%] (Sampling)
Chain 2: Iteration:  1800 / 2000 [ 90%] (Sampling)
Chain 2: Iteration:  2000 / 2000 [100%] (Sampling)
Chain 2:
Chain 2: Elapsed Time: 0.052 seconds (Warm-up)
Chain 2:                  0.047 seconds (Sampling)
Chain 2:                  0.099 seconds (Total)
Chain 2:

```

SAMPLING FOR MODEL 'continuous' NOW (CHAIN 3).

Chain 3:

Chain 3: Gradient evaluation took 1.1e-05 seconds

Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 0.11 seconds.

Chain 3: Adjust your expectations accordingly!

Chain 3:

Chain 3:

Chain 3: Iteration: 1 / 2000 [0%] (Warmup)

Chain 3: Iteration: 200 / 2000 [10%] (Warmup)

Chain 3: Iteration: 400 / 2000 [20%] (Warmup)

Chain 3: Iteration: 600 / 2000 [30%] (Warmup)

Chain 3: Iteration: 800 / 2000 [40%] (Warmup)

Chain 3: Iteration: 1000 / 2000 [50%] (Warmup)

Chain 3: Iteration: 1001 / 2000 [50%] (Sampling)

Chain 3: Iteration: 1200 / 2000 [60%] (Sampling)

Chain 3: Iteration: 1400 / 2000 [70%] (Sampling)

Chain 3: Iteration: 1600 / 2000 [80%] (Sampling)

Chain 3: Iteration: 1800 / 2000 [90%] (Sampling)

Chain 3: Iteration: 2000 / 2000 [100%] (Sampling)

Chain 3:

Chain 3: Elapsed Time: 0.047 seconds (Warm-up)

Chain 3: 0.042 seconds (Sampling)

Chain 3: 0.089 seconds (Total)

Chain 3:

SAMPLING FOR MODEL 'continuous' NOW (CHAIN 4).

Chain 4:

Chain 4: Gradient evaluation took 2.1e-05 seconds

Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 0.21 seconds.

Chain 4: Adjust your expectations accordingly!

Chain 4:

Chain 4:

Chain 4: Iteration: 1 / 2000 [0%] (Warmup)

Chain 4: Iteration: 200 / 2000 [10%] (Warmup)

Chain 4: Iteration: 400 / 2000 [20%] (Warmup)

Chain 4: Iteration: 600 / 2000 [30%] (Warmup)

Chain 4: Iteration: 800 / 2000 [40%] (Warmup)

Chain 4: Iteration: 1000 / 2000 [50%] (Warmup)

Chain 4: Iteration: 1001 / 2000 [50%] (Sampling)

Chain 4: Iteration: 1200 / 2000 [60%] (Sampling)

Chain 4: Iteration: 1400 / 2000 [70%] (Sampling)

Chain 4: Iteration: 1600 / 2000 [80%] (Sampling)

```
Chain 4: Iteration: 1800 / 2000 [ 90%] (Sampling)
Chain 4: Iteration: 2000 / 2000 [100%] (Sampling)
Chain 4:
Chain 4: Elapsed Time: 0.058 seconds (Warm-up)
Chain 4:           0.046 seconds (Sampling)
Chain 4:           0.104 seconds (Total)
Chain 4:
```

```
summary(model_bcat2)
```

Model Info:

```
function:    stan_glm
family:      gaussian [identity]
formula:     weight ~ avg_daily_snacks + environ
algorithm:   sampling
sample:      4000 (posterior sample size)
priors:      see help('prior_summary')
observations: 16
predictors:  3
```

Estimates:

	mean	sd	10%	50%	90%
(Intercept)	3.5	0.1	3.4	3.5	3.7
avg_daily_snacks	0.2	0.1	0.1	0.2	0.2
environOutdoor	0.3	0.2	0.1	0.3	0.5
sigma	0.3	0.1	0.2	0.3	0.4

Fit Diagnostics:

	mean	sd	10%	50%	90%
mean_PPD	3.9	0.1	3.8	3.9	4.1

The mean_ppd is the sample average posterior predictive distribution of the outcome variable

MCMC diagnostics

	mcse	Rhat	n_eff
(Intercept)	0.0	1.0	3785
avg_daily_snacks	0.0	1.0	3047
environOutdoor	0.0	1.0	2937
sigma	0.0	1.0	2680
mean_PPD	0.0	1.0	3807


```
log-posterior    0.0  1.0  1463
```

For each parameter, mcse is Monte Carlo standard error, n_eff is a crude measure of effective

```
describe_posterior(model_bcat2)
```

Summary of Posterior Distribution

Parameter	Median	95% CI	pd	ROPE	% in ROPE	Rhat
(Intercept)	3.53	[3.25, 3.81]	100%	[-0.04, 0.04]	0%	1.000
avg_daily_snacks	0.16	[0.02, 0.30]	98.90%	[-0.04, 0.04]	1.55%	1.001
environOutdoor	0.28	[-0.04, 0.62]	95.65%	[-0.04, 0.04]	4.18%	1.000

```
report::report(model_bcat2)
```

SAMPLING FOR MODEL 'continuous' NOW (CHAIN 1).

Chain 1:

Chain 1: Gradient evaluation took 1.6e-05 seconds

Chain 1: 1000 transitions using 10 leapfrog steps per transition would take 0.16 seconds.

Chain 1: Adjust your expectations accordingly!

Chain 1:

Chain 1:

Chain 1: Iteration: 1 / 2000 [0%] (Warmup)

Chain 1: Iteration: 200 / 2000 [10%] (Warmup)

Chain 1: Iteration: 400 / 2000 [20%] (Warmup)

Chain 1: Iteration: 600 / 2000 [30%] (Warmup)

Chain 1: Iteration: 800 / 2000 [40%] (Warmup)

Chain 1: Iteration: 1000 / 2000 [50%] (Warmup)

Chain 1: Iteration: 1001 / 2000 [50%] (Sampling)

Chain 1: Iteration: 1200 / 2000 [60%] (Sampling)

Chain 1: Iteration: 1400 / 2000 [70%] (Sampling)

Chain 1: Iteration: 1600 / 2000 [80%] (Sampling)

Chain 1: Iteration: 1800 / 2000 [90%] (Sampling)

Chain 1: Iteration: 2000 / 2000 [100%] (Sampling)

Chain 1:

Chain 1: Elapsed Time: 0.057 seconds (Warm-up)

Chain 1: 0.043 seconds (Sampling)

Chain 1: 0.1 seconds (Total)

Chain 1:

SAMPLING FOR MODEL 'continuous' NOW (CHAIN 2).

Chain 2:

Chain 2: Gradient evaluation took 1.1e-05 seconds

Chain 2: 1000 transitions using 10 leapfrog steps per transition would take 0.11 seconds.

Chain 2: Adjust your expectations accordingly!

Chain 2:

Chain 2:

Chain 2: Iteration: 1 / 2000 [0%] (Warmup)

Chain 2: Iteration: 200 / 2000 [10%] (Warmup)

Chain 2: Iteration: 400 / 2000 [20%] (Warmup)

Chain 2: Iteration: 600 / 2000 [30%] (Warmup)

Chain 2: Iteration: 800 / 2000 [40%] (Warmup)

Chain 2: Iteration: 1000 / 2000 [50%] (Warmup)

Chain 2: Iteration: 1001 / 2000 [50%] (Sampling)

Chain 2: Iteration: 1200 / 2000 [60%] (Sampling)

Chain 2: Iteration: 1400 / 2000 [70%] (Sampling)

Chain 2: Iteration: 1600 / 2000 [80%] (Sampling)

Chain 2: Iteration: 1800 / 2000 [90%] (Sampling)

Chain 2: Iteration: 2000 / 2000 [100%] (Sampling)

Chain 2:

Chain 2: Elapsed Time: 0.062 seconds (Warm-up)

Chain 2: 0.071 seconds (Sampling)

Chain 2: 0.133 seconds (Total)

Chain 2:

SAMPLING FOR MODEL 'continuous' NOW (CHAIN 3).

Chain 3:

Chain 3: Gradient evaluation took 1.9e-05 seconds

Chain 3: 1000 transitions using 10 leapfrog steps per transition would take 0.19 seconds.

Chain 3: Adjust your expectations accordingly!

Chain 3:

Chain 3:

Chain 3: Iteration: 1 / 2000 [0%] (Warmup)

Chain 3: Iteration: 200 / 2000 [10%] (Warmup)

Chain 3: Iteration: 400 / 2000 [20%] (Warmup)

Chain 3: Iteration: 600 / 2000 [30%] (Warmup)

Chain 3: Iteration: 800 / 2000 [40%] (Warmup)

Chain 3: Iteration: 1000 / 2000 [50%] (Warmup)

Chain 3: Iteration: 1001 / 2000 [50%] (Sampling)

Chain 3: Iteration: 1200 / 2000 [60%] (Sampling)

Chain 3: Iteration: 1400 / 2000 [70%] (Sampling)

```

Chain 3: Iteration: 1600 / 2000 [ 80%] (Sampling)
Chain 3: Iteration: 1800 / 2000 [ 90%] (Sampling)
Chain 3: Iteration: 2000 / 2000 [100%] (Sampling)
Chain 3:
Chain 3: Elapsed Time: 0.089 seconds (Warm-up)
Chain 3:           0.052 seconds (Sampling)
Chain 3:           0.141 seconds (Total)
Chain 3:

```

SAMPLING FOR MODEL 'continuous' NOW (CHAIN 4).

```

Chain 4:
Chain 4: Gradient evaluation took 1e-05 seconds
Chain 4: 1000 transitions using 10 leapfrog steps per transition would take 0.1 seconds.
Chain 4: Adjust your expectations accordingly!
Chain 4:
Chain 4:
Chain 4: Iteration:    1 / 2000 [  0%] (Warmup)
Chain 4: Iteration:   200 / 2000 [ 10%] (Warmup)
Chain 4: Iteration:   400 / 2000 [ 20%] (Warmup)
Chain 4: Iteration:   600 / 2000 [ 30%] (Warmup)
Chain 4: Iteration:   800 / 2000 [ 40%] (Warmup)
Chain 4: Iteration:  1000 / 2000 [ 50%] (Warmup)
Chain 4: Iteration:  1001 / 2000 [ 50%] (Sampling)
Chain 4: Iteration:  1200 / 2000 [ 60%] (Sampling)
Chain 4: Iteration:  1400 / 2000 [ 70%] (Sampling)
Chain 4: Iteration:  1600 / 2000 [ 80%] (Sampling)
Chain 4: Iteration:  1800 / 2000 [ 90%] (Sampling)
Chain 4: Iteration:  2000 / 2000 [100%] (Sampling)
Chain 4:
Chain 4: Elapsed Time: 0.073 seconds (Warm-up)
Chain 4:           0.098 seconds (Sampling)
Chain 4:           0.171 seconds (Total)
Chain 4:

```

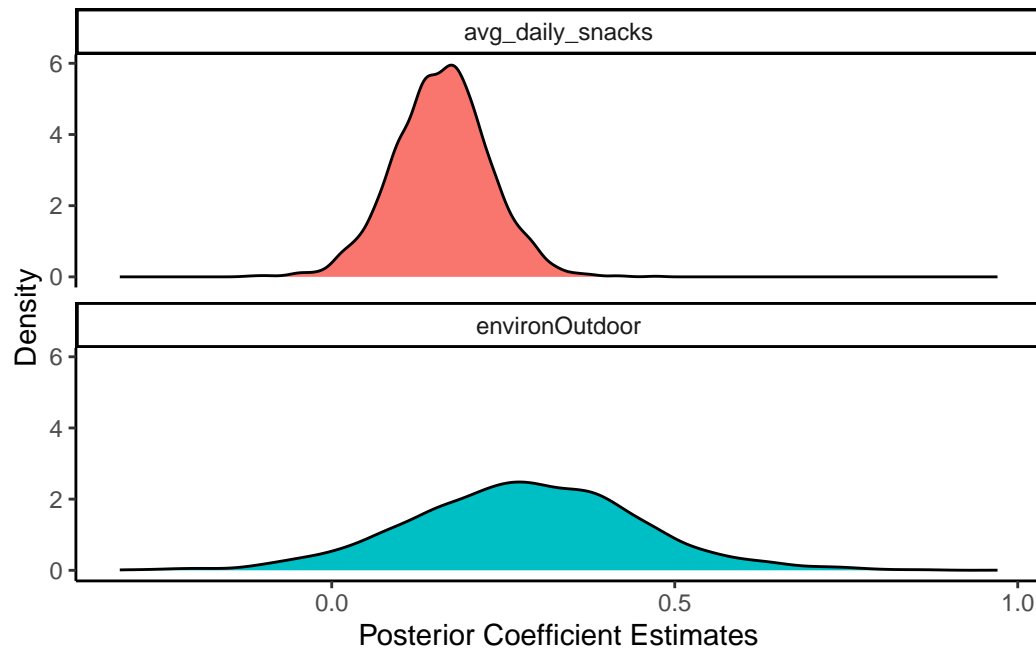
We fitted a Bayesian linear model (estimated using MCMC sampling with 4 chains of 2000 iterations and a warmup of 1000) to predict weight with avg_daily_snacks and environ (formula: `weight ~ avg_daily_snacks + environ`). Priors over parameters were all set as normal (mean = 0.00, SD = 0.80; mean = 0.00, SD = 1.87) distributions. The model's explanatory power is substantial ($R^2 = 0.50$, 95% CI [0.17, 0.74], adj. $R^2 = 0.26$). The model's intercept, corresponding to avg_daily_snacks = 0 and environ = Indoor, is at 3.53 (95% CI [3.25, 3.81]). Within this model:

- The effect of avg daily snacks (Median = 0.16, 95% CI [0.02, 0.30]) has a 98.90% probability of being positive (> 0), 97.72% of being significant (> 0.02), and 76.35% of being large (> 0.11). The estimation successfully converged (Rhat = 1.001) and the indices are reliable (ESS = 3047)
- The effect of environ [Outdoor] (Median = 0.28, 95% CI [-0.04, 0.62]) has a 95.65% probability of being positive (> 0), 94.53% of being significant (> 0.02), and 85.28% of being large (> 0.11). The estimation successfully converged (Rhat = 1.000) and the indices are reliable (ESS = 2937)

Following the Sequential Effect eXistence and sIgnificance Testing (SEXIT) framework, we report the median of the posterior distribution and its 95% CI (Highest Density Interval), along the probability of direction (pd), the probability of significance and the probability of being large. The thresholds beyond which the effect is considered as significant (i.e., non-negligible) and large are |0.02| and |0.11| (corresponding respectively to 0.05 and 0.30 of the outcome's SD). Convergence and stability of the Bayesian sampling has been assessed using R-hat, which should be below 1.01 (Vehtari et al., 2019), and Effective Sample Size (ESS), which should be greater than 1000 (Burkner, 2017).

```
posterior2 <- get_parameters(model_bcat2)

posterior2 |>
  pivot_longer(cols = c(avg_daily_snacks, environOutdoor),
               names_to = "Parameter",
               values_to="estimate") |>
  ggplot() +
  geom_density(aes(x = estimate, fill = Parameter)) +
  theme_classic() +
  labs(x = "Posterior Coefficient Estimates",
       y = "Density") +
  facet_wrap(facets = ~Parameter, ncol = 1) +
  theme(legend.position = "none")
```

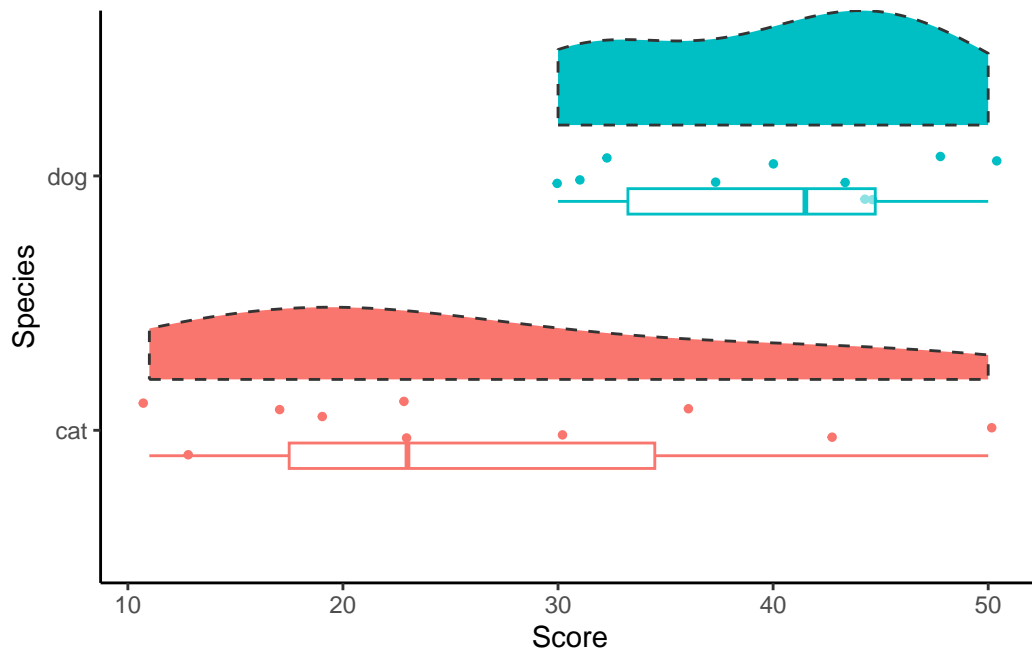


Lecture: Calculating variance

Why does it matter?

```
vardat <- tibble(cat = c(13, 17, 30, 36, 11, 43, 23, 50, 19, 23),
                  dog = c(30, 31, 45, 43, 48, 50, 37, 32, 40, 44))

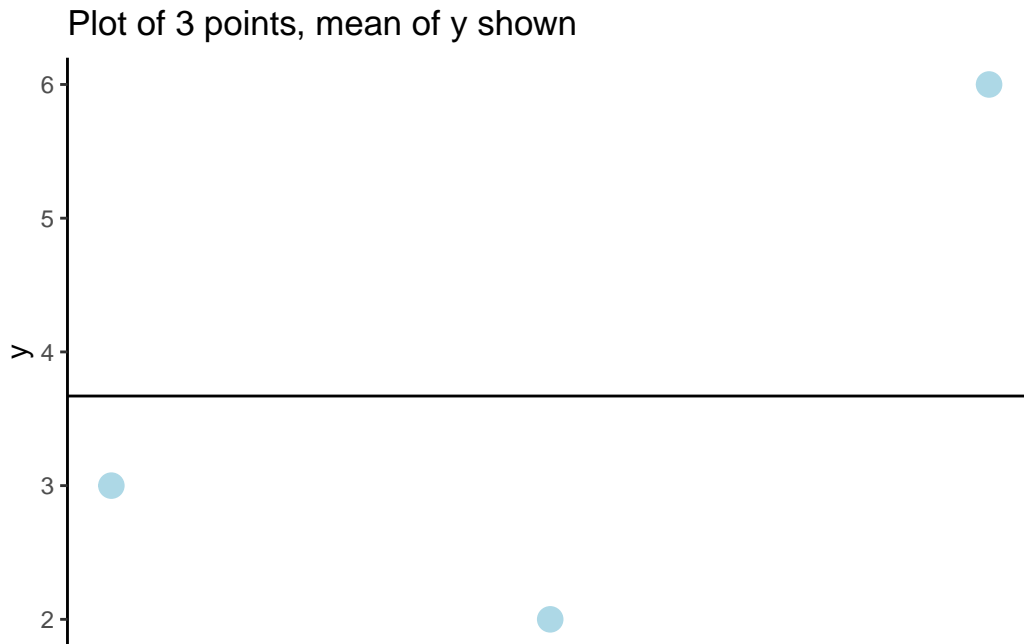
vardat |>
  pivot_longer(cols = c(cat, dog),
               names_to = "Species",
               values_to = "Score") |>
  ggplot(aes(x = Species)) +
  geom_point(aes(y = Score, colour = Species), position = position_jitter(width = .13), size = 100) +
  see::geom_violinhalf(aes(y = Score, fill = Species), linetype = "dashed", position = position_jitter(width = .13)) +
  geom_boxplot(aes(y = Score, alpha = 0.3, colour = Species), position = position_nudge(x = 0.5)) +
  theme_classic() +
  labs(x = "Species", y = "Score") +
  theme(legend.position = "none") +
  coord_flip()
```



Residuals

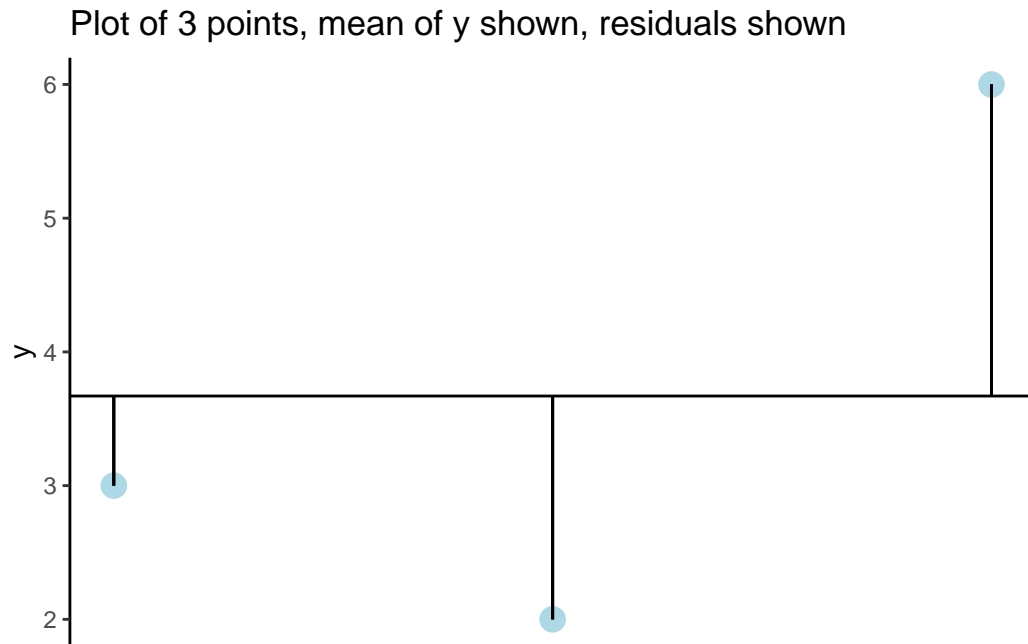
```
resid <- tibble(x = c(1, 2, 3),
                y = c(3, 2, 6))

resid |>
  ggplot(aes(x, y)) +
  geom_point(size = 4, colour = "lightblue") +
  theme_classic() +
  geom_hline(yintercept = 3.67) +
  labs(title = "Plot of 3 points, mean of y shown") +
  theme(axis.text.x=element_blank(),
        axis.ticks.x=element_blank(),
        axis.title.x = element_blank())
```



Adding the residuals

```
resid |>
  ggplot(aes(x, y)) +
  geom_point(size = 4, colour = "lightblue") +
  theme_classic() +
  geom_hline(yintercept = 3.67) +
  geom_segment(aes(x = 1, y = 3.67, xend = 1, yend = 3)) +
  geom_segment(aes(x = 2, y = 3.67, xend = 2, yend = 2)) +
  geom_segment(aes(x = 3, y = 3.67, xend = 3, yend = 6)) +
  labs(title = "Plot of 3 points, mean of y shown, residuals shown") +
  theme(axis.text.x=element_blank(),
        axis.ticks.x=element_blank(),
        axis.title.x = element_blank())
```

Compare Variances

```
vardat |>
  summarise(var_dogs = var(dog),
            var_cat = var(cat))
```

```
# A tibble: 1 x 2
  var_dogs var_cat
  <dbl>    <dbl>
1      52     169.
```

Compare Standard Deviations

```
vardat |>
  summarise(sd_dogs = sd(dog),
            sd_cat = sd(cat))
```

```
# A tibble: 1 x 2
  sd_dogs sd_cat
  <dbl>   <dbl>
1    7.21   13.0
```

Compare Standard Errors

```
std.error <- function(x) sd(x)/sqrt(length(x))

vardat |>
  summarise(se_dogs = std.error(dog),
            se_cat = std.error(cat))
```

```
# A tibble: 1 x 2
  se_dogs se_cat
  <dbl>   <dbl>
1    2.28    4.11
```

Lecture: Meta Analyses

Calculate rs from R2

```
sqrt(0.11)
```

5 Week 4: Considerations for Collecting Data

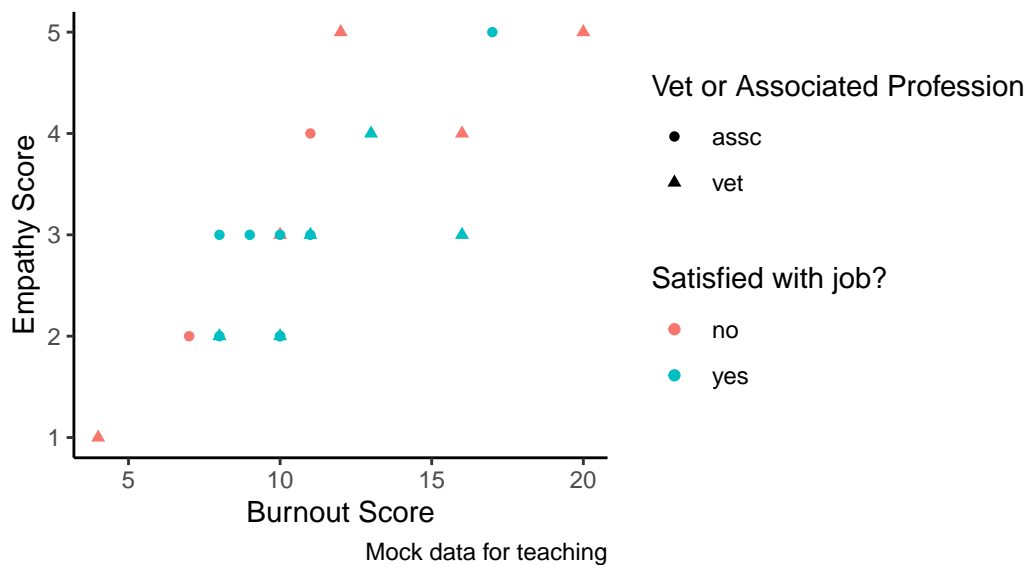
Lecture: Effect Sizes and Covariance

Mock Data and visualisation

```
job_dat <- tibble(job = c("vet", "vet", "vet","vet", "vet", "vet", "vet", "vet", "vet", "vet", "v",
                          "assc", "assc", "assc", "assc", "assc", "assc", "assc", "assc", "assc", "assc",
                          burnout = c(13, 12, 4, 16, 16, 20, 8, 10, 11, 10,
                                      10, 11, 8, 7, 8, 10, 9, 11, 17, 10),
                          empathy = c(4, 5, 1, 4,3, 5, 2, 3,3,2,
                                      2, 3, 3, 2, 2, 3, 3, 4, 5, 2),
                          satisfaction = c("yes", "no", "no", "no", "yes", "no", "yes", "no", "yes",
                                           "yes", "yes", "yes", "no", "yes", "yes", "yes", "no", "y")

job_dat |>
  ggplot(aes(x = burnout, y = empathy, shape = job, colour = satisfaction)) +
  geom_point() +
  theme_classic() +
  labs(title = "Burnout and empathy scores for vets and associated professions",
       subtitle = "Job Satisfaction shown",
       caption = "Mock data for teaching",
       x = "Burnout Score",
       y = "Empathy Score") +
  scale_shape_discrete(name = "Vet or Associated Profession") +
  scale_color_discrete(name = "Satisfied with job?")
```

Burnout and empathy scores for vets and associated professions:
Job Satisfaction shown



Calculate Cohen's d

```
library(effsize)

cohen.d(d = job_dat$burnout, f = job_dat$job)
```

Cohen's d

```
d estimate: -0.5048995 (medium)
95 percent confidence interval:
      lower      upper
-1.4593128  0.4495138
```

Calculate Hedge's g

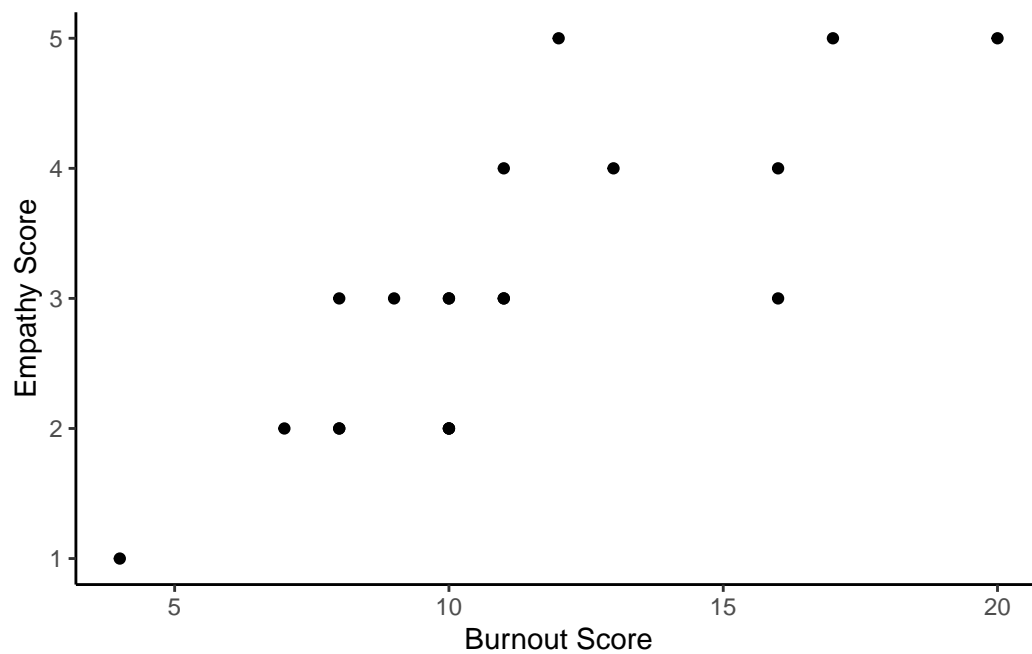
```
cohen.d(d = job_dat$burnout, f = job_dat$job, hedges.correction = TRUE)
```

Hedges's g

g estimate: -0.4835657 (small)
95 percent confidence interval:
lower upper
-1.3964834 0.4293519

Effects of Differences

```
job_dat |>  
  ggplot(aes(x = burnout, y = empathy)) +  
  geom_point() +  
  theme_classic() +  
  labs(x = "Burnout Score", y = "Empathy Score")
```



Correlation coefficient (r)

```
cor(job_dat$burnout, job_dat$empathy, method = "pearson")
```

```
[1] 0.7991678
```

Other Correlation Coefficients

```
cor(job_dat$burnout, job_dat$empathy, method = "spearman")
```

```
[1] 0.8202187
```

```
cor.test(job_dat$burnout, as.numeric(as.factor(job_dat$job)))
```

Pearson's product-moment correlation

```
data: job_dat$burnout and as.numeric(as.factor(job_dat$job))
t = 1.129, df = 18, p-value = 0.2737
alternative hypothesis: true correlation is not equal to 0
95 percent confidence interval:
 -0.2091671  0.6281908
sample estimates:
      cor
0.2571562
```

Cramer's V

```
library(lsr)

job_dat <- job_dat |>
  mutate(burnoutcat = case_when(burnout > 10 ~ "burnout",
                                TRUE ~ "no burnout"))
```



```
job_tbl <- xtabs(~job_dat$job + job_dat$satisfaction + job_dat$burnoutcat)
ftable(job_tbl)
```

		job_dat\$burnoutcat	
		burnout	no burnout
job_dat\$job	job_dat\$satisfaction		
assc	no	1	1
	yes	2	6
vet	no	3	2
	yes	3	2

```
chisq.test(ftable(job_tbl))
```

Pearson's Chi-squared test

```
data: ftable(job_tbl)
X-squared = 2.2222, df = 3, p-value = 0.5276
```

```
cramersV(ftable(job_tbl))
```

```
[1] 0.3333333
```

R²adj Example

```
jobmod <- lm(burnout ~ empathy + satisfaction, data = job_dat)
summary(jobmod)
```

Call:

```
lm(formula = burnout ~ empathy + satisfaction, data = job_dat)
```

Residuals:

Min	1Q	Median	3Q	Max
-3.7526	-1.0832	-0.3836	1.4822	4.7305

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	1.9944	1.8904	1.055	0.306
empathy	2.7516	0.4865	5.656	2.85e-05 ***
satisfactionyes	1.0202	1.1393	0.895	0.383

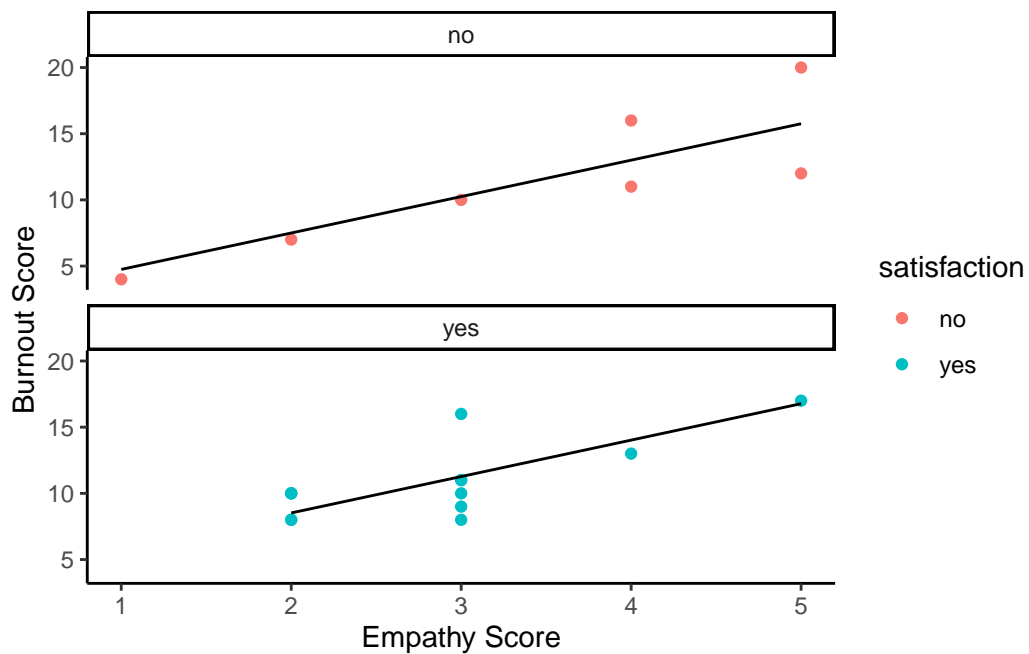
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.354 on 17 degrees of freedom

Multiple R-squared: 0.6549, Adjusted R-squared: 0.6144

F-statistic: 16.13 on 2 and 17 DF, p-value: 0.000118

```
job_dat |>
  mutate(mod = predict(jobmod)) |>
  ggplot() +
    geom_point(aes(x = empathy, y = burnout, colour = satisfaction)) +
    geom_line(aes(x = empathy, y = mod)) +
    theme_classic() +
    facet_wrap(facets = ~ satisfaction, ncol = 1) +
    labs(x = "Empathy Score", y = "Burnout Score")
```



5.1 Covariance {. unnumbered}

```
jobmod2 <- lm(burnout ~ empathy + job, data = job_dat)
summary(jobmod2)
```

Call:

```
lm(formula = burnout ~ empathy + job, data = job_dat)
```

Residuals:

Min	1Q	Median	3Q	Max
-4.6359	-1.3894	-0.4212	1.6035	4.5151

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	2.631	1.552	1.695	0.108
empathy	2.575	0.471	5.469	4.16e-05 ***
jobvet	1.127	1.052	1.072	0.299

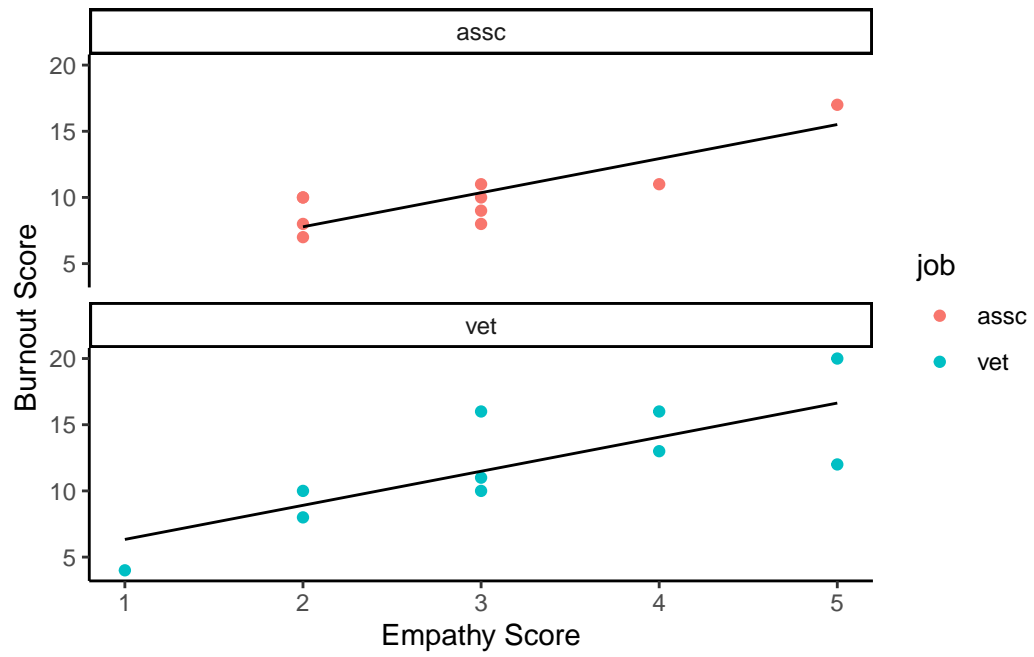
Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 2.331 on 17 degrees of freedom

Multiple R-squared: 0.6615, Adjusted R-squared: 0.6217

F-statistic: 16.61 on 2 and 17 DF, p-value: 0.0001002

```
job_dat |>
  mutate(mod = predict(jobmod2)) |>
  ggplot() +
  geom_point(aes(x = empathy, y = burnout, colour = job)) +
  geom_line(aes(x = empathy, y = mod)) +
  theme_classic() +
  facet_wrap(facets = ~ job, ncol = 1) +
  labs(x = "Empathy Score", y = "Burnout Score")
```



6 Week 5: Sources of Data

Lecture 1 Digital Media Research

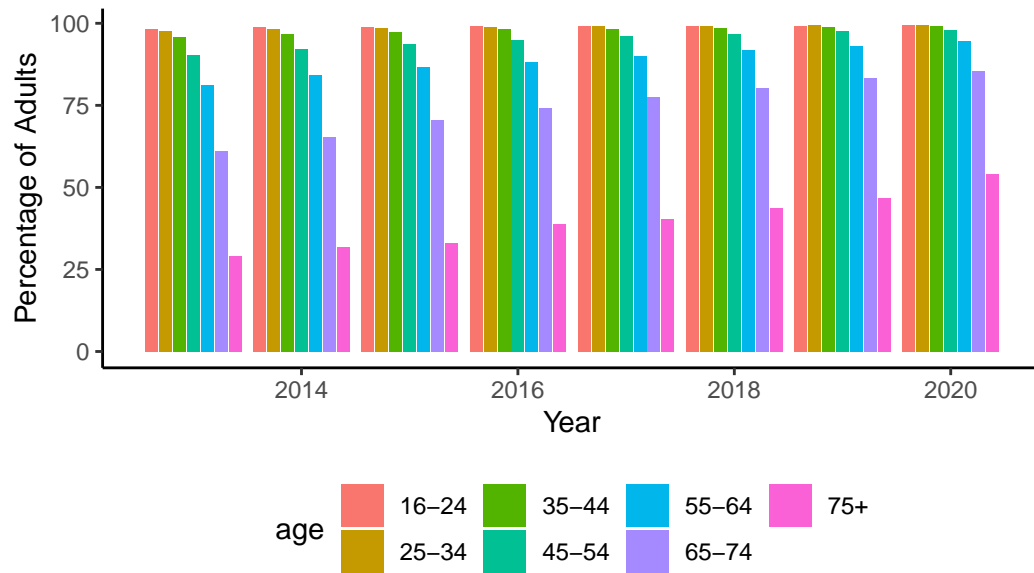
6.1 Who's in digital spaces

```
library(tidyverse)

internet <- tibble(year = c(2013, 2014, 2015, 2016, 2017, 2018, 2019, 2020),
  "16-24" = c(98.3, 98.9, 98.8, 99.2, 99.2, 99.3, 99.2, 99.3),
  "25-34" = c(97.7, 98.3, 98.6, 98.9, 99.1, 99.2, 99.4, 99.5),
  "35-44" = c(95.8, 96.7, 97.3, 98.2, 98.4, 98.6, 98.9, 99.0),
  "45-54" = c(90.2, 92.3, 93.6, 94.9, 96.2, 96.8, 97.5, 97.8),
  "55-64" = c(81.3, 84.2, 86.7, 88.3, 90.0, 91.8, 93.2, 94.5),
  "65-74" = c(61.1, 65.5, 70.6, 74.1, 77.5, 80.2, 83.2, 85.5),
  "75+" = c(29.1, 31.9, 33.0, 38.7, 40.5, 43.6, 46.8, 54.0))

pivot_longer(internet, cols = -year,
  names_to = "age",
  values_to = "perc")

internet |>
  ggplot(aes(x = year, y = perc, fill = age)) +
  geom_bar(stat = "identity", position = "dodge2") +
  theme_classic() +
  theme(legend.position = "bottom") +
  labs(x = "Year", y = "Percentage of Adults",
    caption = "UK adults who used the internet in the last 3 months (Jan-March)\nData from the Office for National Statistics")
```



UK adults who used the internet in the last 3 months (Jan–March)
Data from ONS

7 Week 6: Analysing Qualitative Data

There's no content in this week this year :)

8 Week 7: Analysing Quantitative Data

Lecture 1: Choosing a Statistical Test

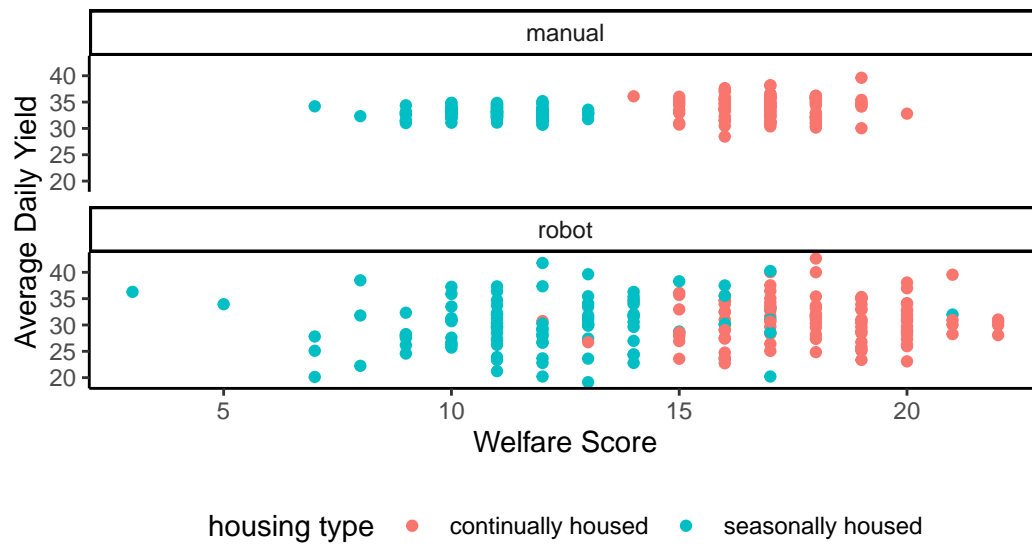
```
library(tidyverse)

cows <- readxl::read_excel("cows.xlsx") |>
  mutate(parlour = as.factor(parlour),
         `housing type` = as.factor(`housing type`))

cows |>
  ggplot(aes(x = `Welfare Score`, y = `Average Daily Yield`, colour = `housing type`)) +
  geom_point() +
  theme_classic() +
  labs(x = "Welfare Score", y = "Average Daily Yield",
       title = "Milk Yield versus Welfare Score",
       subtitle = "For Robotic vs Manual Parlours") +
  facet_wrap(facets = ~parlour, ncol = 1) +
  theme(legend.position = "bottom")
```

Milk Yield versus Welfare Score

For Robotic vs Manual Parlours



Numerical Response

```
cows |>
  summarise(mean_yield = mean(`Average Daily Yield`),
            sd_yield = sd(`Average Daily Yield`))
```

```
# A tibble: 1 x 2
  mean_yield sd_yield
  <dbl>     <dbl>
1       32       3.73
```

```
t.test(cows$`Average Daily Yield`, mu = 28)
```

One Sample t-test

```
data: cows$`Average Daily Yield`
t = 21.448, df = 399, p-value < 2.2e-16
alternative hypothesis: true mean is not equal to 28
```

95 percent confidence interval:

31.63336 32.36664

sample estimates:

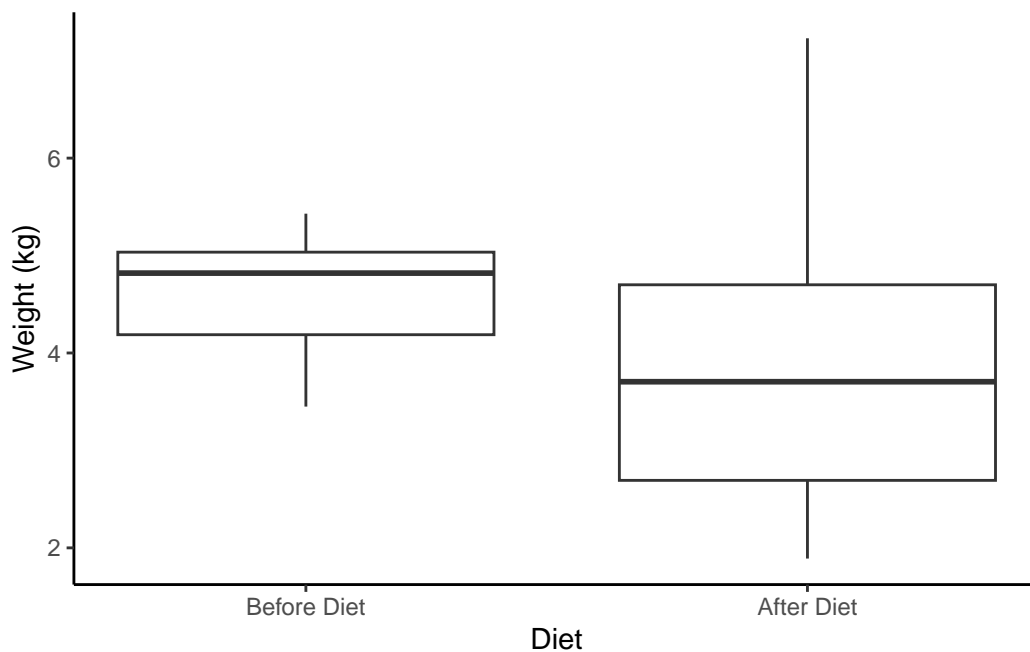
mean of x

32

Numerical Response Categorical Explanatory

```
diet <- tibble (before = c(5.04, 4.63, 4.04, 5.10, 5.43, 4.83, 3.45, 3.49, 5.02, 4.81),  
               after  = c( 4.78, 2.49, 4.46, 2.03, 5.13, 7.23, 3.50, 1.89, 3.30, 3.91))
```

```
diet |>  
  ggplot(aes(y = before)) +  
  geom_boxplot() +  
  geom_boxplot(aes(y = after, x =1)) +  
  theme_classic() +  
  scale_x_continuous(labels =c("Before Diet", "After Diet"), breaks = c(0,1)) +  
  labs(x = "Diet", y = "Weight (kg)")
```



```
diet |>
  summarise(before_mean = mean(before),
            after_mean = mean(after),
            before_sd = sd(before),
            after_sd = sd(after))
```

```
# A tibble: 1 x 4
  before_mean after_mean before_sd after_sd
    <dbl>      <dbl>      <dbl>    <dbl>
1      4.58      3.87      0.689     1.62
```

```
t.test(diet$before, diet$after, paired = TRUE, alternative = "two.sided")
```

Paired t-test

```
data: diet$before and diet$after
t = 1.4615, df = 9, p-value = 0.1779
alternative hypothesis: true mean difference is not equal to 0
95 percent confidence interval:
 -0.3900511  1.8140511
sample estimates:
mean difference
      0.712
```

2-Way ANOVA

```
model1 <- aov(`Average Daily Yield` ~ parlour + `housing type`, data = cows)
summary(model1)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
parlour	1	900	900.0	78.511	< 2e-16 ***
`housing type`	1	100	100.0	8.723	0.00333 **
Residuals	397	4551	11.5		

```
Signif. codes:  0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1
```

Linear model

```
model2 <- lm(`Average Daily Yield` ~ parlour + `housing type`, data = cows)
summary(model2)
```

Call:

```
lm(formula = `Average Daily Yield` ~ parlour + `housing type`,
    data = cows)
```

Residuals:

Min	1Q	Median	3Q	Max
-10.8651	-1.7814	0.0787	1.6805	11.7654

Coefficients:

	Estimate	Std. Error	t value	Pr(> t)
(Intercept)	34.0000	0.2932	115.956	< 2e-16 ***
parlourrobot	-3.0000	0.3386	-8.861	< 2e-16 ***
`housing type`seasonally housed	-1.0000	0.3386	-2.954	0.00333 **

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

Residual standard error: 3.386 on 397 degrees of freedom

Multiple R-squared: 0.1801, Adjusted R-squared: 0.176

F-statistic: 43.62 on 2 and 397 DF, p-value: < 2.2e-16

Numerical Response Numerical Explanatory

Correlation

```
cor.test(cows$`Average Daily Yield`, cows$`Welfare Score`)
```

Pearson's product-moment correlation

data: cows\$`Average Daily Yield` and cows\$`Welfare Score`

t = 1.7643, df = 398, p-value = 0.07845

alternative hypothesis: true correlation is not equal to 0

95 percent confidence interval:

-0.01004724 0.18454894

sample estimates:

```
cor
0.08809126
```

Linear Model

Generalised Linear Model

```
#| eval: true

model4 <- glm(`Average Daily Yield` ~ `Welfare Score`
              + `housing type` + parlour, data = cows)
summary(model4)
```

Categorical Response

Proportion Test

```
prop.test(x = 3, n = 20, p = 0.18, alternative = "two.sided")
```

1-sample proportions test with continuity correction

```
data: 3 out of 20, null probability 0.18
X-squared = 0.0033875, df = 1, p-value = 0.9536
alternative hypothesis: true p is not equal to 0.18
95 percent confidence interval:
 0.03956627 0.38862512
sample estimates:
p
0.15
```

Categorical Response Categorical Explanatory

McNemar's Test

```
work <- matrix(c(2, 5, 38, 35),
               ncol=2,
               byrow=TRUE,
```

```

dimnames = list(c("Dysplasia", "No Dysplasia"),
                 c("Before Work Season", "After Work Season"))

mcnemar.test(work)

```

McNemar's Chi-squared test with continuity correction

data: work
 McNemar's chi-squared = 23.814, df = 1, p-value = 1.061e-06

Fisher's Exact Test

```
fisher.test(x = c(4,16), y = c(2,18))
```

Fisher's Exact Test for Count Data

data: c(4, 16) and c(2, 18)
 p-value = 1
 alternative hypothesis: true odds ratio is not equal to 1
 95 percent confidence interval:
 0.02564066 Inf
 sample estimates:
 odds ratio
 Inf

```

# Calculate Odds Ratio
(4+18) / (16 + 2)

```

[1] 1.222222

Chi2 Test

```

gsd <- matrix(c(16, 12, 84, 86),
               ncol=2,
               byrow=TRUE,
               dimnames = list(c("Dysplasia", "No Dysplasia"),

```



```
c("Inbred", "Less Inbred")))
```

```
chisq.test(gsd)
```

Pearson's Chi-squared test with Yates' continuity correction

```
data: gsd
X-squared = 0.30714, df = 1, p-value = 0.5794
```

```
library(vcd)
assocstats(gsd)
```

	X ²	df	P(> X ²)
Likelihood Ratio	0.57672	1	0.44760
Pearson	0.57481	1	0.44835

Phi-Coefficient : 0.054
Contingency Coeff.: 0.054
Cramer's V : 0.054

Categorical Response Numerical Explanatory

Logistic Regression

```
dysp <- tibble(dysplasia = c(1, 1, 1, 1, 1, 1, 1, 1,
                             0, 0, 0, 0, 0, 0, 0, 0,
                             0, 0, 0, 0, 0, 0, 0, 0),
               inflammation = c(0.91, 0.79, 1.40, 0.71, 1.01, 0.77, 0.85,
                                0.42, 1.02, 0.31, 0.05, 1.17, 0.04, 0.36,
                                0.12, 0.02, 0.05, 0.42, 0.92, 0.72, 1.05))

logit <- glm(dysplasia ~ inflammation, data = dysp, family = "binomial")
summary(logit)
```

Call:

```
glm(formula = dysplasia ~ inflammation, family = "binomial",
     data = dysp)
```

Deviance Residuals:

Min	1Q	Median	3Q	Max
-1.5715	-0.5727	-0.3094	1.0397	1.4914

Coefficients:

	Estimate	Std. Error	z value	Pr(> z)
(Intercept)	-3.190	1.484	-2.150	0.0316 *
inflammation	3.488	1.740	2.004	0.0450 *

Signif. codes: 0 '***' 0.001 '**' 0.01 '*' 0.05 '.' 0.1 ' ' 1

(Dispersion parameter for binomial family taken to be 1)

Null deviance: 26.734 on 20 degrees of freedom
 Residual deviance: 20.534 on 19 degrees of freedom
 AIC: 24.534

Number of Fisher Scoring iterations: 5

```
library(easystats)
report(logit)
```

We fitted a logistic model (estimated using ML) to predict dysplasia with inflammation (formula: `dysplasia ~ inflammation`). The model's explanatory power is moderate (Tjur's $R^2 = 0.24$). The model's intercept, corresponding to inflammation = 0, is at -3.19 (95% CI [-7.09, -0.88], $p = 0.032$). Within this model:

- The effect of inflammation is statistically significant and positive (beta = 3.49, 95% CI [0.65, 7.91], $p = 0.045$; Std. beta = 1.47, 95% CI [0.27, 3.33])

Standardized parameters were obtained by fitting the model on a standardized version of the dataset. 95% Confidence Intervals (CIs) and p-values were computed using a Wald z-distribution approximation.

```
parameters(logit)
```

Parameter	Log-Odds	SE	95% CI	z	p
(Intercept)	-3.19	1.48	[-7.09, -0.88]	-2.15	0.032
inflammation	3.49	1.74	[0.65, 7.91]	2.00	0.045

```
exp(cbind(OddsRatio = coef(logit), confint(logit)))
```

	OddsRatio	2.5 %	97.5 %
(Intercept)	0.04118154	0.0008355444	0.4146414
inflammation	32.71638289	1.9151146706	2735.6121035

Parametric vs Non Parametric

Power Calculations

Assumptions

Residuals

```
residuals <- tibble(resids = resid(model4))

residuals |>
  ggplot(aes(x = resids)) +
  geom_density()+
  theme_classic()

describe_distribution(residuals)
```

9 Weeks 8 & 9: Analytical Softwares

This week has no content yet, please check back later!

10 Week 10: Project Proposals

This week has no content yet, please check back later!

11 References

References

The cover image duck comes from [Pixabay](#), as a Creative Commons 0 image by Clker-Free-Vector-Images-3736

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