Assignment6

## Quarto

library(ggplot2)  
library(dplyr)

Attaching package: 'dplyr'

The following objects are masked from 'package:stats':  
  
 filter, lag

The following objects are masked from 'package:base':  
  
 intersect, setdiff, setequal, union

library(ggforce)  
  
plots <- readr::read\_csv('https://raw.githubusercontent.com/rfordatascience/tidytuesday/master/data/2023/2023-05-02/plots.csv')

Rows: 8 Columns: 2

── Column specification ────────────────────────────────────────────────────────  
Delimiter: ","  
chr (1): treatment  
dbl (1): plot  
  
ℹ Use `spec()` to retrieve the full column specification for this data.  
ℹ Specify the column types or set `show\_col\_types = FALSE` to quiet this message.

species <- readr::read\_csv('https://raw.githubusercontent.com/rfordatascience/tidytuesday/master/data/2023/2023-05-02/species.csv')

Rows: 21 Columns: 15  
── Column specification ────────────────────────────────────────────────────────  
Delimiter: ","  
chr (4): species, scientificname, taxa, commonname  
dbl (11): censustarget, unidentified, rodent, granivore, minhfl, meanhfl, ma...  
  
ℹ Use `spec()` to retrieve the full column specification for this data.  
ℹ Specify the column types or set `show\_col\_types = FALSE` to quiet this message.

surveys <- readr::read\_csv('https://raw.githubusercontent.com/rfordatascience/tidytuesday/master/data/2023/2023-05-02/surveys.csv')

Rows: 28364 Columns: 22  
── Column specification ────────────────────────────────────────────────────────  
Delimiter: ","  
chr (14): treatment, species, sex, reprod, age, testes, vagina, pregnant, n...  
dbl (7): month, day, year, plot, stake, hfl, wgt  
date (1): censusdate  
  
ℹ Use `spec()` to retrieve the full column specification for this data.  
ℹ Specify the column types or set `show\_col\_types = FALSE` to quiet this message.

library(vtable)

Loading required package: kableExtra

Attaching package: 'kableExtra'

The following object is masked from 'package:dplyr':  
  
 group\_rows

species

# A tibble: 21 × 15  
 species scientificname taxa commonname censustarget unidentified rodent  
 <chr> <chr> <chr> <chr> <dbl> <dbl> <dbl>  
 1 BA Baiomys taylori Rode… Northern … 1 0 1  
 2 PB Chaetodipus baileyi Rode… Bailey's … 1 0 1  
 3 PH Chaetodipus hispid… Rode… Hispid po… 1 0 1  
 4 PI Chaetodipus interm… Rode… Rock pock… 1 0 1  
 5 PP Chaetodipus penici… Rode… Desert po… 1 0 1  
 6 DM Dipodomys merriami Rode… Merriam's… 1 0 1  
 7 DO Dipodomys ordii Rode… Ord's kan… 1 0 1  
 8 DS Dipodomys spectabi… Rode… Banner-ta… 1 0 1  
 9 <NA> Neotoma albigula Rode… White-thr… 1 0 1  
10 OL Onychomys leucogas… Rode… Northern … 1 0 1  
# ℹ 11 more rows  
# ℹ 8 more variables: granivore <dbl>, minhfl <dbl>, meanhfl <dbl>,  
# maxhfl <dbl>, minwgt <dbl>, meanwgt <dbl>, maxwgt <dbl>, juvwgt <dbl>

surveys

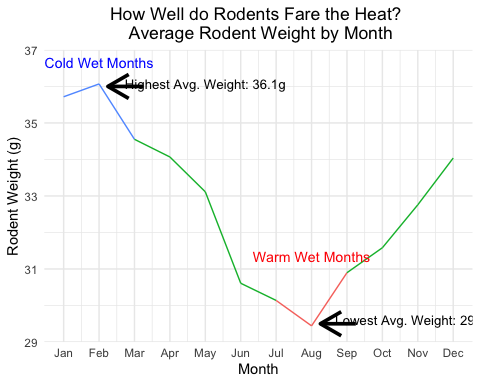
# A tibble: 28,364 × 22  
 censusdate month day year treatment plot stake species sex reprod age   
 <date> <dbl> <dbl> <dbl> <chr> <dbl> <dbl> <chr> <chr> <chr> <chr>  
 1 1978-01-08 1 8 1978 exclosure 3 11 OL <NA> <NA> <NA>   
 2 1978-01-08 1 8 1978 exclosure 3 22 <NA> <NA> <NA> <NA>   
 3 1978-01-08 1 8 1978 exclosure 3 54 PF M <NA> <NA>   
 4 1978-01-08 1 9 1978 control 14 14 OT <NA> <NA> <NA>   
 5 1978-01-08 1 9 1978 control 17 14 DM M Z <NA>   
 6 1978-01-08 1 9 1978 control 17 16 DM F <NA> <NA>   
 7 1978-01-08 1 9 1978 control 17 26 DS F Z <NA>   
 8 1978-01-08 1 9 1978 control 11 31 DM M Z <NA>   
 9 1978-01-08 1 9 1978 control 4 34 DS M Z <NA>   
10 1978-01-08 1 9 1978 control 14 35 OL <NA> <NA> <NA>   
# ℹ 28,354 more rows  
# ℹ 11 more variables: testes <chr>, vagina <chr>, pregnant <chr>,  
# nipples <chr>, lactation <chr>, hfl <dbl>, wgt <dbl>, tag <chr>,  
# note2 <chr>, ltag <chr>, note3 <chr>

library(dplyr)  
library(ggplot2)  
library(ggforce)

surveys$censusdate <- as.Date(surveys$censusdate, format = "%Y-%m-%d")  
  
surveys$month <- format(surveys$censusdate, "%m")  
  
library(dplyr)  
library(ggplot2)  
library(ggforce)  
  
weights\_by\_month <- surveys %>%  
 group\_by(month) %>%  
 summarise(mean\_weight = mean(wgt, na.rm = TRUE))  
  
ggplot(weights\_by\_month, aes(x = as.integer(month), y = mean\_weight, group = 1)) +   
 theme\_minimal() +  
 geom\_line(aes(color = ifelse(as.integer(month) %in% c(1,2), "red", ifelse(as.integer(month) %in% c(7,8), "black", "blue")))) +   
 # had trouble figuring out the color of the lines not sure why it was defaulting to green   
 ggtitle("How Well do Rodents Fare the Heat? \n Average Rodent Weight by Month") +  
 annotate("text", x = 2, y = 36.1, label = "Cold Wet Months",   
 size = 3.75, vjust = -1.5, color = "blue") +  
 annotate("text", x = 8, y = 30.8, label = "Warm Wet Months",   
 size = 3.75, vjust = -1.5, color = "red") +  
 labs(x = "Month", y = "Rodent Weight (g)") +  
 scale\_x\_continuous(breaks = c(9, 10, 11, 12, 1, 2, 3, 4, 5, 6, 7, 8), labels = c("Sep", "Oct", "Nov", "Dec", "Jan", "Feb", "Mar", "Apr", "May", "Jun", "Jul", "Aug")) +  
 annotate("segment", x = 9.25, xend = 8.25, y = 29.5, yend = 29.5,  
 colour = "black", size = 1.3, arrow = arrow()) +  
 annotate("segment", x = 3.25, xend = 2.25, y = 36, yend = 36,  
 colour = "black", size = 1.3, arrow = arrow()) +  
 guides(color = FALSE) +  
 annotate("text", x = 10.9, y = 29.1, label = "Lowest Avg. Weight: 29.4g",   
 size = 3.5, vjust = -1.5, color = "black") +  
 annotate("text", x = 5, y = 35.55, label = "Highest Avg. Weight: 36.1g",   
 size = 3.5, vjust = -1.5, color = "black") +  
 theme(plot.title = element\_text(hjust = 0.5)) +  
 scale\_y\_continuous(limits = c(29, 37), expand = c(0, 0))

Warning: Using `size` aesthetic for lines was deprecated in ggplot2 3.4.0.  
ℹ Please use `linewidth` instead.

Warning: The `<scale>` argument of `guides()` cannot be `FALSE`. Use "none" instead as  
of ggplot2 3.3.4.



weights\_by\_month

# A tibble: 12 × 2  
 month mean\_weight  
 <chr> <dbl>  
 1 01 35.7  
 2 02 36.1  
 3 03 34.6  
 4 04 34.1  
 5 05 33.1  
 6 06 30.6  
 7 07 30.1  
 8 08 29.4  
 9 09 30.9  
10 10 31.6  
11 11 32.8  
12 12 34.0