

# CompThinking2

Eric and Paige

## Load in libraries

```
library(tidyverse)
```

Warning: package 'ggplot2' was built under R version 4.4.3

Warning: package 'purrr' was built under R version 4.4.3

```
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
v dplyr      1.1.4      v readr      2.1.5
v forcats    1.0.0      v stringr    1.5.1
v ggplot2    4.0.1      v tibble     3.2.1
v lubridate  1.9.4      v tidyr      1.3.1
v purrr      1.2.1
-- Conflicts ----- tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()     masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become
```

```
library(here)
```

Warning: package 'here' was built under R version 4.4.3

here() starts at C:/Users/jgard/OneDrive/Paige's stuff 12.20/Graduate School/UCSC/Project pl

```
library(lterdatasampler)
```

Warning: package 'lterdatasampler' was built under R version 4.4.3

## Q1.1

```
x <- 11

# Check if the value of x is greater than 10
if(x > 10)
{
  # Paste takes the value stored in x and combines that with a character string
  print(paste(x, "is greater than 10"))
} else
{
  print(paste(x, "is less than or equal to 10"))
}
```

[1] "11 is greater than 10"

output: "11 is greater than 10"

## Q 1.2

```
vec <- c(-2,42,0,10)
# For 1 through the length of the vector "vec"
for (i in 1:length(vec)) {

  # check the value of using nested if-else statements
  if (vec[i] < 0) {
    # if the element is less than 10
    print("value is negative")
  } else {
    # if the element is exactly equal to 10
    if (vec[i] == 0) {
      # if the element equals 10
      print("value is equal to 0")
    } else {
      # if the element is greater than 10
      print("positive")
    }
  }
}
```

```
[1] "value is negative"
[1] "positive"
[1] "value is equal to 0"
[1] "positive"
```

### Q1.3

Stress was measured as the glucocorticoid metabolite concentration in pika feces. The variable is called `concentration_pg_m` and the units are picogram.

### Q 1.4

Answer: Each row is a feces sample (individual pika poop)

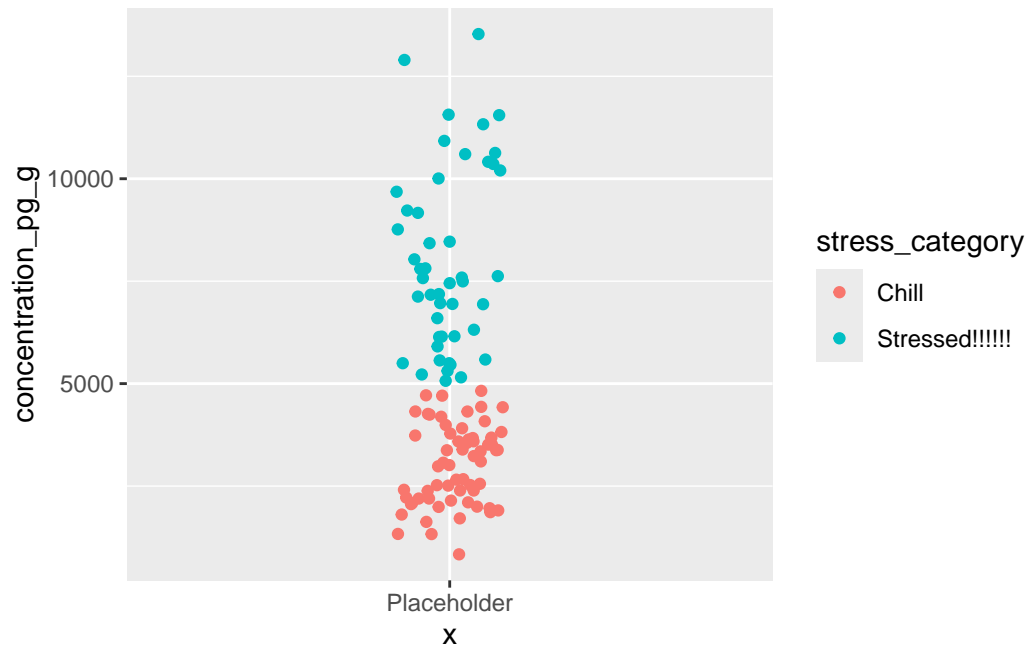
### Q 1.5

```
data("nwt_pikas")
head(nwt_pikas)
```

```
# A tibble: 6 x 8
  date       site      station utm_easting utm_northing sex      concentration_pg_g
  <date>     <fct>     <fct>      <dbl>      <dbl> <fct>      <dbl>
1 2018-06-08 Cable Ga~ Cable ~      451373      4432963 male      11563.
2 2018-06-08 Cable Ga~ Cable ~      451411      4432985 male      10629.
3 2018-06-08 Cable Ga~ Cable ~      451462      4432991 male      10924.
4 2018-06-13 West Kno~ West K~      449317      4434093 male      10414.
5 2018-06-13 West Kno~ West K~      449342      4434141 male      13531.
6 2018-06-13 West Kno~ West K~      449323      4434273 <NA>      7799.
# i 1 more variable: elev_m <dbl>
```

```
nwt_pikas_categ <- nwt_pikas %>%
  # Call the new column stress_category
  mutate(stress_category = case_when(
    # When the value is > 5000, make the new column's value "Stressed!!!!"
    concentration_pg_g > 5000 ~ "Stressed!!!!!!",
    # Otherwise, make the new column's value "Chill"
    .default = "Chill"
  ))
```

```
nwt_pikas_categ %>%
  # We're adding a little placeholder axis just so we can see the point distribution
  ggplot(aes(x = "Placeholder",
             y = concentration_pg_g,
             color = stress_category)) +
  # Add the geom_jitter geom
  geom_jitter(width = 0.1)
```



## Section 2

```
library(lterdatasampler)
library(tidyverse)
```

### Q 2.1

Using the knz bison dataset

```
data("knz_bison")
head(knz_bison)
```

```
# A tibble: 6 x 8
  data_code rec_year rec_month rec_day animal_code animal_sex animal_weight
  <chr>      <dbl>    <dbl>  <dbl> <chr>      <chr>      <dbl>
1 CBH01      1994      11      8 813        F          890
2 CBH01      1994      11      8 834        F         1074
3 CBH01      1994      11      8 B-301      F         1060
4 CBH01      1994      11      8 B-402      F          989
5 CBH01      1994      11      8 B-403      F         1062
6 CBH01      1994      11      8 B-502      F          978
# i 1 more variable: animal_yob <dbl>
```

## Q 2.2

We want the for loop to plot the weight of individuals in each age class. To do this, we first will calculate the age of each animal, then for every i age group, make a ggplot. We will plot animal\_weight on the y-axis, age on the x-axis, and then color by animal\_sex.

## Q 2.3

```
# First, calculate age by subtracting year of sampling from birth year
knz_bison2 <- knz_bison %>%
  mutate(age = rec_year - animal_yob)

# make a vector that

# Next, write a for loop

for (i in sort(unique(knz_bison2$age))) {
  # Fetch the column names of the dataframe, store in a vector "names"
  filt_data <- knz_bison2 %>%
    filter(age == i, !is.na(animal_weight))

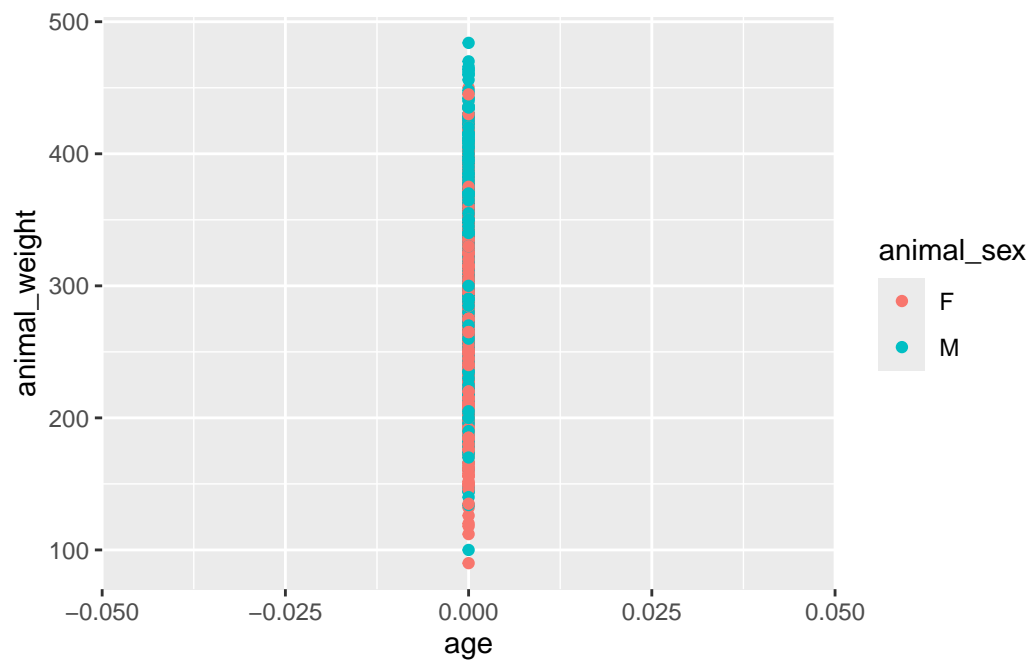
  # plot the mean weight for each age
  plot <- filt_data %>%
    ggplot(aes(x=age,
               y= animal_weight,
```

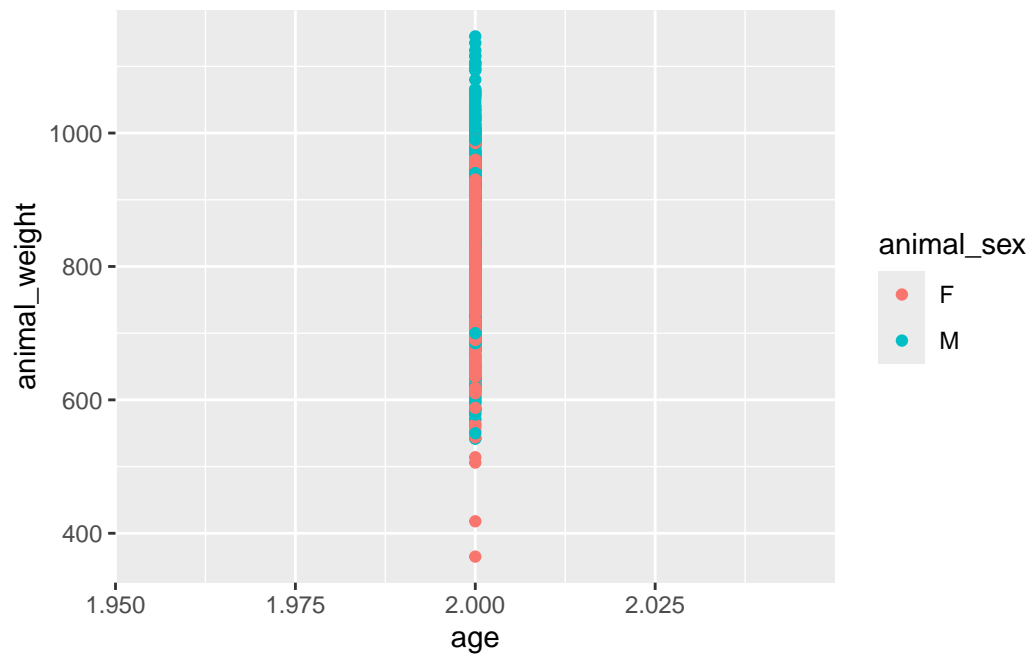
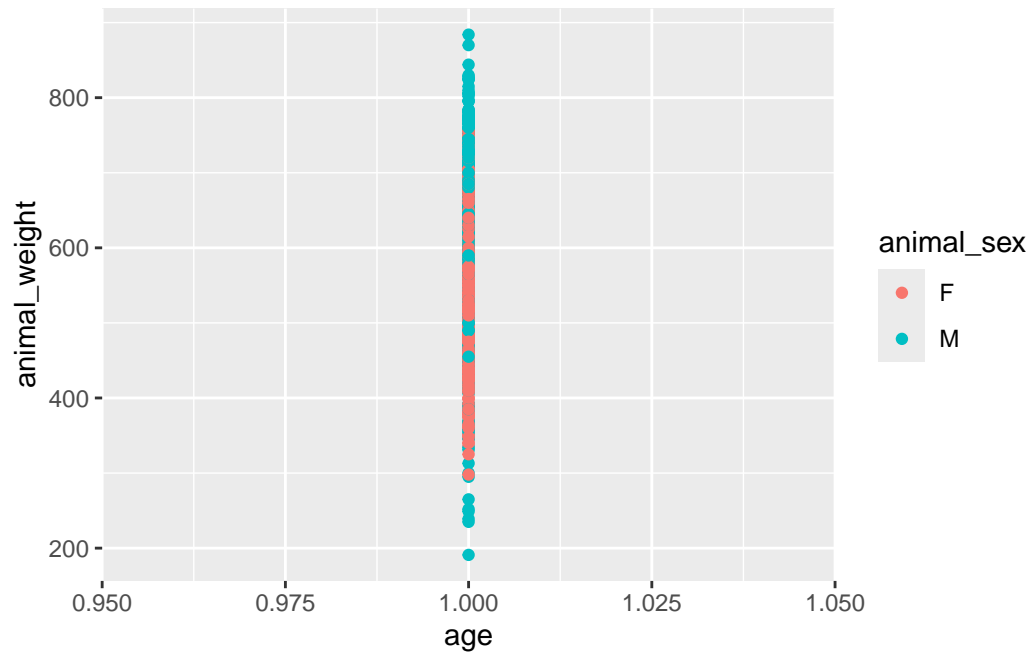
```

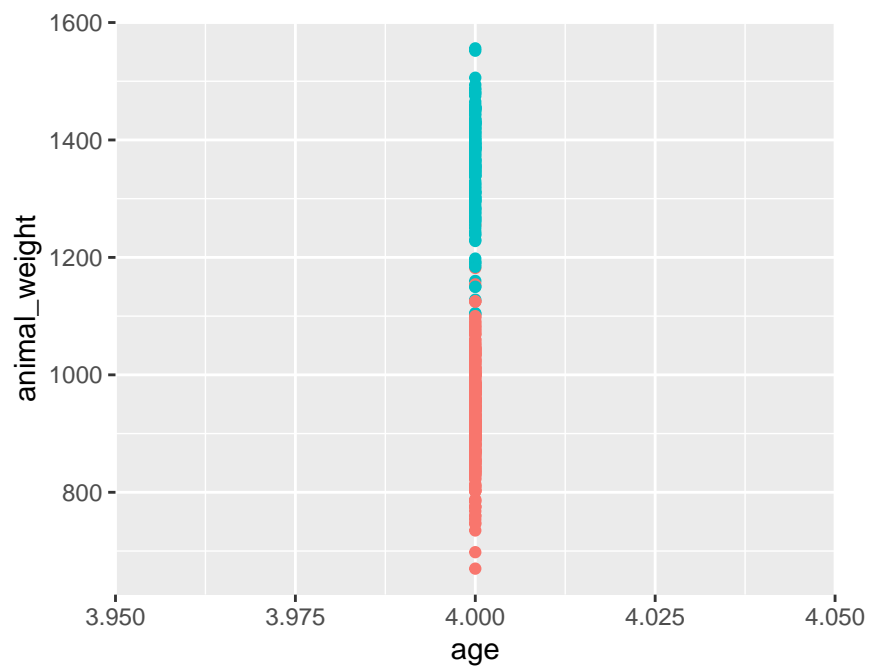
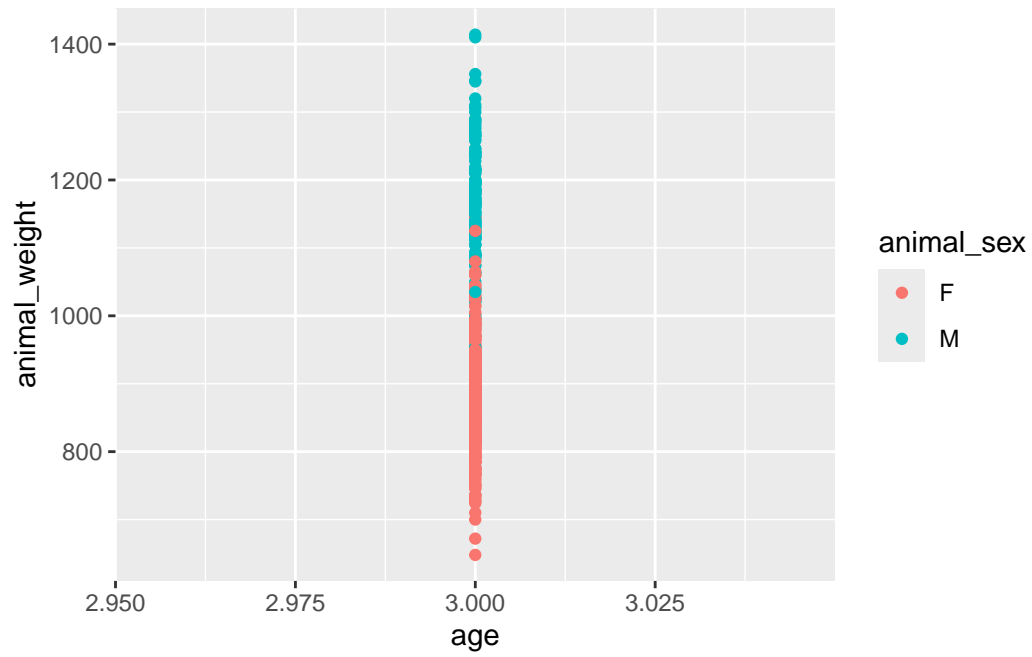
        color = animal_sex))+
  geom_point()

# This prints out column i
# print(plot)
print(plot)
}

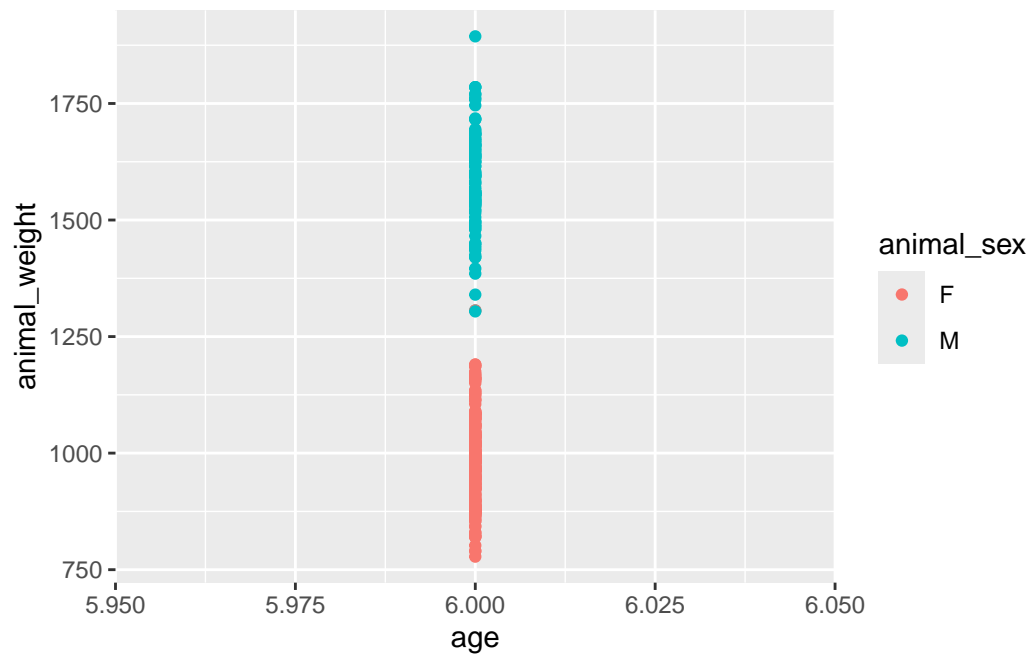
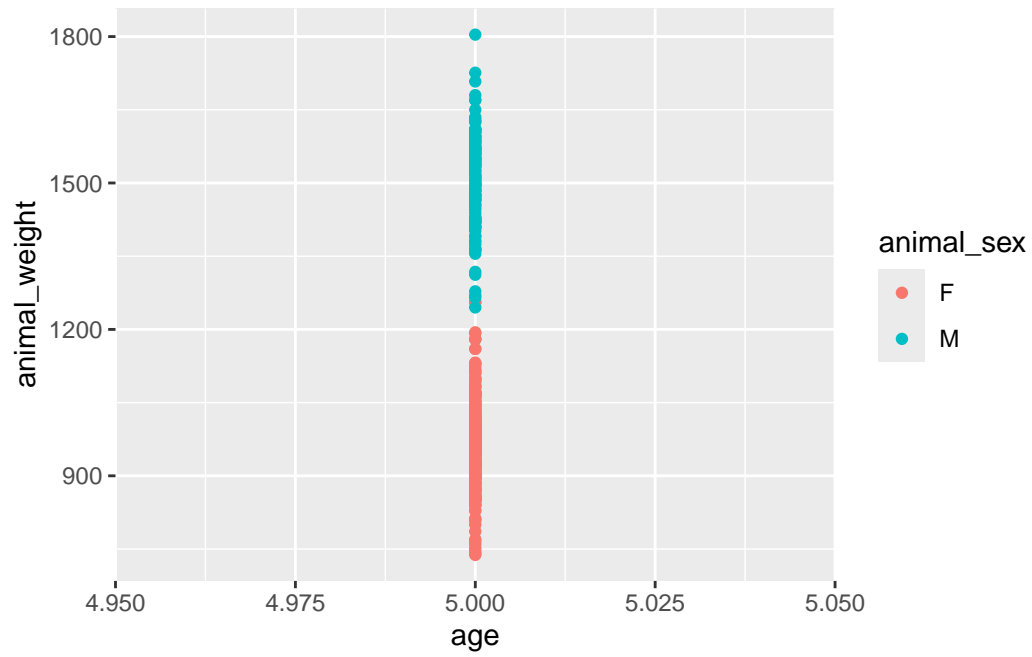
```

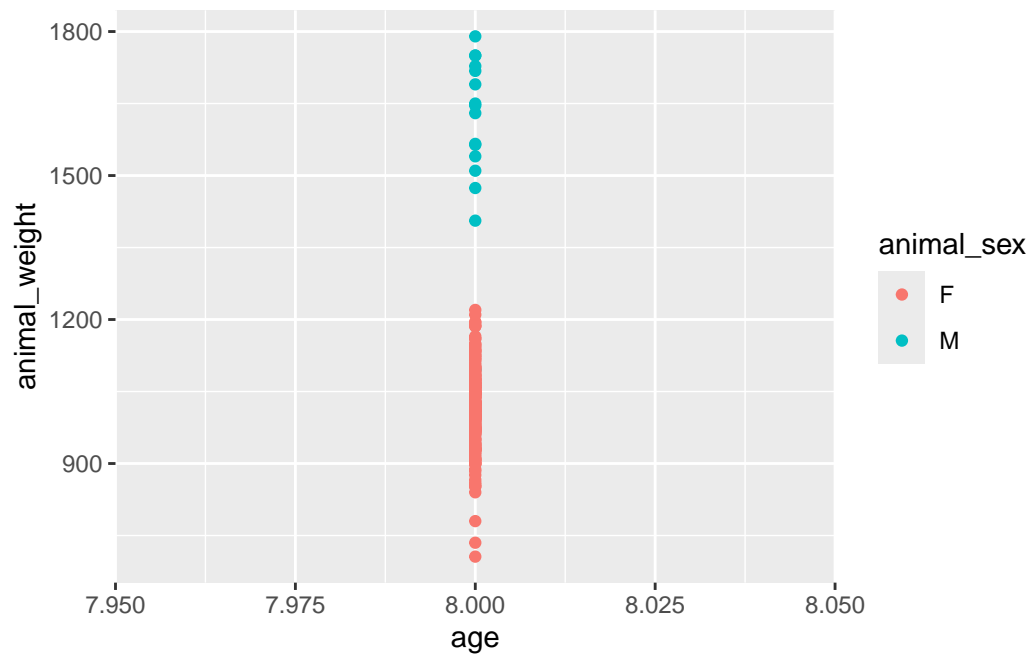
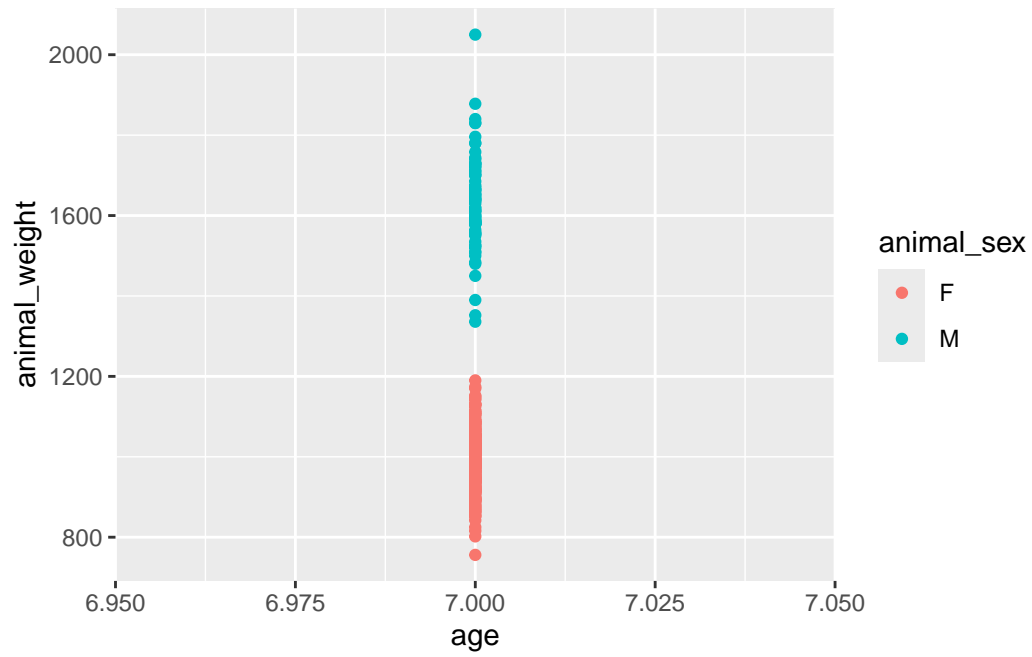


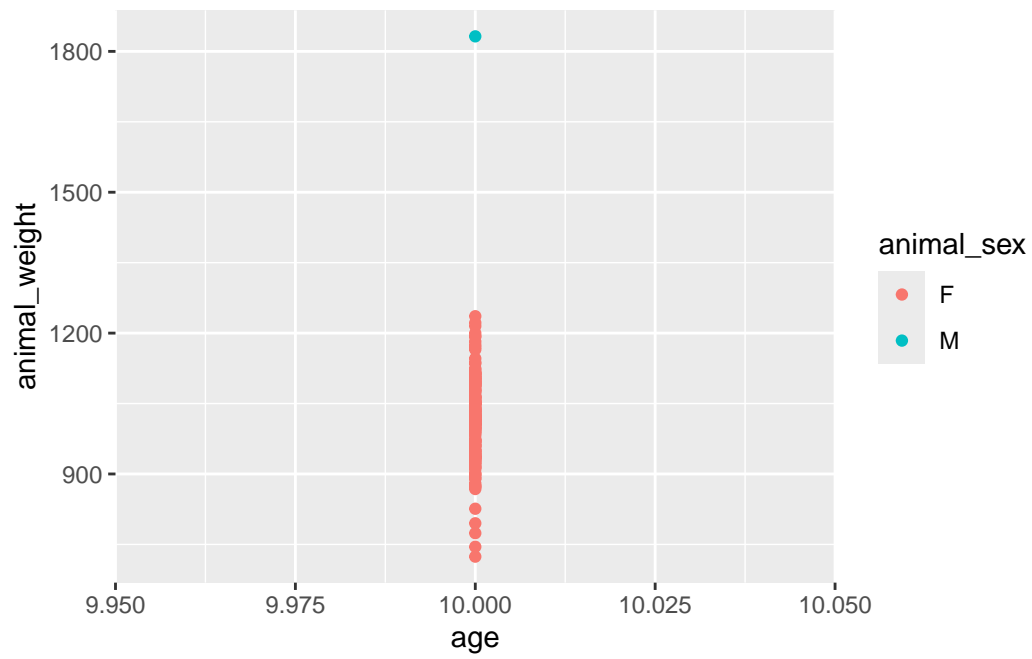
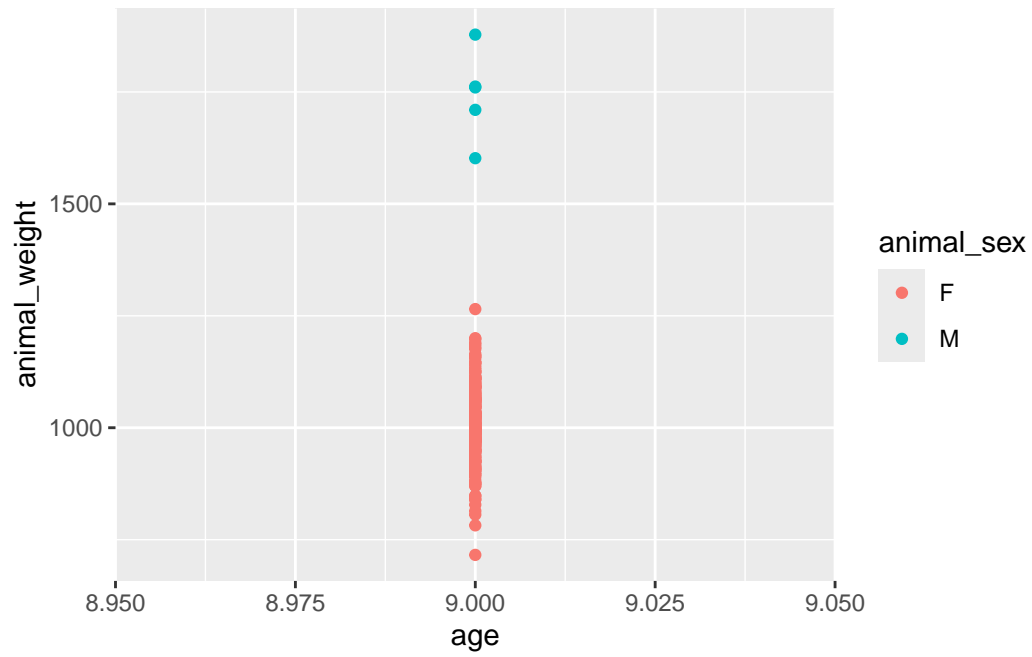


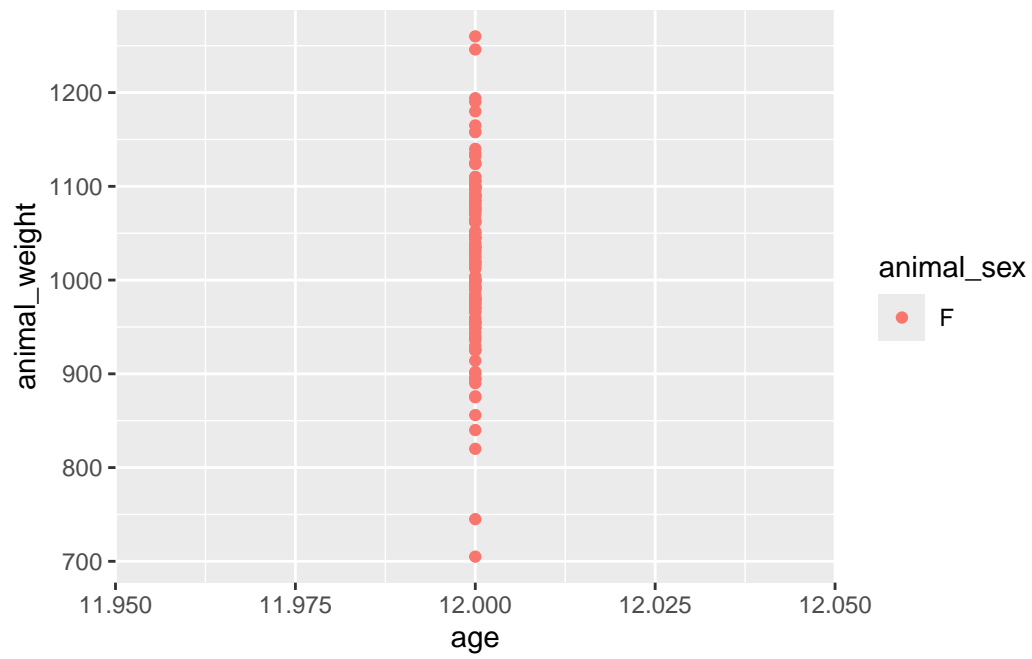
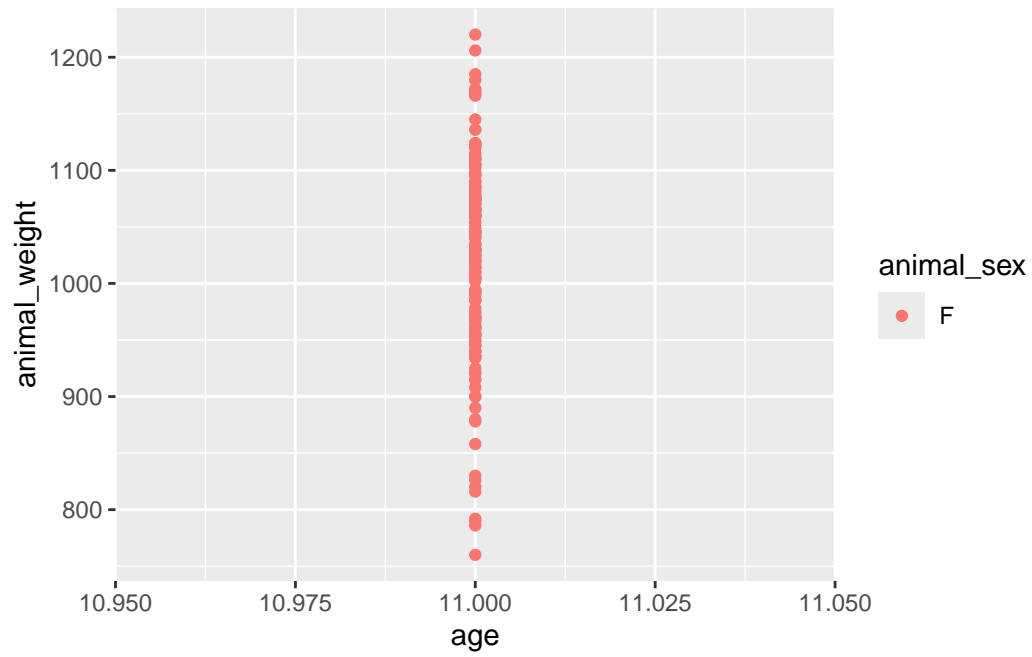


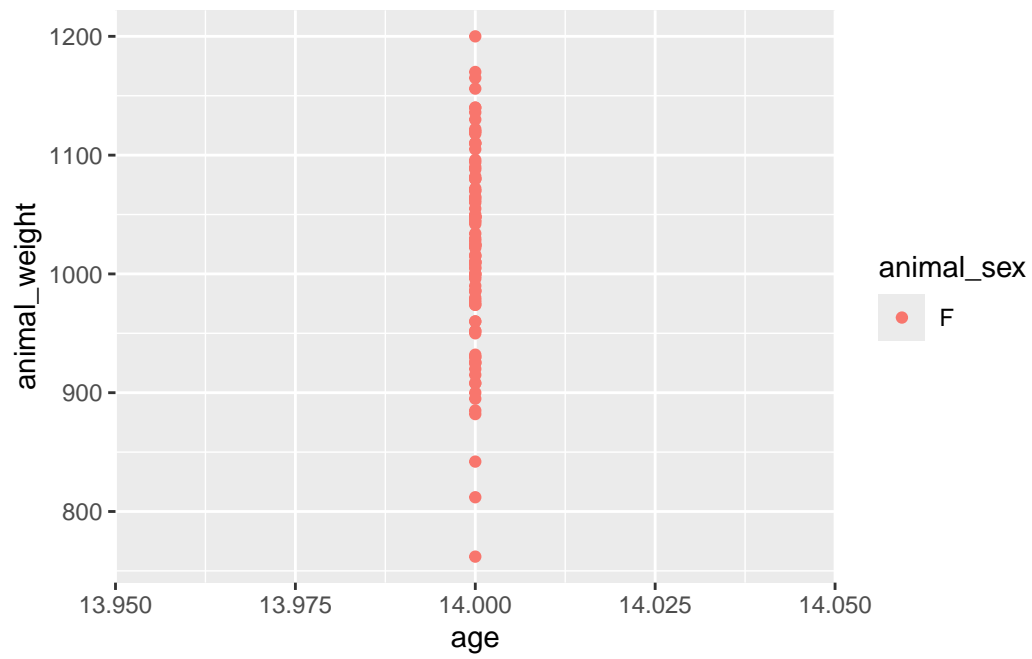
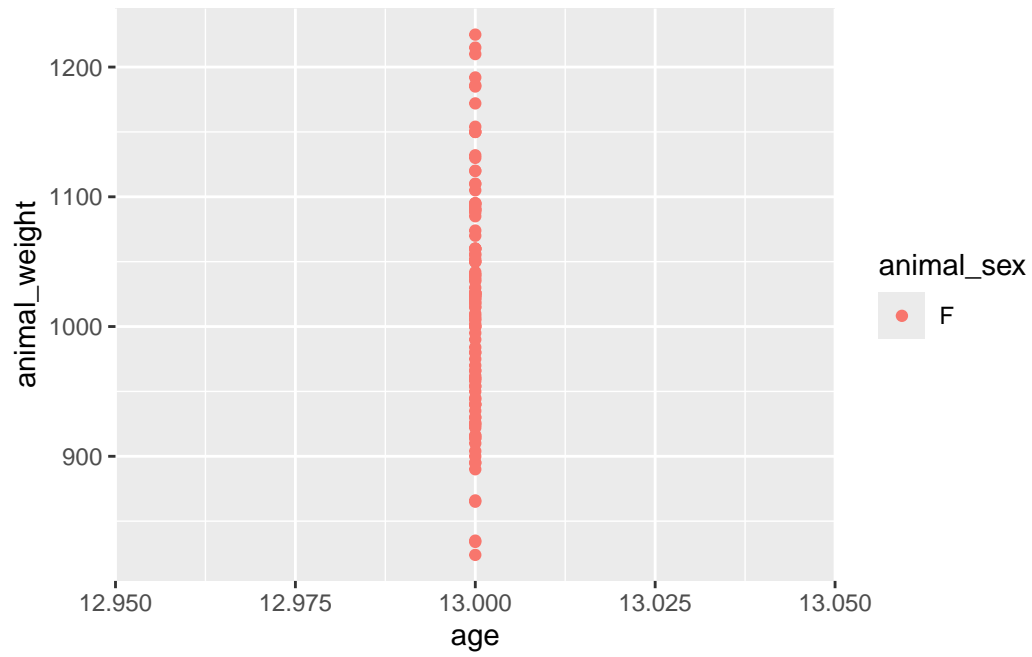


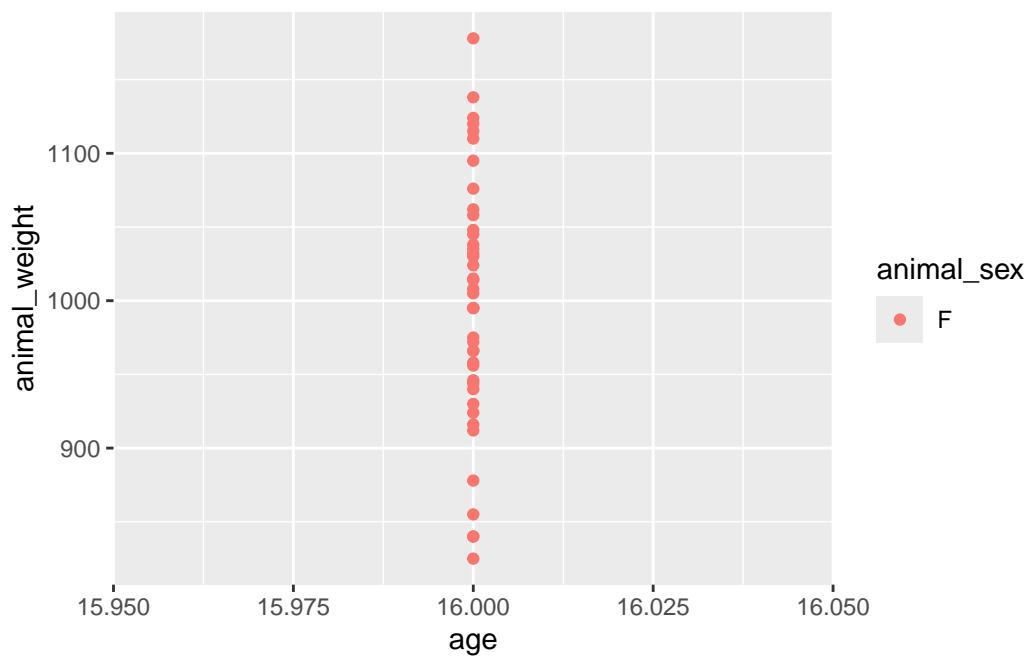
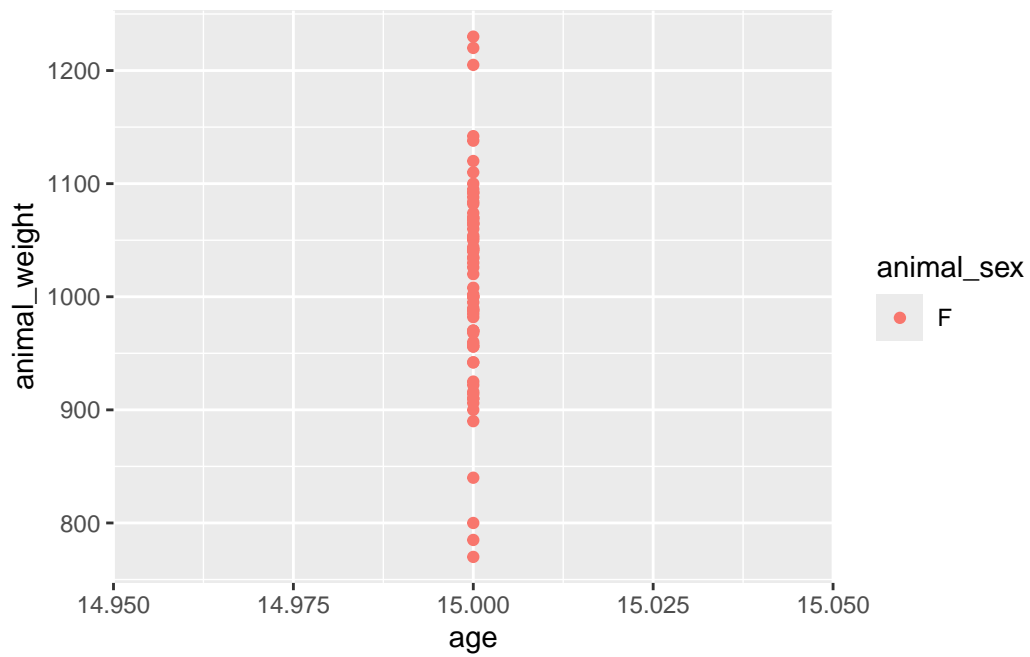


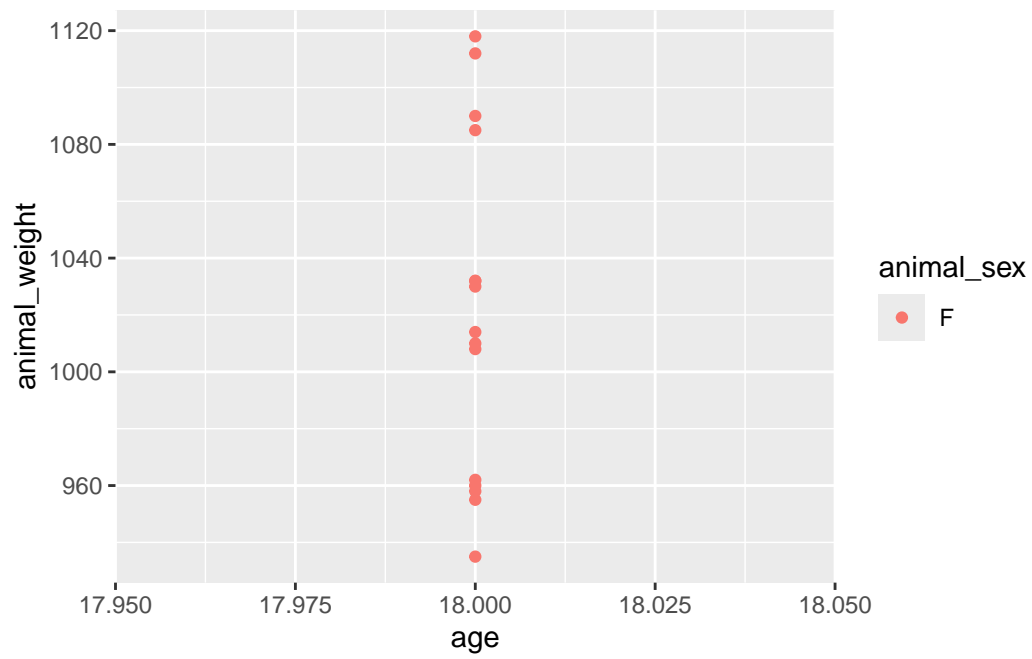
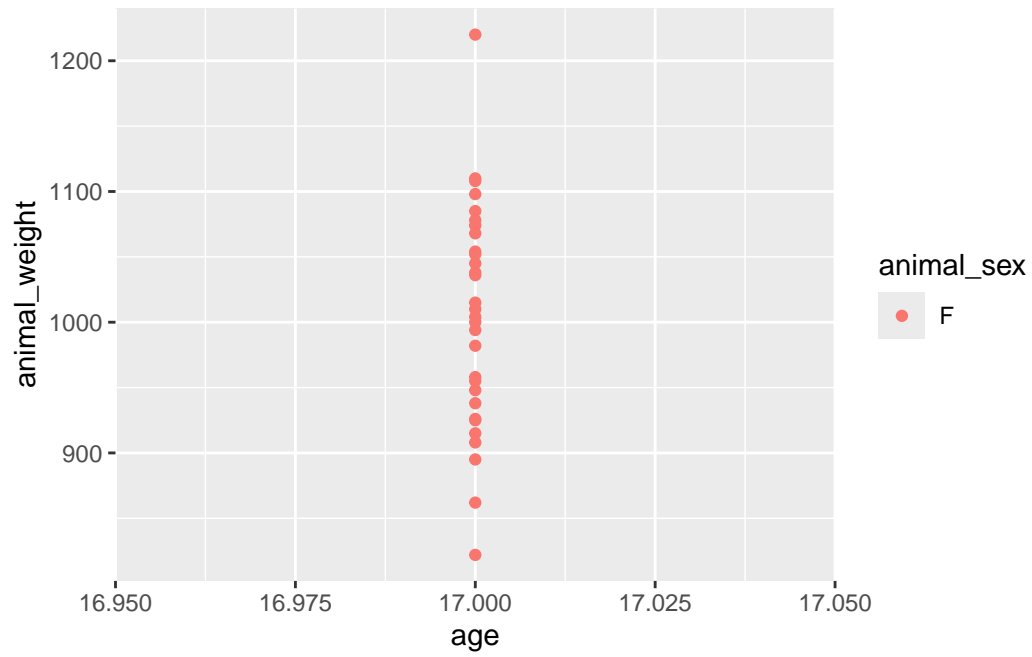


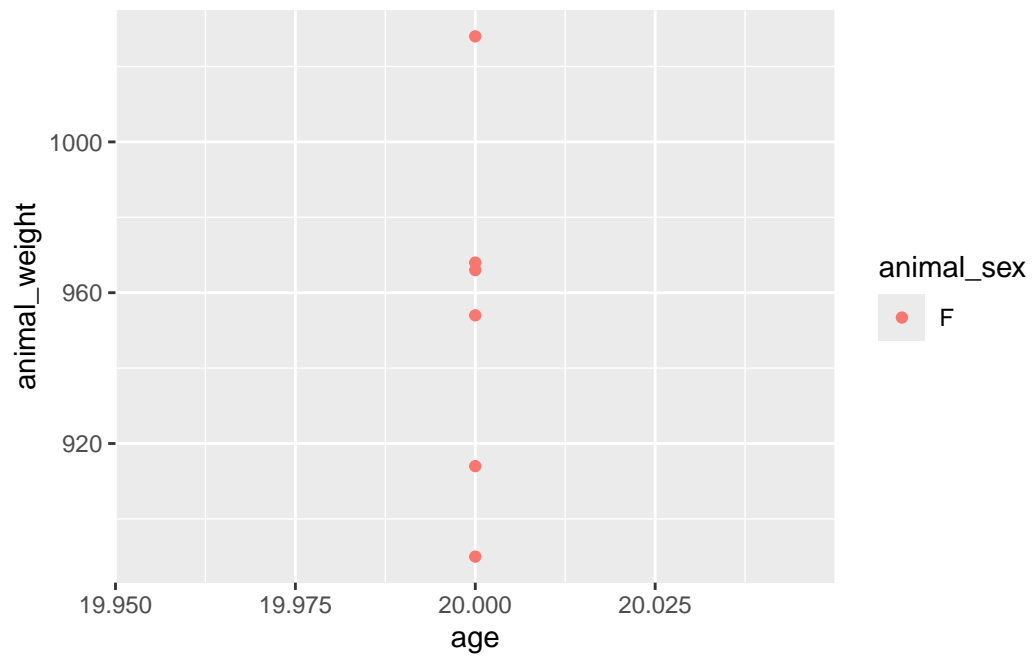
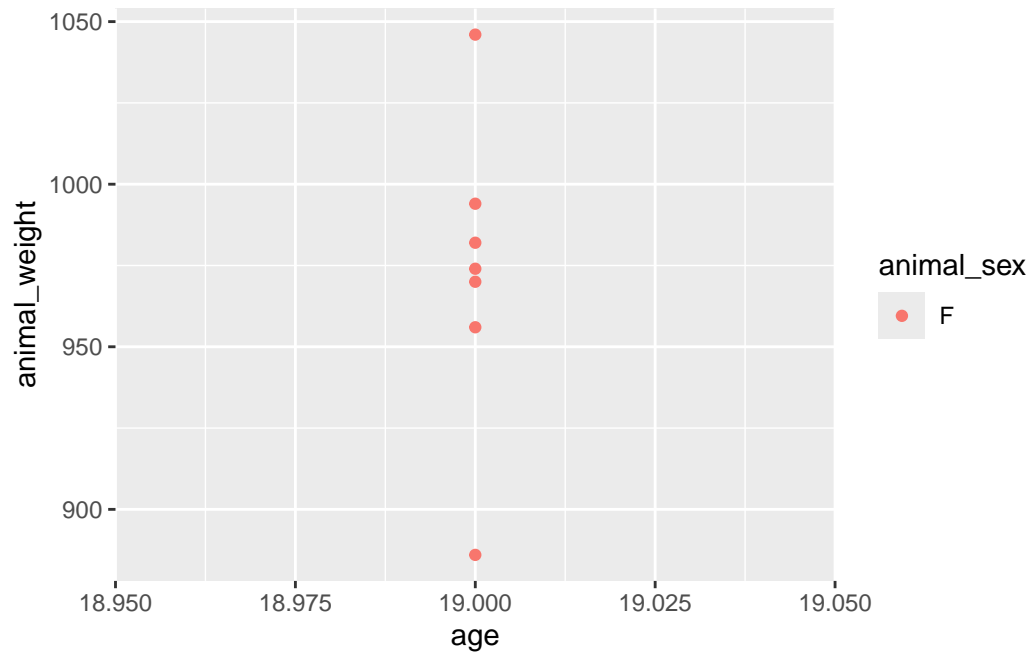




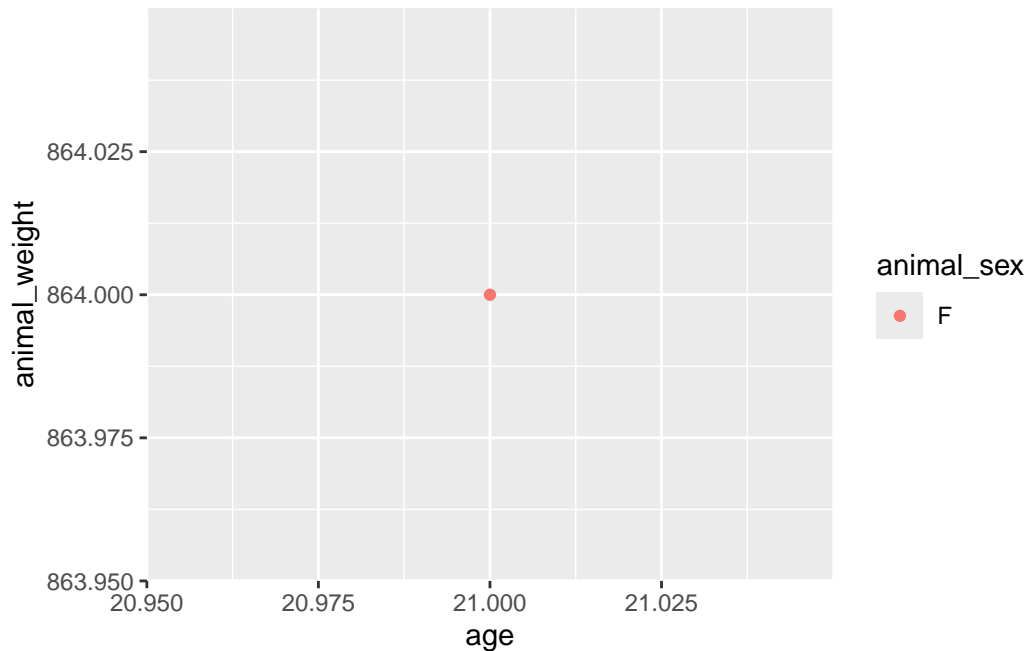












## Q2.4

We want to see how many males at age 1 are >500 lbs, and which are less. Those that are >500 lbs will be labeled “beefy” and those <500lbs will be labeled “lean”. This is best done with a `case_when` function.

First, we will filter a new dataframe for just males at age 1.

## Q 2.5

```
# filter a new dataset for just males at age 1
knz_bison_males <- knz_bison2 %>%
  filter(animal_sex == "M",
         age == 1)

knz_bison_males <- knz_bison_males %>%
  # Call the new column stress_category
  mutate(strength = case_when(
    # When the value is > 500, make the new column's value "Beefy"
    animal_weight > 500 ~ "Beefy",
```

```

    # Otherwise, make the new column's value "Chill"
    .default = "Lean"
  ))
head(knz_bison_males)

```

```

# A tibble: 6 x 10
  data_code rec_year rec_month rec_day animal_code animal_sex animal_weight
  <chr>      <dbl>    <dbl>   <dbl> <chr>      <chr>      <dbl>
1 CBH01      1994        11      8 302        M          359
2 CBH01      1994        11      8 OR 12        M          239
3 CBH01      1994        11      8 OR 14        M          353
4 CBH01      1994        11      8 OR 16        M          442
5 CBH01      1994        11      8 OR 18        M          265
6 CBH01      1994        11      8 OR 20        M          313
# i 3 more variables: animal_yob <dbl>, age <dbl>, strength <chr>

```

## Plot just for fun

```

ggplot(knz_bison_males, aes(x = animal_weight, fill = strength))+
  geom_histogram(binwidth = 20,
                 color= "black")

```

Warning: Removed 1 row containing non-finite outside the scale range (``stat_bin()``).

