Capstone Exercise

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**Differences in weight by sex**

```r
# create summary data of means by gender for M and F animals
mean.weight.by.sex <- portal %>%
    filter(sex == "M" | sex == "F") %>%
    group_by(sex) %>%
    summarise(mean = mean(weight, na.rm = TRUE))

# Calculate mean weight across all males, round the result to 2 decimal places
male.mean.weight <- mean.weight.by.sex %>%
    filter(sex == "M") %>%
    select(mean)
male.mean.weight <- round(male.mean.weight, 3)

# Calculate mean weight across all females, round the result to 2 decimal places
female.mean.weight <- mean.weight.by.sex %>%
    filter(sex == "F") %>%
    select(mean)
female.mean.weight <- round(female.mean.weight, 2)
```

```r
# Calculate difference between the means with a t-test
# If this is significant, then say so in the markdown text below
# If not, then change to state that it is not significant
weight.ttest <- t.test(portal[portal$sex == "F","weight"],
                       portal[portal$sex == "M","weight"],
                       na.rm = TRUE)
```

As you can see in the following figure, the average weight in grams for male species measured was 42.995 and for females it was 42.17. This is a statistically significant difference (p = 0.04).

Boxplot of mean weight across all animals by sex
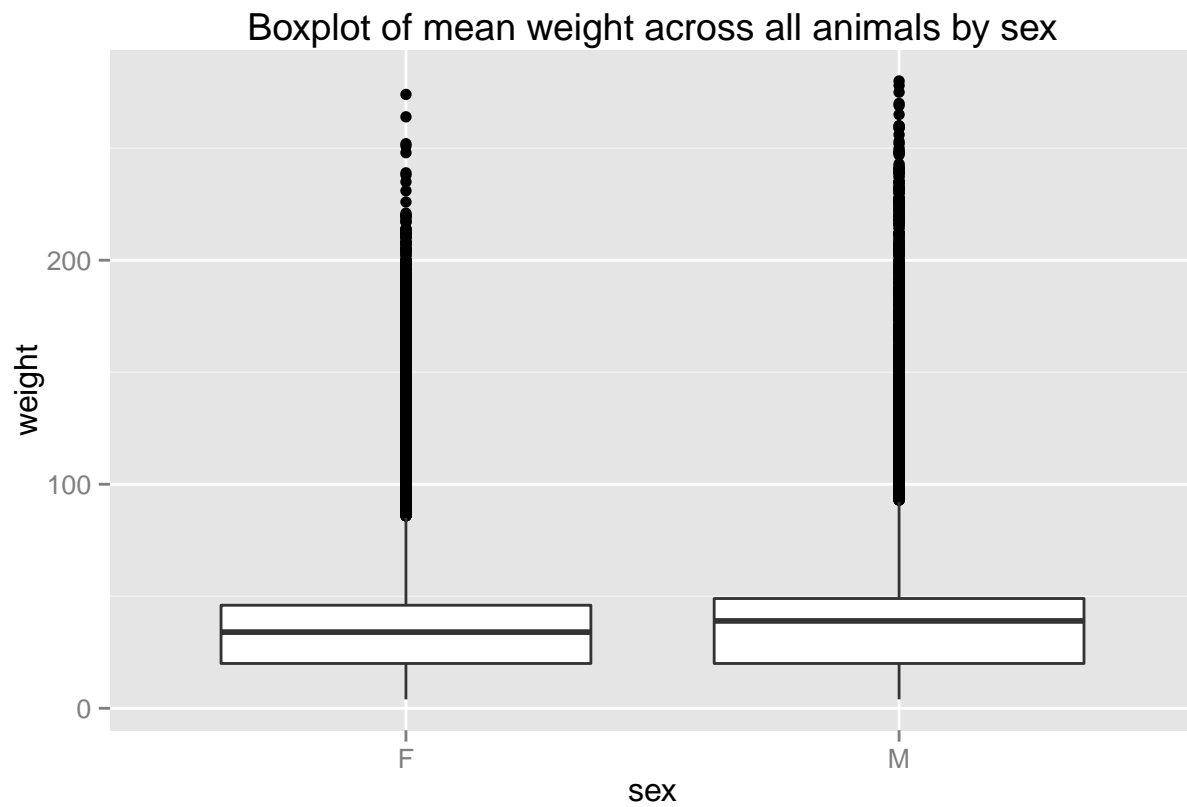
Distribution of measured hindfoot lengths

```r
# Generate a histogram of hindfoot length across all species
ggplot(portal, aes(x = hindfoot_length)) +
    geom_histogram() +
    ggtitle("Histogram of hindfoot lengths")
```

Histogram of hindfoot lengths
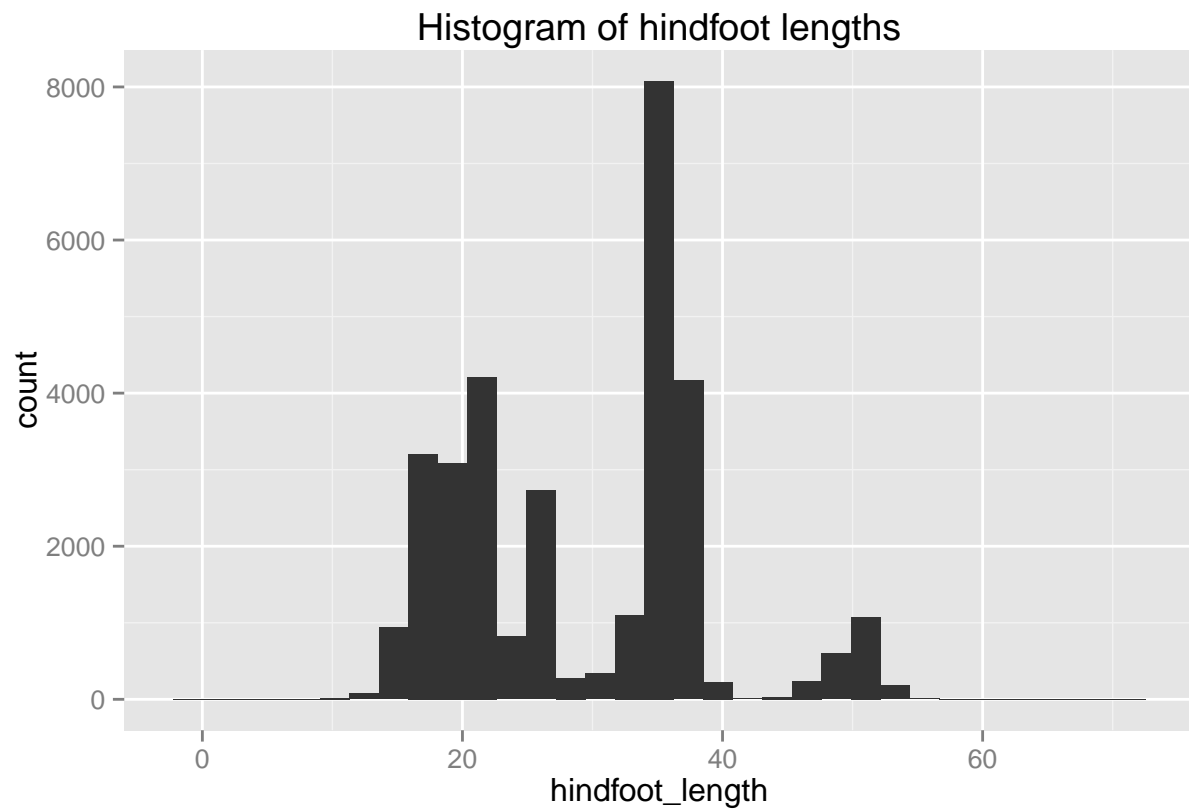

```r
# Generate a histogram of hindfoot length across all species,
# but with narrower binwidths
ggplot(portal, aes(x = hindfoot_length)) +
    geom_histogram(bin = 1) +
    ggtitle("Histogram of hindfoot lengths, using narrower bin widths")
```

Histogram of hindfoot lengths, using narrower bin widths
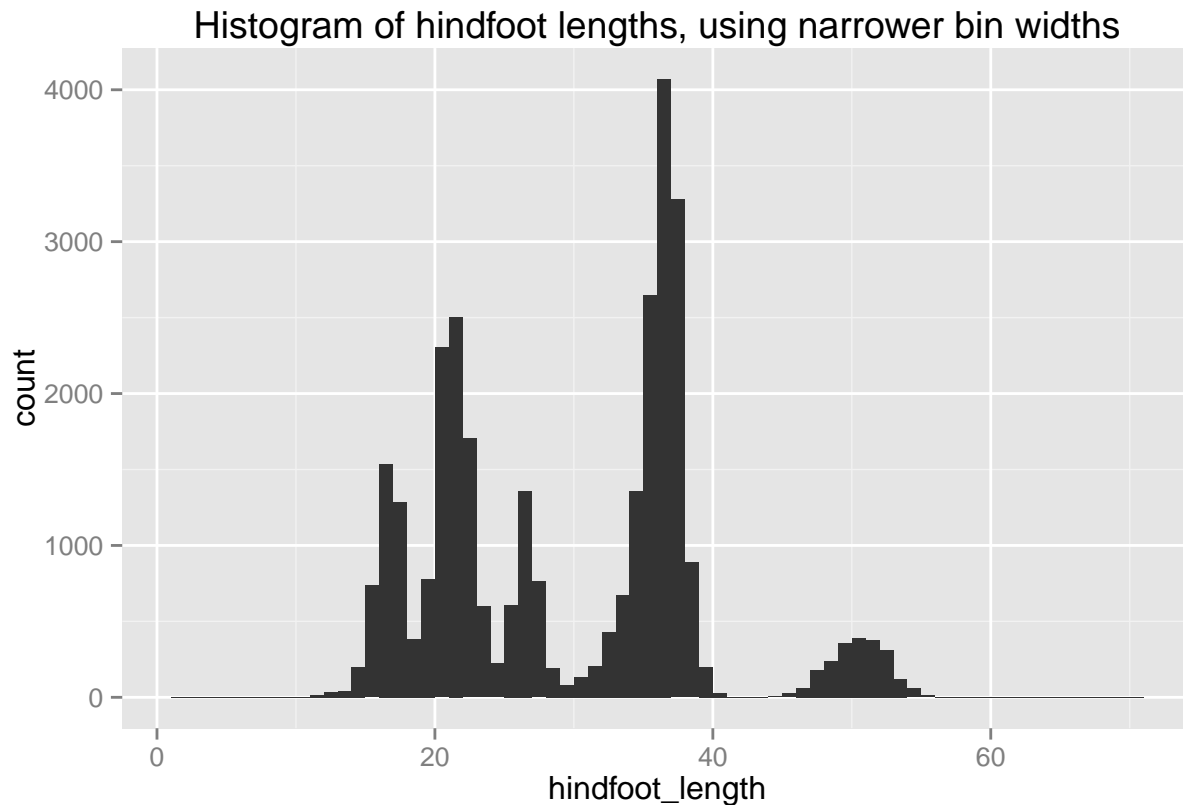
Scatterplot of three selected species

```r
# Choose three species on the next line:
chosen.species <- c("DM", "DO", "DS")

species.names <- portal %>%
    filter(species_id %in% chosen.species) %>%
    group_by(genus, species) %>%
    summarise()
```
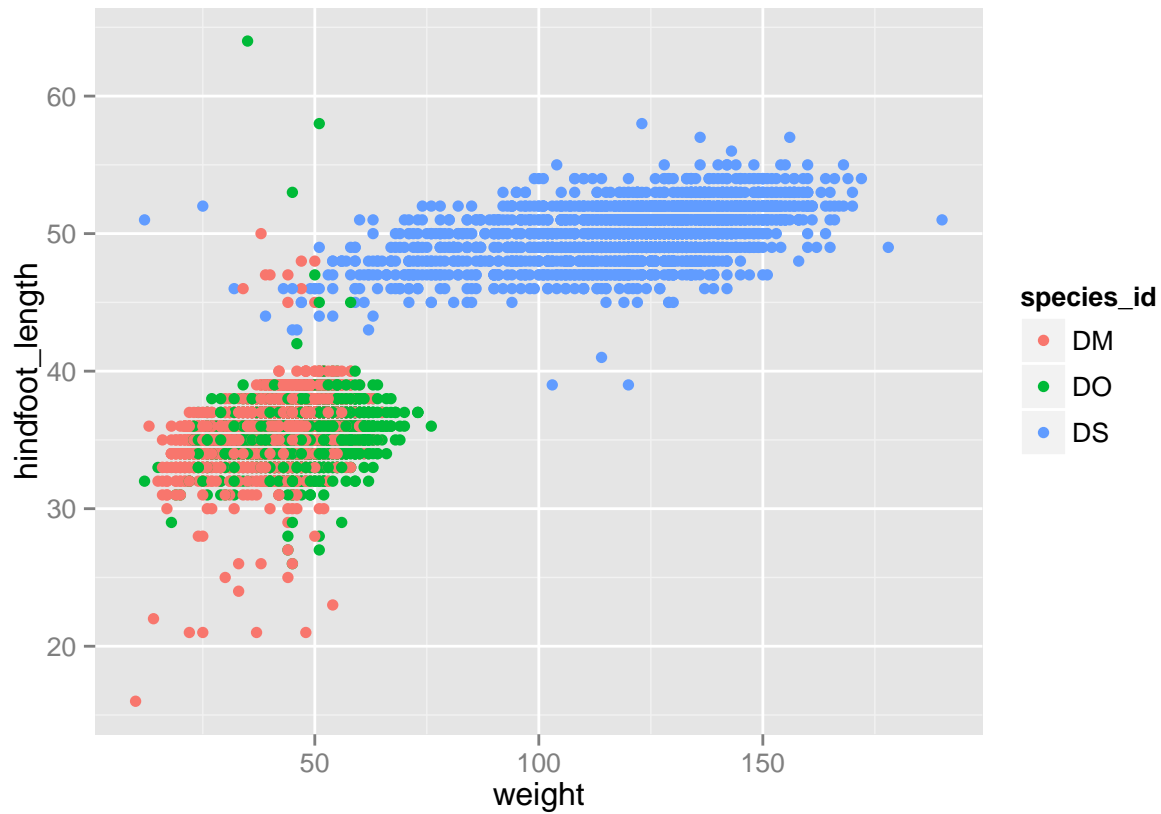
Generate a scatterplot of three chosen species:

- *Dipodomys merriami*
- *Dipodomys ordii*
- *Dipodomys spectabilis*

```r
# create a scatterplot of the three chosen species, coloring by species ID
portal %>%
    filter(species_id %in% chosen.species) %>%
    ggplot(aes(x = weight, y = hindfoot_length, color = species_id)) +
    geom_point()
```

Observation counts for species DM over time, faceted by plot type

```r
# Generate a line plot of the number of species observed in each of the
# different treatment types, for species DM, over time

portal %>%
    filter(species_id == "DM") %>%
    group_by(plot_type, year) %>%
    tally() %>%
    ggplot(aes(x = year, y = n)) +
        geom_line() +
        facet_wrap(~ plot_type)
```
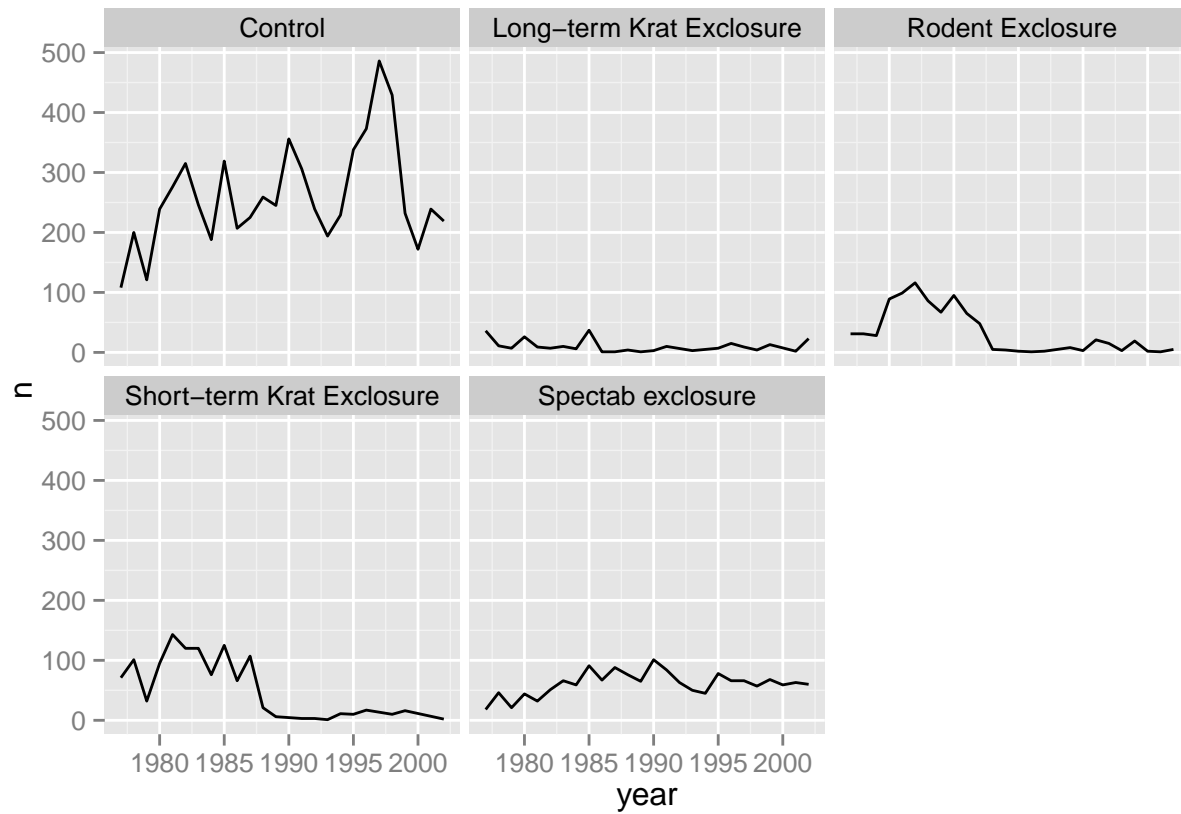
It appears that the Long-term Krat Exclosure treatment was effective at keeping individuals out, and that the Rodent exclosure and Short-term Krat exclosure were also effective, particularly after 1990.