functions-after.Rmd

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Installing library package

```
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(ggplot2)
```

#reading in the csv files

```
surveys <- read.csv(file = "../data-raw/surveys.csv")
species <- read.csv(file = "../data-raw/species.csv")
plots <- read.csv(file = "../data-raw/species.csv")
```

combining surveys and species tables into single data frame

```
combined_df <- inner_join(surveys, species, by ="species_id")
```

writing a function that takes three arguments

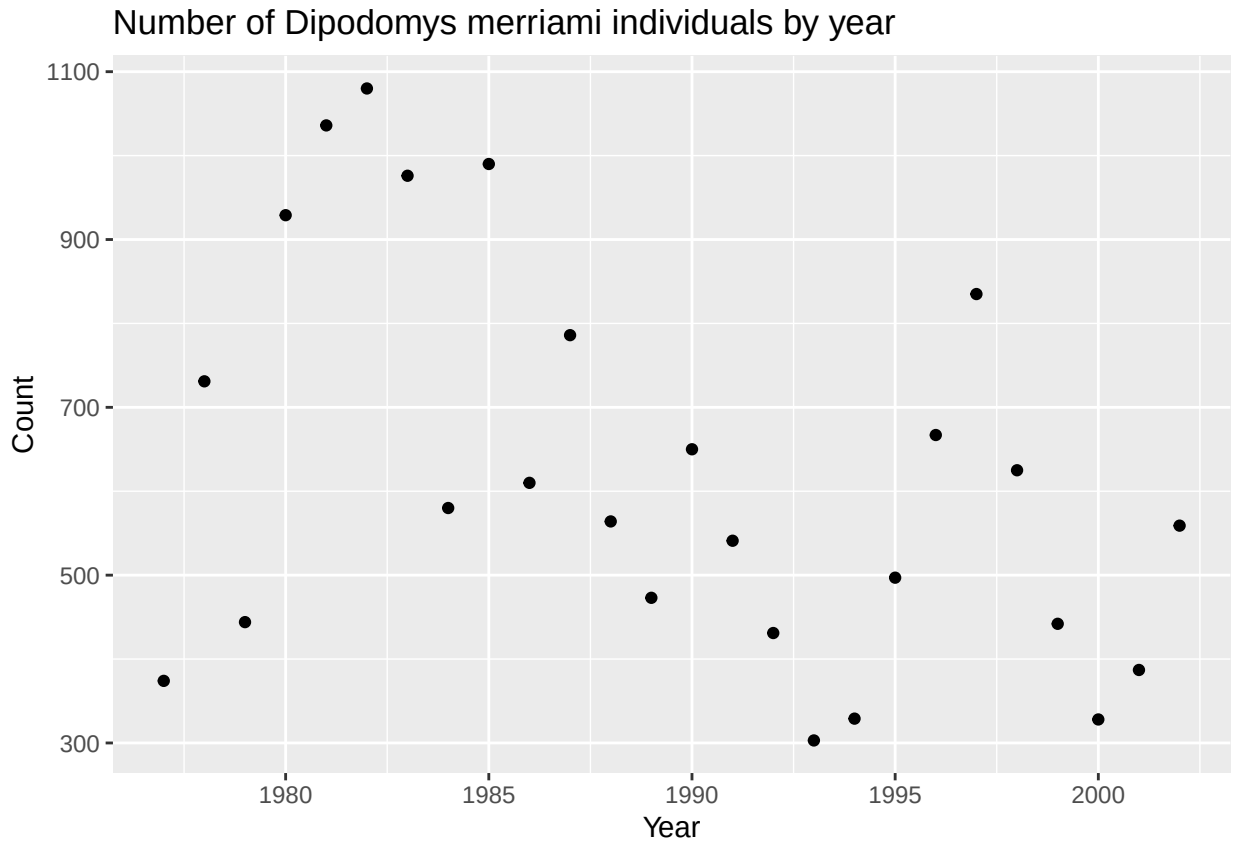
```
get_species_count_by_year <- function(df, genus, species){
  species_df <- df %>%
  filter(genus == "Dipodomys" | species == "merriami")
```

```
  count_df <- species_df %>%
  group_by(year) %>%
  summarize(count = n())
return(count_df)
}
```

using function to get the data frame of time series by year for the genus “Dipodomys” and the species “merriami” and make a graph

```
count_df <- get_species_count_by_year(combined_df, "Dipodomys", "merriami")

ggplot(count_df, aes(x = year, y = count)) +
  geom_point() +
  labs(x = "Year", y = "Count", title = "Number of Dipodomys merriami individuals by year")
```



Using the function to get the data frame series by year for the genus Chaetodipus and species penicillatus and make a graph

```
count_df <- get_species_count_by_year(combined_df, "Chaetodipus", "penicillatus")
ggplot(count_df, aes(x = year, y = count)) +
  geom_line(color = "blue", size = 2) +
  geom_point(color = "blue", size = 1) +
  labs(x = "Year", y = "Number of Individuals", title = "Number of Chaetodipus penicillatus individuals
```

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