functions-after

2023-04-01

```r
surveys <- read.csv(file = "../data raw/surveys.csv")
species <- read.csv (file = "../data raw/species.csv")
plots <- read.csv(file = "../data raw/plots.csv")
```
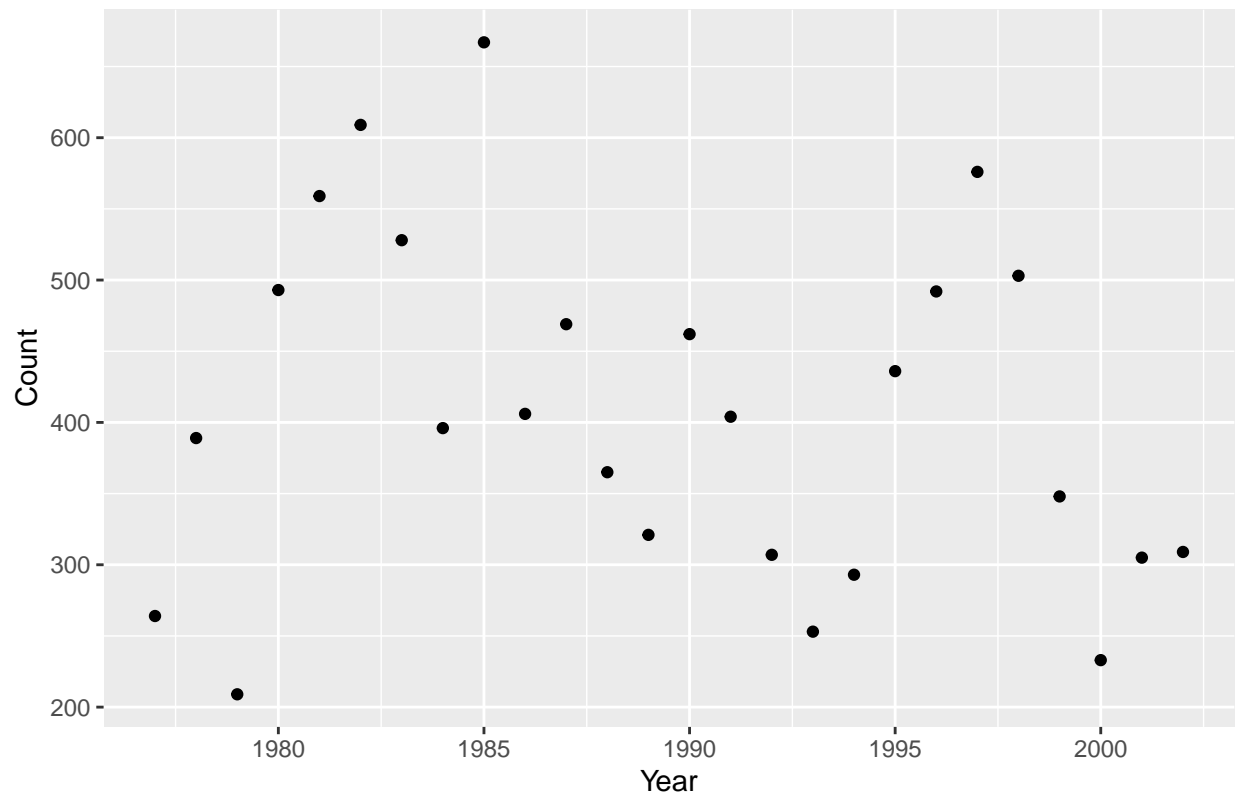
```r
mixed <- inner_join(surveys, species, by = "species_id")
```

```r
library(ggplot2)
```

```r
object <- function(mixed, genus_name, species_name) { mixed %>%
select(year, genus, species) %>%
filter(genus == genus_name, species == species_name) %>% group_by(year) %>%
summarise(count = n()) -> result_data_frame
return(result_data_frame) }
```

```r
Dipodomys_merriami <- object(mixed, "Dipodomys", "merriami")
ggplot(data = Dipodomys_merriami, mapping = aes(x = year, y = count)) +
geom_point() +
labs(x = "Year", y = "Count", title = "Dipodomys merriami - Time Series by Year")
```

Dipodomys merriami – Time Series by Year


```
Chaetodipus_penicillatus <- object(mixed, "Chaetodipus", "penicillatus")
ggplot(data = Chaetodipus_penicillatus, mapping = aes(x = year, y = count)) +
geom_point(size = 1, color = "blue") +
geom_line(size = 2, color = "blue") +
labs(x = "Year", y = "Number of Individuals", title = "Chaetodipus penicillatus - Time Series by Year")
```

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

Chaetodipus penicillatus – Time Series by Year