FunctionHw(3/21)

Anita Dhillon

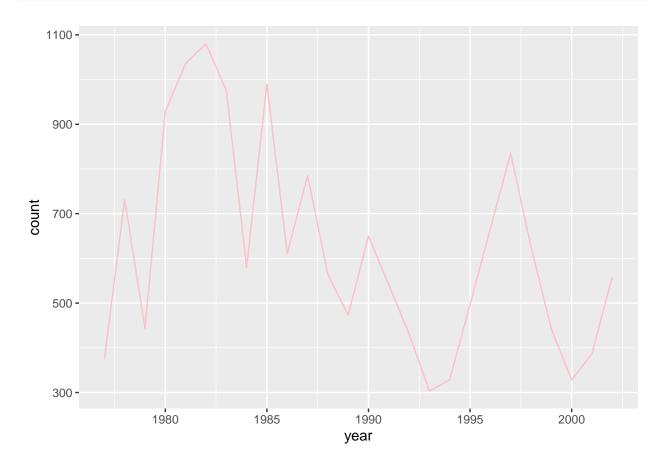
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Function for the Portal Data Set

```
surveys <-read.csv(file = "../data-raw/surveys.csv")</pre>
species <-read.csv(file = "../data-raw/species.csv")</pre>
plots <- read.csv(file = "../data-raw/plots.csv")</pre>
intersect(colnames(surveys), colnames(species))
## [1] "species_id"
a = inner_join(surveys, species, by = "species_id")
head(a)
     record_id month day year plot_id species_id sex hindfoot_length weight
##
## 1
             1
                   7 16 1977
                                               NL
                                                    Μ
## 2
             2
                   7 16 1977
                                               NL
                                                    Μ
                                                                    33
                                                                            NA
                   7 16 1977
                                     2
                                                    F
                                                                    37
## 3
             3
                                               DM
                                                                           NA
                   7 16 1977
                                     7
## 4
             4
                                               DM
                                                    Μ
                                                                    36
                                                                            NA
             5
                   7 16 1977
                                     3
                                               DM
                                                                    35
## 5
                                                    М
                                                                           NA
                   7 16 1977
## 6
             6
                                     1
                                               PF
                                                                    14
                                                                           NA
                                                    Μ
           genus species
##
## 1
        Neotoma albigula Rodent
## 2
        Neotoma albigula Rodent
## 3
       Dipodomys merriami Rodent
       Dipodomys merriami Rodent
       Dipodomys merriami Rodent
## 5
## 6 Perognathus
                   flavus Rodent
my_function <- function(a, genus_name = "Dipodomys", species_name = "merriami") {</pre>
 a %>%
  group_by(year) %>%
  filter(genus == genus_name | species == species_name) %>%
  summarize(count = n()) -> output
  return(output)
my_function(a = a)
## # A tibble: 26 x 2
##
       year count
```

```
##
      <int> <int>
##
   1 1977
             374
   2 1978
             731
##
   3 1979
             444
##
##
      1980
             929
##
   5 1981 1036
##
   6 1982 1080
   7 1983
             976
##
##
   8 1984
             580
##
   9 1985
             990
## 10 1986
             610
## # ... with 16 more rows
```

```
my_function(a =a) %>%
ggplot(mapping = aes(x = year, y = count)) +
geom_line(color = "pink")
```



```
my_function(a = a, "Chaetodipus", "penicillatus") %>%
  ggplot(mapping = aes(x = year, y = count)) +
  geom_point(size = 1, color = "yellow") +
  geom_line(size = 2, color = "red") +
  labs(x = "year", y = "Number of Individuals")
```

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

