Functions homework

Luna L Sanchez Reyes

2022-11-11

1. Loda data table

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

2. Combine data tables

```
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
```

```
combined <- inner_join(surveys, species)
```

```
## Joining, by = "species_id"
```

```
head(combined)
```

```
##   record_id month day year plot_id species_id sex hindfoot_length weight
## 1         1     7  16 1977       2         NL   M              32     NA
## 2         2     7  16 1977       3         NL   M              33     NA
## 3         3     7  16 1977       2         DM   F              37     NA
## 4         4     7  16 1977       7         DM   M              36     NA
## 5         5     7  16 1977       3         DM   M              35     NA
## 6         6     7  16 1977       1         PF   M              14     NA
##         genus   species   taxa
## 1     Neotoma albigula Rodent
## 2     Neotoma albigula Rodent
## 3   Dipodomys merriami Rodent
## 4   Dipodomys merriami Rodent
## 5   Dipodomys merriami Rodent
## 6 Perognathus   flavus Rodent
```

3. Write a function

Review of the skeleton of a function:

```
name_of_function <- function(arguments, for, the, function, here, a, default_argument = default_value)
  Body of teh function()
  create_new_variables <- c()
```

```
    return(results)
}
```

Write a function to create time series from the UHURU data set:

```
function1 <- function(combined, genus_name = "Neotoma", species_name = "albigula") {
  combined %>%
    select(year, genus, species) %>%
    filter(genus == genus_name, species == species_name) %>%
    group_by(year) %>%
    summarize(count = n()) -> data_frame_result

  return(data_frame_result)
}

combined1 <- time_series <- function1
```

```
function1(combined)
```

```
## # A tibble: 26 x 2
##     year count
##    <int> <int>
##  1  1977    31
##  2  1978    48
##  3  1979    30
##  4  1980    57
##  5  1981    63
##  6  1982   111
##  7  1983    98
##  8  1984    64
##  9  1985    45
## 10  1986    60
## # ... with 16 more rows
```
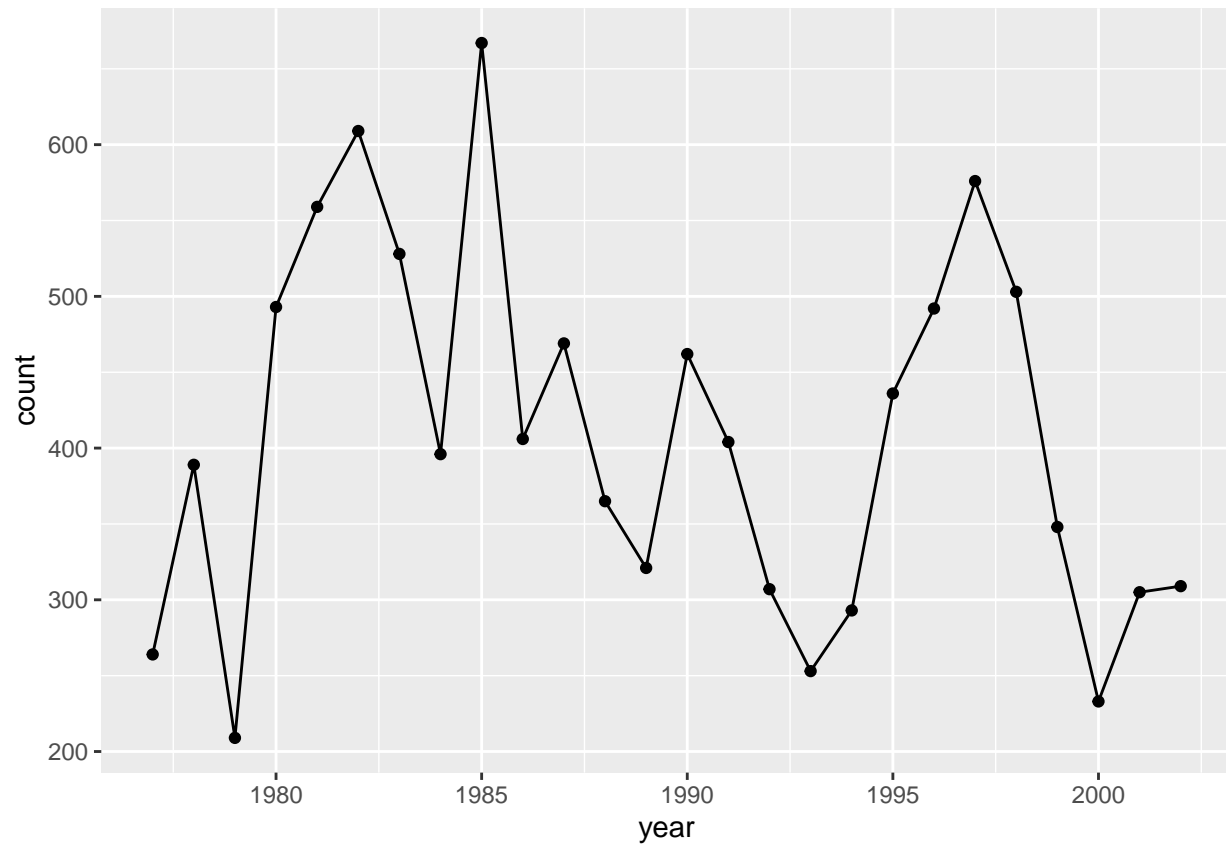
```
test1 <- function1(genus_name = "Dipodomys", combined = combined, species_name = "merriami")

library(ggplot2)
ggplot(test1, mapping = aes(x = year, y = count)) +
  geom_point() +
  geom_line()
```

"Chaetodipus" "penicillatus"

```r
chp_time_series <- combined1(combined = combined, genus_name = "Chaetodipus", species_name = "penicilla

ggplot(chp_time_series, mapping = aes(x = year, y = count)) +
  geom_point() +
  geom_line()
```