

Activity_6

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```
library(tidyverse)
```

```
-- Attaching core tidyverse packages ----- tidyverse 2.0.0 --
v dplyr      1.1.4      v readr      2.1.5
v forcats    1.0.0      v stringr    1.5.1
v ggplot2    4.0.0      v tibble     3.3.0
v lubridate  1.9.4      v tidyr      1.3.1
v purrr      1.1.0
-- Conflicts ----- tidyverse_conflicts() --
x dplyr::filter() masks stats::filter()
x dplyr::lag()     masks stats::lag()
i Use the conflicted package (<http://conflicted.r-lib.org/>) to force all conflicts to become
```

```
library(here)
```

here() starts at /Users/josh1/Desktop/GitAndGithub-DataSci-172026/ds4eeb_Lab4/Activity 6

1. Functions

```
# Create a new function called add_together
# x and y will be the two arguments to the function
add_together <- function(x, y){

  # Add x and y together, store as the object "output"
  output <- x + y

  # Print out whatever is stored in "output"
```

```
    return(output)
}
```

Q1.1)

```
add_together(x=3, y=5)
```

```
[1] 8
```

Q1.2)

```
add_together(x=3, y="five")
```

Error in x + y : non-numeric argument to binary operator

The error is explaining that you cannot input letters or other characters that are not numbers into the add_together function.

Q1.3)

```
#create new function, main_time, with x, y, and z will be the arguments
main_time <- function(x, y, z){
  output2 <- (x-y)^2/z
  return(output2)
}
main_time(x=5, y=2, z=9)
```

```
[1] 1
```

Q1.4)

```
#Defining Vector
bison <- c(1000, 800, 1200, 1400)

#Creating function to find mean
deviation <- function(x){
  output3 <- x-mean(x)
  return(output3)
}

deviation(x=bison)
```

```
[1] -100 -300 100 300
```

2. Iteration

Q2.1)

```
?iris
```

The `?iris` function brings us to the help page of `iris` which tells us that the unit of measurement is centimeters.

Q2.2)

```
iris %>%
  group_by(Species) %>%
  summarize(across(.cols = everything(),
                    .fns = median))
```

```
# A tibble: 3 x 5
  Species    Sepal.Length Sepal.Width Petal.Length Petal.Width
  <fct>          <dbl>         <dbl>         <dbl>         <dbl>
1 setosa          5          3.4          1.5          0.2
2 versicolor    5.9          2.8          4.35         1.3
3 virginica      6.5          3          5.55         2
```

Q2.3)

```
#reading/defining data in csv
cereal <- read_csv("data/cereal.csv")
```

Rows: 77 Columns: 16

-- Column specification -----

Delimiter: ","

chr (3): name, mfr, type

dbl (13): calories, protein, fat, sodium, fiber, carbo, sugars, potass, vita...

i Use `spec()` to retrieve the full column specification for this data.

i Specify the column types or set `show_col_types = FALSE` to quiet this message.

```
cereal |>
  group_by(mfr) |>
  summarize(across(.cols = where(is.numeric),
                    .fns = mean))
```

A tibble: 7 x 14

	mfr	calories	protein	fat	sodium	fiber	carbo	sugars	potass	vitamins	shelf
	<chr>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>	<dbl>
1	Americ~	100	4	1	0	0	16	3	95	25	2
2	Genera~	111.	2.32	1.36	200.	1.27	14.7	7.95	85.2	35.2	2.14
3	Kellog~	109.	2.65	0.609	175.	2.74	15.1	7.57	103.	34.8	2.35
4	Nabisco	86.7	2.83	0.167	37.5	4	16	1.83	121.	8.33	1.67
5	Post	109.	2.44	0.889	146.	2.78	13.2	8.78	114.	25	2.44
6	Quaker~	95	2.62	1.75	92.5	1.34	10	5.25	74.4	12.5	2.38
7	Ralsto~	115	2.5	1.25	198.	1.88	17.6	6.12	89.2	25	2

i 3 more variables: weight <dbl>, cups <dbl>, rating <dbl>

Q2.4)

```
for(i in 1:10){
  print(i^2)
}
```

```
[1] 1
[1] 4
[1] 9
[1] 16
[1] 25
[1] 36
[1] 49
[1] 64
[1] 81
[1] 100
```

Q2.5)

Q2.5a

```
N0 = 300 #initial population size

years = 50 #number of years into the future

N = vector(length = years) # create an empty vector to store pop. sizes

N[1] = N0 #initial population size should be the first N

lambda = 0.95 #growth rate

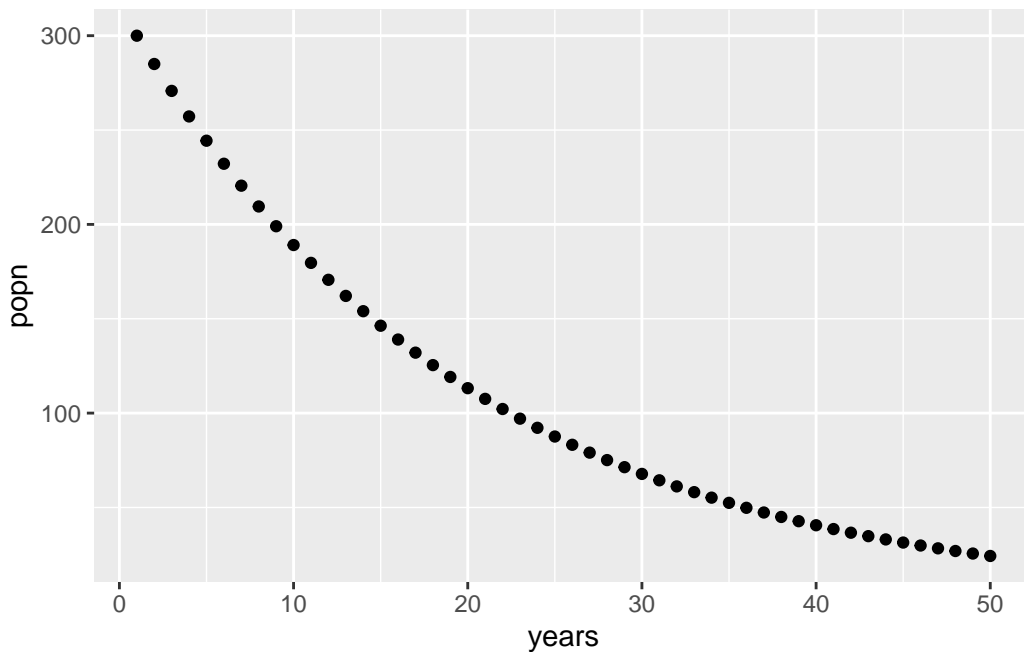
# For every year t in 2 through 20 (remember, "years" also equals 20), apply the following equation
for (t in 2:50) {
  N[t] = N[t - 1] * lambda # Apply the equation
}

# Store the data output as a dataframe for plotting
popn_data <- tibble(years = 1:years, # Make the years column = 1, 2, 3, ..., 50
                    popn = N) # Make the population column the corresponding population vector
```

Q2.5b

```
# Now plot the data with years on the x axis and population on the y axis
popn_data %>%
```

```
ggplot(aes(x = years, y = popn)) +  
  geom_point()
```



The population is declining somewhat exponentially over 50 years. It has declined to under 30 individuals when the current data in the end.

Q2.6)

I prefer the `across()` function because it gives column names of the ones you want to pull and and you can easily edit the function. The `for()` loop feels intricate and clunky. I'm more likely to make mistakes.

Q2.7)

```
# Store a vector of unique species names from the Species column of Iris  
spp_names <- unique(iris$Species)
```

```
# Create a vector that starts with 1 to the length of the spp_names, which is 3, and use i as  
for (i in 1:length(spp_names)) {
```

```

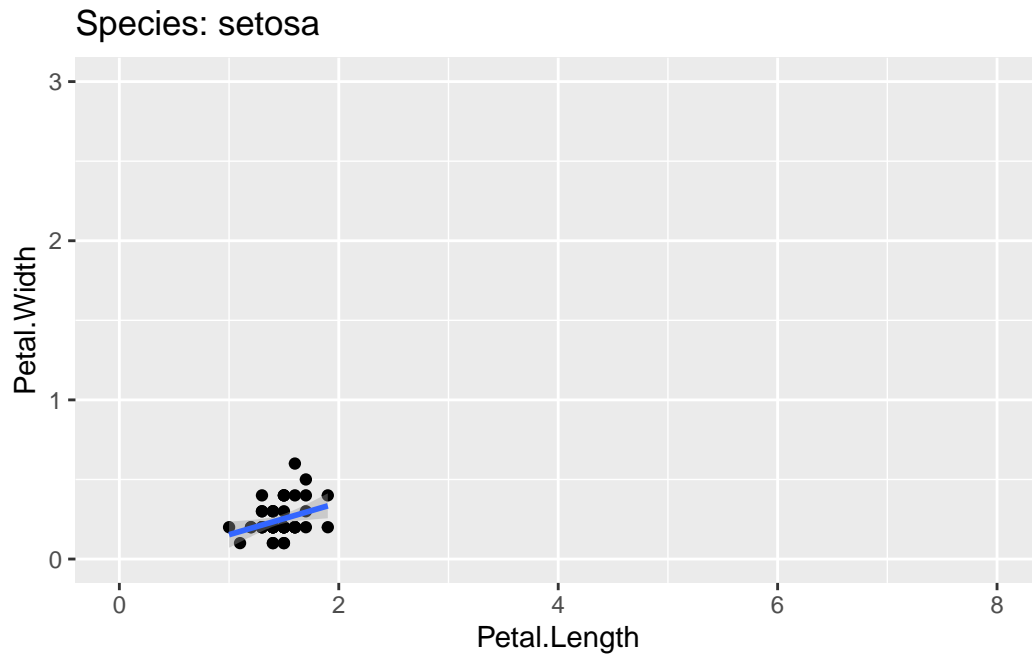
filt_data <- iris %>%
  # Keep only the rows where Species matches the current species
  filter(Species == spp_names[i])

# Build a ggplot object using the filtered data for the current species
plot <- filt_data %>%
  # Initialize the plot: x = Petal.Length, y = Petal.Width
  ggplot(aes(x = Petal.Length,
             y = Petal.Width)) +
  # Add scatterplot points for each observation
  geom_point() +
  # Add a best-fit linear regression line
  geom_smooth(method = "lm") +
  # Set fixed axis limits so all species plots use the same x and y ranges
  lims(x = c(0,8),
       y = c(0,3)) +
  # Add a title that includes the current species name
  ggtitle(paste("Species:", spp_names[i]))

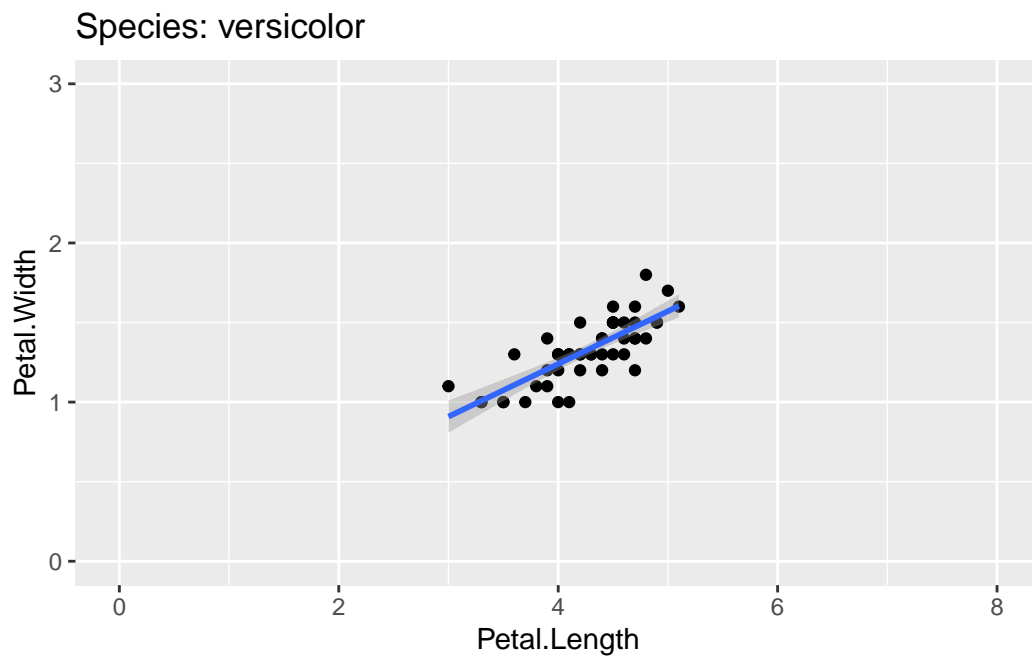
#Display the plot for this species inside the loop
print(plot)
}

```

`geom_smooth()` using formula = 'y ~ x'



``geom_smooth()`` using formula = 'y ~ x'



``geom_smooth()`` using formula = 'y ~ x'

Species: virginica

