ComputationalThinking1

Overview

Welcome! This is the first "computational thinking" lesson, which is about two topics: writing your own functions and performing iterations. I will go over very basic examples of each, but know that these are topics that will be very useful if using R for "programming" sorts of tasks.

You will submit one output for this activity:

1. A **PDF** of a rendered Quarto document with all of your R code. Please create a new Quarto document (e.g. don't use this `README.qmd`), include all of the code that appears in this document, in addition to adding your own code and **answers to all of the questions** in the "Q#" sections. Submit this through Gradescope.

If you have trouble submitting as a PDF, please ask Calvin or Malin for help. If we still can't solve it, you can submit the .qmd file instead.

A reminder: **Please label the code** in your final submission in two ways: 1) denote your answers to each question using headers that correspond to the question you're answering and 2) thoroughly "comment" your code: remember, this means annotating your code directly by typing descriptions of what each line does after a `#`. This will help future you!

Let's start by reading in the relevant packages

```
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   3.5.1     v tibble    3.2.1
v lubridate 1.9.4     v tidyr     1.3.1
v purrr     1.0.4
-- 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 becon
```

```r
library(here)
```

```
here() starts at /Users/waltvance/Library/Mobile Documents/com~apple~CloudDocs/School/UCSC/BI
```

---

1. Functions

Functions take the form of

```
my.function  <- function(arg1, arg2, ... ){

the function's code (body) is nestled between curly braces

return(object)

}
```

To create a function, we start by assigning the function a name with the assignment operator, such as `my.function <-`. This names the function. To save a function, it must be named.

Then, we use the `function()` function (yes, there's a function called `function`) to tell R it will be a function. We list the **arguments** in our function between parentheses and include any default values. These are the function's inputs. Then, in between two curly braces { }, we enter R code that tells R what to do with the inputs, and what to return to the function user (the output).

Working with single values as input

Let's start out with a very simple mathematical example and write a function that takes a number as input, adds 1 to that number, and then returns that new output to us.

- Let's name the function `add_one`.
- Within the brackets of the function, we will supply only one argument: `x`. `x` will be the number that gets taken in as input.
- Within the curly brackets, we will tell the function what to do with `x`. In this case, we will add 1 to it and store it as a data object called `output`.
- Lastly, let's tell the function to return our `output`, aka just print out the results that are stored in the data object

```r
# Create a new function called add_one
# x will be the only input to the function
add_one  <- function(x){

  # Add x and 1 together, store as the object "output"
  output <- x + 1

  # Print out whatever is stored in "output"
  return(output)

}
```

Look in your Environment tab in the top-right; a function called `add_one` should have popped up. That means our function is stored and ready to go!

Let's use our function. We will supply the number `10` to our function as input.

```r
# Supply 10 to our function
add_one(x = 10)
```

```
[1] 11
```

Our very first homemade function! Nice!

Let's make this a little more complicated and add in a second argument. This function will take two numbers as input and add them together. Let's call those arguments `x` and `y`. Separate them with a comma within the `function()` function.

```r
# 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 Feed our new function two numbers

Feed our new function `add_together()` two numbers: Add together a 3 and a 5 within the function

```r
#using the function we created above, x = 3 and y = 5
add_together(3,5)
```

```
[1] 8
```

Q1.2 Feed our new function a number and a character string

What happens if a function receives unexpected input? Feed our new function `add_together()` 3 and "five" instead of 3 and 5. Copy and paste the error code you receive and describe what you think it's telling you.

Important for QMD: When you try to render this document, Quarto will get mad that you're running code that doesn't work. In the code chunk where you add together 3 and "five", substitute the `{r}` for `{r eval=FALSE}` so that it does not evaluate this chunk of code (click "Source" instead of "Visual" in the top left of the document in order to see the `{r}`)

```r
#intentionally putting the incorrect value of "five"
add_together(3,five)
```

A1.2 "Error: object 'five' not found

You can access the source code for a function by typing it's name without parentheses and clicking enter.

```r
#accesses the source code of a custom function
add_together
```

```
function (x, y)
{
    output <- x + y
    return(output)
}
```

Q1.3 Create your own function!

Time to try it yourself! First, create a new function called `math_time` with three arguments, x, y, and z, that executes this equation:

$$(x - y)^2/z$$

Then, run that equation with `x = 5`, `y = 2`, and `z = 9`. What is the output?

```r
#creating a function and naming it math_time, z, y, z are inputs
math_time <- function(x, y, z){

  #inputing a mathmatical function and that creates an object named output
  output <- (x - y)^2/z

  #printing out whatever is stored in output
  return(output)

}
```

```
#running math_time with x = 5, y = 2, and z = 9
math_time(5,2,9)
```

```
[1] 1
```

A1.3 Output = 1

Working with vectors as input

Let's use vectors as input instead of just numbers. Let's write a function to convert a vector of weights from pounds into kilograms. To go from pounds to kilograms, we multiply the vector in pounds by ~0.454. This multiplies every element in the vector by 0.454.

Just like before, we tell the function what we want our argument(s) to be. Let's supply one argument called `weights`.

```
# Create a function called lbs_to_kg that takes a data object 'weights' as input
lbs_to_kg  <- function(weights){

  # Multiply weights by 0.454, store as the object "output"
  output <- weights*0.454

  # Print out whatever is stored in "output"
  return(output)

}
```

Next, let's make a vector of bison weights

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

And feed it to the function:

```
lbs_to_kg(weights = bison)
```

```
[1] 454.0 363.2 544.8 635.6
```

Each element was multiplied by 0.454!

Q1.4 Calculate deviation from a mean

Here's a tricky one: Write a function called `deviation` that takes a vector as an argument. Then, make that function:

1) Calculate a mean value for the vector
2) Subtract that mean from each element in the vector
3) Return the output from 2)

After you've created the function, feed the `bison` vector to it as input.

```
#creating a function named deviation and assigning vector as the argument name
deviation <- function(vector){

  #creates an object called mean that is the mean of the vector input
  mean <- mean(vector)

  #creates an object called output that is the vector input minus the mean calculated above
  output <- vector - mean

  #prints the output from above
  return(output)

}
```

```
#using the deviation function on the bison vector
deviation(bison)
```

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

A1.4 -100 -300 100 300

I hope that you are starting to see a glimmer of the utility of writing functions; they can make things much easier for us, while also making us feel like super cool coders.

2. Iteration

Iteration in R means repeatedly performing the same action but in different ways or on different "things". We've already snuck this in in a couple ways:

- facet_wrap() and facet_grid() draw a plot for each subset variable.
- group_by() and summarize() compute summary statistics for each grouped variable.

---

across()

We'll start with yet another dplyr function, `across()`. To illustrate iterating using the `across()` function, let's look at the built-in iris flower morphometric data. Take a look at the help page to familiarize yourself with the columns.

```r
# Look at the first 6 rows of iris
head(iris)
```

```
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1          5.1         3.5          1.4         0.2  setosa
2          4.9         3.0          1.4         0.2  setosa
3          4.7         3.2          1.3         0.2  setosa
4          4.6         3.1          1.5         0.2  setosa
5          5.0         3.6          1.4         0.2  setosa
6          5.4         3.9          1.7         0.4  setosa
```

Q2.1: What are the units that the sepal and petal columns are measured in?

A2.1: centimeters

Let's say that we want to calculate means for all four of these columns separately for each species. In the last lesson I asked you to first pivot the energy source columns to long format, and then group those variables and summarize them to calculate a mean. However, sometimes having the columns pivoted all together in a single column doesn't make sense. For instance, here, we might want `Petal.length` and `Petal.width` to be distinct columns that can be related to one another (for instance in a graph comparing the two).

One option is summarize each column separately by typing out the equation for each column:

```r
iris %>%
  group_by(Species) %>%
  summarize(Sepal.Length = mean(Sepal.Length),
            Sepal.Width = mean(Sepal.Width),
            Petal.Length = mean(Petal.Length),
            Petal.Width = mean(Petal.Width))
```

```
# A tibble: 3 x 5
  Species    Sepal.Length Sepal.Width Petal.Length Petal.Width
  <fct>             <dbl>       <dbl>        <dbl>       <dbl>
1 setosa             5.01        3.43         1.46       0.246
2 versicolor         5.94        2.77         4.26       1.33
3 virginica          6.59        2.97         5.55       2.03
```

You can imagine that this will get very tedious if you have tens or even hundreds of columns. Instead, you can use `across()`, which iterates across each column that you specify.

You'll use the first two arguments to `across()` every time you use it: the first argument, `.cols`, specifies which columns you want to iterate over, and the second argument, `.fns`, specifies what to do with each column.

```r
iris %>%
  group_by(Species) %>%
  summarize(across(.cols = c(Sepal.Length, Sepal.Width, Petal.Length, Petal.Width),
                   .fns = mean))
```

```
# A tibble: 3 x 5
  Species    Sepal.Length Sepal.Width Petal.Length Petal.Width
  <fct>             <dbl>       <dbl>        <dbl>       <dbl>
1 setosa             5.01        3.43         1.46       0.246
2 versicolor         5.94        2.77         4.26       1.33
3 virginica          6.59        2.97         5.55       2.03
```

As a sneaky shortcut, you can also say `Sepal.Length:Petal.Width` to indicate that you want to iterate across all columns from `Sepal.Length` to `Petal.Width`. (It also works if you specify column number instead of column name, such as `1:4`)

```r
iris %>%
  group_by(Species) %>%
  summarize(across(.cols = Sepal.Length:Petal.Width,
                   .fns = mean))
```

```
# A tibble: 3 x 5
  Species    Sepal.Length Sepal.Width Petal.Length Petal.Width
  <fct>             <dbl>       <dbl>        <dbl>       <dbl>
1 setosa             5.01        3.43         1.46       0.246
2 versicolor         5.94        2.77         4.26       1.33
3 virginica          6.59        2.97         5.55       2.03
```

There are two additional selection techniques that are particularly useful for selecting columns in `across()`: `everything()` and `where()`.

`everything()` is straightforward: it selects every (non-grouping) column:

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

```
# A tibble: 3 x 5
  Species    Sepal.Length Sepal.Width Petal.Length Petal.Width
  <fct>             <dbl>       <dbl>        <dbl>       <dbl>
1 setosa             5.01        3.43         1.46       0.246
2 versicolor         5.94        2.77         4.26       1.33
3 virginica          6.59        2.97         5.55       2.03
```

Note the grouping column(s) (in this case `Species`) are not included in `across()`, because they're automatically preserved by `summarize()`.

Q2.2 Summarize to calculate the median across all columns

Group the `iris` data by `species` and calculate a `median` across all of the columns. (What function do you think you should use to calculate a median?)

```
iris %>%
  #groups the df by the unique values in the species col
  group_by(Species) %>%
  #using the summarize function and across, everything() selects all non-grouped cols, then r
  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
```

`where()` is another way to select columns, and allows you to select columns based on their type:

- `where(is.numeric)` selects all numeric columns.
- `where(is.character)` selects all character string columns.
- `where(is.Date)` selects all date columns.
- `where(is.POSIXct)` selects all date-time columns.
- `where(is.logical)` selects all logical columns.

```
iris %>%
  group_by(Species) %>%
  summarize(across(.cols = where(is.numeric),
                   .fns = mean))
```

```
# A tibble: 3 x 5
  Species    Sepal.Length Sepal.Width Petal.Length Petal.Width
  <fct>             <dbl>       <dbl>        <dbl>       <dbl>
1 setosa             5.01        3.43         1.46       0.246
2 versicolor         5.94        2.77         4.26       1.33
3 virginica          6.59        2.97         5.55       2.03
```

Q2.3 Summarize to calculate the mean across all numeric columns in the cereal data

1) Read in the `cereal` data that we worked with back in the first data wrangling lesson. It is already stored in the `data` folder of this repository.
2) Group the data by manufacturer and calculate a mean value for all of the *numeric* columns in that dataset.

```r
cereal <- read_csv(here("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.
```

```r
head(cereal)
```

```
# A tibble: 6 x 16
  name       mfr   type  calories protein   fat sodium fiber carbo sugars potass
  <chr>      <chr> <chr>    <dbl>   <dbl> <dbl>  <dbl> <dbl> <dbl>  <dbl>  <dbl>
1 100% Bran  Nabi~ C           70       4     1    130  10     5        6    280
2 100% Natu~ Quak~ C          120       3     5     15   2     8        8    135
3 All-Bran   Kell~ C           70       4     1    260   9     7        5    320
4 All-Bran ~ Kell~ C           50       4     0    140  14     8        0    330
5 Almond De~ Rals~ C          110       2     2    200   1    14        8     -1
6 Apple Cin~ Gene~ C          110       2     2    180   1.5  10.5     10     70
# i 5 more variables: vitamins <dbl>, shelf <dbl>, weight <dbl>, cups <dbl>,
#   rating <dbl>
```

```r
cereal %>%
  #creates groups by each manufacturer
  group_by(mfr) %>%
  #selects all cols that are numeric and calculates each groups mean
  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>
```

For-loops

Loop through a simple equation

A commonly used method of coding when you want to repeat a task a defined number of times is the for loop. We have been teaching you how to code largely using `tidyverse` functions; for loops are not particularly common when using `tidyverse` because the creators of it built functions that allow us to do the same or similar iterative tasks in more intuitive ways. For instance, `across()`, from above, as well as `group_by()`/`summarize()` and `facet_wrap()` can accomplish what used to be only doable with for loops (or writing your own functions). Despite this, for loops are a fundamental part of all coding languages, and so we will introduce them here!

The most basic example of a for loop is:

```r
for (i in 1:5) {
  # Print out whatever the value of i is
  print(i)
}
```

```
[1] 1
[1] 2
[1] 3
[1] 4
[1] 5
```

This is a dynamic bit of code where an “index” `i` is iteratively replaced by each value in the vector `1:5` (which is 1, 2, 3, 4, 5).

Let’s dissect what the loop is doing: because the first value in our sequence `1:5` is 1, the loop starts by replacing i with 1 and runs everything between the { }. Loops typically use i as the counter, short for iteration, but you are free to use whatever you like, such as `x`, `number`, or `rhubarb`.

We could do this all manually of course. To manually run the first two iterations of the loop, we would run:

```r
# First iteration where i = 1:
i <- 1
print(i)
```

```
[1] 1
```

```r
# Second iteration where i = 2
i <- 2
print(i)
```

```
[1] 2
```

The for loop makes this all automated though, and loops through the number of values we tell it to, in this case, 5 values.

We can make things a little more complex; let's multiply our i value by 2

```r
for (i in 1:5) {
  print(i*2)
}
```

```
[1] 2
[1] 4
[1] 6
[1] 8
[1] 10
```

As with before, the for loop starts with `i = 1` and runs what we tell it to. When `i = 1`, it prints out `i*2`, which equals 2. Then, when `i = 2`, it prints out `i*2`, which equals 4, and so forth.

Q2.4 Create a for loop that iterates from 1 to 10 and squares the value of the index `i`

Create a for loop that iterates from 1 to 10 and squares the value of the index `i`, then prints out that output

```r
#creates a for loop where the each iteration of i will be the values 1 through 10
for (i in 1:10){
  #prints each of the iterations and squares them
  print(i^2)
}
```

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

Simulate data using a for-loop

One fun way we can use a for loop is by iteratively simulating data. Let's simulate population growth using the equation:

$$N[t] = N[t-1] * lambda$$

The population at time `t` is `N[t]`, and we can calculate it by taking the population from the previous time step `t-1`, which is represented by `N[t-1]`, and multiplying that by a growth rate `lambda`. Think of this as if you had 100 individuals in time `t-1` and you population was growing by 20%, `lambda` would equal 1.2, so your population at time `t` would be: `100*1.2 = 120`. Let's simulate this over 20 time steps.

```r
N0 = 100  #initial population size

years = 20  #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 = 1.2  #growth rate
```

Let's look at that vector we created:

```
print(N)
```

```
 [1] 100   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0   0
[20]   0
```

We can see that the first value is 100, since we assigned `N[1]` to be 100, but all the rest are zeroes. The for loop will iterate from the second value through the the number of years (20) and fill in the rest!

When we use square brackets after a vector, e.g. `N[5]`, we are able to reference that element of the vector, in this case the 5th value in vector N. Just to demonstrate, if we now ask for the 5th element in vector `N`, we will get zero, whereas if we ask for the first, we will get 100

```
N[5]
```

```
[1] 0
```

```
N[1]
```

```
[1] 100
```

Now we will start the for loop: Here we say that element number "t" in the vector N will equal the previous year's N multiplied by lambda. For instance, in year `t = 5`, the newly created population value in year 5 will equal the population in year `t = 4` times `lambda`.

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

Now let's check out what N looks like

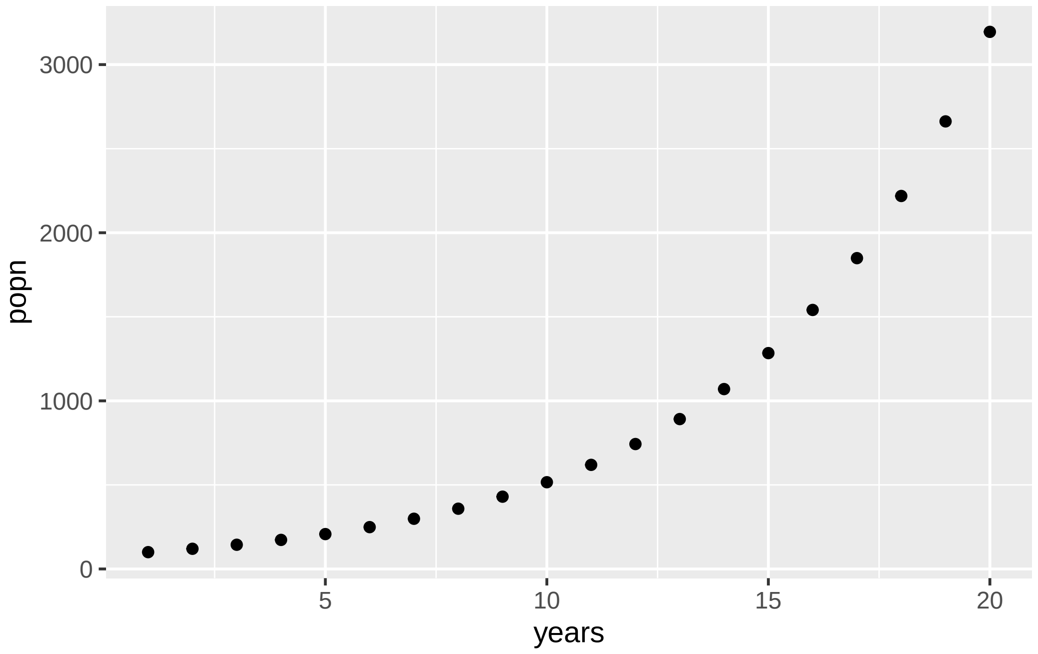
```
N
```

```
 [1]  100.0000  120.0000  144.0000  172.8000  207.3600  248.8320  298.5984
 [8]  358.3181  429.9817  515.9780  619.1736  743.0084  891.6100 1069.9321
[15] 1283.9185 1540.7022 1848.8426 2218.6111 2662.3333 3194.8000
```

Nice, it's all filled in! Let's create a datframe from this data and plot it to look at

```
# Store the data output as a dataframe for plotting
popn_data <- tibble(years = 1:years, # Make the years column = 1, 2, 3, ..., 20
                    popn = N) # Make the population column the corresponding population vecto
```

```
# Now plot the data with years on the x axis and population on the y
popn_data %>%
  ggplot(aes(x = years, y = popn)) +
  geom_point()
```



Q2.5a Rerun the for loop with the following parameters:

Copy and paste the for loop from above, but change the initial parameters so that:

- The initial population size = 300
- The growth rate = 0.95
- The number of years to iterate over = 50

```
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
```

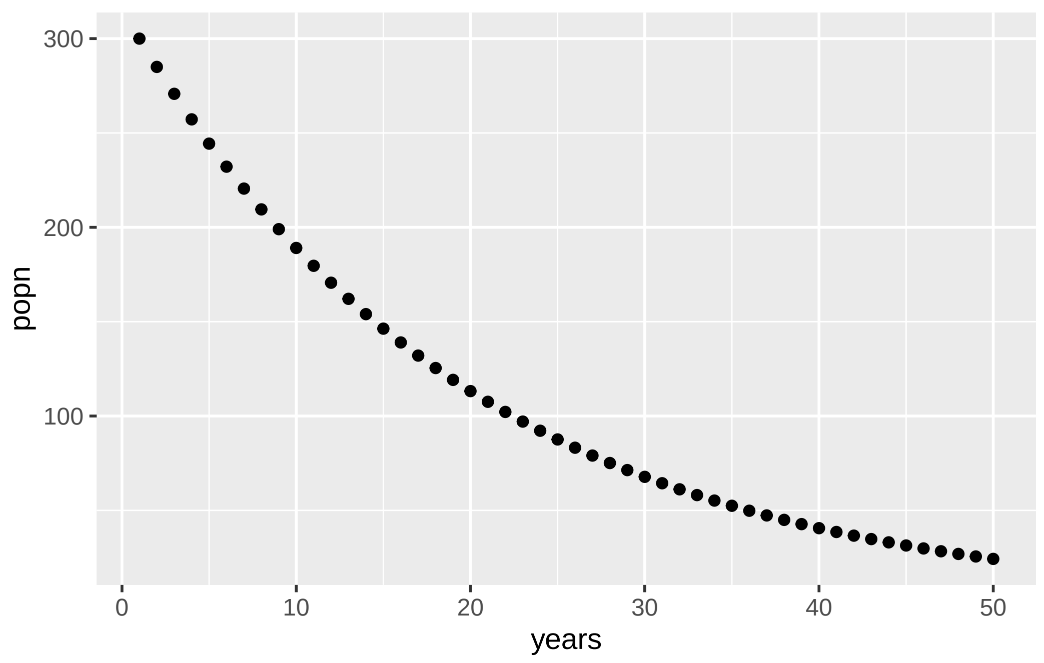
Q2.5b Plot the data and interpret

Plot your data and describe how the population is changing.

```
# For every year t in 2 through 50 (remember, "years" also equals 50), apply the following ec
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, ..., 20
                    popn = N) # Make the population column the corresponding population vect
```

```
# Now plot the data with years on the x axis and population on the y
popn_data %>%
  ggplot(aes(x = years, y = popn)) +
  geom_point()
```



Loop through data frames

Lastly, I want to demonstrate how to loop through dataframes in a couple different ways. Up above, we were referencing certain elements of a vector by index, aka by which number element it was (e.g. `N[5]` is the 5th element in the vector N). Vectors are one dimensional, so you can access any element within it with just one number. Data frames, however, are two dimensional: they have both rows and columns. Let's check out the `iris` data again:

```
head(iris)
```

```
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1          5.1         3.5          1.4         0.2  setosa
2          4.9         3.0          1.4         0.2  setosa
3          4.7         3.2          1.3         0.2  setosa
4          4.6         3.1          1.5         0.2  setosa
5          5.0         3.6          1.4         0.2  setosa
6          5.4         3.9          1.7         0.4  setosa
```

If we apply square brackets to the dataframe to extract elements, we can apply 1 or 2 numbers within them to reference either rows, columns, or both. This takes to form of: `data[row#, column#]`. If we want to access just a row, we leave the column number blank, and vice versa.

For instance, to get the first row:

```
iris[1,]
```

```
  Sepal.Length Sepal.Width Petal.Length Petal.Width Species
1          5.1         3.5          1.4         0.2  setosa
```

To get the data in the third column (which will print out as a vector):

```
iris[,3]
```

```
  [1] 1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 1.5 1.6 1.4 1.1 1.2 1.5 1.3 1.4
 [19] 1.7 1.5 1.7 1.5 1.0 1.7 1.9 1.6 1.6 1.5 1.4 1.6 1.6 1.5 1.5 1.4 1.5 1.2
 [37] 1.3 1.4 1.3 1.5 1.3 1.3 1.3 1.6 1.9 1.4 1.6 1.4 1.5 1.4 4.7 4.5 4.9 4.0
 [55] 4.6 4.5 4.7 3.3 4.6 3.9 3.5 4.2 4.0 4.7 3.6 4.4 4.5 4.1 4.5 3.9 4.8 4.0
 [73] 4.9 4.7 4.3 4.4 4.8 5.0 4.5 3.5 3.8 3.7 3.9 5.1 4.5 4.5 4.7 4.4 4.1 4.0
 [91] 4.4 4.6 4.0 3.3 4.2 4.2 4.2 4.3 3.0 4.1 6.0 5.1 5.9 5.6 5.8 6.6 4.5 6.3
[109] 5.8 6.1 5.1 5.3 5.5 5.0 5.1 5.3 5.5 6.7 6.9 5.0 5.7 4.9 6.7 4.9 5.7 6.0
[127] 4.8 4.9 5.6 5.8 6.1 6.4 5.6 5.1 5.6 6.1 5.6 5.5 4.8 5.4 5.6 5.1 5.1 5.9
[145] 5.7 5.2 5.0 5.2 5.4 5.1
```

And to get the exact value in the cell in the 1st row and 3rd column:

```
iris[1,3]
```

```
[1] 1.4
```

We can replace all of these numbers with the `i` index to iteratively perform some action on a number of rows or columns that we want.

For instance, let's print out all of the values for each column, 1 through 5. I've added a little bit of text that will print out to tell us what column we're on

```r
for (i in 1:5) {

  # This prints out a statement saying "Here's column i",
  #but the i gets replaced with the number that it's currently at
  print(paste("Here's column",i))

  # This prints out column i
  print(iris[,i])
}
```

```
[1] "Here's column 1"
  [1] 5.1 4.9 4.7 4.6 5.0 5.4 4.6 5.0 4.4 4.9 5.4 4.8 4.8 4.3 5.8 5.7 5.4 5.1
 [19] 5.7 5.1 5.4 5.1 4.6 5.1 4.8 5.0 5.0 5.2 5.2 4.7 4.8 5.4 5.2 5.5 4.9 5.0
 [37] 5.5 4.9 4.4 5.1 5.0 4.5 4.4 5.0 5.1 4.8 5.1 4.6 5.3 5.0 7.0 6.4 6.9 5.5
 [55] 6.5 5.7 6.3 4.9 6.6 5.2 5.0 5.9 6.0 6.1 5.6 6.7 5.6 5.8 6.2 5.6 5.9 6.1
 [73] 6.3 6.1 6.4 6.6 6.8 6.7 6.0 5.7 5.5 5.5 5.8 6.0 5.4 6.0 6.7 6.3 5.6 5.5
 [91] 5.5 6.1 5.8 5.0 5.6 5.7 5.7 6.2 5.1 5.7 6.3 5.8 7.1 6.3 6.5 7.6 4.9 7.3
[109] 6.7 7.2 6.5 6.4 6.8 5.7 5.8 6.4 6.5 7.7 7.7 6.0 6.9 5.6 7.7 6.3 6.7 7.2
[127] 6.2 6.1 6.4 7.2 7.4 7.9 6.4 6.3 6.1 7.7 6.3 6.4 6.0 6.9 6.7 6.9 5.8 6.8
[145] 6.7 6.7 6.3 6.5 6.2 5.9
[1] "Here's column 2"
  [1] 3.5 3.0 3.2 3.1 3.6 3.9 3.4 3.4 2.9 3.1 3.7 3.4 3.0 3.0 4.0 4.4 3.9 3.5
 [19] 3.8 3.8 3.4 3.7 3.6 3.3 3.4 3.0 3.4 3.5 3.4 3.2 3.1 3.4 4.1 4.2 3.1 3.2
 [37] 3.5 3.6 3.0 3.4 3.5 2.3 3.2 3.5 3.8 3.0 3.8 3.2 3.7 3.3 3.2 3.2 3.1 2.3
 [55] 2.8 2.8 3.3 2.4 2.9 2.7 2.0 3.0 2.2 2.9 2.9 3.1 3.0 2.7 2.2 2.5 3.2 2.8
 [73] 2.5 2.8 2.9 3.0 2.8 3.0 2.9 2.6 2.4 2.4 2.7 2.7 3.0 3.4 3.1 2.3 3.0 2.5
 [91] 2.6 3.0 2.6 2.3 2.7 3.0 2.9 2.9 2.5 2.8 3.3 2.7 3.0 2.9 3.0 3.0 2.5 2.9
[109] 2.5 3.6 3.2 2.7 3.0 2.5 2.8 3.2 3.0 3.8 2.6 2.2 3.2 2.8 2.8 2.7 3.3 3.2
[127] 2.8 3.0 2.8 3.0 2.8 3.8 2.8 2.8 2.6 3.0 3.4 3.1 3.0 3.1 3.1 3.1 2.7 3.2
[145] 3.3 3.0 2.5 3.0 3.4 3.0
[1] "Here's column 3"
  [1] 1.4 1.4 1.3 1.5 1.4 1.7 1.4 1.5 1.4 1.5 1.5 1.6 1.4 1.1 1.2 1.5 1.3 1.4
 [19] 1.7 1.5 1.7 1.5 1.0 1.7 1.9 1.6 1.6 1.5 1.4 1.6 1.6 1.5 1.5 1.4 1.5 1.2
 [37] 1.3 1.4 1.3 1.5 1.3 1.3 1.3 1.6 1.9 1.4 1.6 1.4 1.5 1.4 4.7 4.5 4.9 4.0
 [55] 4.6 4.5 4.7 3.3 4.6 3.9 3.5 4.2 4.0 4.7 3.6 4.4 4.5 4.1 4.5 3.9 4.8 4.0
 [73] 4.9 4.7 4.3 4.4 4.8 5.0 4.5 3.5 3.8 3.7 3.9 5.1 4.5 4.5 4.7 4.4 4.1 4.0
 [91] 4.4 4.6 4.0 3.3 4.2 4.2 4.2 4.3 3.0 4.1 6.0 5.1 5.9 5.6 5.8 6.6 4.5 6.3
[109] 5.8 6.1 5.1 5.3 5.5 5.0 5.1 5.3 5.5 6.7 6.9 5.0 5.7 4.9 6.7 4.9 5.7 6.0
[127] 4.8 4.9 5.6 5.8 6.1 6.4 5.6 5.1 5.6 6.1 5.6 5.5 4.8 5.4 5.6 5.1 5.1 5.9
[145] 5.7 5.2 5.0 5.2 5.4 5.1
[1] "Here's column 4"
  [1] 0.2 0.2 0.2 0.2 0.2 0.4 0.3 0.2 0.2 0.1 0.2 0.2 0.1 0.1 0.2 0.4 0.4 0.3
 [19] 0.3 0.3 0.2 0.4 0.2 0.5 0.2 0.2 0.4 0.2 0.2 0.2 0.2 0.4 0.1 0.2 0.2 0.2
 [37] 0.2 0.1 0.2 0.2 0.3 0.3 0.2 0.6 0.4 0.3 0.2 0.2 0.2 0.2 1.4 1.5 1.5 1.3
 [55] 1.5 1.3 1.6 1.0 1.3 1.4 1.0 1.5 1.0 1.4 1.3 1.4 1.5 1.0 1.5 1.1 1.8 1.3
 [73] 1.5 1.2 1.3 1.4 1.4 1.7 1.5 1.0 1.1 1.0 1.2 1.6 1.5 1.6 1.5 1.3 1.3 1.3
 [91] 1.2 1.4 1.2 1.0 1.3 1.2 1.3 1.3 1.1 1.3 2.5 1.9 2.1 1.8 2.2 2.1 1.7 1.8
[109] 1.8 2.5 2.0 1.9 2.1 2.0 2.4 2.3 1.8 2.2 2.3 1.5 2.3 2.0 2.0 1.8 2.1 1.8
[127] 1.8 1.8 2.1 1.6 1.9 2.0 2.2 1.5 1.4 2.3 2.4 1.8 1.8 2.1 2.4 2.3 1.9 2.3
[145] 2.5 2.3 1.9 2.0 2.3 1.8
[1] "Here's column 5"
  [1] setosa     setosa     setosa     setosa     setosa     setosa    
  [7] setosa     setosa     setosa     setosa     setosa     setosa    
 [13] setosa     setosa     setosa     setosa     setosa     setosa    
 [19] setosa     setosa     setosa     setosa     setosa     setosa    
 [25] setosa     setosa     setosa     setosa     setosa     setosa    
 [31] setosa     setosa     setosa     setosa     setosa     setosa    
 [37] setosa     setosa     setosa     setosa     setosa     setosa    
 [43] setosa     setosa     setosa     setosa     setosa     setosa    
 [49] setosa     setosa     versicolor versicolor versicolor versicolor
 [55] versicolor versicolor versicolor versicolor versicolor versicolor
 [61] versicolor versicolor versicolor versicolor versicolor versicolor
 [67] versicolor versicolor versicolor versicolor versicolor versicolor
 [73] versicolor versicolor versicolor versicolor versicolor versicolor
 [79] versicolor versicolor versicolor versicolor versicolor versicolor
 [85] versicolor versicolor versicolor versicolor versicolor versicolor
 [91] versicolor versicolor versicolor versicolor versicolor versicolor
 [97] versicolor versicolor versicolor versicolor virginica  virginica 
[103] virginica  virginica  virginica  virginica  virginica  virginica 
[109] virginica  virginica  virginica  virginica  virginica  virginica 
[115] virginica  virginica  virginica  virginica  virginica  virginica 
[121] virginica  virginica  virginica  virginica  virginica  virginica 
[127] virginica  virginica  virginica  virginica  virginica  virginica 
[133] virginica  virginica  virginica  virginica  virginica  virginica 
[139] virginica  virginica  virginica  virginica  virginica  virginica 
[145] virginica  virginica  virginica  virginica  virginica  virginica 
Levels: setosa versicolor virginica
```

We can expand on this by performing some sort of operation on the columns that we are extracting. Let's now take the mean of each column before printing it, but this time only iterate up to i = 4, since we know that column 5 is the column with species names in them:

```
for (i in 1:4) {
  # This prints out a statement saying "Here's column i", but the i gets replaced with the nu
  print(paste("Here's column",i))

  # This prints out column i
  print(mean(iris[,i]))
}
```

```
[1] "Here's column 1"
[1] 5.843333
[1] "Here's column 2"
[1] 3.057333
[1] "Here's column 3"
[1] 3.758
[1] "Here's column 4"
[1] 1.199333
```

Now we have a mean value for every column. We could have easily done this with our across function too:

```
iris %>%
  summarize(across(.cols = 1:4,
                   .fns = mean))
```

```
  Sepal.Length Sepal.Width Petal.Length Petal.Width
1     5.843333    3.057333        3.758    1.199333
```

Q2.6 Which do you prefer?

Which makes more sense to you: summarizing with a for loop or with the summarize/across functions?

A nice thing to remember with for loops is that you can do many things within the loop. For instance, here I will create a vector of column names and print out the "i"th element. Since i is going to equal the same number when I print out the column name vs the column values, it will match up nicely.

```
for (i in 1:4) {
  # Fetch the column names of the dataframe, store in a vector "names"
  names <- colnames(iris)

  # Print out the "i"th element of the vector to print alongside the output
  print(names[i])

  # This prints out column i
  print(mean(iris[,i]))
}
```

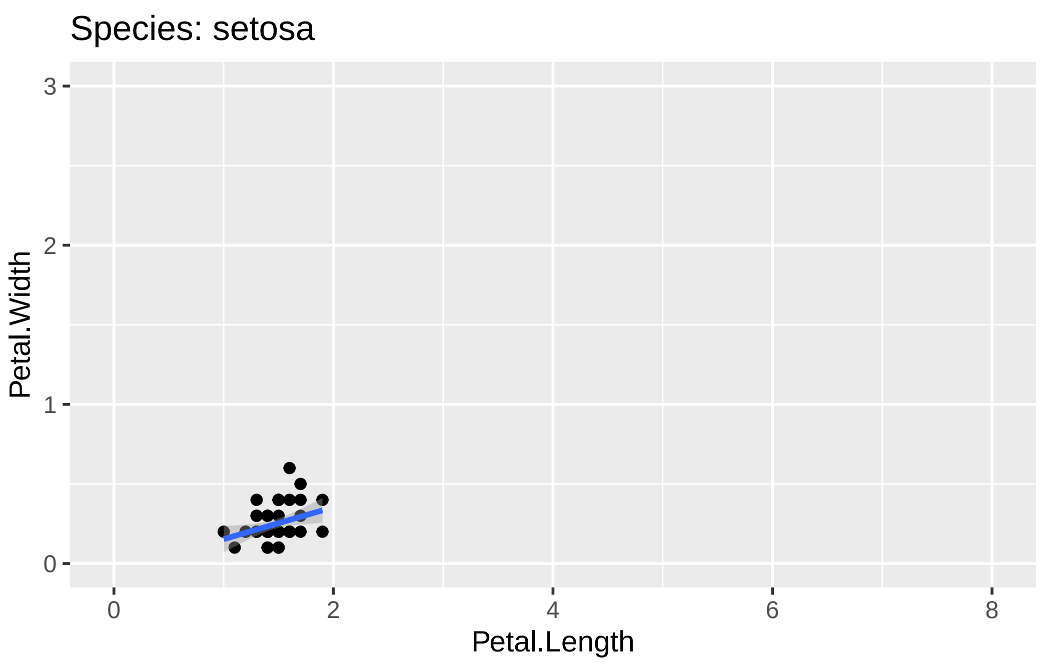
```
[1] "Sepal.Length"
[1] 5.843333
[1] "Sepal.Width"
[1] 3.057333
[1] "Petal.Length"
[1] 3.758
[1] "Petal.Width"
[1] 1.199333
```

Q2.7 Annotate this code with what you think it's doing

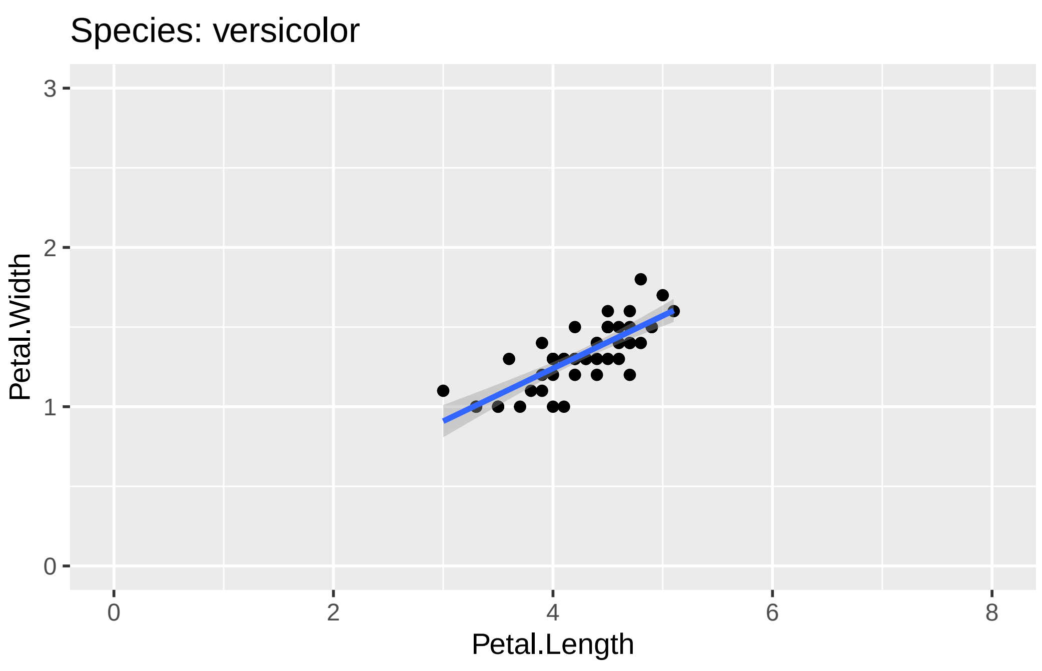
For the last question, I have created a chunk of code here that does a few things. Go through and on each line where you see a pound sign, comment what you think each line is doing. I've done the first for you as an example. Remember that you can highlight small bits of code to run those particular portions, even within a for loop (e.g. highlighting `iris$Species` within the `unique()` function and hitting run will only run `iris$Species` or highlighting and running `spp_names` will show you what is stored in `spp_names`).

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

# creates a for loop where i iterates between 1 and the number of unique species names
for (i in 1:length(spp_names)) {

  filt_data <- iris %>%
    # creates an object called filt_data that filters for rows that have the name of the spe
    filter(Species == spp_names[i])

  # creates an object called plot that uses data from filt_data
  plot <- filt_data %>%
    # creates a ggplot with petal length on the x asis and petal width on the y
    ggplot(aes(x = Petal.Length,
               y = Petal.Width)) +
    # tells ggplot to apply points to the graph from the filt_data
    geom_point() +
    # creates a line on the graph, calculated using a linear model
    geom_smooth(method = "lm") +
    # tells ggplot what the values of the axises be
    lims(x = c(0,8),
         y = c(0,3)) +
    # gives each plot a title that is "Species (the name of species for iteration i)
    ggtitle(paste("Species:", spp_names[i]))

  # prints each plot
  print(plot)
}
```

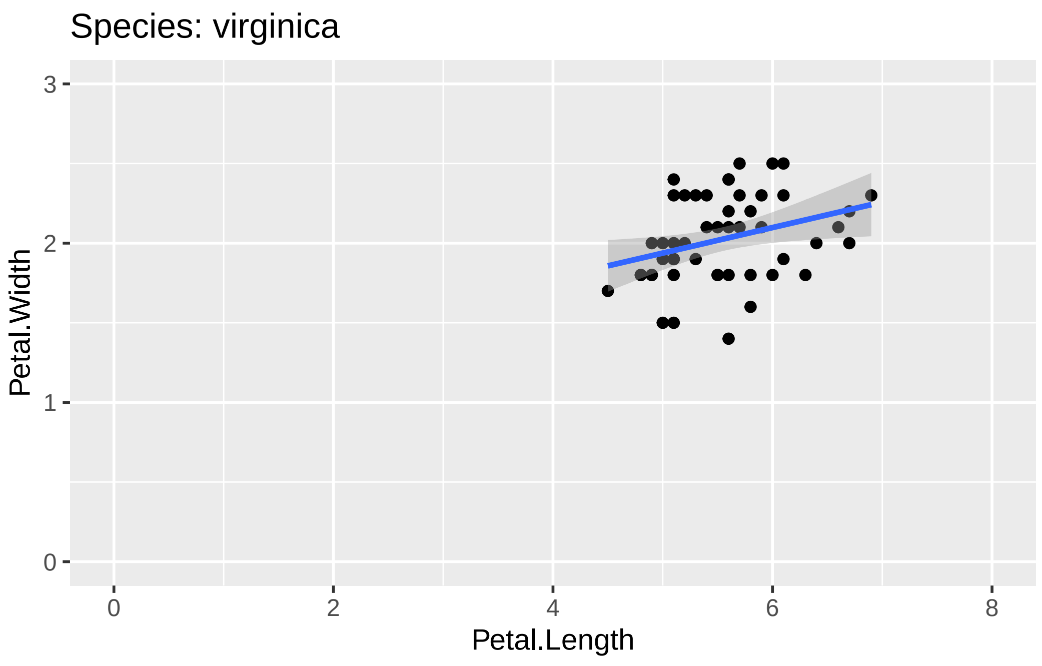
```
`geom_smooth()` using formula = 'y ~ x'
```



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



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



Congrats on getting to the end!!!

——-##