GIS in R: Fundamentals and Economic Applications

Dr. Gaby Perez-Quesada

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Welcome!

This book was created in order to host all of the materials for AREC 493 class.

Spatial data is increasingly essential for understanding economic activity, policy and development. This course introduces students to the use of R as a Geographic Information System (GIS) for economic analysis. Students will learn core GIS concepts alongside the basics of R programming, with a focus on practical applications in economics. The course closely integrates *tidyverse* functions with GIS tools to develop efficient and intuitive coding. Topics include spatial data processing, covering the import, management, and manipulation of raster and vector data, as well as visualization of spatial data through maps to identify spatial patterns. By the end, students will have the skills to integrate spatial analysis into economic research, enabling them to work with powerful and flexible tools for investigating real-world economic questions.

Be aware that the book is currently being written and will be completed by the end of the semester. Let me know if you think any changes are necessary!

1 Syllabus

1.1 Course Information

Course: AREC 493

Instructor: Dr. Gaby Perez-Quesada

Email: gperezqu@utk.edu

Term: Spring 2026

Times: T & R, 2:30-3:45pm

Location: Morgan Hall 212B

Office Hours: T & R, 3:45-5:00pm

1.2 Learning Objectives

- Use R and ***tidyverse*** tools to import, clean, and manipulate spatial data efficiently and reproducibly
- Explain and apply core GIS concepts, including spatial data types, projections, and coordinate reference systems
- Work with vector and raster datasets, performing basic operations, analysis, and integration between data types
- Visualize spatial data effectively through maps to identify and interpret spatial patterns
- Access and process real-world spatial datasets from public sources for applied economic analysis

1.3 Prerequisites

AREC 270. Prior coursework in basic statistics or econometrics is recommended. Students should be comfortable with fundamental concepts such as descriptive statistics, regression analysis, and interpreting empirical results.

1.4 Lecture Topics

(*Subject to change based on progression through the material*)

Getting started with R

- Get started with running code
- Install and load libraries
- Load in data from files, the internet, or libraries
- Write good code and responsibly use AI in your coding
- Look at your data and get basic statistical results
- Manipulate your data and get it ready for analysis

GIS fundamentals

- Types of spatial data
- Projections and coordinate reference system

The basics of vector data handling using *sf* package

- Vector data (points, lines, polygons)
- Import and export vector data
- (re)projection of spatial datasets
- Single-layer geometrical operations (e.g., create buffers)

Spatial interactions of vector datasets

- Understand topological relations of multiple *sf* objects
- Spatially subset a layer based on another layer
- Extracting values form one layer to another layer

The basics of raster data handling using *raster* and *terra* packages

- Import and export raster data
- Stack raster data
- Quick plotting

Spatial interactions of vector and raster datasets

- Cropping a raster layer to the geographic extent of a vector layer
- Extracting values form a raster to a vector later

Creating maps using *ggplot2* package

- Visualizing spatial data with ggplot2

Download and process publicly available datasets

- USDA NASS QuickStat (*tidyUSDA*)
- PRISM (*prism*)
- Daymet (*daymetr*)
- Cropland Data Layer (*CropScapeR*)
- Census (*tidycensus*)

1.5 Course Materials

This course will follow a set of high-quality, freely available online resources, alongside DataCamp Classroom. Students are encouraged to consult these materials to complement lectures and exercises.

Introduction to R

- R for Data Science
- Introduction to Working with Data: R version

R for GIS

- R as GIS for Economists
- Spatial Statistics for Data Science: Theory and Practice with R

1.6 Grading

Assignments: 30%

Midterm Exam: 25%

Participation: 15%

Final Project: 30%

1.7 Academic Integrity

In accordance with the college's academic honesty policy, students are expected to submit original work for all assignments. Any form of academic dishonesty will not be tolerated. Plagiarism includes copying answers, phrases, sentence structures, or ideas from any source without proper attribution.

This also applies to the use of artificial intelligence tools such as ChatGPT. While you may use AI to assist with coding or to explore solutions, you must not simply feed it questions and

submit the generated responses as your own work. All submitted assignments should reflect your understanding and effort.

1.8 Generative AI Tools in Coursework

Open Use Guidelines: Embrace and encourage AI use in assignments, with the requirement that students disclose any AI assistance.

AI policy: permitted in this course with attribution

In this course, students are allowed to use Generative AI Tools like ChatGPT to support their work. To maintain academic integrity, students must disclose any AI-generated material they use and properly attribute it, including in-text citations, quotations, and references.

A student should include the following statement in assignments to indicate use of a Generative AI Tool: "The author(s) would like to acknowledge the use of [Generative AI Tool Name], a language model developed by [Generative AI Tool Provider], in the preparation of this assignment. The [Generative AI Tool Name] was used in the following way(s) in this assignment [e.g., coding, brainstorming, grammatical correction, citation, which portion of the assignment]."

1.9 Accommodations for Students with Disabilities

I am available to discuss appropriate academic accommodations that may be required for student with disabilities. The University of Tennessee, Knoxville, is committed to providing an inclusive learning environment for all students. If you anticipate or experience a barrier in this course due to a chronic health condition, a learning, hearing, neurological, mental health, vision, physical, or other kind of disability, or a temporary injury, you are encouraged to contact Student Disability Services (SDS) at 865-974-6087 or sds@utk.edu. An SDS Coordinator will meet with you to develop a plan to ensure you have equitable access to this course. If you are already registered with SDS, please contact your instructor to discuss implementing accommodations included in your course access letter.

1.10 Online@UT

Students are required to routinely access their UTK email account and the course website located on the Online@UT (Canvas) portal

2 Getting Started with R

2.1 Why use R?

As stated on the R Project website, R is a programming language and environment for statistical computing and graphics. It's flexible, easy to build on, and supported by a large, welcoming community.

Cost

R is free and open-source for everyone.

Reproducibility

Using a programming language for data management and analysis, rather than relying on Excel or other point-and-click tools, makes your work easier to reproduce, helps you catch mistakes more quickly, and can save you a lot of time and effort.

Community

The R community is huge and supportive. New packages and tools to tackle real-world problems are developed all the time, and the community helps test, improve, and share them.

2.2 Installation: R and RStudio

To get started, you'll need to have R running on your computer. There are a few options, but **RStudio** is a popular choice that makes working with R much easier.

Installing RStudio takes two steps. First, you'll need to install the R language itself.

How to install R

Visit this website https://www.r-project.org and download the latest version of R suitable for your computer. *Note*: Any mirror will work fine, but perhaps pick one close to you.

Once that's done, you can **install RStudio**

Go to this website https://posit.co/download/rstudio-desktop/ and download the latest free Desktop version of RStudio suitable for your computer.

2.3 Navigating RStudio

Open RStudio. RStudio is divided into four main *panes*, each showing different information like your code, console, and files.

The source pane

By default, this pane appears in the upper-left corner. It's where you can write, run, and save your scripts (your scripts are basically the sets of commands you want R to execute. You can also use this pane to view your datasets (data frames) while working.

The R console pane

The R Console (usually in the lower-left pane) is where the R "engine" lives. When you run commands here, you'll see results, warnings, or error messages right away. You can type commands directly in the Console, but unlike scripts, these commands won't be saved for later, so it's best for quick tests or checks.

The environment pane

By default, this pane appears in the upper-right. It's mainly used to get a quick look at the objects in your R environment during the current session. These objects can include datasets you've imported, created, or modified, as well as parameters or vectors and lists you've defined. You can click the little arrow next to a data frame to explore its variables.

Plots, Viewer, Packages, and Help pane

The lower-right pane contains several useful tabs. The *Plots* tab displays your charts, graphs, and maps, while the *Viewer* tab shows interactive or HTML outputs. The *Help* tab gives access to R documentation and help files, and the *Files* tab works like a mini file explorer, letting you open, move, or delete files. Finally, the *Packages* tab lets you see which R packages are installed, add new ones, update or remove them, and load or unload them for your session.

2.4 Scripts

Scripts are a fundamental part of programming. They're files that store the commands you want R to run, like creating or modifying datasets and generating visualizations. You can save a script and run it again later, which comes with some big advantages:

Portability: you can easily share your work with others by sending them your script.

Reproducibility: using scripts makes it clear exactly what steps you took, so you, or anyone else, can repeat your analysis with confidence.

Example script

```r
3 + 4
```

```
[1] 7
```

```r
a <- 3 + 4 # you can annotate around your code!
```

2.5 Quarto

Quarto is a tool that lets you combine your R code, text, and visualizations in a single document. It's perfect for creating reports, tutorials, or assignments where you want your analysis and explanations to live side by side. With Quarto, you can run your code, include the results, and produce a polished document; all in one place, making your work easy to share and easy to reproduce.

We will use Quarto document (.qmd) to write and edit your code!

Free online resources:

Tutorial: Hello Quarto

R for Data Science: Quarto

2.6 Working directory

The working directory (wd) is the root folder location used by R for your work, where R looks for and save files by default. R will save new files and outputs to this location, and will look for files to import (e.g. datasets) here as well.

The `wd` information appears at the top pf the Console pane. You can also print the current `wd` by running `getwd()` function.


```r
getwd()
```

```
[1] "/Users/gperezqu/Library/CloudStorage/OneDrive-UniversityofTennessee/University of Tennes
```

A recommended (and very efficient) approach is to use R projects. When you work inside the R project, your `wd` is automatically set to the project's root folder, which contains the `.rproj` file. This happens whenever you open RStudio by double-clicking the ".rproj" file, so you don't need to set the working directory yourself.

2.7 Create your R project

1. Create a folder in your computer (e.g., Project1)
2. Open RStudio
3. Click File → New Project
4. Click Browse
5. Select the folder you created (`Project1`)
6. Click Create Project

RStudio will now:

- Open the project
- Create a `.rproj` in the folder
- Set the `wd` automatically

7. Confirm you're in the project

You should see:

- the project name in the top-right corner of RStudio
- a file ending in `.rproj` in the Files pane

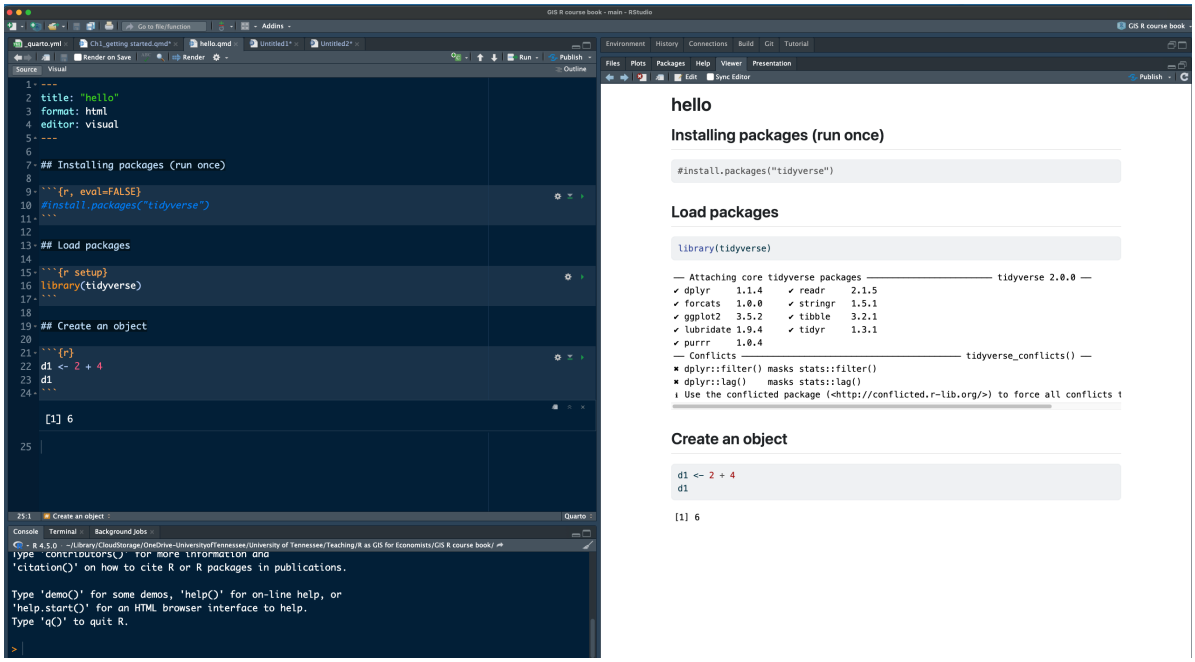
8. Create your first `Quarto` document

- Click File → New File → Quarto Document…
- Choose: Format: HTML; Engine: Knitr
- Click Create
- Save as → `hello`

Always open your project **by double-clicking** the `.rproj` file, not by opening RStudio first and setting the `wd` manually.

2.8 Quarto file (`.qmd`) overview

Below is a Quarto document (the `.qmd` file on the left) and its rendered output as an HTML page (on the right). The `.qmd` file is where you write your content and code, and when you render it, Quarto turns it into a polished document. You're not limited to HTML, you can also render the same file as a PDF, a Word document, and more.



- Select `Preview in Viewer Pane` if you want to see the rendered output on the `Viewer Pane`.
- Click on the `Render` button to render the file and preview the output.
- Two modes of the RStudio editor: `visual` (on the left) and `source` (on the right). `visual`: what-you-see-is-what-you-mean (WYSIWYM) experience, so you can format text without worrying about markdown syntax. `source`: plain-text markdown code.

3 hello Quarto

3.1 Headings

In this paper….

3.1.1 subsection

Some more text… This is **bold** text

My name is **Gaby…**

Use `#` symbols for section titles. Leave a blank line after headings for readability.

Section title

Subsection title

Smaller heading (more # = smaller heading)

3.2 Bold and italic text

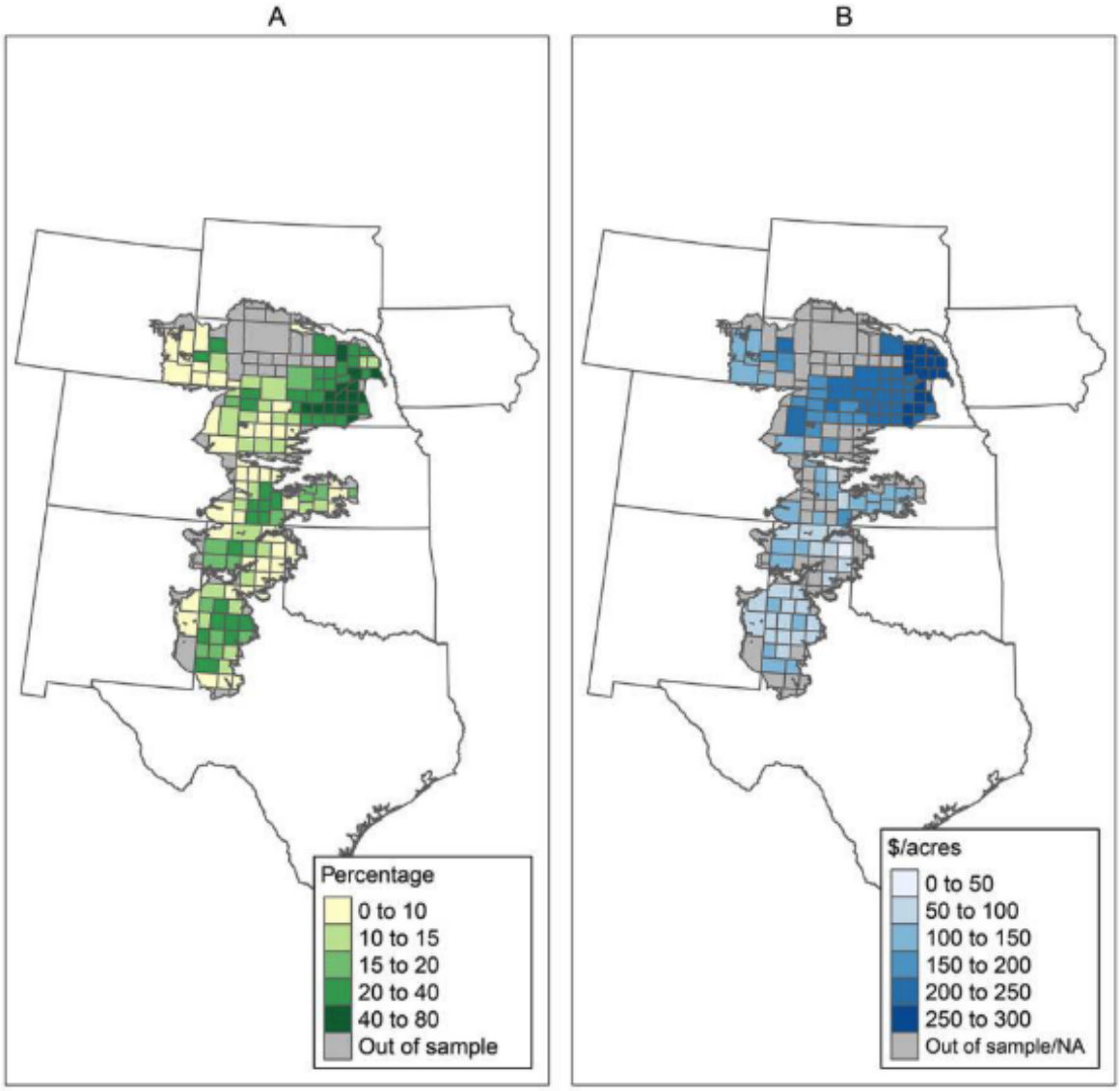
If you are using `Source`: **`text`** and *italic*

If you are using `Visual`: Click Format → Bold

3.3 Adding figures and links

Find any image and save it as `.png` in your R project.

The figure below shows that…



You can learn more about this paper here.

How to include figures and links when using `Visual`?

3.4 Code chuncks

R code chunks are marked with `{r}`. Type the chunk by hand or using keyboard shortcut.

Mac: Command + Option + I

Windows: Ctrl + Alt + I

```
# your R code goes here
# comment
```

3.5 Common chunck options

- eval = FALSE → show code, don't run it
- echo = FALSE → run code, don't show it
- include = FALSE → run code, show nothing
- message = FALSE → hide package messages
- warning = FALSE → hide warnings

Example:

```
d1 <- 4 + 8
d1
```

```
[1] 12
```

```
[1] 12
```

3.6 Installing packages (run once) and loading library

```
#install.packages("tidyverse")
library(tidyverse) # Load packages
```

```
Warning: package 'tibble' was built under R version 4.5.2
```

```
Warning: package 'purrr' was built under R version 4.5.2
```

```
Warning: package 'dplyr' was built under R version 4.5.2
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.2.0     v readr     2.1.5
v forcats   1.0.0     v stringr   1.5.1
v ggplot2   3.5.2     v tibble    3.3.1
v lubridate 1.9.4     v tidyr     1.3.1
v purrr     1.2.1
-- 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 becor
```

3.7 Create an object

Everything in R is an object, and R is an object-oriented language. An object exists once you assign a value to it.

After an object is created, it appears in the Environment pane. From there, you can use the object in your code (inspect it, manipulate it, change it, or redefine it by assigning it a new value).

```
# Defining an object (<-)
d1 <- 2 + 4
d1
```

```
[1] 6
```

3.8 Using built-in datasets in R

```
#data() # list of datasets
data(mtcars) # load mtcars

# create an object
my.data <- mtcars

# Inspect it
head(my.data)
```

	mpg	cyl	disp	hp	drat	wt	qsec	vs	am	gear	carb
Mazda RX4	21.0	6	160	110	3.90	2.620	16.46	0	1	4	4
Mazda RX4 Wag	21.0	6	160	110	3.90	2.875	17.02	0	1	4	4
Datsun 710	22.8	4	108	93	3.85	2.320	18.61	1	1	4	1
Hornet 4 Drive	21.4	6	258	110	3.08	3.215	19.44	1	0	3	1
Hornet Sportabout	18.7	8	360	175	3.15	3.440	17.02	0	0	3	2
Valiant	18.1	6	225	105	2.76	3.460	20.22	1	0	3	1

4 R Basics

4.1 Create an object

Everything in R is an object, and R is an object-oriented language. An object exists once you assign a value to it.

After an object is created, it appears in the Environment pane. From there, you can use the object in your code (inspect it, manipulate it, change it, or redefine it by assigning it a new value).

```
library(tidyverse)
```

```
Warning: package 'tibble' was built under R version 4.5.2
```

```
Warning: package 'purrr' was built under R version 4.5.2
```

```
Warning: package 'dplyr' was built under R version 4.5.2
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.2.0     v readr     2.1.5
v forcats   1.0.0     v stringr   1.5.1
v ggplot2   3.5.2     v tibble    3.3.1
v lubridate 1.9.4     v tidyr     1.3.1
v purrr     1.2.1
-- 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 becor
```

```
# Defining an object (<-)
d1 <- 2 + 4
d1
```

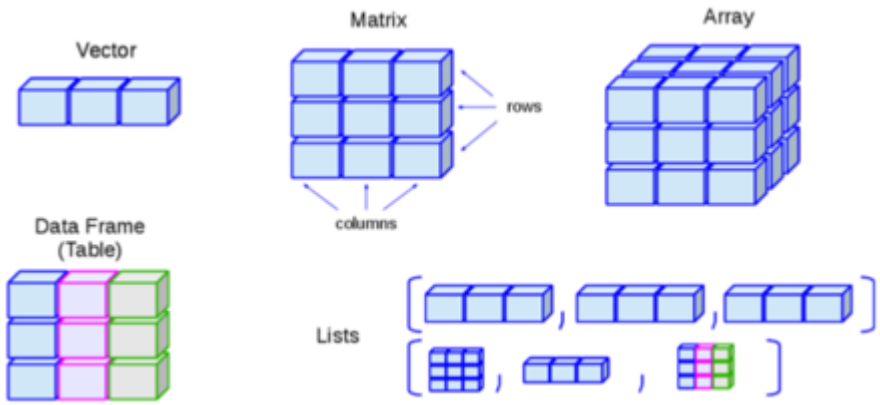
```
[1] 6
```

```r
#data()
# Using built-in datasets in R
data(mtcars) # load mtcars

# create an object
my.data <- mtcars
# Inspect it
head(my.data)
```

```
                   mpg cyl disp  hp drat    wt  qsec vs am gear carb
Mazda RX4         21.0   6  160 110 3.90 2.620 16.46  0  1    4    4
Mazda RX4 Wag     21.0   6  160 110 3.90 2.875 17.02  0  1    4    4
Datsun 710        22.8   4  108  93 3.85 2.320 18.61  1  1    4    1
Hornet 4 Drive    21.4   6  258 110 3.08 3.215 19.44  1  0    3    1
Hornet Sportabout 18.7   8  360 175 3.15 3.440 17.02  0  0    3    2
Valiant           18.1   6  225 105 2.76 3.460 20.22  1  0    3    1
```

4.2 Object structure

Objects can be as simple as a single value (e.g., `d1`), or they can hold more structured data, such as vectors, tables, or datasets, like the examples shown in the figure below (borrowed from this online R tutorial).



4.2.1 Data types

In this course, we will be using mostly vector and data frame.

Vector: a collection of values of the same type (e.g., numbers or text) stored together in one object.

```
# Numeric vector
numbers <- c(1, 2, 3, 4, 5)
numbers
```

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

```
class(numbers)
```

```
[1] "numeric"
```

```
# Character vector
names <- c("Alice", "Bob", "Charlie")
class(names)
```

```
[1] "character"
```

data.frame: a table of data where each column is a vector, and all columns have the same number of rows.

```
data(mtcars) # load mtcars

# create an object
my.data <- mtcars
class(my.data)
```

```
[1] "data.frame"
```

4.2.2 Variables types

Variable	Description	Example
integer	Whole numbers	5, 160, -30
numeric	Decimals	0.5, -0.38, 234.567
character	Text	“A”, “Nice”, “welcome”
logical	Booleans	TRUE or FALSE

Variable	Description	Example
factor	Categorical	“green”, “blue”, “red”
empty	–	NULL

Examples

```
class(d1)
```

```
[1] "numeric"
```

```
# Numeric (decimal)
num <- 3.14
num2 <- 56 # R treats all numbers without a decimal as numeric by default

class(num)
```

```
[1] "numeric"
```

```
class(num2)
```

```
[1] "numeric"
```

```
# Integer
int <- as.integer(num)
class(int)
```

```
[1] "integer"
```

```
int <- 56L # L tells R to store this as an integer
class(int)
```

```
[1] "integer"
```

```r
x <- 89
x <- 289

# Character (text)
char_var <- "welcome"

# Logical (TRUE/FALSE)
log_var <- TRUE

# Factor (categorical)
fact_var <- factor(c("green", "blue", "red"))

# variables type in my.data
class(my.data$hp)
```

```
[1] "numeric"
```

```r
class(my.data$mpg)
```

```
[1] "numeric"
```

4.3 Functions

Functions are at the core of using R. Want to calculate, plot, or transform something? There's probably a function for it. R comes with lots built in, you can add more with packages, and you can even make your own! Learn more here.

A function is like a little machine: you give it some inputs, it does something with them, and then it gives you an output. What comes out depends on the function you're using.

Inputs → [function] → Output

Simple functions

```r
# Function: sum()
# Inputs: numbers
# Action: adds them together
# Output: the total
sum(4, 7, 10)
```

```
[1] 21
```

```r
result <- sum(4, 7, 10)
result
```

```
[1] 21
```

```r
# Function: as.numeric()
# Inputs: char_nums
# Action: convert to numeric
# Output: num_nums

# Convert a character vector to numeric
char_nums <- c("1", "2", "3", "4")
class(char_nums)
```

```
[1] "character"
```

```r
# Convert to numeric
num_nums <- as.numeric(char_nums)
class(num_nums)
```

```
[1] "numeric"
```

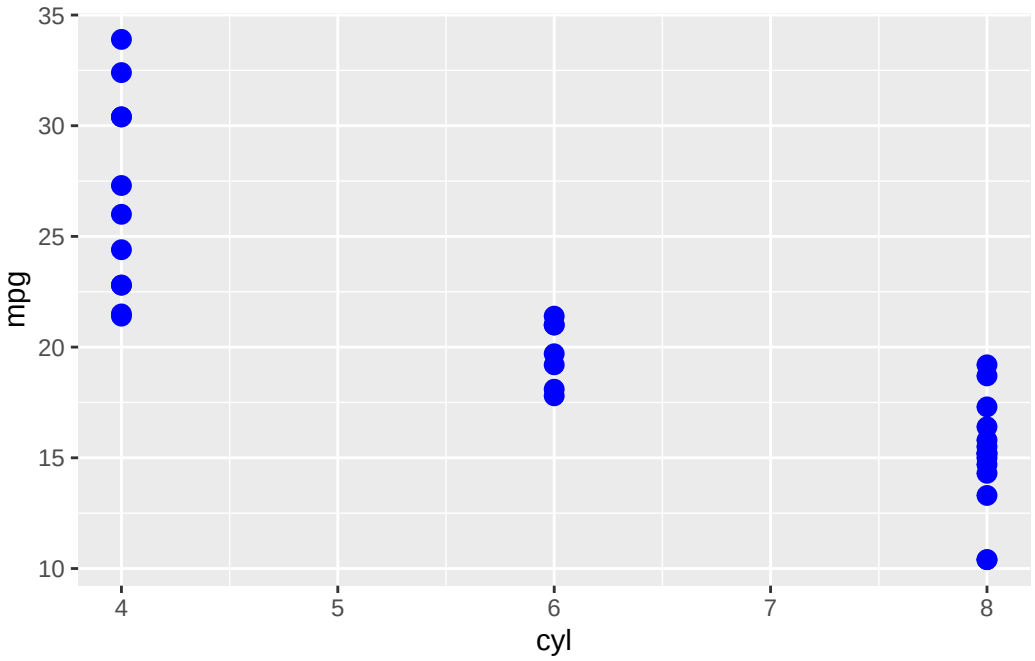
Custom function

```r
# Define a function that doubles a number
double_it <- function(x) {
  x * 2
}

# Use the function
double_it(4576)
```

```
[1] 9152
```

```r
# Functions with multiple arguments
# Load ggplot2 package (install first if you don't have it)
library(ggplot2)

# Use the built-in dataset 'mtcars'
```

```r
# We'll plot miles per gallon (mpg) vs number of cylinders (cyl)
ggplot(data = mtcars,              # Required argument: dataset
       mapping = aes(x = cyl, y = mpg)) +  # Required: aesthetics
  geom_point(color = "blue", size = 3)     # Optional arguments inside geom_point()
```



4.4 Piping (%>%)

Instead of nesting functions inside each other, you can write code step by step, which is often easier to read.

`%>%` (the "then" operator): pipes send an object from function to function.

Using **Tidyverse** + `%>%` you can do complex tasks in easy-to-read, step-by-step code.

Tidyverse is is a collection of R packages designed to work well together.

Example without a pipe

```r
# Find the average mpg of cars with 6 cylinders
mean(subset(my.data, cyl == 6)$mpg)
```

```
[1] 19.74286
```

Example with a pipe

```
my.data %>%
  filter(cyl == 6) %>%
  pull(mpg) %>%
  mean()
```

```
[1] 19.74286
```

```
# save the avg mpg as an object
avg.mpg <- mtcars %>%
  filter(cyl == 6) %>%
  pull(mpg) %>%
  mean()

class(avg.mpg)
```

```
[1] "numeric"
```

5 Data Wrangling

This chapter walks through the most common steps involved in taking raw data and turning it into analysis-ready data. You'll learn how to import datasets, clean and transform variables, handle missing values, combine multiple data sources, and filter data to answer specific questions. Along the way, we'll introduce essential R data-management functions-mostly from the **tidyverse**-and show how to chain them together using pipes to create clear, readable workflows.

5.1 Loading data from a file

Often your data will be stored in a file that you need to load into R. Common examples include:

File type	Extension	Common function	Package
Excel spreadsheet	`.xlsx`	`read_excel()`	**readxl**
Comma-separated values	`.csv`	`read_csv()`	**readr**
Stata dataset	`.dta`	`read_dta()`	**haven**

Note: You can use read_csv() and read_excel() after loading tidyverse. You can also use **rio** package, which has an `import()` function that works for just about any data file type you might want.

```
library(tidyverse)
```

```
Warning: package 'tibble' was built under R version 4.5.2
```

```
Warning: package 'purrr' was built under R version 4.5.2
```

```
Warning: package 'dplyr' was built under R version 4.5.2
```

```
-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.2.0     v readr     2.1.5
v forcats   1.0.0     v stringr   1.5.1
v ggplot2   3.5.2     v tibble    3.3.1
v lubridate 1.9.4     v tidyr     1.3.1
v purrr     1.2.1
-- 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 becor
```

```
water <- read_csv("../data/water_data.csv")
```

```
Rows: 76736 Columns: 6
-- Column specification --------------------------------------------------------
Delimiter: ","
dbl (6): year, field, price_water, q_water, center_pivot, county

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.
```

```
#water <- read_csv("water_data.csv")

ls(water)
```

```
[1] "center_pivot" "county"       "field"        "price_water"  "q_water"
[6] "year"
```

5.2 Looking at the data

```
class(water)
```

```
[1] "spec_tbl_df" "tbl_df"      "tbl"         "data.frame"
```

```
head(water)
```

```
# A tibble: 6 x 6
   year field price_water q_water center_pivot county
  <dbl> <dbl>       <dbl>   <dbl>        <dbl>  <dbl>
1  1992     1       0.585    14.6            0     12
2  1993     1       0.639    10.8            0     12
3  1994     1       0.644    17.0            1     12
4  1995     1       0.570    18.7            1     12
5  1996     1       0.760    21.4            1     12
6  1997     1       0.768    15              1     12
```

```
water %>% glimpse()
```

```
Rows: 76,736
Columns: 6
$ year         <dbl> 1992, 1993, 1994, 1995, 1996, 1997, 1998, 1999, 2000, 200~
$ field        <dbl> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 4, 4, 4, ~
$ price_water  <dbl> 0.5845152, 0.6391169, 0.6440908, 0.5702707, 0.7600425, 0.~
$ q_water      <dbl> 14.58335, 10.79831, 17.02275, 18.71972, 21.36000, 15.0000~
$ center_pivot <dbl> 0, 0, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, ~
$ county       <dbl> 12, 12, 12, 12, 12, 12, 12, 12, 12, 12, 12, 12, 12, 12, 1~
```

```
summary(water)
```

```
      year          field         price_water         q_water      
 Min.   :1992   Min.   :    1   Min.   :0.01553   Min.   : 0.000005  
 1st Qu.:1996   1st Qu.: 6015   1st Qu.:0.20199   1st Qu.:10.110240  
 Median :2000   Median :12099   Median :0.51795   Median :14.066380  
 Mean   :2000   Mean   :12058   Mean   :0.71312   Mean   :14.048993  
 3rd Qu.:2004   3rd Qu.:18118   3rd Qu.:0.98047   3rd Qu.:17.824100  
 Max.   :2007   Max.   :24086   Max.   :5.42991   Max.   :30.000000  
  center_pivot        county     
 Min.   :0.0000   Min.   : 1.00  
 1st Qu.:1.0000   1st Qu.: 7.00  
 Median :1.0000   Median :22.00  
 Mean   :0.9261   Mean   :20.83  
 3rd Qu.:1.0000   3rd Qu.:33.00  
 Max.   :1.0000   Max.   :41.00  
```

```
nrow(water)
```

```
[1] 76736
```

```r
ncol(water)
```

```
[1] 6
```

```r
# type of variables in water
class(water$year)
```

```
[1] "numeric"
```

```r
unique(water$year)
```

```
 [1] 1992 1993 1994 1995 1996 1997 1998 1999 2000 2001 2002 2003 2004 2005 2006
[16] 2007
```

5.3 Cleaning variable names

```r
water <- water %>%
  rename(county_code = county) #rename
```

5.4 Selecting and filtering data

```r
# Create a subset with only two variables: year and county_code
sub1 <- water %>%
  select(year, county_code)

# Get rid of the field variable
sub2 <- water %>%
  select(-field)

# Create a subset containing only year=2000
sub.2000 <- water %>%
  filter(year == 2000)
```

5.5 Creating variables

```
water <- water %>%
  mutate(year2 = year + 1,
         year3 = year2 + 3) # takes our year variable and adds 1 to it

# create a subset center_pivot == 1 and create a new variable = total cost
cost <- water %>%
  filter(center_pivot == 1) %>%
  mutate(tot.cost = price_water*q_water)

options(scipen = 999)
summary(cost$tot.cost)
```

```
      Min.    1st Qu.     Median       Mean    3rd Qu.       Max.
  0.000001   2.452759   6.182512  11.046254  15.240035 141.681762
```

5.6 Aggregating data

A dataset's observation level is simply what each row of the data represents. For example, `water` dataset contains one row per field for a given year, then the observation level is field-year.

Each row corresponds to one field in one specific year. Sometimes your data are more detailed than what you need for your analysis, and you may want to zoom out. For instance, you might start with field-year data but want to analyze outcomes at the field level overall. To do that, you need to aggregate the data.

In the tidyverse, this is usually done with `group_by()`, which tells R to perform calculations separately within each group. You'll then typically use `summarize()` to combine multiple rows into a single row per group. The resulting dataset will have an observation level based on whatever variable(s) you used in `group_by()`.

```
# get average total water cost by field
# averaged over all the years
avg.cost <- cost %>%
  group_by(field) %>%
  summarize(avg.cost = mean(tot.cost)) # add sum
```

5.7 Multi-row calculations

It's pretty common to need to use more than one row of data (but not the entire dataset) to calculate something you care about. For example, to calculate statistics by group, we can use `group_by()` to do by-group calculations. However, if we want to calculate by group and create a new column with that calculation rather than change the observation level, we want to follow that `group_by()` with a `mutate()` instead of a summarize.

```
cost <- cost %>%
  group_by(field) %>%
  mutate(avg.cost = mean(tot.cost, na.rm = T),
         tot.use = sum(q_water))

# What if I need the avg cost and total use by field-year?
```

```
# Your time to practice
# 1) Create a subset that includes only years > 1999
# 2) create a new variable: q_water10 = (q_water + 10)
# 3) create a two new variables: min.use and min.price by year
```

```
data1 <- water %>%
  filter(year > 1999) %>%
  mutate(q_water10 = q_water + 10) %>%
  group_by(year) %>%
  mutate(min.use = min(q_water),
         min.price = min(price_water))
```

5.8 Re-code values using logic and conditions

Specific values

To re-code with simple logical criteria, you can use `replace()` within mutate().

```
# avg cost is changed for field = 24

avg.cost <- avg.cost %>%
  mutate(avg.cost = replace(avg.cost, field == 24, 8.564))
```

Another function for simple logic is `ifelse()`. It applies a simple condition to a whole vector at once and return one value if the condition is true and another if it's false. It's especially useful for creating or transforming variables based on rules.

Let's create a new variable, `type`, that takes the value 1 when `q_water`> mean(q_water), and 0 otherwise.

```
# calculate the mean of q_water
summary(water$q_water)
```

```
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
 0.000005 10.110240 14.066380 14.048993 17.824100 30.000000
```

```
water <- water %>%
  mutate(type = ifelse(q_water > 14.05, 1, 0))

class(water$type)
```

```
[1] "numeric"
```

```
# Convert type to factor variable and create labels.
water <- water %>%
  mutate(type = factor(type, levels = c(0, 1), labels = c("low", "high")))

?factor
class(water$type)
```

```
[1] "factor"
```

Complex logic

Use `case_when()` when you need to recode a variable into many groups or apply more complex logical rules. The function checks each row of the data and assigns a new value based on the conditions you specify.

Each `case_when()` rule has a condition on the left and a value on the right, separated by a tilde (~):

- Conditions go on the left-hand side (LHS)
- Assigned values go on the right-hand side (RHS)
- Rules are separated by commas

Now, we want to create `type2` but taking three values, low, medium and high.

```r
summary(water$q_water)
```

```
     Min.   1st Qu.    Median      Mean   3rd Qu.      Max.
 0.000005 10.110240 14.066380 14.048993 17.824100 30.000000
```

```r
water <- water %>%
  mutate(type2 = case_when(
    q_water < 12 ~ 0,
    q_water >= 12 & q_water < 15 ~ 1,
    q_water >= 15 ~ 2
  ))

# using ifelse
water <- water %>%
  mutate(type.test = ifelse(q_water < 12, 0, ifelse(q_water >= 12 & q_water < 15, 1,2)))

# Convert type to factor variable and create labels.
water <- water %>%
  mutate(type_fac = factor(type2, levels = c(0, 1, 2), labels = c("low", "medium", "high")))

# or create a factor variable directly
water <- water %>%
  mutate(type2 = factor(case_when(
    q_water < 12 ~ 0,
    q_water >= 12 & q_water < 15 ~ 1,
    q_water >= 15 ~ 2),
    levels = c(0, 1, 2),
    labels = c("low", "medium", "high")))
```

5.9 Missing values

When we are cleaning our data, we need to handle missing values. They are represented by special values: `NA`, `NULL`, `NaN` and `Inf`.

Examples

R command	Outcome
`5 / 0`	Inf
`0 / 0`	NaN

R command	Outcome
`5 / NA`	NA

Useful functions

Let's build an example dataset and use some important functions to deal with missing values.

```
df <- tibble(
  id     = 1:10,
  score  = c(10, 9, NA, 7, 6, NA, 8, 9, NA, 5),
  group  = c("A", "A", "A", "B", "B", "B", "A", "A", "B", "B"))

df
```

```
# A tibble: 10 x 3
      id score group
   <int> <dbl> <chr>
 1     1    10 A
 2     2     9 A
 3     3    NA A
 4     4     7 B
 5     5     6 B
 6     6    NA B
 7     7     8 A
 8     8     9 A
 9     9    NA B
10    10     5 B
```

Detect missing values `is.na()`

```
df %>%
  mutate(score_na = is.na(score))
```

```
# A tibble: 10 x 4
      id score group score_na
   <int> <dbl> <chr> <lgl>
 1     1    10 A     FALSE
 2     2     9 A     FALSE
 3     3    NA A     TRUE
 4     4     7 B     FALSE
```

```
 5     5     6 B     FALSE
 6     6    NA B     TRUE
 7     7     8 A     FALSE
 8     8     9 A     FALSE
 9     9    NA B     TRUE
10    10     5 B     FALSE
```

```r
is.na(df)
```

```
         id score group
 [1,] FALSE FALSE FALSE
 [2,] FALSE FALSE FALSE
 [3,] FALSE  TRUE FALSE
 [4,] FALSE FALSE FALSE
 [5,] FALSE FALSE FALSE
 [6,] FALSE  TRUE FALSE
 [7,] FALSE FALSE FALSE
 [8,] FALSE FALSE FALSE
 [9,] FALSE  TRUE FALSE
[10,] FALSE FALSE FALSE
```

Keep only complete values `!is.na()`, `drop_na()`

```r
df_comp <- df %>%
  filter(!is.na(score))

df_comp <- df %>%
  drop_na(score)
```

Ignore missing values in calculations `na.rm = TRUE`

```r
df %>%
  summarise(mean_socre = mean(score))
```

```
# A tibble: 1 x 1
  mean_socre
       <dbl>
1         NA
```

```r
df %>%
  summarise(mean_socre = mean(score, na.rm = T))
```

```
# A tibble: 1 x 1
  mean_socre
       <dbl>
1       7.71
```

Your turn to practice: calculate the average score by group.

```r
df %>%
  group_by(group) %>%
  summarise(group_socre = mean(score, na.rm = T))
```

```
# A tibble: 2 x 2
  group group_socre
  <chr>       <dbl>
1 A               9
2 B               6
```

```r
# if you want to save the outcome
group_socre <- df %>%
  group_by(group) %>%
  summarise(group_socre = mean(score, na.rm = T))
```

5.10 Joining data

Often, you'll work with multiple datasets that describe the same observations (for example, the same people, places, or time periods). To combine these datasets, you use a merge (or join) based on one or more key variables that appear in both datasets. These key variables act like an ID that tells R which rows belong together. At least one of the datasets should have only one row per key value, so R knows exactly how to match the observations without ambiguity.

```r
# let's create a new dataset to merge with water
water2 <- water %>%
  select(year, field) %>% # IDs variables
  mutate(
    x = rnorm(n()),
    y = rnorm(n()))
```

We now have a second dataset that includes variables `x` and `y`, and we want to bring those variables back into our original `water` dataset. To do this, we use `joins` functions, which are provided by the **dplyr** package (included in the **tidyverse**).

Join functions can be used in two ways: as standalone commands that create a new data frame, or inside a pipe (`%>%`) as part of a larger data-cleaning workflow.

In this example, we use `left_join()` as a standalone command to create a new data frame called `joined_data`. The first data frame listed (`water`) is the baseline dataset we want to keep, and the second data frame (`water.2`) is joined to it.

The `by =` argument tells R which columns to use to match rows between the two datasets. These columns must exist in both data frames and should uniquely identify the observations so the rows line up correctly.

```
joined_data <- left_join(water, water2, by = c("year", "field")) # note we use two IDs varial
```

Left and right joins

`left_join()`, `right_join()`

Left and right joins are commonly used to add new information to an existing dataset.

The order of the datasets matters:

- In a left join, the first dataset is the baseline.
- In a right join, the second dataset is the baseline.

All rows from the baseline dataset are kept. Data from the other dataset is added only when there is a match on the identifier column(s). Rows in the secondary dataset that do not match are dropped.

If one row in the secondary dataset matches multiple baseline rows, the same information is added to each matching row. If a baseline row matches multiple rows in the secondary dataset, new rows will be created, increasing the size of the data.

Should we use a left join or a right join? To answer this question, ask yourself: Which dataset do I want to keep all rows from?

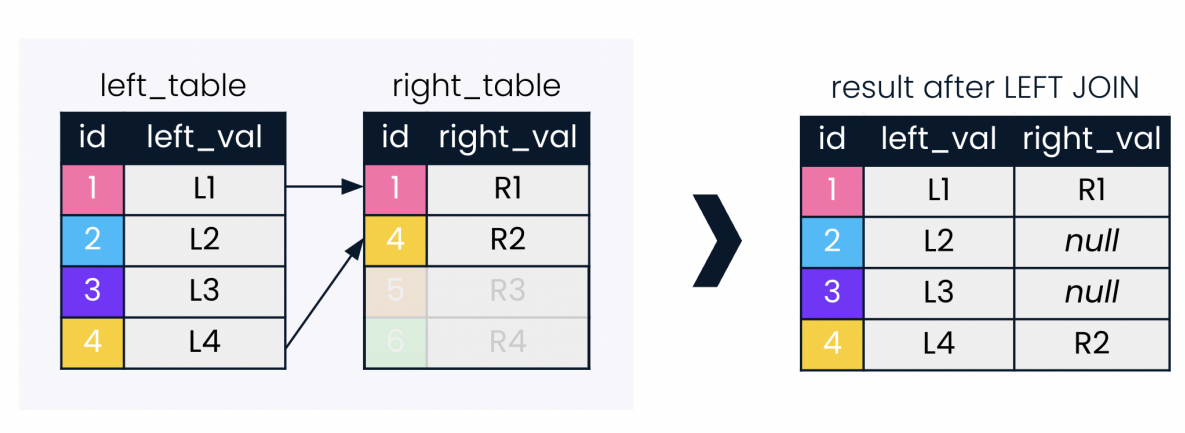


Figure 5.1: Source: Datacamp

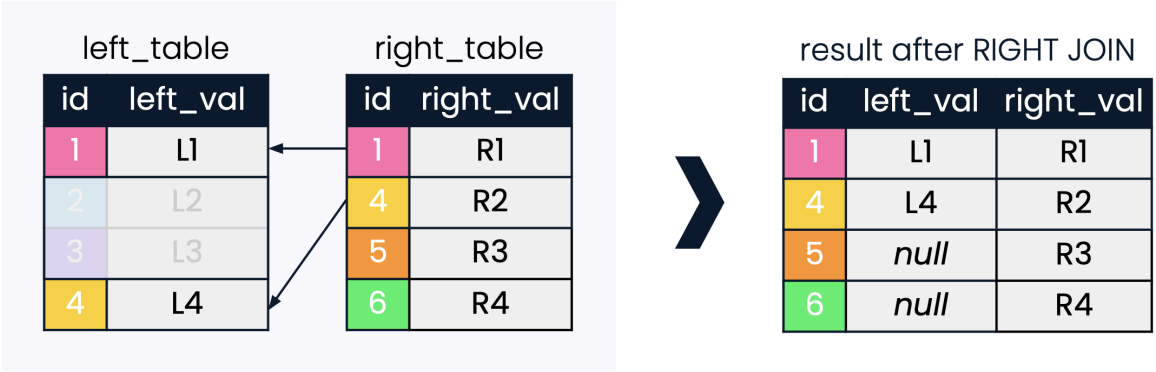


Figure 5.2: Source: Datacamp

Full joins

`full_join()`

A full join is the most inclusive type of join. It keeps all rows from both datasets.

If a row appears in one dataset but not the other, it is still included in the result. Any missing information created by these unmatched rows is filled in with NA. Because full joins can increase both the number of rows and columns, it's a good idea to keep an eye on the output to catch issues like mismatched variable names, case sensitivity, or small differences in character values.

In a full join, the dataset listed first in the command is treated as the baseline. While this does not change which rows are returned, it can affect the order of rows and columns and which identifier columns are kept.

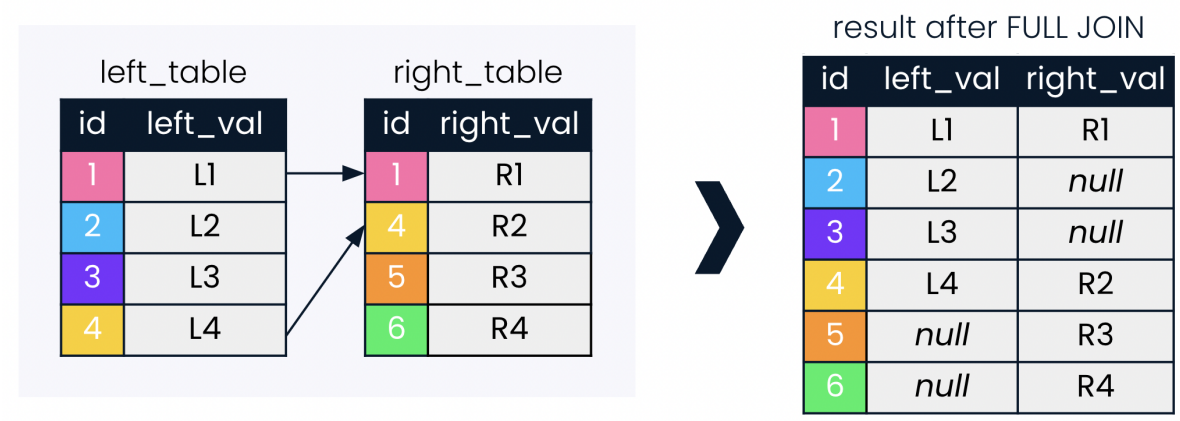


Figure 5.3: Source: Datacamp

Inner join

`inner_join()`

An inner join is the most restrictive type of join—it keeps only rows that have matching values in both datasets.

Because of this, the number of rows in the resulting dataset may be smaller than in the original (baseline) dataset.

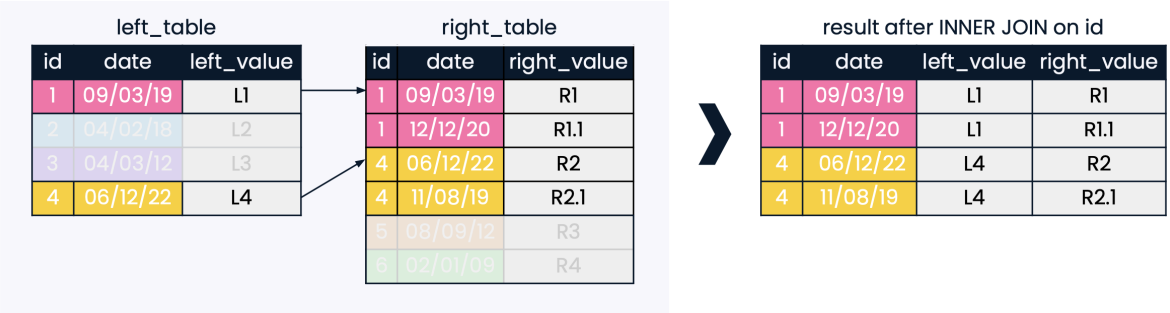


Figure 5.4: Source: Datacamp

6 Data Visualization

7 Introducing ggplot

ggplot2 is the most widely used data-visualization package in R. At the heart of it is the ggplot() function. The "gg" stands for the grammar of graphics, a way of building plots by combining clear components (data, mappings, geometric shapes, scales, and more). Instead of drawing a figure in one step, you assemble it layer by layer. This might feel unusual at first, but it gives you enormous flexibility.

Another big advantage is that **ggplot2** works beautifully with the **tidyverse** ecosystem. Many companion packages extend what you can do—adding new themes, annotations, color systems, interactivity, and specialized plot types.

There are several resources and tutorials where you can learn more about ggplot:

- ggplot2
- The R Graph Gallery
- dataviz
- R for Data Science

Installation

The easiest way to get ggplot2 is to install the whole **tidyverse** (install.packages("tidyverse")). Alternatively, install just **ggplot2** (install.packages("ggplot2")).

8 Basics of ggplot

Plotting with **ggplot2** is based on building a figure by adding layers. Each new part of the plot is added to the previous ones using the plus sign (+).

Instead of drawing everything in a single command, you start with a base plot and then keep improving it step by step. The final result is a plot object that you can save, print, modify, or export.

Even though ggplot figures can become very sophisticated, most of them follow a simple structure.

Basic skeleton code:

```
# plot data from my_data columns as red points
ggplot(data = my_data)+                    # use the dataset "my_data"
  geom_point(                              # add a layer of points (dots)
    mapping = aes(x = var1, y = var2),     # "map" data column to axes
    color = "red")+                        # other specification for the geom
  labs()+                                  # here you add titles, axes labels, etc.
  theme()                                  # here you adjust color, font, size etc of non-data
```

9 Total population data from tidycensus

Now that we want to look at population data for many years, it would be tedious and repetitive to call `get_acs()` separately for each year. Instead of doing it manually, we can automate the process by "mapping" a function over a vector of years. This way, the same code runs for each year, and we can collect all the results in a single dataset efficiently.

In **purrr** package, `map()` is a tool for repeating a function over a list or vector of inputs. Instead of writing a loop, you can apply a function to every element and get a list of results. It makes your code shorter, cleaner, and easier to read. See additional resources: Purrr in R and map functions.

Sometimes, the output of `map()` is a list of data frames. That's useful, but often we want a single, combined data frame to work with in tidyverse pipelines. That's where `map_df()` comes in.

`map_df()` does the same job as `map()`, but it automatically binds all the results together row-wise into one tidy data frame. This is perfect for our population example, where we pull data for multiple years and want a single dataset with a "year" column.

The `map()` function takes the following arguments:

- .x: The data structure to which the function to be applied will be applied
- .f: The function to apply
- ...: Additional arguments required by the function

In the code below:

- we map a function over every year in `years`
- for each year, we pull total population with `get_acs()`
- `map_df()` combines all the results into one single data frame `pop_state`

```
library(tidycensus) # load packages
```

```
Warning: package 'tidycensus' was built under R version 4.5.2
```

```
library(tidyverse)
```

```
Warning: package 'tibble' was built under R version 4.5.2

Warning: package 'purrr' was built under R version 4.5.2

Warning: package 'dplyr' was built under R version 4.5.2

-- Attaching core tidyverse packages ------------------------ tidyverse 2.0.0 --
v dplyr     1.2.0     v readr     2.1.5
v forcats   1.0.0     v stringr   1.5.1
v ggplot2   3.5.2     v tibble    3.3.1
v lubridate 1.9.4     v tidyr     1.3.1
v purrr     1.2.1
-- 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 becor
```

```r
library(purrr)
```

Get the data we will plot:

```r
# choose the years you want
years <- 2012:2022

pop_state <- map_df(years, function(y) {
  get_acs(
     geography = "state",
     variables = "B01003_001",
     year = y,
     survey = "acs5") %>%
     select(GEOID, NAME, estimate) %>%
     mutate(year = y)})
```

```
Getting data from the 2008-2012 5-year ACS

Getting data from the 2009-2013 5-year ACS

Getting data from the 2010-2014 5-year ACS

Getting data from the 2011-2015 5-year ACS
```

```
Getting data from the 2012-2016 5-year ACS

Getting data from the 2013-2017 5-year ACS

Getting data from the 2014-2018 5-year ACS

Getting data from the 2015-2019 5-year ACS

Getting data from the 2016-2020 5-year ACS

Getting data from the 2017-2021 5-year ACS

Getting data from the 2018-2022 5-year ACS
```

```r
unique(pop_state$year)
```

```
 [1] 2012 2013 2014 2015 2016 2017 2018 2019 2020 2021 2022
```

Simplified example using `map_df()`:

- input vector: 1, 2, 3
- function: square of x
- output: a single data frame; `map_df()` stacks them

```r
map_df(1:3, function(x) {tibble(number = x, square = x^2) })
```

```
# A tibble: 3 x 2
  number square
   <int>  <dbl>
1      1      1
2      2      4
3      3      9
```

Let's create a few subset of the data:

```r
tn <- pop_state %>% # only TN
  filter(NAME == "Tennessee") %>%
  rename(pop = estimate)

# select 3 states
tn_ga_sc <- pop_state %>%
  filter(NAME %in% c("Tennessee", "Georgia", "South Carolina")) %>%
  rename(pop = estimate)
```

10 Creating a ggplot

When working with **ggplot2**, every plot starts with the ggplot() function. Think of this as setting up a blank canvas. Inside `ggplot()`, the first thing we tell R is which dataset we want to use (e.g., `tn`).

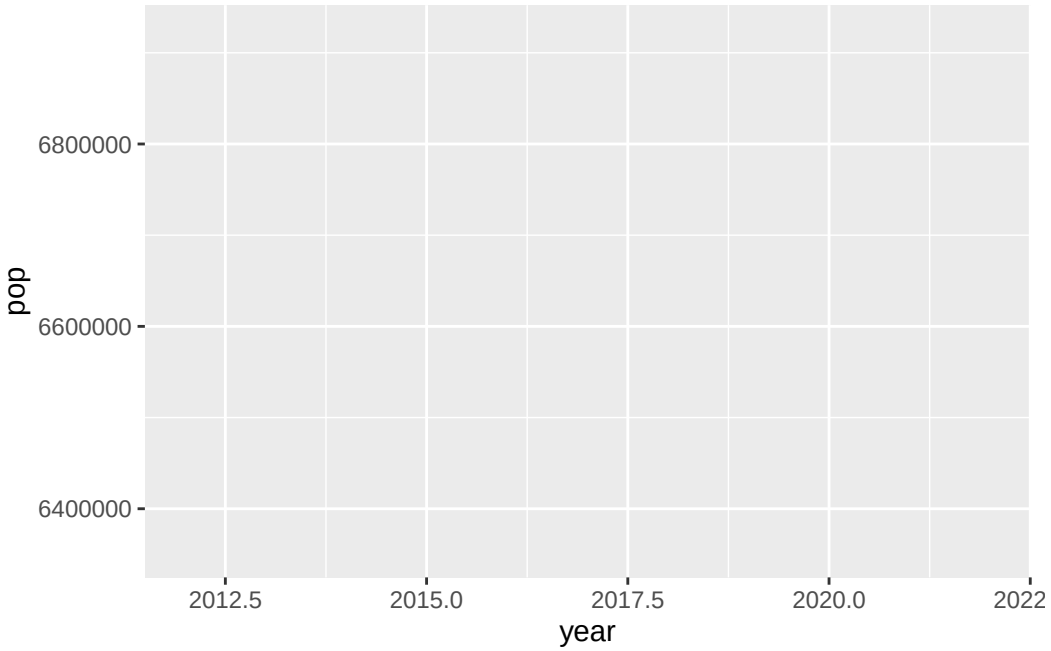
The code below creates an empty plot that's connected to the `tn` dataset. Right now, nothing appears on the screen. This is because we've told R what data to use, but we haven't told it how to display it yet.

The magic of ggplot happens when we start adding layers to show the data visually.

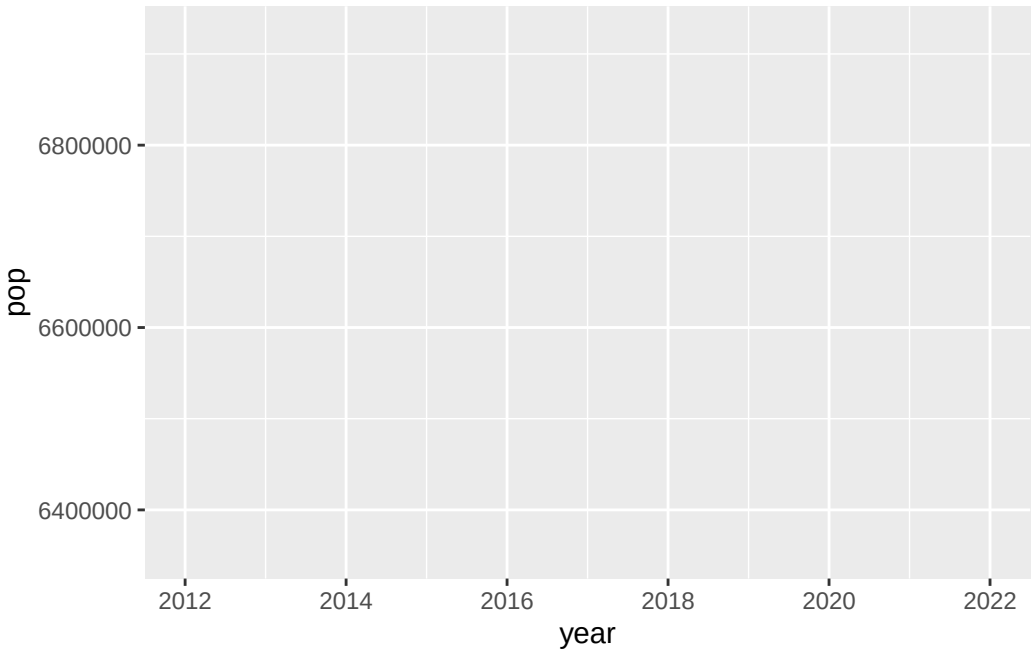
```
ggplot(tn)
```


Next, we need to tell `ggplot()` how we want our data to appear on the graph. This is where aesthetic mappings come in. In ggplot, we use the `aes()` function (short for "aesthetics") to explain how variables in our dataset should be connected to visual elements in the plot.

```
ggplot(data = tn,
       mapping = aes(x = year, y = pop)) # what happen with year?
```




```
ggplot(data = tn,
       mapping = aes(x = year, y = pop)) +
  scale_x_continuous(breaks = seq(min(tn$year), max(tn$year), by = 2))
```

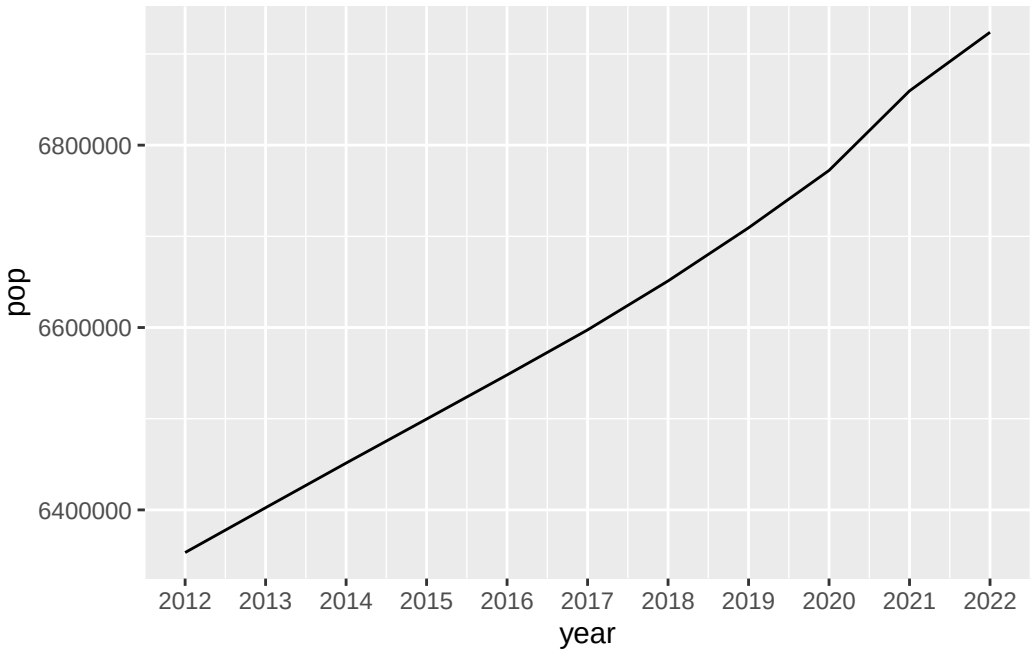


Now we need to choose a *geom* (short for geometric object). A *geom* is simply the type of shape that ggplot uses to display your data.

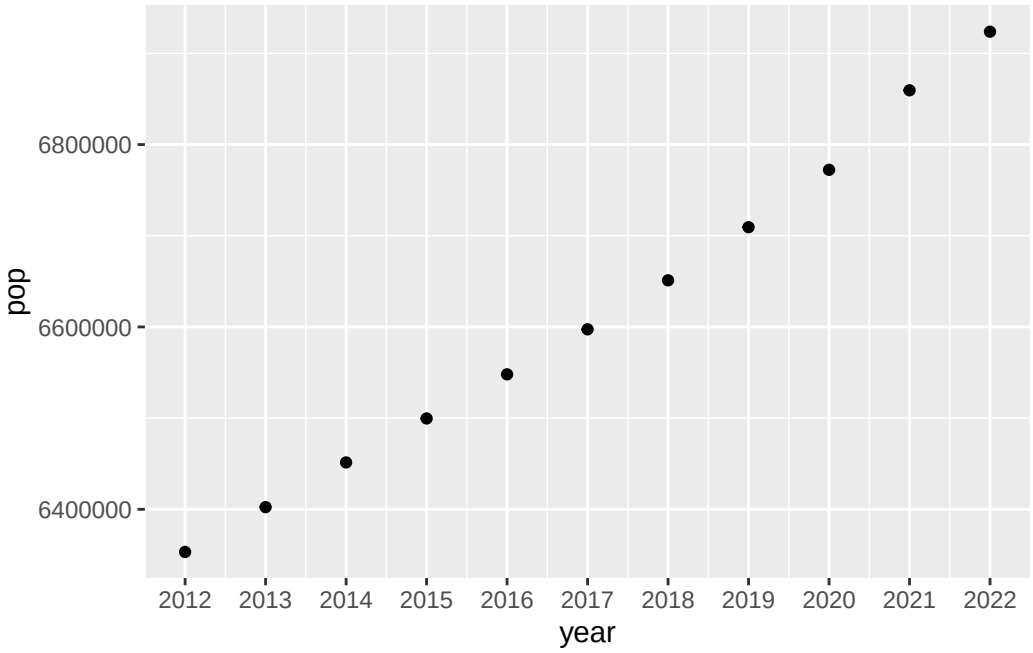
In ggplot2, *geoms* are added with functions that start with `geom_`. For example: - Bar charts use `geom_bar()` - Line charts use `geom_line()` - Boxplots use `geom_boxplot()` - Scatterplots use `geom_point()`

So when you decide what kind of plot you want, you're really deciding which geom to add.

```
ggplot(
  data = tn,
  mapping = aes(x = year, y = pop)) +
  scale_x_continuous(breaks = seq(min(tn$year), max(tn$year), by = 1)) +
  geom_line()
```




```
ggplot(
  data = tn,
  mapping = aes(x = year, y = pop)) +
  scale_x_continuous(breaks = seq(min(tn$year), max(tn$year), by = 1)) +
  geom_point()
```

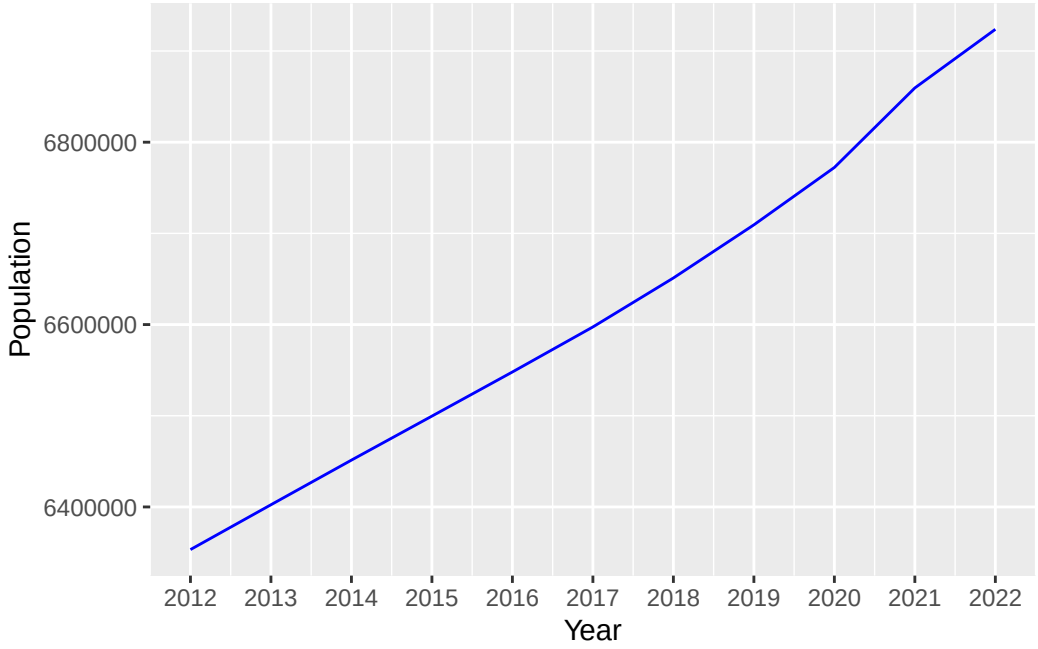


11 Adding aesthetics and layers

Now, we want to change the appearance of the line and the axis labels. Note that:

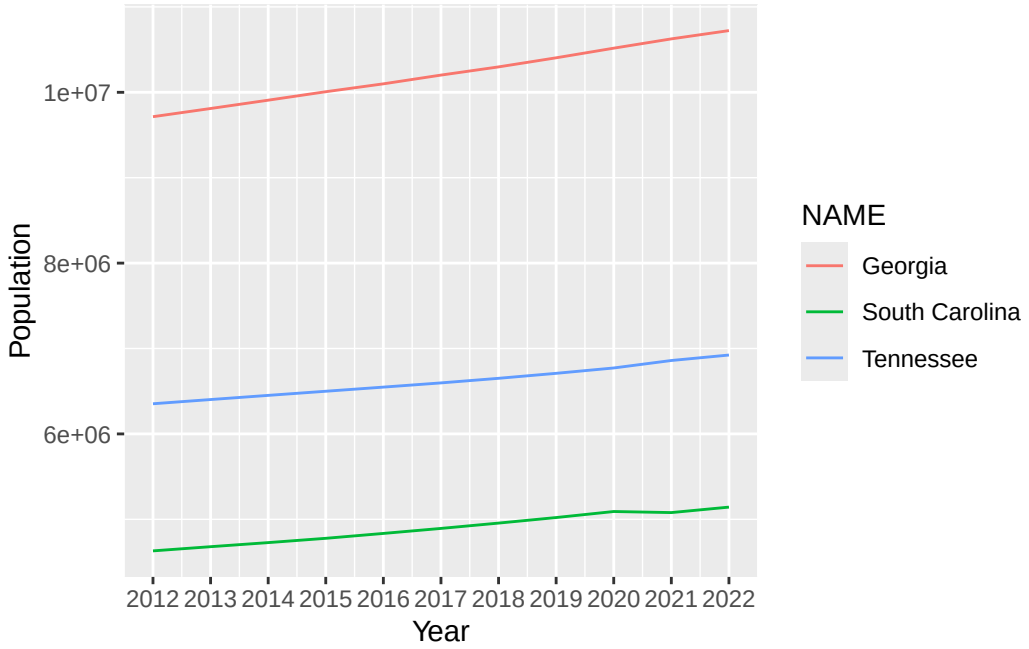
- When we put `color = "blue"` inside `geom_line()` but outside `aes()`, we are setting a fixed color
- If we put color inside `aes()`, ggplot would expect a variable and would color lines based on data

```
ggplot(
  data = tn,
  mapping = aes(x = year, y = pop)) +
  scale_x_continuous(breaks = seq(min(tn$year), max(tn$year), by = 1)) +
  geom_line(color = "blue") +
  labs(x = "Year", y = "Population")
```



Now, instead of looking at just one state, we're using a dataset that includes three states. We want one line for each state so we can compare them over time.

```r
ggplot(
  data = tn_ga_sc,
  mapping = aes(x = year, y = pop, colour = NAME)) +
  scale_x_continuous(breaks = seq(min(tn$year), max(tn$year), by = 1)) +
  geom_line() +
  labs(x = "Year", y = "Population")
```



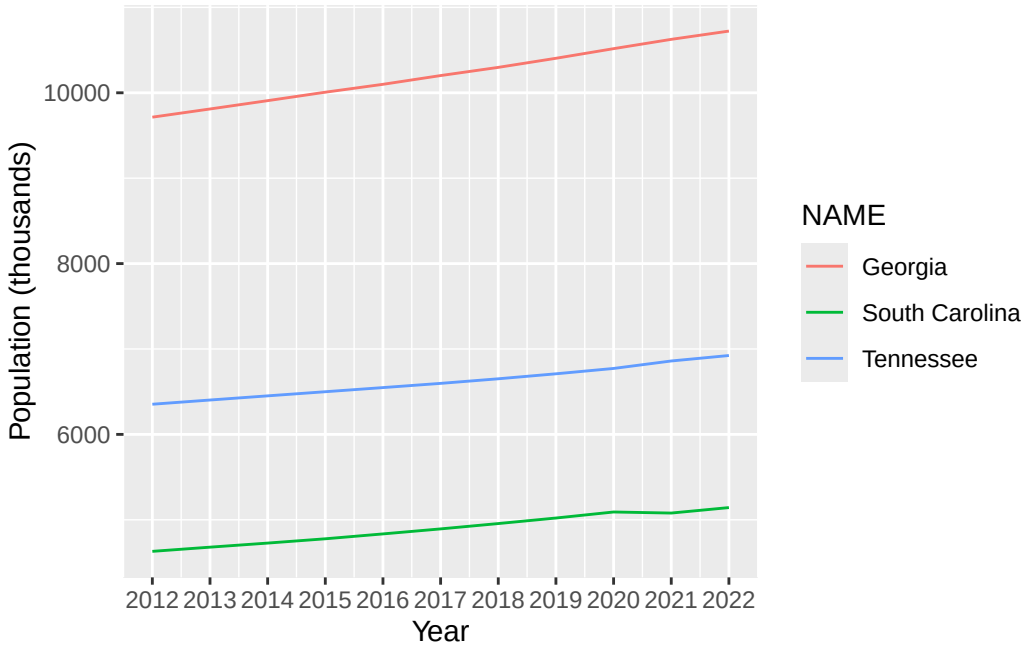
Large numbers can make a graph harder to read. So, instead of plotting large values, we can rescale the data to make the axis cleaner and easier to interpret.

```r
summary(tn_ga_sc$pop)
```

```
   Min. 1st Qu.  Median    Mean 3rd Qu.    Max.
4630351 5078903 6597381 7239605 9907756 10722325
```

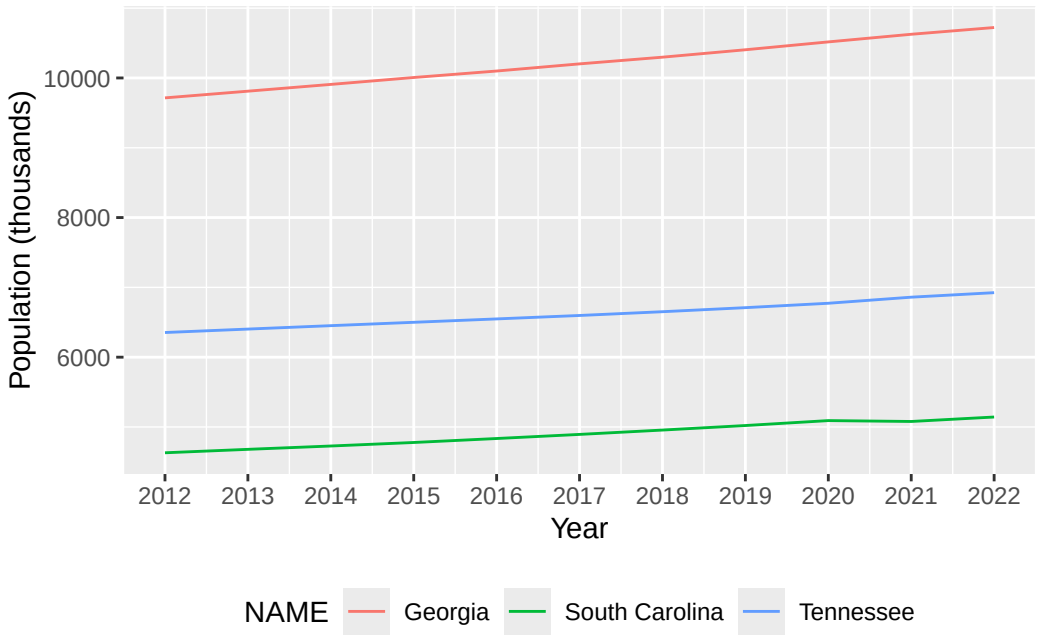
```r
tn_ga_sc <- tn_ga_sc %>%
  mutate(pop2 = pop/1000)

ggplot(
  data = tn_ga_sc,
  mapping = aes(x = year, y = pop2, colour = NAME)) +
  scale_x_continuous(breaks = seq(min(tn$year), max(tn$year), by = 1)) +
```

```
  geom_line() +
  labs(x = "Year", y = "Population (thousands)")
```



What if we want to move the legend to the bottom? We can use `theme()` function.

```
ggplot(
  data = tn_ga_sc,
  mapping = aes(x = year, y = pop2, colour = NAME)) +
  scale_x_continuous(breaks = seq(min(tn$year), max(tn$year), by = 1)) +
  geom_line() +
  labs(x = "Year", y = "Population (thousands)") +
  theme(legend.position = "bottom")
```


Population (thousands)
10000
8000
6000
2012
2013
2014
2015
2016
2017
2018
2019
2020
2021
2022
Year
NAME
Georgia
South Carolina
Tennessee

References