Python and R

Clay Ford, Jacob Goldstein-Greenwood, Oyinkansola Adenekan, Samantha Lomuscio

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Welcome

This book provides parallel examples in Python and R to help users of one platform more easily learn how the other platform "works" when it comes to data analysis.

Chapter 1

Basics

This chapter covers the very basics of Python and R.

1.1 Math

Mathematical operators are the same except for exponents, integer division, and remainder division (modulo).

Python

Python uses `**` for exponentiation, `//` for integer division, and `%` for remainder division.

```
> 3**2
9
> 5 // 2
2
> 5 % 2
1
```

In Python, the `+` operator can also be used to combine strings. See this TBD section.

R

Python uses `^` for exponentiation, `%/%` for integer division, and `%%` for remainder division.

```
> 3^2
[1] 9
> 5 %/% 2
[1] 2
> 5 %% 2
[1] 1
```

1.2 Assignment

Python uses `=` for assignment while R can use either `=` or `<-` for assignment. The latter "assignment arrow" is preferred in most R style guides to distinguish it between assignment and setting the value of a function argument. According to R's documentation, "The operator `<-` can be used anywhere, whereas the operator `=` is only allowed at the top level (e.g., in the complete expression typed at the command prompt) or as one of the subexpressions in a braced list of expressions." See `?assignOps`.

Python

```
> x = 12
```

R

```
> x <- 12
```

1.3 Printing a value

To see the value of an object created via assignment, you can simply enter the object at the console and hit enter for both Python and R, though it is common in Python to explicitly use the `print()` function.

Python

```
> x
12
```

R

```
> x
[1] 12
```

1.4 Packages

User-created functions can be bundled and distributed as packages. Packages need to be installed only once. Thereafter they're "imported" (Python) or "loaded" (R) in each new session when needed.

Packages with large user bases are often updated to add functionality and fix bugs. The updates are not automatically installed. Staying apprised of library/package updates can be challenging. Some suggestions are following developers on Twitter, signing up for newsletters, or periodically checking to see what updates are available.

Packages often depend on other packages. These are known as "dependencies." Sometimes packages are updated to accommodate changes to other packages they depend on.

Python

R

The main repository for R packages is the Comprehensive R Archive Network (CRAN). Another repository is Bioconductor, which provides tools for working with genomic data. Many packages are also distributed on GitHub.

To install packages from CRAN use the `install.packages()` function. In RStudio, you can also go to Tools…Install Packages… for a dialog that will autocomplete package names as you type.

```
> # install the vcd package, a package for Visualizing Categorical Data
> install.packages("vcd")
>
> # load the package
> library(vcd)
>
> # see which packages on your computer have updates available
> old.packages()
>
> # download and install available package updates;
```

```
> # set ask = TRUE to verify installation of each package
> update.packages(ask = FALSE)
```

To install R packages from GitHub use the `install_github()` function from the **devtools** package. You need to include the username of the repo owner followed by a forward slash and the name of the package. Typing two colons between a package and a function in the package allows you to use that function without loading the package. That's how we use the `install_github()` below.

```
> install.packages("devtools")
> devtools::install_github("username/packagename")
```

Occasionally when installing package updates you will be asked "Do you want to install from sources the package which needs compilation?" R packages on CRAN are *compiled* for Mac and Windows operating systems. That can take a day or two after a package has been submitted to CRAN. If you try to install a package that has not been compiled then you'll get asked the question above. If you click *Yes*, R will try to compile the package on your computer. This will only work if you have the required build tools on your computer. For Windows this means having Rtools installed. Mac users should already have the necessary build tools. Unless you absolutely need the latest version of a package, it's probably fine to click *No*.

1.5 Logic

Python and R share the same operators for making comparisons:

- `==` (equals)
- `!=` (not equal to)
- `<` (less than)
- `<=` (less than or equal to)
- `>` (greater than)
- `>=` (greater than or equal to)

Likewise they share the same operators for logical AND and OR:

- `&` (AND)
- `|` (OR)

However R also has `&&` and `||` operators for programming control-flow.

Python and R have different operators for negation and xor (exclusive OR).

Python

R

1.6 Generating a sequence of values

In Python, one option for generating a sequence of values is `arange()` from **NumPy**. In R, a common approach is to use `seq()`. The sequences can be incremented by indicating a `step` argument in `arange()` or a `by` argument in `seq()`. Be aware that the end of the start/stop interval in `arange()` is *open*, but both sides of the from/to interval in `seq()` are *closed*.

Python

```
> import numpy as np
+ x = np.arange(start = 1, stop = 11, step = 2)
+ x
array([1, 3, 5, 7, 9])
```

R

```
> x <- seq(from = 1, to = 11, by = 2)
> x
[1]  1  3  5  7  9 11
```

1.7 Calculating means and medians

The **NumPy** Python library has functions for calculating means and medians, and base R has functions for doing the same.

Python

Mean, using function from **NumPy** library

```
> import numpy as np
+ x = [90, 105, 110]
+ x_avg = np.mean(x)
+ print(x_avg)
101.66666666666667
```

Median, using function from **NumPy** library

```
> x = [98, 102, 20, 22, 304]
+ x_med = np.median(x)
+ print(x_med)
98.0
```

R

Mean, using function from base R

```
> x <- c(90, 105, 110)
> x_avg <- mean(x)
> x_avg
[1] 101.6667
```

Median, using function from base R

```
> x <- c(98, 102, 20, 22, 304)
> x_med <- median(x)
> x_med
[1] 98
```

1.8 Writing your own functions

Python and R allow and encourage users to create their own functions. Functions can be created, named, and stored in memory and used throughout a session. Or they can be created on-the-fly "anonymously" and used once.

Python

Functions in Python are defined by using the `def` keyword followed by the name we choose for our function with its arguments inside parentheses. We must include a `return()` statement after the body of our function to indicate the end of the function. The return statement takes an optional argument in it's parenthesis that will be the output of the function. Here we create a function to calculate the standard error of a mean (SEM) and call it `SEM`.

```
> def SEM(x):
+   import numpy as np # import statement included inside the function to ensure it's
+   s = x.std(ddof=1) # find standard deviation of the input array, specify delta degr
+   n = x.shape[0] # extract the length of the input array (x.shape returns a numpy ar
```

```
+   sem = s / np.sqrt(n) # calculate the SEM
+   return(sem) # return the calculated SEM value
```

Now let's try our function out on some test data.

```
> d = np.array([3,4,4,7,9,6,2,5,7])
+ SEM(d)
0.7412035591181296
```

R

Functions in R can be created and named using `function()`. Add arguments inside the parentheses. Longer functions with multiple lines can be wrapped in curly braces `{}`.

Below we create a function to calculate the standard error of a mean (SEM) and name it `sem`. It takes one argument: `x`, a vector of numbers. Both the function name and argument name(s) can be whatever we like, as long as they follow R's naming conventions.

```
> sem <- function(x){
+   s <- sd(x)
+   n <- length(x)
+   s/sqrt(n)
+ }
```

Now we can try it out on some test data.

```
> d <- c(3,4,4,7,9,6,2,5,7)
> sem(d)
[1] 0.7412036
```

Functions that will be used on different data and/or by different users often need built-in error-checking to return informative error messages. This simple example checks if the data are not numeric and returns a special error message.

```
> sem <- function(x){
+   if(!is.numeric(x)) stop("x must be numeric")
+   s <- sd(x)
+   n <- length(x)
+   s/sqrt(n)
+ }
> sem(c(1, 4, 6, "a"))
Error in sem(c(1, 4, 6, "a")): x must be numeric
```

R functions can also return more than one result. Below we return a list that holds the mean and SEM, but we could also return a vector, a data frame, or other data structure. Notice we also add an additional argument, `...`, known as the three dots argument. This allows us to pass arguments for `sd` and `mean` directly through our own function. Below we pass through `na.rm = TRUE` to drop missing values.

```
> sem <- function(x, ...){
+   if(!is.numeric(x)) stop("x must be numeric")
+   s <- sd(x, ...)
+   n <- length(x)
+   se <- s/sqrt(n)
+   mean <- mean(x, ...)
+   list(mean = mean, SEM = se)
+ }
>
> d <- c(1, 4, 6, 8, NA, 4, 4, 8, 6)
> sem(d, na.rm = TRUE)
$mean
[1] 5.125

$SEM
[1] 0.7855339
```

Functions can also be created on-the-fly as "anonymous" functions. This simply means the functions are not saved as objects in memory. These are often used with R's family of `apply` functions. As before, the functions can be created with `function()`. We can also use the backslash `\` as a shorthand for `function()`. We demonstrate both below with a data frame.

```
> # generate some example data
> d <- data.frame(x1 = c(3, 5, 7, 1, 5, 4),
+                 x2 = c(6, 9, 8, 9, 2, 5),
+                 x3 = c(1, 9, 9, 7, 8, 4))
> d
  x1 x2 x3
1  3  6  1
2  5  9  9
3  7  8  9
4  1  9  7
5  5  2  8
6  4  5  4
```

Now find the standard error of the mean for the three columns using an anonymous function with `lapply`. The "l" means the result will be a list. We apply the function to each column of the data frame.

```
> lapply(d, function(x)sd(x)/sqrt(length(x)))
$x1
[1] 0.8333333

$x2
[1] 1.118034

$x3
[1] 1.308094
```

We can also use the backslash as a shorthand for `function()`.

```
> lapply(d, \(x)sd(x)/sqrt(length(x)))
$x1
[1] 0.8333333

$x2
[1] 1.118034

$x3
[1] 1.308094
```

Chapter 2

Data Structures

This chapter compares and contrasts data structures in Python and R.

2.1 One-dimensional data

A one-dimensional data structure can be visualized as a column in a spreadsheet or as a list of values.

Python

There are many ways to organize one-dimensional data in Python. The of the most common one-dimensional data structures are lists, numpy arrays, and pandas Series. All three are ordered and mutable, and can contain data of different types.

Lists in Python do not need to be explicitly declared, they are indicated by the use of square brackets.

```
> l = [1,2,3,'hello']
```

Values in lists can be accessed by using square brackets. Python indexing begins at 0, so to extract the first element, we would use the index 0. Python also allows for negative indexing, using an index of -1 will return the last value in the list. Indexing a range in Python is not inclusive of the last index.

```
> # extract first element
+ l[0]
+
```

```
+ #extract last element
1
> l[-1]
+
+ # extract 2nd and 3rd elements
'hello'
> l[1:3]
[2, 3]
```

Numpy arrays, on the other hand, need to be declared using the `numpy.array()` function and the **numpy** package needs to be imported.

```
> import numpy as np
+
+ arr = np.array([1,2,3,'hello'])
+ print(arr)
['1' '2' '3' 'hello']
```

Accessing data in a numpy array is the same as indexing a list.

```
> # extract first element
+ arr[0]
+
+ # extract last element
'1'
> arr[-1]
+
+ # extract 2nd and 3rd elements
'hello'
> arr[1:3]
array(['2', '3'], dtype='<U11')
```

Pandas Series also need to be declared using the `pandas.Series()` function. Like **numpy**, the **pandas** package must be imported as well. The pandas package is built on numpy, so we can input data into a pandas Series using a numpy array. We can extract data from the Series by using the index similar to indexing a list and numpy array.

```
> import pandas as pd
+ import numpy as np
+
+ data = np.array([1,2,3,"hello"])
+ ser1 = pd.Series(data)
+ print(ser1)
```

```
+
+ # extract first element
0        1
1        2
2        3
3    hello
dtype: object
> ser1[0]
+
+ # extract 2nd and 3rd elements
'1'
> ser1[1:3]
1    2
2    3
dtype: object
```

To extract the last element of a pandas Series using `-1`, we need to use the `iloc` function.

```
> ser1.iloc[-1]
'hello'
```

We can relabel the indices of the Series to whatever we like using the `index` attribute within the `Series` function.

```
> import pandas as pd
+ import numpy as np
+
+ ser2 = pd.Series(data, index=['a','b','c','d'])
+ print(ser2)
a        1
b        2
c        3
d    hello
dtype: object
```

We can then use our own specified indices to select and index our data. Indexing with our labels can be done in two ways. One similar to indexing arrays and lists with square brackets using the `.loc` function, and the other follows this form: `Series.label_name`.

```
>
+ # extract element in row b
+ ser2.loc["b"]
```

```
+
+ # extract elements from row b to the end
'2'
> ser2.loc["b":]
+
+ # extract element in row "d"
b        2
c        3
d    hello
dtype: object
> ser2.d
+
+ # extract element in row "b"
'hello'
> ser2.b
'2'
```

One thing to note is that mathematical operations cannot be carried out on lists, but can be carried out on numpy arrays and pandas Series. In general, lists are better for short data sets that you will not be operating on mathematically. Numpy arrays and pandas Series are better for long data sets, and for data sets that will be operated on mathematically.

R

In R a one-dimensional data structure is called a *vector*. We can create a vector using the `c()` function. A vector in R can only contain one type of data (all numbers, all strings, etc). The columns of data frames are vectors. If multiple types of data are put into a vector, the data will be coerced according to the hierarchy `logical` < `integer` < `double` < `complex` < `character`. This means if you mix, say, integers and character data, all the data will be coerced to character.

```
> x1 <- c(23, 43, 55)
> x1
[1] 23 43 55
>
> # all values coerced to character
> x2 <- c(23, 43, 'hi')
> x2
[1] "23" "43" "hi"
```

Values in a vector can be accessed by position using indexing brackets. R indexes elements of a vector starting at 1. Index values are inclusive. For example, `2:3` selects the second and third elements.

```
> # extract the 2nd value
> x1[2]
[1] 43
>
> # extract the 2nd and 3rd value
> x1[2:3]
[1] 43 55
```

2.2 Two-dimensional data

Two-dimensional data are rectangular in nature, consisting of rows and columns. These can be the type of data you might find in a spreadsheet with a mix of data types in columns; they can also be matrices as you might encounter in matrix algebra.

Python

In Python, two common two-dimensional data structures include the *numpy array* and the *pandas DataFrame*.

A two-dimensional numpy array is made in a similar way to the one-dimensional array using the `numpy.array` function.

```
> import numpy as np
+
+ arr2d = np.array([[1,2,3,"hello"],[4,5,6,"world"]])
+ print(arr2d)
[['1' '2' '3' 'hello']
 ['4' '5' '6' 'world']]
```

Selecting data for a two-dimensional numpy array follows the same form as indexing a one-dimensional array.

```
> import numpy as np
+
+ # extract first element
+ arr2d[0,0]
+
+ # extract last element
'1'
> arr2d[-1, -1]
+
+ # extract 2nd and 3rd columns
```

```
'world'
> arr2d[:,1:3]
array([['2', '3'],
       ['5', '6']], dtype='<U11')
```

A pandas DataFrame is made using the `pandas.DataFrame` function in a similar way to the pandas Series.

```
> import pandas as pd
+ import numpy as np
+
+ data = np.array([[1,2,3,"hello"],[4,5,6,"world"]])
+ df = pd.DataFrame(data)
+ print(df)
   0  1  2      3
0  1  2  3  hello
1  4  5  6  world
```

Selecting data from a DataFrame is similar to that of the Series.

```
> # extract first element
+ df.loc[0,0]
+
+ # extract column 1
'1'
> df.loc[0]
+
+ # extract row 1
0        1
1        2
2        3
3    hello
Name: 0, dtype: object
> df.loc[0,0]
'1'
```

Like the pandas Series, we can change the indices and the column names of the DataFrame and can use those to select and index our data.

We change the indices again using the `index` attribute in the `pandas.DataFrame` function:

```
> import pandas as pd
+ import numpy as np
+
```

```
+ data = np.array([[1,2,3,"hello"],[4,5,6,"world"]])
+ df = pd.DataFrame(data, index=["a","b"])
+ print(df)
   0  1  2      3
a  1  2  3  hello
b  4  5  6  world
```

We can change the column names using the `columns` attribute in the `pandas.DataFrame` function:

```
> import pandas as pd
+ import numpy as np
+
+ data = np.array([[1,2,3,"hello"],[4,5,6,"world"]])
+ df = pd.DataFrame(data, index=["a","b"], columns=["column 1","column 2", "column 3", "column 4'
+ print(df)
  column 1 column 2 column 3 column 4
a        1        2        3    hello
b        4        5        6    world
```

One thing to note is that numpy arrays can actually have N dimensions, whereas pandas DataFrames can only have two. Numpy arrays will be the better choice for data with more than two dimensions.

R

Two-dimensional data structures in R include the *matrix* and *data frame*. A matrix can contain only one data type. A data frame can contain multiple vectors each of which can consist of different data types.

Create a matrix with the `matrix()` function. Create a data frame with the `data.frame()` function. Most imported data comes into R as a data frame.

```
> # matrix; populated down by column by default
> m <- matrix(data = c(1,3,5,7), nrow = 2, ncol = 2)
> m
     [,1] [,2]
[1,]    1    5
[2,]    3    7
>
> # data frame
> d <- data.frame(name = c("Rob", "Cindy"),
+                 age = c(35, 37))
> d
```

```
   name age
1   Rob  35
2 Cindy  37
```

Values in a matrix and data frame can be accessed by position using indexing brackets. The first number(s) refers to rows; the second number(s) refers to columns. Leaving row or column numbers empty selects all rows or columns.

```
> # extract value in row 1, column 2
> m[1,2]
[1] 5
>
> # extract values in row 2
> d[2,]
   name age
2 Cindy  37
```

2.3 Three-dimensional and higher data

Three-dimensional and higher data can be visualized as multiple rectangular structures stratified by extra variables. These are sometimes referred to as *arrays*. Analysts usually prefer two-dimensional data frames to arrays. Data frames can accommodate multidimensional data by including the additional dimensions as variables.

Python

To create a three-dimensional and higher data structure in Python, we again use a numpy array. We can think of the three-dimensional array as a stack of two-dimensional arrays. We construct this in the same way as the one- and two-dimensional arrays.

```
> import numpy as np
+
+ arr3d = np.array([[[1, 2, 3], [4, 5, 6]], [[7, 8, 9], [10, 11, 12]]])
+ arr3d
array([[[ 1,  2,  3],
        [ 4,  5,  6]],

       [[ 7,  8,  9],
        [10, 11, 12]]])
```

We can also construct a three-dimensional numpy array using the `reshape` function on an existing array. The argument of `reshape` is where you input your desired dimensions - strata, rows, columns. Here, the `arange` function is used to create a numpy array containing the numbers 1 through 12 (to recreate the same array shown above).

```
> arr3d_2 = np.arange(1,13).reshape(2,2,3)
+ arr3d_2
array([[[ 1,  2,  3],
        [ 4,  5,  6]],

       [[ 7,  8,  9],
        [10, 11, 12]]])
```

Indexing the three-dimensional array follows the same format as the two-dimensional arrays. Since we can think of the three-dimensional array as a stack of two-dimensional arrays, we can extract each "stacked" two-dimensional array. Here we extract the first of the "stacked" two-dimensional arrays:

```
> # extract first strata (first "stacked" 2-D array)
+ arr3d[0]
array([[1, 2, 3],
       [4, 5, 6]])
```

We can also extract entire rows and columns, and individual array elements:

```
> # extract 1st row of 2nd strata (second "stacked" 2-D array)
+ arr3d[1, 0]
+
+ # extract 1st column of 2nd strata
array([7, 8, 9])
> arr3d[1, :, 0]
+
+ # extract the number 6 (1st strata, 2nd row, 3rd column)
array([ 7, 10])
> arr3d[0, 1, 2]
6
```

The three-dimensional arrays can be converted to two-dimensional arrays again using the `reshape` function:

```
> arr3d_2d = arr3d.reshape(4,3)
+ arr3d_2d
array([[ 1,  2,  3],
```

```
       [ 4,  5,  6],
       [ 7,  8,  9],
       [10, 11, 12]])
```

R

The `array()` function in R can create three-dimensional and higher data structures. Arrays are like vectors and matrices in that they can only contain one data type. In fact matrices and arrays are sometimes described as vectors with instructions on how to layout the data.

We can specify the dimension number and size using the `dim` argument. Below we specify 2 rows, 3 columns, and 2 strata using a vector: `c(2,3,2)`. This creates a three-dimensional data structure. The data in the example are simply the numbers 1 through 12.

```
> a1 <- array(data = 1:12, dim = c(2,3,2))
> a1
, , 1

     [,1] [,2] [,3]
[1,]    1    3    5
[2,]    2    4    6

, , 2

     [,1] [,2] [,3]
[1,]    7    9   11
[2,]    8   10   12
```

Values in arrays can be accessed by position using indexing brackets.

```
> # extract value in row 1, column 2, strata 1
> a1[1,2,1]
[1] 3
>
> # extract column 2 in both strata
> # result is returned as matrix
> a1[,2,]
     [,1] [,2]
[1,]    3    9
[2,]    4   10
```

The dimensions can be named using the `dimnames()` function. Notice the names must be a *list*.

```
> dimnames(a1) <- list("X" = c("x1", "x2"),
+                      "Y" = c("y1", "y2", "y3"),
+                      "Z" = c("z1", "z2"))
> a1
, , Z = z1

    Y
X    y1 y2 y3
  x1  1  3  5
  x2  2  4  6

, , Z = z2

    Y
X    y1 y2 y3
  x1  7  9 11
  x2  8 10 12
```

The `as.data.frame.table()` function can collapse an array into a two-dimensional structure that may be easier to use with standard statistical and graphical routines. The `responseName` argument allows you to provide a suitable column name for the values in the array.

```
> as.data.frame.table(a1, responseName = "value")
    X  Y  Z value
1  x1 y1 z1     1
2  x2 y1 z1     2
3  x1 y2 z1     3
4  x2 y2 z1     4
5  x1 y3 z1     5
6  x2 y3 z1     6
7  x1 y1 z2     7
8  x2 y1 z2     8
9  x1 y2 z2     9
10 x2 y2 z2    10
11 x1 y3 z2    11
12 x2 y3 z2    12
```

2.4 General data structures

Both R and Python provide general “catch-all” data structures that can contain any number, shape, and type of data.

Python

R

The most general data structure in R is the *list*. A list is an ordered collection of objects, which are referred to as the *components*. The components can be vectors, matrices, arrays, data frames, and other lists. The components are always numbered but can also have names. The results of statistical functions are often returned as lists.

We can create lists with the `list()` function. The list below contains three components: a vector named "x", a matrix named "y", and a data frame named "z". Notice the `m` and `d` objects were created in the two-dimensional data section earlier in this chapter.

```
> l <- list(x = c(1,2,3),
+           y = m,
+           z = d)
> l
$x
[1] 1 2 3

$y
     [,1] [,2]
[1,]    1    5
[2,]    3    7

$z
   name age
1   Rob  35
2 Cindy  37
```

We can refer to list components by their order number or name (if present). To use order number, use indexing brackets. Single brackets returns a list. Double brackets return the component itself.

```
> # second element returned as list
> l[2]
$y
     [,1] [,2]
[1,]    1    5
[2,]    3    7
>
> # second element returned as itself (matrix)
> l[[2]]
     [,1] [,2]
```

```
[1,]    1    5
[2,]    3    7
```

Use the $ operator to refer to components by name. This returns the component itself.

```
> l$y
     [,1] [,2]
[1,]    1    5
[2,]    3    7
```

Finally it is worth noting that a data frame is a special case of a list consisting of components with the same length. The `is.list()` function returns TRUE if an object is a list and FALSE otherwise.

```
> # object d is data frame
> d
   name age
1   Rob  35
2 Cindy  37
> str(d)
'data.frame':   2 obs. of  2 variables:
 $ name: chr  "Rob" "Cindy"
 $ age : num  35 37
>
> # but a data frame is a list
> is.list(d)
[1] TRUE
```

Chapter 3

Importing, Export, and Save Data

This chapter reviews importing external data into Python and R, including CSV, Excel, and other structured data files. There is often more than one way to import data into Python and R. The examples below highlight one way that we frequently see used.

The data we use for demonstration is New York State Math Test Results by Grade from 2006 - 2011, downloaded from data.gov on September 30, 2021.

3.1 CSV

Comma separated value (CSV) files are text files with fields separated by commas. They are useful for "rectangular" data where rows represent observations and columns represent variables or features.

Python

The **pandas** function `read_csv()` is a common approach to importing CSV files into Python.

```
> import pandas as pd
+ d = pd.read_csv('data/ny_math_test.csv')
+ d.loc[0:2, ["Grade", "Year", "Mean Scale Score"]]
  Grade  Year  Mean Scale Score
0     3  2006               700
1     4  2006               699
2     5  2006               691
```

R

There are many ways to import a csv file. A common way is to use the base R function `read.csv()`.

```
> d <- read.csv("data/ny_math_test.csv")
> d[1:3, c("Grade", "Year", "Mean.Scale.Score")]
  Grade Year Mean.Scale.Score
1     3 2006              700
2     4 2006              699
3     5 2006              691
```

Notice the spaces in the column names have been replaced with periods.

Two packages that provide alternatives to `read.csv()` are **readr** and **data.table**. The **readr** function `read_csv()` returns a tibble. The **data.table** function `fread()` returns a data.table.

3.2 XLS/XLSX (Excel)

Excel files are native to Microsoft Excel. Prior to 2007, Excel files had an extension of XLS. With the launch of Excel 2007, the extension was changed to XLSX. Excel files can have multiple sheets of data. This needs to be accounted for when importing into Python and R.

Python

The **pandas** function `read_excel()` is a common approach to importing Excel files into Python. The `sheet_name` argument allows you to specify which sheet you want to import. You can specify sheet by its (zero-indexed) ordering or by its name. Since this Excel file only has one sheet we do not need to use the argument. In addition, specifying `sheet_name=None` will read in all sheets and return a dict data structure where the *key* is the sheet name and the *value* is a DataFrame.

```
> import pandas as pd
> d = pd.read_excel('data/ny_math_test.xlsx')
> d.loc[0:2, ["Grade", "Year", "Mean Scale Score"]]
>
```

R

readxl is a well-documented and actively maintained package for importing Excel files into R. The workhorse function is `read_excel()`. The `sheet` argument allows you to specify which sheet you want to import. You can specify sheet by its ordering or by its name. Since this Excel file only has one sheet we do not need to use the argument.

```
> library(readxl)
> d_xls <- read_excel("data/ny_math_test.xlsx")
> d_xls[1:3, c("Grade", "Year", "Mean Scale Score")]
# A tibble: 3 x 3
  Grade  Year `Mean Scale Score`
  <chr> <dbl>              <dbl>
1 3      2006                700
2 4      2006                699
3 5      2006                691
```

The result is a *tibble*, a tidyverse data frame.

It's worth noting we can use the `range` argument to specify a range of cells to import. For example, if the top left corner of the data was B5 and the bottom right corner of the data was J54, we could enter `range="B5:J54"` to just import that section of data.

3.3 JSON

JSON (**J**ava**S**cript **O**bject **N**otation) is a flexible format for storing data. JSON files are text and can be viewed in any text editor. Because of their flexibility JSON files can be quite complex in the way they store data. Therefore there is no one-size-fits-all method for importing JSON files into Python or R.

Python

Below is one approach to importing our "ny_math_test.json" example file. We first import Python's built-in **json** package and use its `loads()` function to read in the lines of the json file. The file is accessed using the `open` function and its associated `read` method.

Next we use the **pandas** function `json_normalize()` to convert the 'data' structure of the json data into a DataFrame.

Finally we add column names to the DataFrame.

```
> import json
+ # load data using Python JSON module
+ with open('data/ny_math_test.json','r') as f:
+     data = json.loads(f.read())
```

```
+
+ import pandas as pd
+ d_json = pd.json_normalize(data, record_path =['data'])
+
+ # add column names
+ names = list()
+ for i in range(23):
+   names.append(data['meta']['view']['columns'][i]['name'])
+ d_json.columns = names
+
+ d_json.loc[0:2, ["Grade", "Year", "Mean Scale Score"]]
  Grade  Year Mean Scale Score
0     3  2006              700
1     4  2006              699
2     5  2006              691
```

Again, this is just one approach that assumes we want a DataFrame.

R

jsonlite is one of several R packages available for importing JSON files into R. The `read_json()` function takes a JSON file and returns a list or data frame depending on the structure of the data file and its arguments. We set `simplifyVector = TRUE` so the data is simplified into a matrix.

```
> library(jsonlite)
> d_json <- read_json('data/ny_math_test.json', simplifyVector = TRUE)
```

The `d_json` object is a list with two elements: "meta" and "data". The "data" element is a matrix that contains the data of interest. The "meta" element contains the column names for the data (among much else). Notice we had to "drill down" in the list to find the column names. We assign column names to the matrix using the `colnames()` function and then convert the matrix to a data frame using the `as.data.frame()` function.

```
> colnames(d_json$data) <- d_json$meta$view$columns$fieldName
> d_json <- as.data.frame(d_json$data)
> d_json[1:3,c("grade", "year", "mean_scale_score")]
  grade year mean_scale_score
1     3 2006              700
2     4 2006              699
3     5 2006              691
```

3.4 XML

XML (e**X**tensible **M**arkup **L**anguage) is a markup language that was designed to store data. XML files are text and can be viewed in any text editor or a web browser. Because of their flexibility XML files can be quite complex in the way they store data. Therefore there is no one-size-fits-all for importing XML files into Python or R.

Python

The **pandas** library provides the `read_xml` function for importing XML files. The `ny_math_test.xml` file identifies records with nodes named "row". The 168 rows are nested in one node also called "row". Therefore we use the `xpath` argument to specify that we want to elect all row elements that are descendant of the single row element.

```
> import pandas as pd
+ d_xml = pd.read_xml('data/ny_math_test.xml', xpath="row//row")
+
+ d_xml.loc[0:2, ["grade", "year", "mean_scale_score"]]
  grade  year  mean_scale_score
0     3  2006               700
1     4  2006               699
2     5  2006               691
```

R

xml2 is a relatively small but powerful package for importing and working with XML files. The `read_xml()` function imports an XML file and returns a list of *pointers* to XML *nodes*. There are a number of ways to proceed once you import an XML file, such as using the `xml_find_all()` function to find nodes that match an xpath expression. Below we take a simple approach and convert the XML nodes into a list using the `as_list()` function that is part of the **xml2** package. Once we have the XML nodes in a list, we can use the `bind_rows()` function in the **dplyr** package to create a data frame. Notice we have to drill down into the list to select the element that contains the data. After this we need to do one more thing: *unlist* each the columns into vectors. We do this by applying the `unlist` function to each column of `d`. We save the result by assigning to `d[]`, which overwrites each element (or column) of `d` with the unlisted result.

```
> library(xml2)
> d_xml <- read_xml('data/ny_math_test.xml')
> d_list <- as_list(d_xml)
```

```
> d <- dplyr::bind_rows(d_list$response$row)
> d[] <- lapply(d, unlist)
> d[1:3,c("grade", "year", "mean_scale_score")]
# A tibble: 3 x 3
  grade year  mean_scale_score
  <chr> <chr> <chr>
1 3     2006  700
2 4     2006  699
3 5     2006  691
```

The result is a *tibble*, a tidyverse data frame. We would most likely want to proceed to converting certain columns to numeric.

3.5 Exporting/Writing/Saving data and variables

To write There are several ways to export/write/save files from Python and R. The following examples highlight some of these ways.

Python

The pandas function `to_csv()` saves a pandas DataFrame as a csv file.

```
> # pass a file name to the function
+ d.to_csv("data.csv")
```

The Python package pickle allows you to write (save) any variable from the Python environment and read (load) any variable you have written into the Python environment.

To write a variable using pickle ...

```
> import pickle
+
+ # define the file name
+ file_name = 'data.pickle'
+
+ # write the variable to the file system
+ with open(file_name, 'wb') as file_:
+     pickle.dump(d, file_, protocol=pickle.HIGHEST_PROTOCOL)
```

To read the same variable using pickle ...

```
>
+ # read the specified file from the file system and load into variable
+ with open('data.pickle', 'rb') as file_:
+     d = pickle.load(file_)
```

R

Chapter 4

Data Manipulation

This chapter looks at various strategies for modifying and deriving variables in data. Unless otherwise stated, examples are for DataFrames (Python) and data frames (R) and use the mtcars data frame that is included with R.

```
> # Python
+ import pandas
+ mtcars = pandas.read_csv('data/mtcars.csv')
```

```
> # R
> data(mtcars)
> # drop row names to match Python version of data
> rownames(mtcars) <- NULL
```

4.1 Names of variables and their types

View and inspect the names of variables and their type (numeric, string, logical, etc.) This is useful to ensure that variables have the expected type.

Python

The `.info()` function in pandas lists information on the DataFrame.

Setting the argument `verbose` to `True` prints the name of the columns, their length excluding `NULL` values, and their data type (`dtype`) in a table. The function lists the unique data types in the DataFrame, and it prints how much memory the DataFrame takes up.

```
> mtcars.info(verbose=True)
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 32 entries, 0 to 31
Data columns (total 11 columns):
 #   Column  Non-Null Count  Dtype
---  ------  --------------  -----
 0   mpg     32 non-null     float64
 1   cyl     32 non-null     int64
 2   disp    32 non-null     float64
 3   hp      32 non-null     int64
 4   drat    32 non-null     float64
 5   wt      32 non-null     float64
 6   qsec    32 non-null     float64
 7   vs      32 non-null     int64
 8   am      32 non-null     int64
 9   gear    32 non-null     int64
 10  carb    32 non-null     int64
dtypes: float64(5), int64(6)
memory usage: 2.9 KB
```

By default, the `verbose` argument is set to `False`. Then, the function lists the unique data types in the DataFrame, and it prints how much memory the DataFrame takes up. This setting excludes the table describing each column.

```
> mtcars.info()
<class 'pandas.core.frame.DataFrame'>
RangeIndex: 32 entries, 0 to 31
Data columns (total 11 columns):
 #   Column  Non-Null Count  Dtype
---  ------  --------------  -----
 0   mpg     32 non-null     float64
 1   cyl     32 non-null     int64
 2   disp    32 non-null     float64
 3   hp      32 non-null     int64
 4   drat    32 non-null     float64
 5   wt      32 non-null     float64
 6   qsec    32 non-null     float64
 7   vs      32 non-null     int64
 8   am      32 non-null     int64
 9   gear    32 non-null     int64
 10  carb    32 non-null     int64
dtypes: float64(5), int64(6)
memory usage: 2.9 KB
```

R

The `str()` function in R lists the names of the variables, their type, the first few values, and the dimensions of the data frame.

```
> str(mtcars)
'data.frame':   32 obs. of  11 variables:
 $ mpg : num  21 21 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 ...
 $ cyl : num  6 6 4 6 8 6 8 4 4 6 ...
 $ disp: num  160 160 108 258 360 ...
 $ hp  : num  110 110 93 110 175 105 245 62 95 123 ...
 $ drat: num  3.9 3.9 3.85 3.08 3.15 2.76 3.21 3.69 3.92 3.92 ...
 $ wt  : num  2.62 2.88 2.32 3.21 3.44 ...
 $ qsec: num  16.5 17 18.6 19.4 17 ...
 $ vs  : num  0 0 1 1 0 1 0 1 1 1 ...
 $ am  : num  1 1 1 0 0 0 0 0 0 0 ...
 $ gear: num  4 4 4 3 3 3 3 4 4 4 ...
 $ carb: num  4 4 1 1 2 1 4 2 2 4 ...
```

To see just the names of the data frame, use the `names()` function.

```
> names(mtcars)
 [1] "mpg"  "cyl"  "disp" "hp"   "drat" "wt"   "qsec" "vs"   "am"   "gear"
[11] "carb"
```

To see just the dimensions of the data frame, use the `dim()` function. It returns the number of rows and columns, respectively.

```
> dim(mtcars)
[1] 32 11
```

4.2 Access variables

How to work with a specific column of data.

Python

The period operator `.` provides access to a column in a DataFrame as a vector. This returns pandas series. A pandas series can do everything a numpy array can do.

```
> mtcars.mpg
0     21.0
1     21.0
2     22.8
3     21.4
4     18.7
5     18.1
6     14.3
7     24.4
8     22.8
9     19.2
10    17.8
11    16.4
12    17.3
13    15.2
14    10.4
15    10.4
16    14.7
17    32.4
18    30.4
19    33.9
20    21.5
21    15.5
22    15.2
23    13.3
24    19.2
25    27.3
26    26.0
27    30.4
28    15.8
29    19.7
30    15.0
31    21.4
Name: mpg, dtype: float64
```

Indexing also provides access to columns as a pandas Series. Single and double quotations both work.

```
> mtcars['mpg']
0     21.0
1     21.0
2     22.8
3     21.4
4     18.7
5     18.1
```

```
6     14.3
7     24.4
8     22.8
9     19.2
10    17.8
11    16.4
12    17.3
13    15.2
14    10.4
15    10.4
16    14.7
17    32.4
18    30.4
19    33.9
20    21.5
21    15.5
22    15.2
23    13.3
24    19.2
25    27.3
26    26.0
27    30.4
28    15.8
29    19.7
30    15.0
31    21.4
Name: mpg, dtype: float64
```

Operations on numpy arrays are faster than operations on pandas series. But using pandas series should be fine, in terms of performance, in many cases. This is important for large data sets on which many operations are performed. The `.values` function returns a numpy array.

```
> mtcars['mpg'].values
array([21. , 21. , 22.8, 21.4, 18.7, 18.1, 14.3, 24.4, 22.8, 19.2, 17.8,
       16.4, 17.3, 15.2, 10.4, 10.4, 14.7, 32.4, 30.4, 33.9, 21.5, 15.5,
       15.2, 13.3, 19.2, 27.3, 26. , 30.4, 15.8, 19.7, 15. , 21.4])
```

Double indexing returns a pandas DataFrame, instead of a numpy array or pandas series.

```
> mtcars[['mpg']]
    mpg
0   21.0
```

```
1   21.0
2   22.8
3   21.4
4   18.7
5   18.1
6   14.3
7   24.4
8   22.8
9   19.2
10  17.8
11  16.4
12  17.3
13  15.2
14  10.4
15  10.4
16  14.7
17  32.4
18  30.4
19  33.9
20  21.5
21  15.5
22  15.2
23  13.3
24  19.2
25  27.3
26  26.0
27  30.4
28  15.8
29  19.7
30  15.0
31  21.4
```

The `head()` and `tail()` functions return the first 5 or last 5 values. Use the `n` argument to change the number of values. This function works on numpy array, pandas series and pandas DataFrames.

```
> # first 6 values
+ mtcars.mpg.head()
0    21.0
1    21.0
2    22.8
3    21.4
4    18.7
Name: mpg, dtype: float64
```

```
> # last row of DataFrame
+ mtcars.tail(n=1)
     mpg  cyl   disp   hp  drat    wt  qsec  vs  am  gear  carb
31  21.4    4  121.0  109  4.11  2.78  18.6   1   1     4     2
```

R

The dollar sign operator, `$`, provides access to a column in a data frame as a vector.

```
> mtcars$mpg
 [1] 21.0 21.0 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 17.8 16.4 17.3 15.2 10.4
[16] 10.4 14.7 32.4 30.4 33.9 21.5 15.5 15.2 13.3 19.2 27.3 26.0 30.4 15.8 19.7
[31] 15.0 21.4
```

Double indexing brackets also provide access to columns as a vector.

```
> mtcars[["mpg"]]
 [1] 21.0 21.0 22.8 21.4 18.7 18.1 14.3 24.4 22.8 19.2 17.8 16.4 17.3 15.2 10.4
[16] 10.4 14.7 32.4 30.4 33.9 21.5 15.5 15.2 13.3 19.2 27.3 26.0 30.4 15.8 19.7
[31] 15.0 21.4
```

Single indexing brackets work as well, but return a data frame instead of a vector (if used with a data frame).

```
> mtcars["mpg"]
    mpg
1  21.0
2  21.0
3  22.8
4  21.4
5  18.7
6  18.1
7  14.3
8  24.4
9  22.8
10 19.2
11 17.8
12 16.4
13 17.3
14 15.2
15 10.4
16 10.4
17 14.7
```

```
18 32.4
19 30.4
20 33.9
21 21.5
22 15.5
23 15.2
24 13.3
25 19.2
26 27.3
27 26.0
28 30.4
29 15.8
30 19.7
31 15.0
32 21.4
```

Single indexing brackets also allow selection of rows when used with a comma. The syntax is `rows, columns`

```
> # first three rows
> mtcars[1:3, "mpg"]
[1] 21.0 21.0 22.8
```

Finally single indexing brackets allow us to select multiple columns. Request columns either by name or position using a vector.

```
> mtcars[c("mpg", "cyl")]
    mpg cyl
1  21.0   6
2  21.0   6
3  22.8   4
4  21.4   6
5  18.7   8
6  18.1   6
7  14.3   8
8  24.4   4
9  22.8   4
10 19.2   6
11 17.8   6
12 16.4   8
13 17.3   8
14 15.2   8
15 10.4   8
16 10.4   8
17 14.7   8
```

```
18 32.4   4
19 30.4   4
20 33.9   4
21 21.5   4
22 15.5   8
23 15.2   8
24 13.3   8
25 19.2   8
26 27.3   4
27 26.0   4
28 30.4   4
29 15.8   8
30 19.7   6
31 15.0   8
32 21.4   4
> # same as mtcars[1:2]
```

The `head()` and `tail()` functions return the first 6 or last 6 values. Use the `n` argument to change the number of values. They work with vectors or data frames.

```
> # first 6 values
> head(mtcars$mpg)
[1] 21.0 21.0 22.8 21.4 18.7 18.1
```

```
> # last row of data frame
> tail(mtcars, n = 1)
    mpg cyl disp  hp drat   wt qsec vs am gear carb
32 21.4   4  121 109 4.11 2.78 18.6  1  1    4    2
```

4.3 Rename variables

How to rename variables or “column headers”.

Python

Column names can be chnaged using the function `.rename()`. Below, we change the column names “cyl” and “wt” to “cylinder” and “WT”, respectively.

```
> mtcars.rename(columns={"cyl":"cylinder", "wt":"WT"})
     mpg  cylinder   disp   hp  drat     WT   qsec  vs  am  gear  carb
0   21.0         6  160.0  110  3.90  2.620  16.46   0   1     4     4
```

```
1   21.0         6  160.0  110  3.90  2.875  17.02  0  1   4   4
2   22.8         4  108.0   93  3.85  2.320  18.61  1  1   4   1
3   21.4         6  258.0  110  3.08  3.215  19.44  1  0   3   1
4   18.7         8  360.0  175  3.15  3.440  17.02  0  0   3   2
5   18.1         6  225.0  105  2.76  3.460  20.22  1  0   3   1
6   14.3         8  360.0  245  3.21  3.570  15.84  0  0   3   4
7   24.4         4  146.7   62  3.69  3.190  20.00  1  0   4   2
8   22.8         4  140.8   95  3.92  3.150  22.90  1  0   4   2
9   19.2         6  167.6  123  3.92  3.440  18.30  1  0   4   4
10  17.8         6  167.6  123  3.92  3.440  18.90  1  0   4   4
11  16.4         8  275.8  180  3.07  4.070  17.40  0  0   3   3
12  17.3         8  275.8  180  3.07  3.730  17.60  0  0   3   3
13  15.2         8  275.8  180  3.07  3.780  18.00  0  0   3   3
14  10.4         8  472.0  205  2.93  5.250  17.98  0  0   3   4
15  10.4         8  460.0  215  3.00  5.424  17.82  0  0   3   4
16  14.7         8  440.0  230  3.23  5.345  17.42  0  0   3   4
17  32.4         4   78.7   66  4.08  2.200  19.47  1  1   4   1
18  30.4         4   75.7   52  4.93  1.615  18.52  1  1   4   2
19  33.9         4   71.1   65  4.22  1.835  19.90  1  1   4   1
20  21.5         4  120.1   97  3.70  2.465  20.01  1  0   3   1
21  15.5         8  318.0  150  2.76  3.520  16.87  0  0   3   2
22  15.2         8  304.0  150  3.15  3.435  17.30  0  0   3   2
23  13.3         8  350.0  245  3.73  3.840  15.41  0  0   3   4
24  19.2         8  400.0  175  3.08  3.845  17.05  0  0   3   2
25  27.3         4   79.0   66  4.08  1.935  18.90  1  1   4   1
26  26.0         4  120.3   91  4.43  2.140  16.70  0  1   5   2
27  30.4         4   95.1  113  3.77  1.513  16.90  1  1   5   2
28  15.8         8  351.0  264  4.22  3.170  14.50  0  1   5   4
29  19.7         6  145.0  175  3.62  2.770  15.50  0  1   5   6
30  15.0         8  301.0  335  3.54  3.570  14.60  0  1   5   8
31  21.4         4  121.0  109  4.11  2.780  18.60  1  1   4   2
```

Alternatively, column names can be changed by replacing the vector of column names with a new vector. Below, we create a vector of columns that replaces "drat" with "axle_ratio" using conditional match and indexing and "disp" with "DISP" using indexing.

```
> column_names = mtcars.columns.values
+
+ # using conditional match
+ column_names[column_names == "drat"] = "axle_ratio"
+
+ # using indexing
+ column_names[2] = "DISP"
+
```

```
+ mtcars.columns = column_names
+ mtcars.columns
Index(['mpg', 'cyl', 'DISP', 'hp', 'axle_ratio', 'wt', 'qsec', 'vs', 'am',
       'gear', 'carb'],
      dtype='object')
```

You can

R

Variable names can be changed by their index (ie, order of columns in the data frame). Below the second column is "cyl". We change the name to "cylinder".

```
> names(mtcars)[2]
[1] "cyl"
> names(mtcars)[2] <- "cylinders"
> names(mtcars)
 [1] "mpg"       "cylinders" "disp"      "hp"        "drat"      "wt"
 [7] "qsec"      "vs"        "am"        "gear"      "carb"
```

Variable names can also be changed by conditional match. Below we find the variable name that matches "drat" and change to "axle_ratio".

```
> names(mtcars)[names(mtcars) == "drat"]
[1] "drat"
> names(mtcars)[names(mtcars) == "drat"] <- "axle_ratio"
> names(mtcars)
 [1] "mpg"        "cylinders"  "disp"       "hp"         "axle_ratio"
 [6] "wt"         "qsec"       "vs"         "am"         "gear"
[11] "carb"
```

More than one variable name can be changed using a vector of positions or matches.

```
> names(mtcars)[c(6,8)] <- c("weight", "engine")
>
> # or
> # names(mtcars)[names(mtcars) %in% c("wt", "vs")] <- c("weight", "engine")
>
> names(mtcars)
 [1] "mpg"        "cylinders"  "disp"       "hp"         "axle_ratio"
 [6] "weight"     "qsec"       "engine"     "am"         "gear"
[11] "carb"
```

See also the `rename()` function in the **dplyr** package.

4.4 Create, replace and remove variables

We often need to create variables that are functions of other variables, or replace existing variables with an updated version.

Python

Adding a new variable using the indexing notation and assigning a result adds a new column.

```
> # add column for Kilometer per liter
+ mtcars['kpl'] = mtcars.mpg/2.352
```

Doing the same with an *existing* column name updates the values in a column.

```
> # update to liters per 100 Kilometers
+ mtcars['kpl'] = 100/mtcars.kpl
```

Alternatively, the `.` notation can be used to update the values in a column.

```
> # update to liters per 50 Kilometers
+ mtcars.kpl = 50/mtcars.kpl
```

To remove a column, use the `.drop()` function.

```
> # drop the kpl variable
+ mtcars.drop(columns=['kpl'])
     mpg  cyl   DISP   hp  axle_ratio     wt   qsec  vs  am  gear  carb
0   21.0    6  160.0  110        3.90  2.620  16.46   0   1     4     4
1   21.0    6  160.0  110        3.90  2.875  17.02   0   1     4     4
2   22.8    4  108.0   93        3.85  2.320  18.61   1   1     4     1
3   21.4    6  258.0  110        3.08  3.215  19.44   1   0     3     1
4   18.7    8  360.0  175        3.15  3.440  17.02   0   0     3     2
5   18.1    6  225.0  105        2.76  3.460  20.22   1   0     3     1
6   14.3    8  360.0  245        3.21  3.570  15.84   0   0     3     4
7   24.4    4  146.7   62        3.69  3.190  20.00   1   0     4     2
8   22.8    4  140.8   95        3.92  3.150  22.90   1   0     4     2
9   19.2    6  167.6  123        3.92  3.440  18.30   1   0     4     4
10  17.8    6  167.6  123        3.92  3.440  18.90   1   0     4     4
11  16.4    8  275.8  180        3.07  4.070  17.40   0   0     3     3
12  17.3    8  275.8  180        3.07  3.730  17.60   0   0     3     3
13  15.2    8  275.8  180        3.07  3.780  18.00   0   0     3     3
14  10.4    8  472.0  205        2.93  5.250  17.98   0   0     3     4
```

```
15  10.4    8  460.0  215        3.00  5.424  17.82  0   0     3     4
16  14.7    8  440.0  230        3.23  5.345  17.42  0   0     3     4
17  32.4    4   78.7   66        4.08  2.200  19.47  1   1     4     1
18  30.4    4   75.7   52        4.93  1.615  18.52  1   1     4     2
19  33.9    4   71.1   65        4.22  1.835  19.90  1   1     4     1
20  21.5    4  120.1   97        3.70  2.465  20.01  1   0     3     1
21  15.5    8  318.0  150        2.76  3.520  16.87  0   0     3     2
22  15.2    8  304.0  150        3.15  3.435  17.30  0   0     3     2
23  13.3    8  350.0  245        3.73  3.840  15.41  0   0     3     4
24  19.2    8  400.0  175        3.08  3.845  17.05  0   0     3     2
25  27.3    4   79.0   66        4.08  1.935  18.90  1   1     4     1
26  26.0    4  120.3   91        4.43  2.140  16.70  0   1     5     2
27  30.4    4   95.1  113        3.77  1.513  16.90  1   1     5     2
28  15.8    8  351.0  264        4.22  3.170  14.50  0   1     5     4
29  19.7    6  145.0  175        3.62  2.770  15.50  0   1     5     6
30  15.0    8  301.0  335        3.54  3.570  14.60  0   1     5     8
31  21.4    4  121.0  109        4.11  2.780  18.60  1   1     4     2
```

R

Adding a new variable name after the dollar sign notation and assigning a result adds a new column.

```
> # add column for Kilometer per liter
> mtcars$kpl <- mtcars$mpg/2.352
```

Doing the same with an *existing* variable updates the values in a column.

```
> # update to liters per 100 Kilometers
> mtcars$kpl <- 100/mtcars$kpl
```

To remove a variable, assign it `NULL`.

```
> # drop the kpl variable
> mtcars$kpl <- NULL
```

4.5 Create strings from numbers

You may have data that is numeric but that needs to be treated as a string.

Python

You can change the data type of a column in a DataFrame using the `astype` function.

```
> mtcars['am'] = mtcars['am'].astype(str)
+ type(mtcars.am[0]) # check the type of the first item in 'am' column
<class 'str'>
```

R

The `as.character()` function takes a vector and converts it to string format.

```
> head(mtcars$am)
[1] 1 1 1 0 0 0
> head(as.character(mtcars$am))
[1] "1" "1" "1" "0" "0" "0"
```

Note we just demonstrated conversion. To save the conversion we need to *assign* the result to the data frame.

```
> # add new string variable am_ch
> mtcars$am_ch <- as.character(mtcars$am)
> head(mtcars$am_ch)
[1] "1" "1" "1" "0" "0" "0"
```

The `factor()` function can also be used to convert a numeric vector into a categorical variable. The result is not exactly a string, however. A factor is made of integers with character labels. Factors are useful for character data that have a fixed set of levels (eg, "grade 1", grade 2", etc)

```
> # convert to factor
> head(mtcars$am)
[1] 1 1 1 0 0 0
> head(factor(mtcars$am))
[1] 1 1 1 0 0 0
Levels: 0 1
>
> # convert to factor with labels
> head(factor(mtcars$am, labels = c("automatic", "manual")))
[1] manual    manual    manual    automatic automatic automatic
Levels: automatic manual
```

Again we just demonstrated factor conversion. To save the conversion we need to assign to the data frame.

```
> # create factor variable am_fac
> mtcars$am_fac <- factor(mtcars$am, labels = c("automatic", "manual"))
> head(mtcars$am_fac)
[1] manual    manual    manual    automatic automatic automatic
Levels: automatic manual
```

TODO: add zip code conversion using `str_pad()` (or base R option?)

4.6 Create numbers from strings

String variables that ought to be numbers usually have some character data in the values such as units (eg, "4 cm"). To create numbers from strings it's important to remove any character data that cannot be converted to a number.

Python

The `astype(float)` or `astype(int)` function will coerce strings to numerical representation.

For demonstration, let's say we have the following numpy array.

```
> import numpy as np
+ weight = np.array(["125 lbs.", "132 lbs.", "156 lbs."])
```

The `astype(float)` function throws an error due to the presence of strings. The `astype()` function is for numpy arrays.

```
> try:
+   weight.astype(float)
+ except ValueError:
+   print("ValueError: could not convert string to float: '125 lbs.'")
ValueError: could not convert string to float: '125 lbs.'
```

One way to approach this is to first remove the strings from the objects and then use `astype(float)`. Below we use the `strip()` function to find " lbs." using a list comprehension.

```
> # [] indicates a list in python
+ # np.array() changes the list back into an array
+ weight = np.array([w.strip(" lbs.") for w in weight])
```

Now we can use the `astype()` function to change the elements in weight from `str` to `float`.

```
> weight.astype(float)
array([125., 132., 156.])
```

R

The `as.numeric()` function will attempt to coerce strings to numeric type *if possible*. Any non-numeric values are coerced to NA.

For demonstration, let's say we have the following vector.

```
> weight <- c("125 lbs.", "132 lbs.", "156 lbs.")
```

The `as.numeric()` function returns all NA due to presence of character data.

```
> as.numeric(weight)
Warning: NAs introduced by coercion
[1] NA NA NA
```

There are many ways to approach this. A common approach is to first remove the characters and then use `as.numeric()`. Below we use the `sub` function to find "lbs." and replace with nothing.

```
> weightN <- gsub("lbs.", "", weight)
> as.numeric(weightN)
[1] 125 132 156
```

The `parse_number()` function in the **readr** package can often take care of these situations automatically.

```
> readr::parse_number(weight)
[1] 125 132 156
```

4.7 Change case

How to change the case of strings. The most common case transformations are lower case, upper case, and title case.

Python

The `lower()`, `upper()`, and `title()` functions convert case to lower, upper, and title, respectively. We can use a list comprehension to apply these functions to each string in a list.

```
> col_names = [col.upper() for col in mtcars.columns]
+ mtcars.columns = col_names
```

R

The `tolower()` and `toupper()` functions convert case to lower and upper, respectively.

```
> names(mtcars) <- toupper(names(mtcars))
> names(mtcars)
 [1] "MPG"          "CYLINDERS"  "DISP"         "HP"           "AXLE_RATIO"
 [6] "WEIGHT"       "QSEC"       "ENGINE"       "AM"           "GEAR"
[11] "CARB"         "AM_CH"      "AM_FAC"
```

```
> names(mtcars) <- tolower(names(mtcars))
> names(mtcars)
 [1] "mpg"          "cylinders"  "disp"         "hp"           "axle_ratio"
 [6] "weight"       "qsec"       "engine"       "am"           "gear"
[11] "carb"         "am_ch"      "am_fac"
```

The **stringr** package provides a convenient title case conversion function, `str_to_title()`, which capitalizes the first letter of each string.

```
> stringr::str_to_title(names(mtcars))
 [1] "Mpg"          "Cylinders"  "Disp"         "Hp"           "Axle_ratio"
 [6] "Weight"       "Qsec"       "Engine"       "Am"           "Gear"
[11] "Carb"         "Am_ch"      "Am_fac"
```

4.8 Drop duplicate rows

How to find and drop duplicate elements.

Python

The `duplicated()` function determines which rows of a DataFrame are duplicates of previous rows.

First, we create a DataFrame with a duplicate row by using the pandas `concat()` function. `concat()` combines DataFrames by rows or columns, row by default.

```
> # create DataFrame with duplicate rows
+ import pandas as pd
+ mtcars2 = pd.concat([mtcars.iloc[0:3,0:6], mtcars.iloc[0:1,0:6]])
```

The `duplicated()` function returns a logical vector. TRUE indicates a row is a duplicate of a previous row.

```
> # create DataFrame with duplicate rows
+ mtcars2.duplicated()
0    False
1    False
2    False
0     True
dtype: bool
```

R

The `duplicated()` function "determines which elements of a vector or data frame are duplicates of elements with smaller subscripts". (from `?duplicated`)

```
> # create data frame with duplicate rows
> mtcars2 <- rbind(mtcars[1:3,1:6], mtcars[1,1:6])
> # last row is duplicate of first
> mtcars2
   mpg cylinders disp  hp axle_ratio weight
1 21.0         6  160 110       3.90  2.620
2 21.0         6  160 110       3.90  2.875
3 22.8         4  108  93       3.85  2.320
4 21.0         6  160 110       3.90  2.620
```

The `duplicated()` function returns a logical vector. TRUE indicates a row is a duplicate of a previous row.

```
> # last row is duplicate
> duplicated(mtcars2)
[1] FALSE FALSE FALSE  TRUE
```

The TRUE/FALSE vector can be used to extract or drop duplicate rows. Since TRUE in indexing brackets will keep a row, we can use `!` to negate the logicals and keep those that are "NOT TRUE"

```
> # drop the duplicate and update the data frame
> mtcars3 <- mtcars2[!duplicated(mtcars2),]
> mtcars3
   mpg cylinders disp  hp axle_ratio weight
1 21.0         6  160 110       3.90  2.620
2 21.0         6  160 110       3.90  2.875
3 22.8         4  108  93       3.85  2.320
```

```
> # extract and investigate the duplicate row
> mtcars2[duplicated(mtcars2),]
  mpg cylinders disp  hp axle_ratio weight
4  21         6  160 110        3.9   2.62
```

The anyDuplicated() function returns the row number of duplicate rows.

```
> anyDuplicated(mtcars2)
[1] 4
```

4.9 Randomly sample rows

How to take a random sample of rows from a data frame. The sample is usually either a fixed size or a proportion.

Python

The pandas package provide a function for taking a sample of fixed size or a proportion. To sample with replacement, set `replace = TRUE`.

Additionally, the random sample will change every time the code is run. To always generate the same "random" sample, set `random_state` to any positive integer.

To create a sample with a fixed number of rows, use the `n` argument.

```
> # sample 5 rows from mtcars
+ mtcars.sample(n=5, replace=True)
     MPG  CYL   DISP   HP  AXLE_RATIO  ...  VS  AM  GEAR CARB        KPL
10  17.8    6  167.6  123        3.92  ...   1   0     4    4  3.784014
26  26.0    4  120.3   91        4.43  ...   0   1     5    2  5.527211
19  33.9    4   71.1   65        4.22  ...   1   1     4    1  7.206633
11  16.4    8  275.8  180        3.07  ...   0   0     3    3  3.486395
20  21.5    4  120.1   97        3.70  ...   1   0     3    1  4.570578

[5 rows x 12 columns]
```

To create a sample of a proportion, use the `frac` argument.

```
> # sample 20% of rows from mtcars
+ mtcars.sample(frac = 0.20, random_state=1)
     MPG  CYL   DISP   HP  AXLE_RATIO  ...  VS  AM  GEAR CARB       KPL
27  30.4    4   95.1  113        3.77  ...   1   1     5    2  6.462585
3   21.4    6  258.0  110        3.08  ...   1   0     3    1  4.549320
22  15.2    8  304.0  150        3.15  ...   0   0     3    2  3.231293
18  30.4    4   75.7   52        4.93  ...   1   1     4    2  6.462585
23  13.3    8  350.0  245        3.73  ...   0   0     3    4  2.827381
17  32.4    4   78.7   66        4.08  ...   1   1     4    1  6.887755

[6 rows x 12 columns]
```

The numpy function `random.choice()` in combination with the `loc()` function can be used to sample from a DataFrame.

The `random.choice()` function creates a random sample according to the given parameters. The `loc()` function is used to access rows and columns by index.

```
> # import the numpy package
+ import numpy as np
+
+ # create a random sample of size 5 with replacement
+ random_sample = np.random.choice(len(mtcars), (5,), replace=True)
+
+ # use random_sample to sample from mtcars
+ mtcars.loc[random_sample,]
     MPG  CYL   DISP   HP  AXLE_RATIO    WT   QSEC  VS  AM  GEAR  CARB       KPL
30  15.0    8  301.0  335        3.54  3.57  14.60   0   1     5     8  3.188776
10  17.8    6  167.6  123        3.92  3.44  18.90   1   0     4     4  3.784014
26  26.0    4  120.3   91        4.43  2.14  16.70   0   1     5     2  5.527211
10  17.8    6  167.6  123        3.92  3.44  18.90   1   0     4     4  3.784014
4   18.7    8  360.0  175        3.15  3.44  17.02   0   0     3     2  3.975340
```

The random sample will change every time the code is run. To always generate the same "random" sample, use the `random.seed()` function with any positive integer.

```
> # setting seed to always get same random sample
+ np.random.seed(123)
+
+ # create a random sample of size 5 with replacement
+ sample = np.random.choice(len(mtcars), (5,), replace=True)
+ mtcars.loc[sample,]
     MPG  CYL   DISP   HP  AXLE_RATIO    WT   QSEC  VS  AM  GEAR  CARB       KPL
```

```
30   15.0     8  301.0  335        3.54  3.57  14.60  0  1     5     8  3.188776
13   15.2     8  275.8  180        3.07  3.78  18.00  0  0     3     3  3.231293
30   15.0     8  301.0  335        3.54  3.57  14.60  0  1     5     8  3.188776
2    22.8     4  108.0   93        3.85  2.32  18.61  1  1     4     1  4.846939
28   15.8     8  351.0  264        4.22  3.17  14.50  0  1     5     4  3.358844
```

R

There are many ways to sample rows from a data frame in R. The **dplyr** package provides a convenience function, `slice_sample()`, for taking either a fixed sample size or a proportion.

```
> # sample 5 rows from mtcars
> dplyr::slice_sample(mtcars, n = 5)
   mpg cylinders  disp  hp axle_ratio weight  qsec engine am gear carb am_ch
1 19.2         8 400.0 175       3.08  3.845 17.05      0  0    3    2     0
2 17.3         8 275.8 180       3.07  3.730 17.60      0  0    3    3     0
3 21.4         4 121.0 109       4.11  2.780 18.60      1  1    4    2     1
4 18.1         6 225.0 105       2.76  3.460 20.22      1  0    3    1     0
5 18.7         8 360.0 175       3.15  3.440 17.02      0  0    3    2     0
     am_fac
1 automatic
2 automatic
3    manual
4 automatic
5 automatic
>
> # sample 20% of rows from mtcars
> dplyr::slice_sample(mtcars, prop = 0.20)
   mpg cylinders  disp  hp axle_ratio weight  qsec engine am gear carb am_ch
1 10.4         8 472.0 205       2.93  5.250 17.98      0  0    3    4     0
2 15.2         8 304.0 150       3.15  3.435 17.30      0  0    3    2     0
3 10.4         8 460.0 215       3.00  5.424 17.82      0  0    3    4     0
4 30.4         4  95.1 113       3.77  1.513 16.90      1  1    5    2     1
5 15.0         8 301.0 335       3.54  3.570 14.60      0  1    5    8     1
6 21.5         4 120.1  97       3.70  2.465 20.01      1  0    3    1     0
     am_fac
1 automatic
2 automatic
3 automatic
4    manual
5    manual
6 automatic
```

To sample with replacement, set `replace = TRUE`.

The base R functions `sample()` and `runif()` can be combined to sample sizes or approximate proportions.

```
> # sample 5 rows from mtcars
> # get random row numbers
> i <- sample(nrow(mtcars), size = 5)
> # use i to select rows
> mtcars[i,]
    mpg cylinders  disp  hp axle_ratio weight  qsec engine am gear carb am_ch
25 19.2         8 400.0 175       3.08  3.845 17.05      0  0    3    2     0
16 10.4         8 460.0 215       3.00  5.424 17.82      0  0    3    4     0
2  21.0         6 160.0 110       3.90  2.875 17.02      0  1    4    4     1
4  21.4         6 258.0 110       3.08  3.215 19.44      1  0    3    1     0
9  22.8         4 140.8  95       3.92  3.150 22.90      1  0    4    2     0
      am_fac
25 automatic
16 automatic
2     manual
4  automatic
9  automatic
```

```
> # sample about 20% of rows from mtcars
> # generate random values on range of [0,1]
> i <- runif(nrow(mtcars))
> # use i < 0.20 logical vector to
> # select rows that correspond to TRUE
> mtcars[i < 0.20,]
    mpg cylinders  disp  hp axle_ratio weight  qsec engine am gear carb am_ch
1  21.0         6 160.0 110       3.90  2.620 16.46      0  1    4    4     1
2  21.0         6 160.0 110       3.90  2.875 17.02      0  1    4    4     1
7  14.3         8 360.0 245       3.21  3.570 15.84      0  0    3    4     0
11 17.8         6 167.6 123       3.92  3.440 18.90      1  0    4    4     0
22 15.5         8 318.0 150       2.76  3.520 16.87      0  0    3    2     0
28 30.4         4  95.1 113       3.77  1.513 16.90      1  1    5    2     1
      am_fac
1     manual
2     manual
7  automatic
11 automatic
22 automatic
28    manual
```

The random sample will change every time the code is run. To always generate the same “random” sample, use the `set.seed()` function with any positive integer.

```
> # always get the same random sample
> set.seed(123)
> i <- runif(nrow(mtcars))
> mtcars[i < 0.20,]
    mpg cylinders  disp  hp axle_ratio weight  qsec engine am gear carb am_ch
6  18.1         6 225.0 105       2.76   3.46 20.22      1  0    3    1     0
15 10.4         8 472.0 205       2.93   5.25 17.98      0  0    3    4     0
18 32.4         4  78.7  66       4.08   2.20 19.47      1  1    4    1     1
30 19.7         6 145.0 175       3.62   2.77 15.50      0  1    5    6     1
      am_fac
6  automatic
15 automatic
18    manual
30    manual
```

Chapter 5

Combine, Reshape and Merge

This chapter looks at various strategies for combining, reshaping, and merging data.

5.1 Combine rows

Combining rows may be thought of as "stacking" rectangular data structures.

Python

R

The `rbind()` function "binds" rows. It takes two or more objects. To row bind data frames the column names must match, otherwise an error is returned. If columns being stacked have differing variable types, the values will be coerced according to `logical` < `integer` < `double` < `complex` < `character`. (E.g., if you stack a set of rows with type `logical` in column J on a set of rows with type `character` in column J, the output will have column J as type `character`.)

```
> d1 <- data.frame(x = 4:6, y = letters[1:3])
> d2 <- data.frame(x = 3:1, y = letters[4:6])
> rbind(d1, d2)
  x y
1 4 a
2 5 b
```

```
3 6 c
4 3 d
5 2 e
6 1 f
```

See also the `bind_rows()` function in the **dplyr** package.

5.2 Combine columns

Combining columns may be thought of as setting rectangular data structures next to each other.

Python

R

The `cbind()` function "binds" columns. It takes two or more objects. To column bind data frames, the number of rows must match; otherwise, the object with fewer rows will have rows "recycled" (if possible) or an error will be returned.

```
> d1 <- data.frame(x = 10:13, y = letters[1:4])
> d2 <- data.frame(x = c(23,34,45,44))
> cbind(d1, d2)
   x y  x
1 10 a 23
2 11 b 34
3 12 c 45
4 13 d 44
```

```
> # example of recycled rows (d1 is repeated twice)
> d1 <- data.frame(x = 10:13, y = letters[1:4])
> d2 <- data.frame(x = c(23,34,45,44,99,99,99,99))
> cbind(d1, d2)
   x y  x
1 10 a 23
2 11 b 34
3 12 c 45
4 13 d 44
5 10 a 99
6 11 b 99
7 12 c 99
8 13 d 99
```

See also the `bind_cols()` function in the **dplyr** package.

5.3 Reshaping data

The next two sections discuss how to reshape data from wide to long and from long to wide. "Wide" data are structured such that multiple values associated with a given unit (e.g., a person, a cell culture, etc.) are placed in the same row:

```
   name time_1_score time_2_score
1 larry            3            0
2   moe            6            3
3 curly            2            1
```

Long data, conversely, are structured such that all values are contained in one column, with another column identifying what value is given in any particular row ("time 1," "time 2," etc.):

```
     id time score
1 larry    1     3
2 larry    2     0
3   moe    1     6
4   moe    2     3
5 curly    1     2
6 curly    2     1
```

Shifting between these two data formats is often necessary for implementing certain statistical techniques or representing data with particular visualizations.

5.3.1 Wide to long

Python

R

In base R, the `reshape()` function can take data from wide to long or long to wide. The **tidyverse** also provides reshaping functions: `pivot_longer()` and `pivot_wider()`. The **tidyverse** functions have a degree of intuitiveness and usability that may make them the go-to reshaping tools for many R users. We give examples below using both base R and **tidyverse**.

Say we begin with a wide data frame, `df_wide`, that looks like this:

```
  id sex wk1 wk2 wk3
1  1   m  16   7  15
2  2   m  12  19  10
3  3   f   8  15   7
```

To lengthen a data frame using `reshape()`, a user provides arguments specifying the columns that identify values' origins (person, cell culture, etc.), the columns containing values to be lengthened, and the desired names for output columns in long data:

```
> df_long <- reshape(df_wide,
+                          direction = 'long',
+                          idvar = c('id', 'sex'), # column(s) that uniquely identifies,
+                          varying = c('wk1', 'wk2', 'wk3'), # variables that contain th
+                          v.names = 'val', # desired name of column in long data that c
+                          timevar = 'week') # desired name of column in long data that
> df_long
      id sex week val
1.m.1  1   m    1  16
2.m.1  2   m    1  12
3.f.1  3   f    1   8
1.m.2  1   m    2   7
2.m.2  2   m    2  19
3.f.2  3   f    2  15
1.m.3  1   m    3  15
2.m.3  2   m    3  10
3.f.3  3   f    3   7
```

The **tidyverse** function for taking data from wide to long is `pivot_longer()`. To lengthen `df_wide` using `pivot_longer()`, a user would write:

```
> library(tidyverse)
> df_long_PL <- pivot_longer(df_wide,
+                               cols = -c('id', 'sex'), # columns that contain the value
+                               names_to = 'week', # desired name of column in long data
+                               values_to = 'val') # desired name of column in long data
> df_long_PL
# A tibble: 9 x 4
     id sex   week    val
  <int> <chr> <chr> <int>
1     1 m     wk1      16
2     1 m     wk2       7
3     1 m     wk3      15
4     2 m     wk1      12
5     2 m     wk2      19
6     2 m     wk3      10
7     3 f     wk1       8
8     3 f     wk2      15
9     3 f     wk3       7
```

`pivot_longer()` is particularly useful (a) when dealing with wide data that contain multiple sets of repeated measures in each row that need to be lengthened separately (e.g., two monthly height measurements and two monthly weight measurements for each person) and (b) when column names and/or column values in the long data need to be extracted from column names of the wide data using regular expressions.

For example, say we begin with a wide data frame, `animals_wide`, in which every row contains two values for each of two different measures:

```
     animal lives_in_water jan_playfulness feb_playfulness jan_excitement
1   dolphin           TRUE             6.0             5.5            7.0
2 porcupine          FALSE             3.5             4.5            3.5
3  capybara          FALSE             4.0             5.0            4.0
  feb_excitement
1            7.0
2            3.5
3            4.0
```

`pivot_longer()` can be used to convert this data frame to a long format where there is one column for each of the measures, playfulness and excitement:

```
> animals_long_1 <- pivot_longer(animals_wide,
+                               cols = -c('animal', 'lives_in_water'),
+                               names_to = c('month', '.value'), # ".value" is placeholder for str
+                               names_pattern = '(.+)_(.+)') # specify structure of wide column na
> animals_long_1
# A tibble: 6 x 5
  animal    lives_in_water month playfulness excitement
  <chr>     <lgl>          <chr>       <dbl>      <dbl>
1 dolphin   TRUE           jan           6          7
2 dolphin   TRUE           feb           5.5        7
3 porcupine FALSE          jan           3.5        3.5
4 porcupine FALSE          feb           4.5        3.5
5 capybara  FALSE          jan           4          4
6 capybara  FALSE          feb           5          4
```

Alternatively, `pivot_longer()` can be used to convert this data frame to a long format where there is one column containing all the playfulness and excitement values:

```
> animals_long_2 <- pivot_longer(animals_wide,
+                                 cols = -c('animal', 'lives_in_water'),
+                                 names_to = c('month', 'measure'),
+                                 names_pattern = '(.+)_(.+)',
+                                 values_to = 'val')
```

```
> animals_long_2
# A tibble: 12 x 5
   animal    lives_in_water month measure       val
   <chr>     <lgl>          <chr> <chr>       <dbl>
 1 dolphin   TRUE           jan   playfulness   6
 2 dolphin   TRUE           feb   playfulness   5.5
 3 dolphin   TRUE           jan   excitement    7
 4 dolphin   TRUE           feb   excitement    7
 5 porcupine FALSE          jan   playfulness   3.5
 6 porcupine FALSE          feb   playfulness   4.5
 7 porcupine FALSE          jan   excitement    3.5
 8 porcupine FALSE          feb   excitement    3.5
 9 capybara  FALSE          jan   playfulness   4
10 capybara  FALSE          feb   playfulness   5
11 capybara  FALSE          jan   excitement    4
12 capybara  FALSE          feb   excitement    4
```

5.3.2 Long to wide

Python

R

Say we begin with a long data frame, `df_long`, that looks like this:

```
> df_long
      id sex week val
1.m.1  1   m    1  16
2.m.1  2   m    1  12
3.f.1  3   f    1   8
1.m.2  1   m    2   7
2.m.2  2   m    2  19
3.f.2  3   f    2  15
1.m.3  1   m    3  15
2.m.3  2   m    3  10
3.f.3  3   f    3   7
```

To take data from long to wide with base R's `reshape()`, a user would write:

```
> df_wide <- reshape(df_long,
+                    direction = 'wide',
+                    idvar = c('id', 'sex'), # column(s) that determine which rows sho
+                    v.names = 'val', # column containing values to widen
+                    timevar = 'week', # column from which resulting wide column names
```

```
+                     sep = '_') # the `sep` argument allows a user to specify how the contents oj
> df_wide
      id sex val_1 val_2 val_3
1.m.1  1   m    16     7    15
2.m.1  2   m    12    19    10
3.f.1  3   f     8    15     7
```

The **tidyverse** function for taking data from long to wide is `pivot_wider()`. To widen `df_long` using `pivot_longer()`, a user would write:

```
> library(tidyverse)
> df_wide_PW <- pivot_wider(df_long,
+                           id_cols = c('id', 'sex'),
+                           values_from = 'val',
+                           names_from = 'week',
+                           names_prefix = 'week_') # `names_prefix` specifies a string to paste
> df_wide_PW
# A tibble: 3 x 5
     id sex   week_1 week_2 week_3
  <int> <chr>  <int>  <int>  <int>
1     1 m         16      7     15
2     2 m         12     19     10
3     3 f          8     15      7
```

`pivot_wider()` offers a lot of usability when widening relatively complicated long data structures. For example, say we want to widen both of the long versions of the animals data frame created above.

To widen the version of the long data that has a column for each of the measures (playfulness and excitement):

```
> animals_long_1
# A tibble: 6 x 5
  animal    lives_in_water month playfulness excitement
  <chr>     <lgl>          <chr>       <dbl>      <dbl>
1 dolphin   TRUE           jan           6          7
2 dolphin   TRUE           feb           5.5        7
3 porcupine FALSE          jan           3.5        3.5
4 porcupine FALSE          feb           4.5        3.5
5 capybara  FALSE          jan           4          4
6 capybara  FALSE          feb           5          4
> animals_wide <- pivot_wider(animals_long_1,
+                             id_cols = c('animal', 'lives_in_water'),
+                             values_from = c('playfulness', 'excitement'),
+                             names_from = 'month',
```

```
+                              names_glue = '{month}_{.value}') # `names_glue` allow fo
> animals_wide
# A tibble: 3 x 6
  animal    lives_in_water jan_playfulness feb_playfulness jan_excitement
  <chr>     <lgl>                    <dbl>           <dbl>          <dbl>
1 dolphin   TRUE                       6               5.5            7
2 porcupine FALSE                      3.5             4.5            3.5
3 capybara  FALSE                      4               5              4
# ... with 1 more variable: feb_excitement <dbl>
```

To widen the version of the long data that has one column containing all the values of playfulness and excitement together:

```
> animals_long_2
# A tibble: 12 x 5
   animal    lives_in_water month measure       val
   <chr>     <lgl>          <chr> <chr>       <dbl>
 1 dolphin   TRUE           jan   playfulness   6
 2 dolphin   TRUE           feb   playfulness   5.5
 3 dolphin   TRUE           jan   excitement    7
 4 dolphin   TRUE           feb   excitement    7
 5 porcupine FALSE          jan   playfulness   3.5
 6 porcupine FALSE          feb   playfulness   4.5
 7 porcupine FALSE          jan   excitement    3.5
 8 porcupine FALSE          feb   excitement    3.5
 9 capybara  FALSE          jan   playfulness   4
10 capybara  FALSE          feb   playfulness   5
11 capybara  FALSE          jan   excitement    4
12 capybara  FALSE          feb   excitement    4
> animals_wide <- pivot_wider(animals_long_2,
+                              id_cols = c('animal', 'lives_in_water'),
+                              values_from = 'val',
+                              names_from = c('month', 'measure'),
+                              names_sep = '_')
> animals_wide
# A tibble: 3 x 6
  animal    lives_in_water jan_playfulness feb_playfulness jan_excitement
  <chr>     <lgl>                    <dbl>           <dbl>          <dbl>
1 dolphin   TRUE                       6               5.5            7
2 porcupine FALSE                      3.5             4.5            3.5
3 capybara  FALSE                      4               5              4
# ... with 1 more variable: feb_excitement <dbl>
```

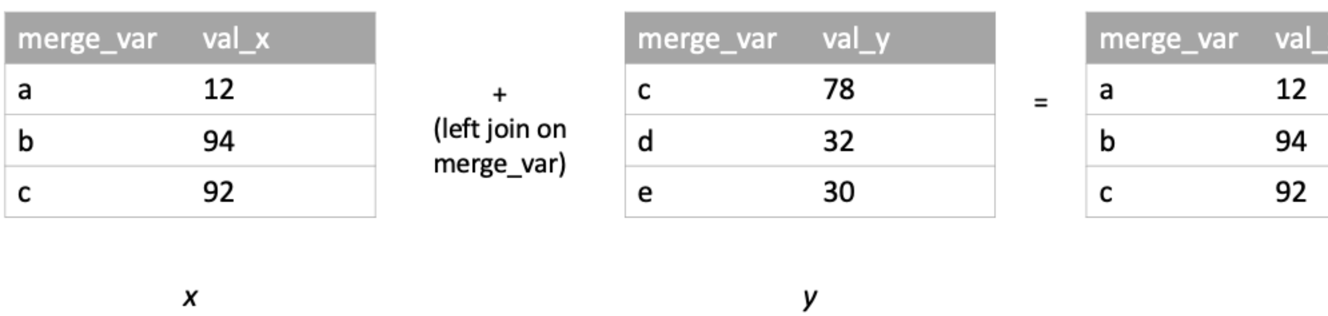
5.4 Merge/Join

The merge/join examples below all make use of the following sample data frames:

```
> # x
> x
  merge_var val_x
1         a    12
2         b    94
3         c    92
> # y
> y
  merge_var val_y
1         c    78
2         d    32
3         e    30
```

5.4.1 Left Join

A left join of x and y keeps all rows of x and merges rows of y into x where possible based on the merge criterion:



Python

```
> import pandas as pd
+ pd.merge(x, y, how = 'left')
  merge_var  val_x  val_y
0         a   12.0    NaN
```

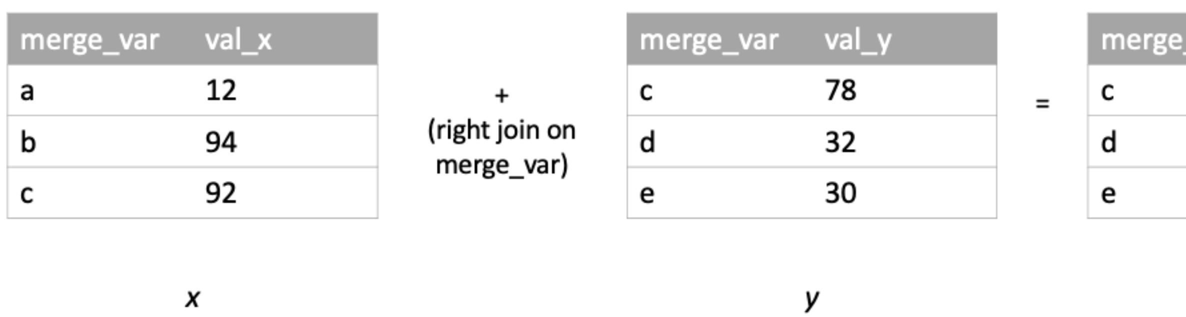
```
1          b   94.0    NaN
2          c   92.0   78.0
```

R

```
> # all.x = T results in a left join
> merge(x, y, by = 'merge_var', all.x = T)
  merge_var val_x val_y
1         a    12    NA
2         b    94    NA
3         c    92    78
```

5.4.2 Right Join

A right join of x and y keeps all rows of y and merges rows of x into y where possible based on the merge criterion:



Python

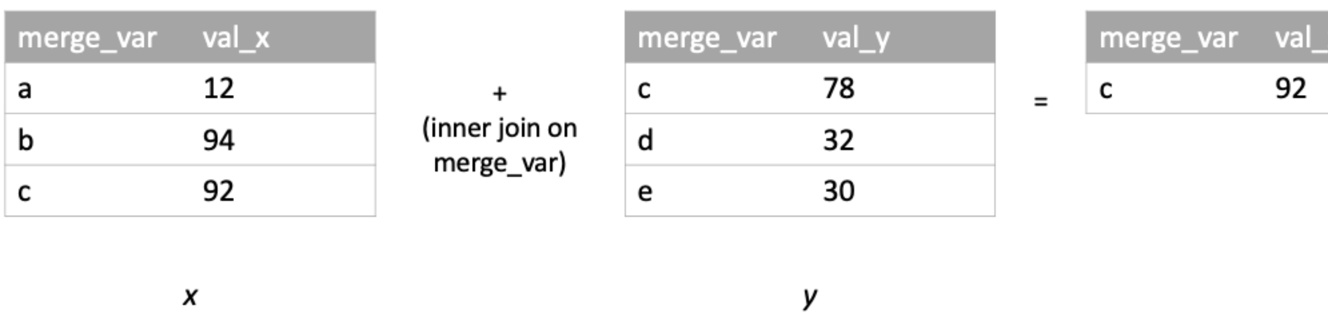
```
> import pandas as pd
+ pd.merge(x, y, how = 'right')
  merge_var  val_x  val_y
0         c   92.0   78.0
1         d    NaN   32.0
2         e    NaN   30.0
```

R

```
> # all.y = T results in a right join
> merge(x, y, by = 'merge_var', all.y = T)
  merge_var val_x val_y
1         c    92    78
2         d    NA    32
3         e    NA    30
```

5.4.3 Inner Join

An inner join of x and y returns merged rows for which a match can be on the merge criterion *in both tables*:



Python

```
> import pandas as pd
+ pd.merge(x, y, how = 'inner')
  merge_var  val_x  val_y
0         c   92.0   78.0
```

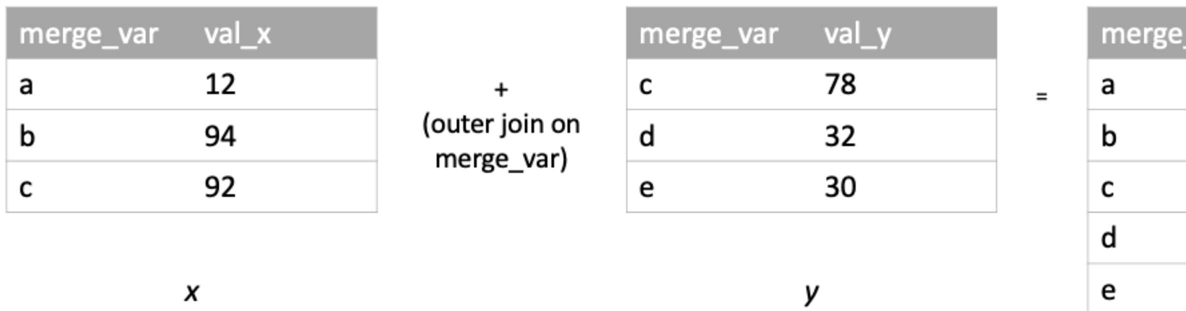
R

```
> # by default, merge() executes an inner join
> # (more specifically, a natural join, which is a kind of
> # inner join in which the merge-criterion column is not
> # repeated, despite being initially present in both tables)
```

```
> merge(x, y, by = 'merge_var')
  merge_var val_x val_y
1         c    92    78
```

5.4.4 Outer Join

An outer join of x and y keeps all rows from both tables, merging rows where possible based on the merge criterion:



Python

```
> import pandas as pd
+ pd.merge(x, y, how = 'outer')
  merge_var  val_x  val_y
0         a   12.0    NaN
1         b   94.0    NaN
2         c   92.0   78.0
3         d    NaN   32.0
4         e    NaN   30.0
```

R

```
> # all = T (or all.x = T AND all.y = T) results in an outer join
> merge(x, y, by = 'merge_var', all = T)
  merge_var val_x val_y
1         a    12    NA
2         b    94    NA
3         c    92    78
```

```
4          d    NA    32
5          e    NA    30
```

Chapter 6

Aggregation and Group Operations

This chapter looks at manipulating and summarizing data by groups.

6.1 Cross tabulation

Cross tabulation is the process of determining frequencies per group (or values based on frequencies, like proportions), with groups delineated by one or more variables (e.g., nationality and sex).

The Python and R examples of cross tabulation below both make use of the following dataset, `dat`:

```
> dat
  nationality sex
1    Canadian   m
2      French   f
3      French   f
4    Egyptian   m
5    Canadian   f
```

Python

The **pandas** package contains a `crosstab()` function for cross tabulation with two or more variables. The `groupby()`, also in **pandas**, facilitates cross tabulation by one or more variables when used in combination with `count()`.

```
> import pandas as pd
+ pd.crosstab(dat.nationality, dat.sex)
sex          f  m
nationality
Canadian     1  1
Egyptian     0  1
French       2  0
> dat.groupby(by = 'nationality').nationality.count()
nationality
Canadian    2
Egyptian    1
French      2
Name: nationality, dtype: int64
> dat.groupby(by = ['nationality', 'sex']).nationality.count()
+ # Or: dat.groupby(by = ['nationality', 'sex']).sex.count()
nationality  sex
Canadian     f      1
             m      1
Egyptian     m      1
French       f      2
Name: nationality, dtype: int64
```

R

The `table()` function performs cross tabulation in R. A user can enter a single grouping variable or enter multiple grouping variables separated by a comma(s). The `xtabs()` function also computes cross-tabs; a user enters the variables to be used for grouping in formula notation.

```
> table(dat$nationality)

Canadian Egyptian   French
       2        1        2
> table(dat$nationality, dat$sex)

           f m
  Canadian 1 1
  Egyptian 0 1
  French   2 0
> xtabs(formula = ~nationality + sex, data = dat)
           sex
nationality f m
   Canadian 1 1
   Egyptian 0 1
```

```
  French    2 0
```

6.2 Group summaries

Computing statistical summaries per group.

Python

R

The `aggregate()` function allows a user to easily generate by-group statistical summaries based on one or more grouping variables. Grouping variables can be declared as a list in the function's `by` argument. Alternatively, the grouping variables (and the variable to be summarized) can be passed to `aggregate()` in formula notation: `var_to_be_aggregated ~ grouping_var_1 + ... + grouping_var_N`. The summarizing function (e.g., `mean()`; `median()`; etc.) is declared in the `FUN` argument.

```
> # One grouping variable
> # Calculating mean of `mpg` in each `cyl` group
> aggregate(x = mtcars$mpg,
+           by = list(cyl = mtcars$cyl),
+           FUN = "mean")
  cyl        x
1   4 26.66364
2   6 19.74286
3   8 15.10000
```

Adding `drop=FALSE` ensures all combinations of levels are returned if no data exist at that combination. Below the final row is `NA` since there are no 8 cylinder cars with a "straight" engine (vs = 1).

```
> # Two or more grouping variables
> # Calculating max of `mpg` in each `cyl`*`vs` group
> aggregate(x = mtcars$mpg,
+           by = list(cyl = mtcars$cyl, vs = mtcars$vs),
+           FUN = "max", drop = FALSE)
  cyl vs    x
1   4  0 26.0
2   6  0 21.0
3   8  0 19.2
4   4  1 33.9
```

```
5   6  1 21.4
6   8  1   NA
```

```
> # Or, specify the variable to summarize and the grouping variables in formula notati
> aggregate(mpg ~ cyl, data = mtcars, FUN = mean)
> aggregate(mpg ~ cyl + vs, data = mtcars, FUN = max)
```

The **tidyverse** also offers a summarizing function, `summarize()` (or `summarise()`, for the Britons), which is in the **dplyr** package. After grouping a data frame/tibble (with, e.g., **dplyr**'s `group_by()` function), a user passes it to `summarize()`, specifying in the function call how the summary statistic should be calculated.

```
> library(dplyr)
> mtcars %>%
+   group_by(cyl, vs) %>%
+   summarize(avg_mpg = mean(mpg))
`summarise()` has grouped output by 'cyl'. You can override using the `.groups` argumen
# A tibble: 5 x 3
# Groups:   cyl [3]
    cyl    vs avg_mpg
  <dbl> <dbl>   <dbl>
1     4     0    26
2     4     1    26.7
3     6     0    20.6
4     6     1    19.1
5     8     0    15.1
```

A benefit of `summarize()` is that it allows a user to specify relatively complicated summary calculations without needing to write an external function.

```
> mtcars %>%
+   group_by(cyl, vs) %>%
+   summarize(avg_mpg = mean(mpg),
+             complicated_summary_calculation =
+               min(mpg)^0.5 *
+               mean(wt)^0.5 +
+               mean(disp)^(1/mean(hp)))
`summarise()` has grouped output by 'cyl'. You can override using the `.groups` argumen
# A tibble: 5 x 4
# Groups:   cyl [3]
    cyl    vs avg_mpg complicated_summary_calculation
  <dbl> <dbl>   <dbl>                           <dbl>
1     4     0    26                              8.51
```

```
2    4    1    26.7                            8.07
3    6    0    20.6                            8.41
4    6    1    19.1                            8.81
5    8    0    15.1                            7.48
```

6.3 Centering and Scaling

Centering refers to rescaling a column or vector of values such that their mean is 0. This is sometimes performed to aid interpretation of linear model coefficients.

Scaling refers to rescaling a column or vector of values such that their mean is 0 and their standard deviation is 1. This is sometimes performed to put multiple variables on the same scale and is often recommended for procedures such as principal components analysis (PCA).

Python

R

The `scale()` function can both center and scale variables.

To center a variable (without scaling it), call `scale()` with the `center` argument set to `TRUE` and the `scale` argument set to `FALSE`. The variable's mean will be subtracted off of each of the variable values. (Note: If desired, the `center` argument can be set to a numeric value instead of `TRUE`/`FALSE`; in that case, each variable value will have the argument value subtracted off of it.)

```
> centered_mpg <- scale(mtcars$mpg, center = T, scale = F)
> mean(centered_mpg)
[1] 4.440892e-16
```

To scale a variable (while also centering it), call `scale()` with the `center` and `scale` arguments set to `TRUE` (these are the default argument values). The variable's mean will be subtracted off of each of the variable values, and each value will then be divided by the variable's standard deviation. (Note: As with the `center` argument, the `scale` argument can also be set to a numeric value instead of `TRUE`/`FALSE`; in that case, the divisor will be the argument value instead of the standard deviation.)

```
> scaled_mpg <- scale(mtcars$mpg, center = T, scale = T)
> mean(scaled_mpg)
[1] 7.112366e-17
> sd(scaled_mpg)
[1] 1
```

Chapter 7

Basic Plotting and Visualization

This chapter looks at creating basic plots to explore and better understand data. Visualization in Python and R is a gigantic and evolving topic. We don't pretend to present a comprehensive comparison.

The plots below make use of the **palmerpenguins** data set, which contains various measurements for 344 penguins across three islands in the Antarctic Palmer Archipelago. The data were collected by Kristen Gorman and colleagues, and they were made available under a CC0 public domain license by Allison Horst, Alison Hill, and Kristen Gorman.

For the R sections below, we provide code showing how to make each plot using base R and using **ggplot2**.

Here's a glimpse at the data set:

```
> head(penguins)
# A tibble: 6 x 8
  species island bill_length_mm bill_depth_mm flipper_length_~ body_mass_g sex
  <fct>   <fct>           <dbl>         <dbl>            <int>       <int> <fct>
1 Adelie  Torge~           39.1          18.7              181        3750 male
2 Adelie  Torge~           39.5          17.4              186        3800 fema~
3 Adelie  Torge~           40.3          18                195        3250 fema~
4 Adelie  Torge~           NA            NA                 NA          NA <NA>
5 Adelie  Torge~           36.7          19.3              193        3450 fema~
6 Adelie  Torge~           39.3          20.6              190        3650 male
# ... with 1 more variable: year <int>
```

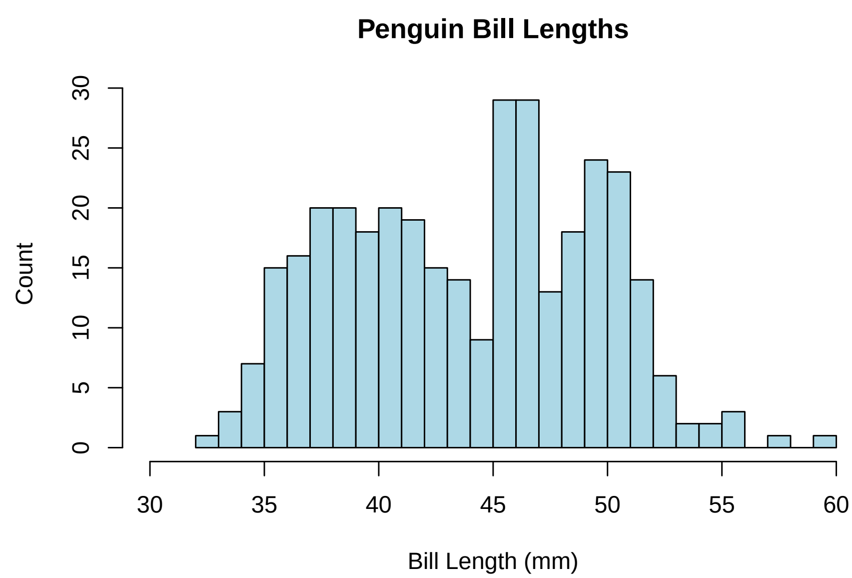
7.1 Histograms

Visualizing the distribution of numeric data.

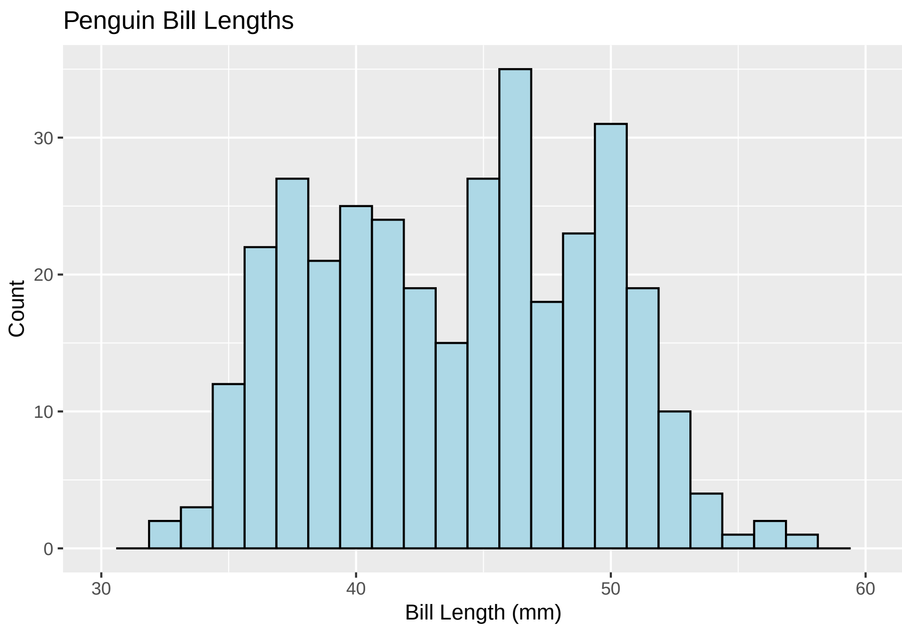
Python

R

```
> hist(penguins$bill_length_mm, breaks = 25, col = 'lightblue', xlim = c(30, 60),
+      main = 'Penguin Bill Lengths', xlab = 'Bill Length (mm)', ylab = 'Count')
```




```
> ggplot(penguins, aes(x = bill_length_mm)) +
+   geom_histogram(fill = 'lightblue', color = 'black', bins = 25) +
+   xlim(30, 60) + labs(title = 'Penguin Bill Lengths', x = 'Bill Length (mm)', y = 'Co
```



7.2 Barplots

Visualizing the distribution of categorical data.

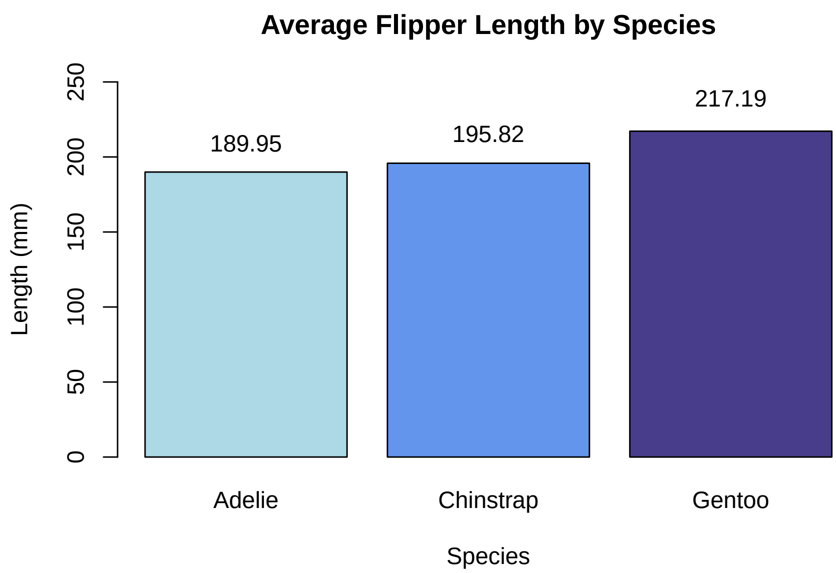
Python

R

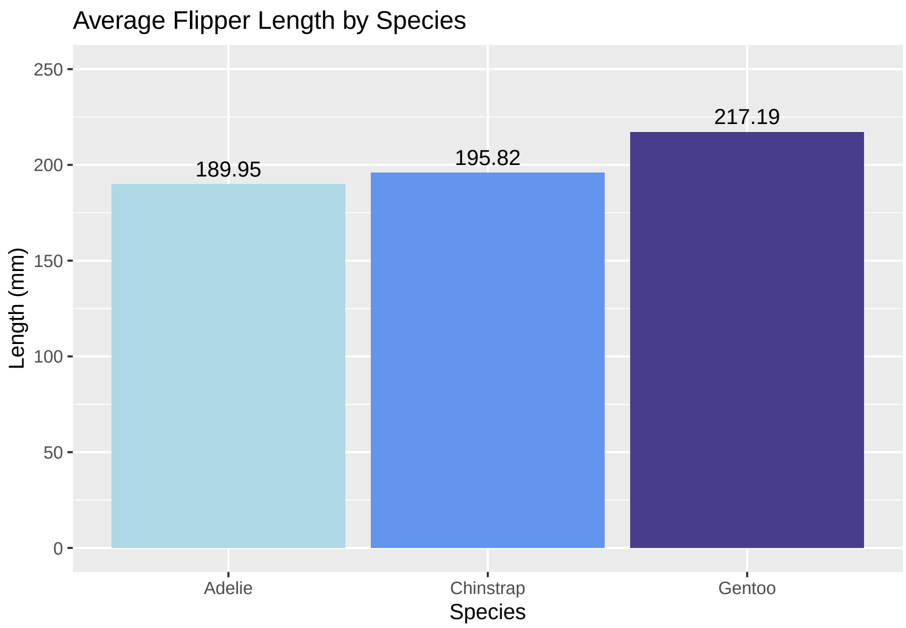
To form barplots, we'll first take the **penguins** data set and...

```
> flippers <- aggregate(penguins$flipper_length_mm, by = list(penguins$species), function(x) mea
> colnames(flippers) <- c('species', 'avg_flipper_length')
```

```
> penguin_plot <- barplot(flippers$avg_flipper_length, names.arg = flippers$species,
+         col = c('lightblue', 'cornflowerblue', 'darkslateblue'),
+         main = 'Average Flipper Length by Species', xlab = 'Species', ylab = 'Length (mm)',
+         ylim = c(0, 250))
> text(x = penguin_plot, y = flippers$avg_flipper_length*1.1, labels = round(flippers$avg_flipper
```




```
> ggplot(flippers, aes(x = species, y = avg_flipper_length)) +
+   geom_bar(aes(fill = species), stat = 'identity') +
+   scale_fill_manual(values = c('lightblue', 'cornflowerblue', 'darkslateblue')) +
+   labs(title = 'Average Flipper Length by Species', x = 'Species', y = 'Length (mm)'
+   theme(legend.position = 'none') + ylim(0, 250) +
+   geom_text(aes(label = round(avg_flipper_length, digits = 2), vjust = -0.5))
```



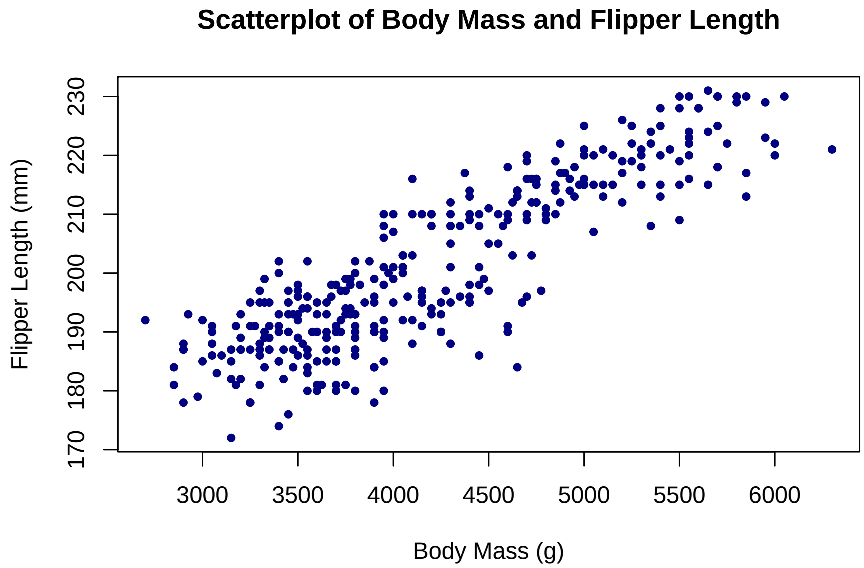
7.3 Scatterplot

Visualizing the relationship between two numeric variables.

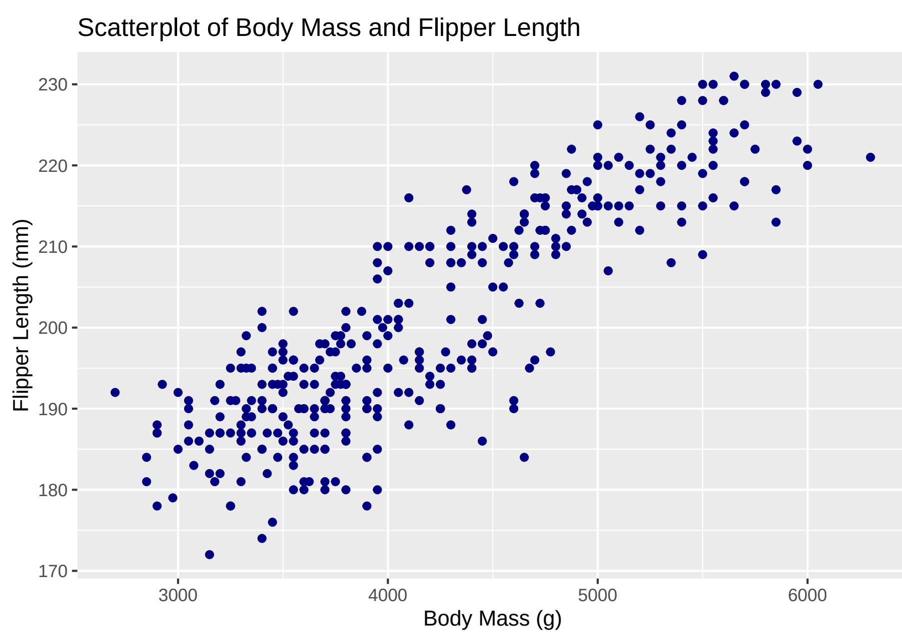
Python

R

```
> plot(penguins$body_mass_g, penguins$flipper_length_mm, col = 'navy', pch = 20,
+      main = 'Scatterplot of Body Mass and Flipper Length', xlab = 'Body Mass (g)', ylab = 'Flip
```




```
> ggplot(penguins, aes(x = body_mass_g, y = flipper_length_mm)) +
+   geom_point(color = 'navy') +
+   labs(title = 'Scatterplot of Body Mass and Flipper Length', x = 'Body Mass (g)', y
```



7.4 Stripcharts

Visualizing the relationship between a numeric variable and a categorical variable.

Python

R

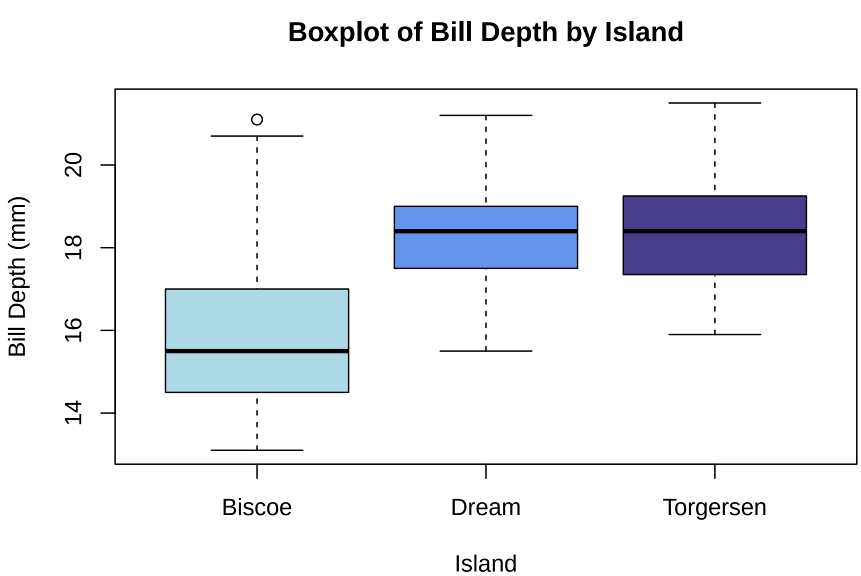
7.5 Boxplots

Visualizing the relationship between a numeric variable and a categorical variable via 5 number summaries.

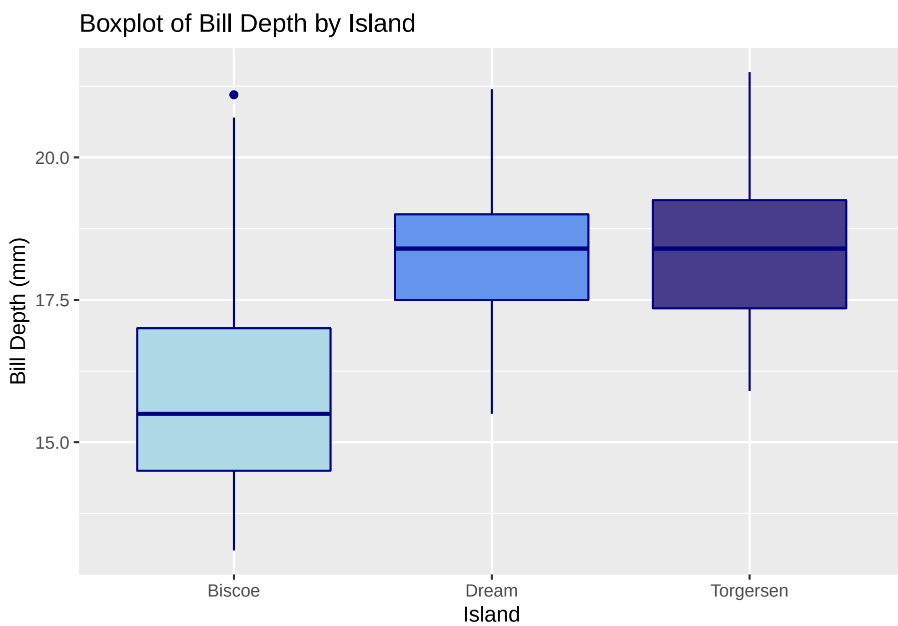
Python

R

```
> boxplot(penguins$bill_depth_mm ~ penguins$island, col = c('lightblue', 'cornflowerblue', 'darks
+         main = 'Boxplot of Bill Depth by Island', xlab = 'Island', ylab = 'Bill Depth (mm)')
```



```
> ggplot(penguins, aes(x = island, y = bill_depth_mm)) +
+   geom_boxplot(aes(fill = island), color = 'navy') +
+   scale_fill_manual(values = c('lightblue', 'cornflowerblue', 'darkslateblue')) +
+   labs(title = 'Boxplot of Bill Depth by Island', x = 'Island', y = 'Bill Depth (mm)
+   theme(legend.position = 'none')
```



7.6 Conditional or Faceted plots

Two or more plots of subsets of data.

Chapter 8

Statistical Inference and Modeling

This chapter looks at performing and interpreting common statistical analyses.

8.1 Comparing group means

Comparing the means of two or more groups to see if or how they differ. Two means can be analyzed with a t test. Three or more can be analyzed with ANOVA. Both the t test and ANOVA are special cases of a linear model.

Python

R

8.2 Comparing group proportions

Comparing the proportions of two or more groups to see if or how they differ.

Python

R

8.3 linear modeling

Analyzing if or how the variability a numeric variable depends on one or more predictor variables.

Python

R

8.4 Logistic regression

Analyzing if or how the variability of a binary variable depends on one or more predictor variables.

Python

R