Introduction to Python

Adapted from the Data & Software Carpentry, and the Montana State University Data Science Worksho
Adapted by Devin Goodwin and SCRS

About Python, R, and RStudio Briefly

`Python` is a popular programming language commonly used for statistical analysis, data visualization, and machine learning. The many ways to interact with `Python` are called Integrated Development Environments (IDE's). IDE choice depends on the context, the nature of the project, and/or personal preference, among other factors. Here are a few IDE's for interacting with `Python`.

- IDLE (Python's Integrated Development and Learning)
- PyCharm
- Jupyter Notebook
- Visual Studio Code
- Google Colab
- RStudio

Additionally, `Python` has broad applications beyond data analysis and can be used for web development, automation, and more. Ultimately, the choice between `R` and `Python` will depend on your specific needs and preferences. Since this series of workshops were developed in `RStudio` and `RStudio` uses `R` behind the scenes, both need to be installed on your computer if you decide to use `RStudio` as your IDE of choice. Otherwise the any code in a `Python` *chunk* will work in any `Python` IDE. Both `R` and `RStudio` are cross-platform, so that everyone's versions look and operate the same regardless of their operating system!

For more details on the installation of `R` and `RStudio`, you have hopefully completed the steps discussed here . The short version for downloading is to first go to to `R` installed and then go to to install RStudio.

Install `Python` by going to https://www.python.org/downloads/ and download the latest version for your operating system.

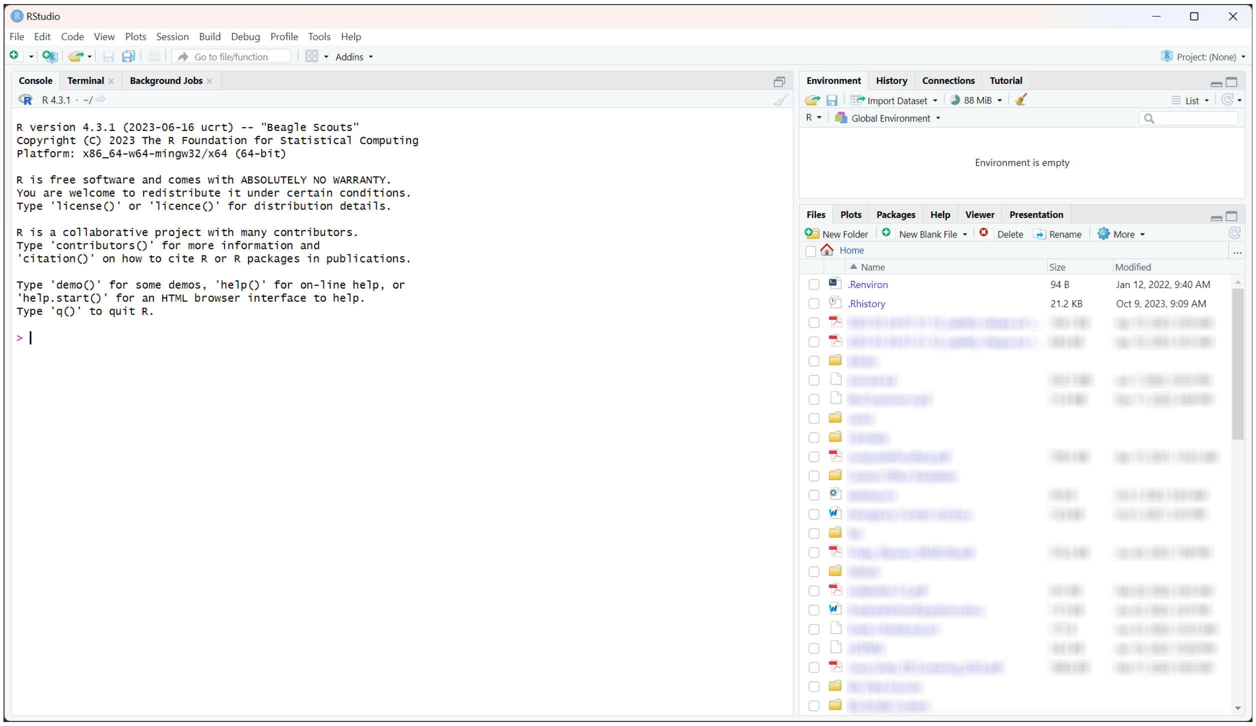
If you did not complete that or do not have a computer available, you can also borrow a laptop from the MSU library (or maybe from a good friend) for the workshop. It needs to be a computer that is running Linux, Windows, or a somewhat recent macOS. Unfortunately, a Chromebook or iPad are not sufficient for installing and running R.

Prepare for the Workshop

Please take these steps if you haven't already done so:

1. Install `R`
2. Install RStudio
3. Download the ZIP file provided for the workshop
4. ***Unzip the file and save the contents locally***
5. Open RStudio
6. Install reticulate
7. Run the code to install miniconda
8. Install python packages

When you open RStudio for the first time, if you have not previously used it or attended the **Introduction to R** workshop, you will see three panels.



```
R version 4.3.1 (2023-06-16 ucrt) -- "Beagle Scouts"
Copyright (C) 2023 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

R is free software and comes with ABSOLUTELY NO WARRANTY.
You are welcome to redistribute it under certain conditions.
Type 'license()' or 'licence()' for distribution details.

R is a collaborative project with many contributors.
Type 'contributors()' for more information and
'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

> |
```

Environment is empty

Name	Size	Modified
.Renviron	94 B	Jan 12, 2022, 9:40 AM
.Rhistory	21.2 KB	Oct 9, 2023, 9:09 AM

[redacted]

Figure 1: Initial RStudio layout

The next thing you need to do is navigate to the unzipped folder and open the RMD file.

Go to **File > Open File...** and browse to where you unzipped the folder and select the **RMD** file.

Once you do that your window should look like this:

Most of you should see a yellow bar saying ***Package reticulate required but is not installed."*** with options ***Install*** or ***Don't Show Again***, if you haven't already installed this package.

`>>> CLICK ON Install NOW! <<<`

RStudio Orientation and Layout

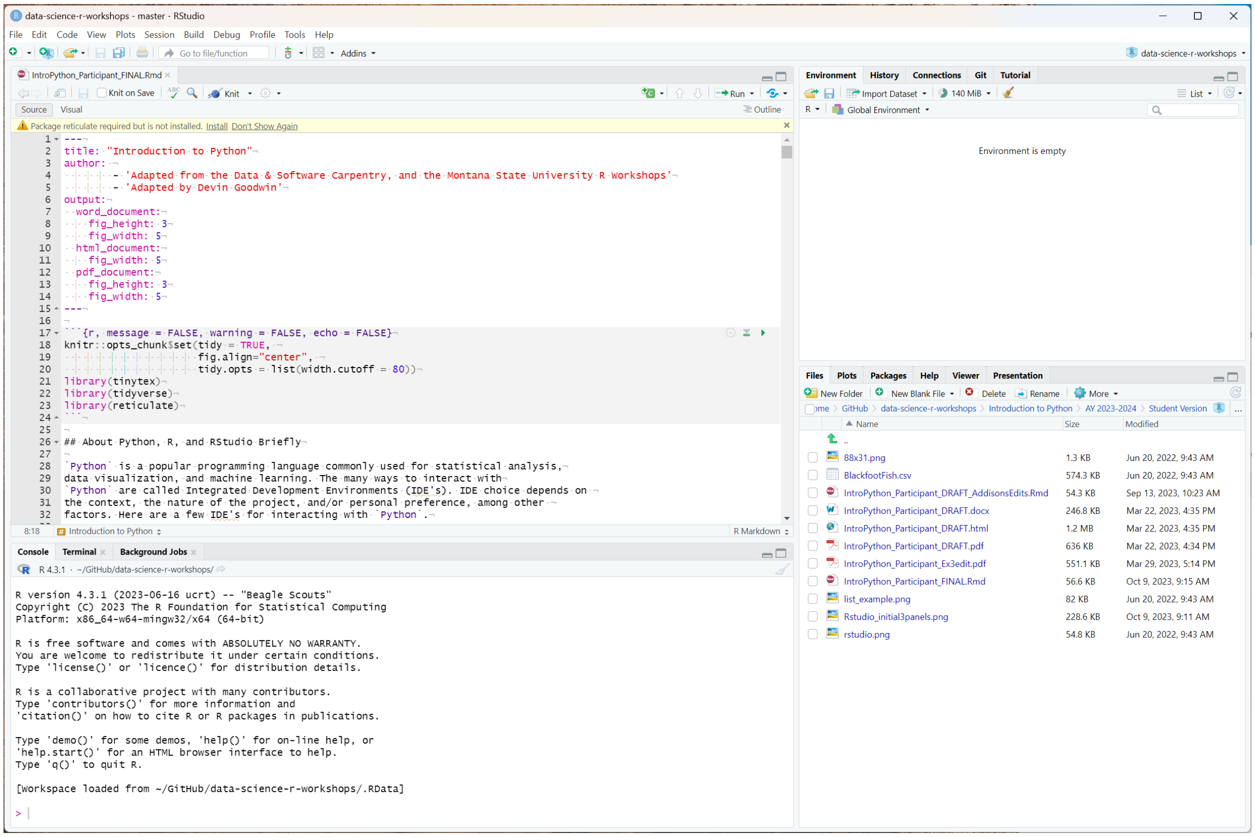
However you get to it, RStudio has four possible panels, where each can be viewed at the same time and has multiple tabs available.

- the **Editor** for your scripts and documents (top-left)
- the `R` **Console** (bottom-left)
- your **Environment (Objects/Variables)/History** (top-right)
- and your **Files/Plots/Packages/Help/Viewer** (bottom-right).

The next step is to set up the system to install Python and load in Python packages:

```r
# Only need to run the following once:
reticulate::install_miniconda()
```

```
## Error: Miniconda is already installed at path "C:/Users/greta/AppData/Local/r-miniconda".
## - Use `reticulate::install_miniconda(force = TRUE)` to overwrite the previous installation.
```


data-science-r-workshops - master - RStudio
File Edit Code View Plots Session Build Debug Profile Tools Help
Go to file/function
Addins
data-science-r-workshops
IntroPython_Participant_FINAL.Rmd
Knit on Save
Knit
Run
Source
Visual
Outline
Environment History Connections Git Tutorial
Import Dataset
140 MiB
List
Global Environment
Environment is empty
Files Plots Packages Help Viewer Presentation
New Folder
New Blank File
Delete
Rename
More
8:18
Introduction to Python
R Markdown
Console Terminal Background Jobs

Package reticulate required but is not installed. Install Don't Show Again

~~~
---
title: "Introduction to Python"
author: 
        - 'Adapted from the Data & Software Carpentry, and the Montana State University R Workshops'
        - 'Adapted by Devin Goodwin'
output:
  word_document:
    fig_height: 3
    fig_width: 5
  html_document:
    fig_width: 5
  pdf_document:
    fig_height: 3
    fig_width: 5
---

```{r, message = FALSE, warning = FALSE, echo = FALSE}
knitr::opts_chunk$set(tidy = TRUE, 
                      fig.align="center", 
                      tidy.opts = list(width.cutoff = 80))
library(tinytex)
library(tidyverse)
library(reticulate)
```

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data visualization, and machine learning. The many ways to interact with
`Python` are called Integrated Development Environments (IDE's). IDE choice depends on 
the context, the nature of the project, and/or personal preference, among other 
factors. Here are a few IDE's for interacting with `Python`.
~~~

R 4.3.1 · ~/GitHub/data-science-r-workshops/

```
R version 4.3.1 (2023-06-16 ucrt) -- "Beagle Scouts"
Copyright (C) 2023 The R Foundation for Statistical Computing
Platform: x86_64-w64-mingw32/x64 (64-bit)

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'citation()' on how to cite R or R packages in publications.

Type 'demo()' for some demos, 'help()' for on-line help, or
'help.start()' for an HTML browser interface to help.
Type 'q()' to quit R.

[Workspace loaded from ~/GitHub/data-science-r-workshops/.RData]

> 
```

ome > GitHub > data-science-r-workshops > Introduction to Python > AY 2023-2024 > Student Version

Name	Size	Modified
..		
88x31.png	1.3 KB	Jun 20, 2022, 9:43 AM
BlackfootFish.csv	574.3 KB	Jun 20, 2022, 9:43 AM
IntroPython_Participant_DRAFT_AddisonsEdits.Rmd	54.3 KB	Sep 13, 2023, 10:23 AM
IntroPython_Participant_DRAFT.docx	246.8 KB	Mar 22, 2023, 4:35 PM
IntroPython_Participant_DRAFT.html	1.2 MB	Mar 22, 2023, 4:35 PM
IntroPython_Participant_DRAFT.pdf	636 KB	Mar 22, 2023, 4:34 PM
IntroPython_Participant_Ex3edit.pdf	551.1 KB	Mar 29, 2023, 5:14 PM
IntroPython_Participant_FINAL.Rmd	56.6 KB	Oct 9, 2023, 9:15 AM
list_example.png	82 KB	Jun 20, 2022, 9:43 AM
Rstudio_initial3panels.png	228.6 KB	Oct 9, 2023, 9:11 AM
rstudio.png	54.8 KB	Jun 20, 2022, 9:43 AM

Figure 2: RStudio layout for this workshop

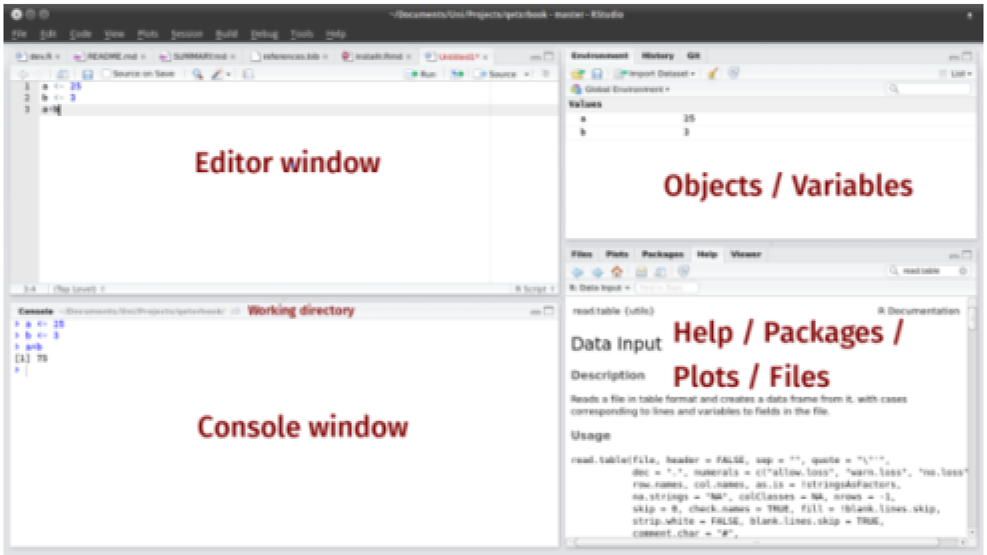


Figure 3: RStudio layout

```r
library(reticulate)  # Integrates Python with R
py_install(packages = c("pandas", "scipy", "numpy", "matplotlib"))
```

```
## Warning in system2(command = python, args = shQuote(script), stdout = TRUE, :
## running command
## '"C:/Users/greta/AppData/Local/Programs/Python/Python312/python.exe"
## "C:/Users/greta/AppData/Local/R/win-library/4.3/reticulate/config/config.py"'
## had status 1

## Error in python_config_impl(python) :
##   Error 1 occurred running C:/Users/greta/AppData/Local/Programs/Python/Python312/python.exe:

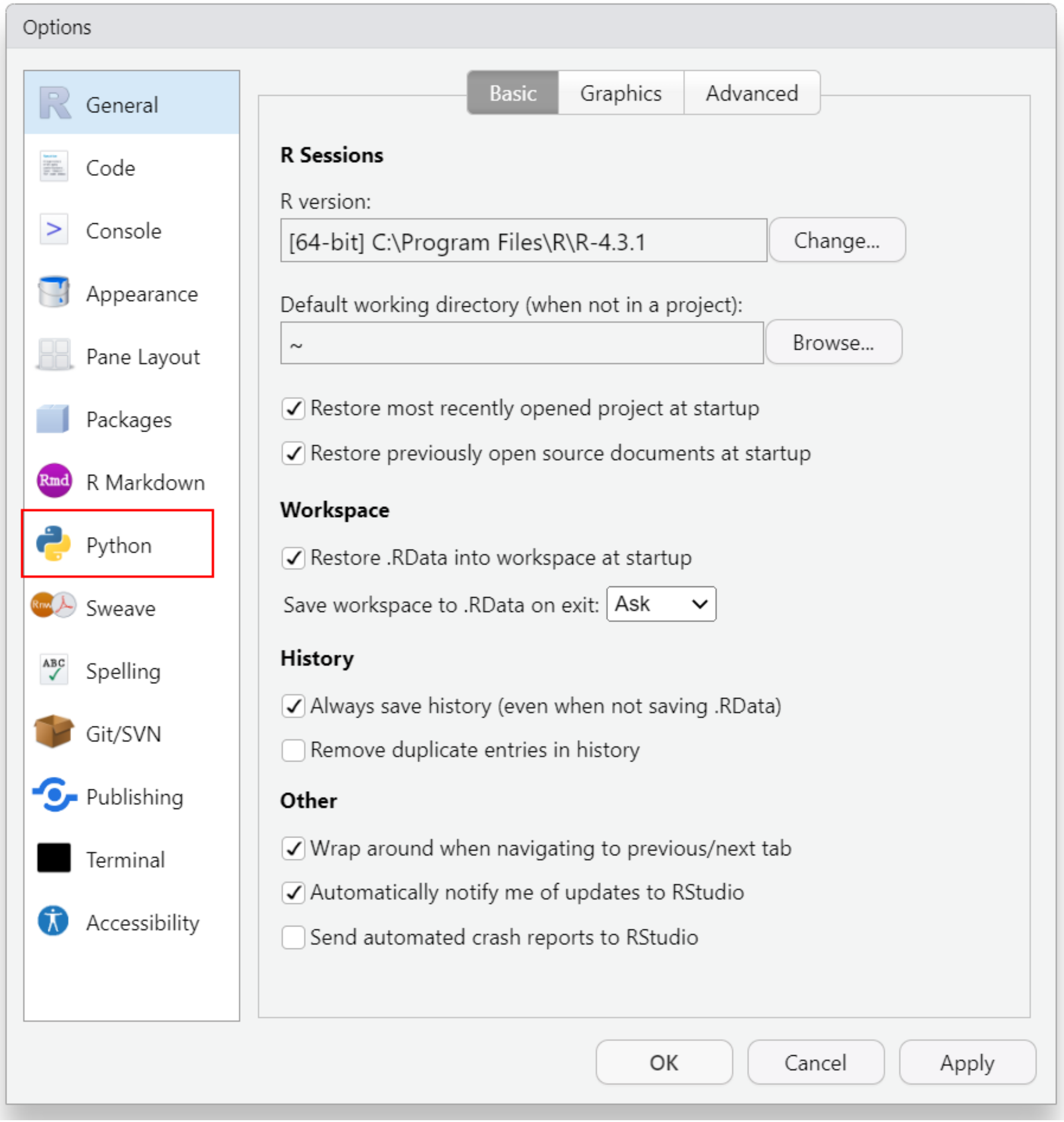
## Warning in system2(command = python, args = shQuote(script), stdout = TRUE, :
## running command
## '"C:/Users/greta/AppData/Local/Programs/Python/Python312/python.exe"
## "C:/Users/greta/AppData/Local/R/win-library/4.3/reticulate/config/config.py"'
## had status 1

## Error in python_config_impl(python) :
##   Error 1 occurred running C:/Users/greta/AppData/Local/Programs/Python/Python312/python.exe:

## + "C:/Users/greta/AppData/Local/r-miniconda/condabin/conda.bat" "install" "--yes" "--prefix" "C:/Use
```

Lastly, we need to make sure that RStudio knows about your Python Interpreter.

Go to **Tools > Global Options. . . .** You should see a dialog box like the one below, and notice **Python** in the list on the left.



R Sessions

R version:

[64-bit] C:\Program Files\R\R-4.3.1

Default working directory (when not in a project):

~

☑ Restore most recently opened project at startup

☑ Restore previously open source documents at startup

Workspace

☑ Restore .RData into workspace at startup

Save workspace to .RData on exit: Ask

History

☑ Always save history (even when not saving .RData)

☐ Remove duplicate entries in history

Other

☑ Wrap around when navigating to previous/next tab

☑ Automatically notify me of updates to RStudio

☐ Send automated crash reports to RStudio

Click on **Python**, and make sure that you select a python interpreter if one is not already selected for you.

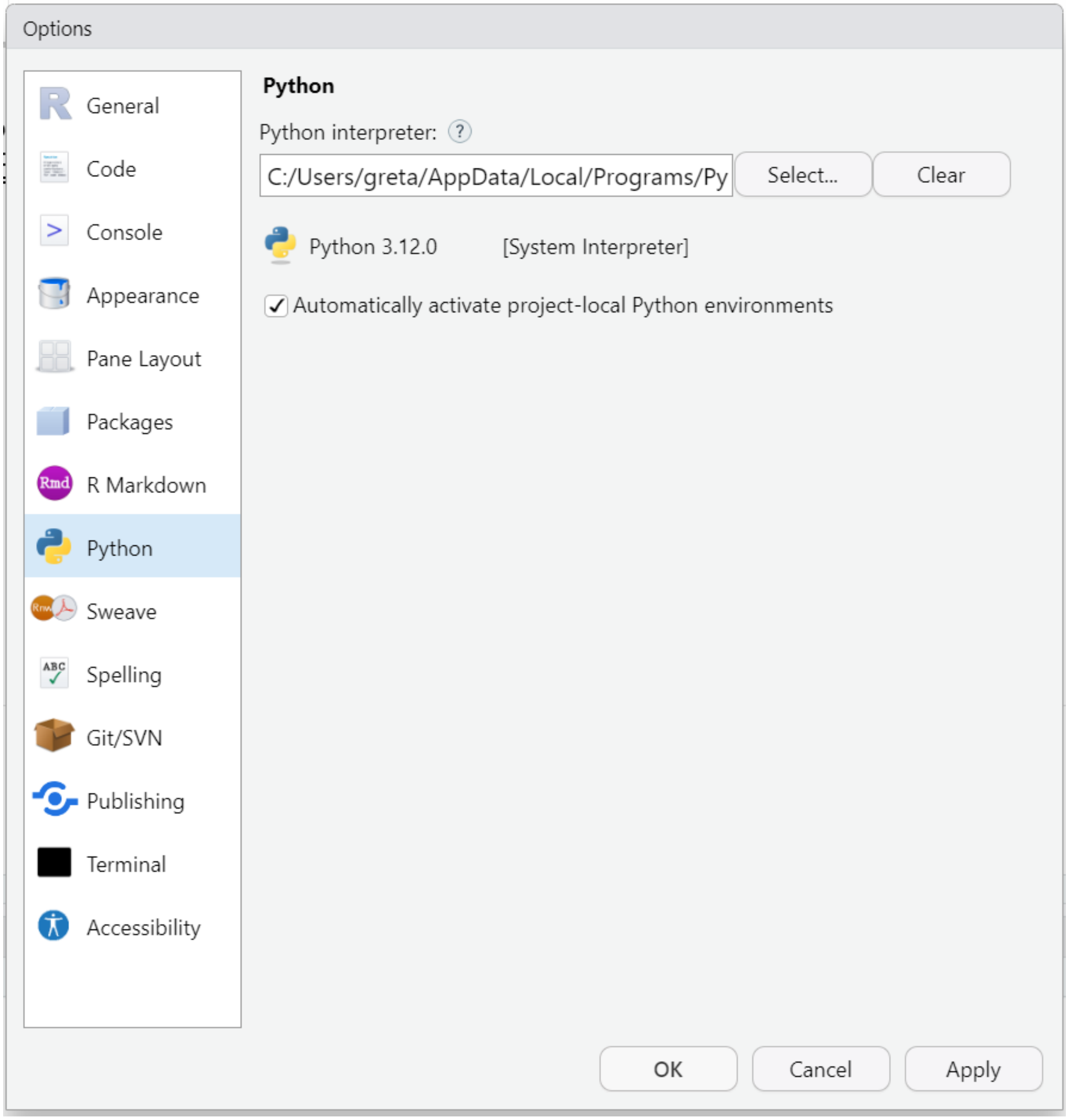
Working in `RStudio`

The document we provided for you is an Rmarkdown (.Rmd) document. It allows you to work in a reproducible fashion, with both code (placed in what are called code chunks) and descriptions of results in the same file. The grey sections that have three single quotes then `{r}` will delineate a code chunk.

~~~
```{r}
1 + 1
```
~~~

The `{r}` specifies which language you will be using, so since we will be working with `Python` we set our chunks as follows:

~~~
```{python}`python ''`
~~~



Python

Python interpreter:

C:/Users/greta/AppData/Local/Programs/Py

Python 3.12.0 [System Interpreter]

☑ Automatically activate project-local Python environments

Figure 4: Global Options - Python Interpreter

~~~~
1 + 1
```
~~~~

Type all of your code in these code chunks and other documentation and interpretation of results outside of the code chunks (like we are doing here). Although there are more complex ways to work in RStudio, you should start today with saving this .Rmd file into a folder that also contains any data and other figures you might want to read into this document. When you do that, RStudio will know where to look to read in the data so you do not need to know the path for its physical location on your computer. Once we are done with our local work, we can also use the `Knit` button to compile our work into HTML, Word (DOCX), or PDF documents. We will demonstrate this at the end of the workshop - but this will only work if all the code "runs" and what we have provided you has some errors in it. One other great (and fairly new) feature in these files is that it does live spell-checknig - I mean spell-checking - by underlining suspect words. We will also discuss RStudio "Projects" that take this one step further in terms of organizing your work built around this markdown framework. It is important to understand the various ways to do your work in R using RStudio.

`RStudio` recognizes where the variable lives, that is under what environment you can find it stored in the Environment panel, you can click the drop down tab `R` where you will see the different environment options. Similarly for the Console, the compiler will be determined by the type of chunk you defined.

Next set up the system:

```r
# Only need to run the following once:
Sys.setenv(RETICULATE_PYTHON = "C:/Users/greta/AppData/Local/Programs/Python/Python312/python.exe")
library(reticulate)  # Integrates Python with R
reticulate::install_miniconda()
py_install(packages = c("pandas", "scipy", "numpy", "matplotlib"))
```

Example: In `R`:

```r
library(reticulate)  # Integrates Python with R
x = 2
y = 3
z = x + y
```

In `Python`:

```python
x = 3
y = 2
z = x + y
```

And notice in your different environments that variables are not overwritten as `RStudio` recognizes the corresponding environment. Also, notice that in your `Python` environment the resulting output is stored in an `R` interface object called Data. This is because RStudio uses the `reticulate` package to integrate `Python` with `R`, and this package automatically creates an `R` interface object to store the output from `Python`.

If `R` is ready to accept commands, the `R` console (in the bottom-left) will show a `>` prompt (`>>>` in `Python` environment). When `R` receives a command (by typing, copy-pasting, or using the shortcut), it will execute it, and when finished will display the results and show the `>` symbol (or `>>>`) once again. If `R` is still waiting for you to provide it with additional instructions, a `+` (⋯ in `Python` environment) will appear in the console. This should tell you that you didn't finish your command. You could have forgotten to close your parenthesis or a quotation. If this happens and you are unsure of what went wrong, click inside the console and hit the `Esc` key. Then you can start over and figure out where you went wrong!

Calculator

Practice: Enter each of the following commands and confirm that the response is the correct answer. Try to do this in the console and by executing the code in the code chunk, both line by line and all at once.

```
1 + 2
```

```
## 3
```

```
16 * 9
```

```
## 144
```

```
20 / 5
```

```
## 4.0
```

```
18.5 - 7.21
```

```
## 11.29
```

```
2 ^ 2
```

```
## 0
```

Notice how 2^2≠ (is not equal to) 4! In Python the exponent operator is not the expected *caret* ^ symbol, but rather exponentiation is defined by *double star* **:

```
2 ** 2
```

```
## 4
```

Also notice algebraic operations are not space-sensitive, this is helpful when trying to format, and read code in Python.

Like R, Python has a wide range of libraries and packages (often referred as Modules) that make it a powerful tool for data analysis. To install and import Python modules in RStudio:

1.- Install the reticulate package: The reticulate package is a package that provides a way to use Python within RStudio. You can install it by running the following command in the R console:

install.packages("reticulate")

```
install.packages("reticulate")
```

```
## Warning: package 'reticulate' is in use and will not be installed
```

2.- Install the required Python packages: You can install Python packages using the pip command in the Python console within RStudio. For example, if you want to install the pandas package (more on this later), you can run the following command:

~~~
```{r}

library(reticulate)
py_install("pandas")

```
~~~

```
library(reticulate)
py_install("pandas")
```

```
## + "C:/Users/greta/AppData/Local/r-miniconda/condabin/conda.bat" "install" "--yes" "--prefix" "C:/Use
```

Where py_install() is an R function provided by the reticulate package, which allows you to install Python packages from within R.

3.- Once the package is installed, you can import it in a Python chunk using the import() function. For example:

~~~
```{python}`python '''`

import pandas as pd

```
~~~

```python
import pandas as pd
```

This will import the pandas package and give it an alias `pd`, which you can use to access its functions and objects. Aliases are useful because they are fewer characters to type as you have to use either the package name or alias anytime you call a function. ***So choose your alias wisely!***

4.- Note that the `reticulate` package requires a `Python` installation to be available on your system, and it uses the `use_python()` function to specify the path to the `Python` binary. You can use `use_python()` to specify a specific `Python` version or environment, or you can let `reticulate` automatically locate a suitable `Python` installation. For example:

~~~
```{r}

library(reticulate)
use_python("/usr/bin/python3")

```
~~~

If you have problems getting Python installed, it may be because you had a previous installation. We recommend that if you are having issues, to uninstall Python and reinstall by following the steps listed above.

Now that we know how to import and load `Python` modules, let us work with some examples of commonly used modules, such as the `math` module. The math module is a built-in module in `Python` that provides various mathematical functions and constants such as the square root, trigonometric, logarithmic, and exponential functions. The general syntax for `Python` when calling a function from a specific module is `module.attribute`.

Try the following code:

```python
import math
math.sqrt(2)
```

```
## 1.4142135623730951
```

```python
math.cos(math.pi)
```

```
## -1.0
```

```python
math.factorial(4)
```

```
## 24
```

```python
math.cos(math.pi/4) ** 2 + math.sin(math.pi/4) ** 2
```

```
## 1.0000000000000002
```

Creating Objects

These operations, however, are not very interesting. To do more useful things in `Python`, we need to assign values to an object. To create an object, we tell `RStudio` the object's name, followed by an equal sign (`=`), and finally the value of the object. This would look something like this:

```
x = 6
```

Once we execute/run this line of code, we notice that a new object appears in our (Python) environment window. This window shows all of the objects that you have created during your session. The value of x appears next to it, since it is a scalar.

Remarks:

- If you are familiar with R language you might think of using the assignment arrow <- instead of =, however, in Python this is not a proper syntax.
    - Python is case sensitive, so if you name your variable cat but then try to run the code Cat + 2, you will get an error saying that Cat does not exist.
    - You also want your object's name to be explanatory, but not too long. Think current_temperature verses current_temp. Do you really want to type out temperature every time?
    - Finally, you cannot begin any object's name with a number. You can end a name with a number (e.g. clean_data2), but does that give you much information about what is in the contents of clean_data2 relative to clean_data?
    - The name cannot contain any punctuation symbols, except for . and _ (. is not recommended)
    - You should not name your object the same as any common functions you may use (mean, stdev, etc.)
- Using a consistent coding style makes your code clearer to read for your future self and your collaborators.

Clean Code

Yes, writing code may be completely new to you, but there is a difference between code that looks nice and code that does not. Generally, object names should be nouns and function names should be verbs. It is also important that your code looks presentable, so that a friend/college/professor can read it and understand what you are doing. For these reasons, there are style guides for writing code in R. The two main style guides are Google's (link) and PEP 8, the official Python style guide, maintained by the Python Software Foundation: (link) Optionally, you can install pylint to automatically check and correct for issues in your code styling. More on packages to come!

Working with Objects

When you assign a value to an object (like we did previously) Python does not output anything by default. If you want to see the output you can use the command print(value), then Python will output the value of the object you created.

```
x = 6

print(x)
```

```
## 6
```

Once the object has been created, you can use it! Run the following lines of code:

```
2.2 * x
```

```
## 13.200000000000001
```

```
4 + x
```

```
## 10
```

We can also overwrite an object's value, so that it has a new value. In the code below create a new object y and then we give x a new value of 2.

```
y = x + 6

x = 2
```

Exercise 1: What is the current value of y? 12 or 8?

```
#Exercise 1 code here!

print(y)
```

```
## 12
```

```
# or

y
```

```
## 12
```

Working with Different Data Types

A vector in Python, formally a list or a NumPy array is the basic data type in Python. A vector is a series of values, which can be either numbers or characters, but every entry of the vector must be the same data type. Python can tell that you are building a vector when you use the squared brackets separating each element with a comma [a,b,...,c], list() or numpy.array([]) functions, which concatenates a series of entries together.

Install the Numpy module in Python command window using the syntax !pip install (this may take a few moments):

```
!pip install numpy
```

Remarks: *When you include ! at the beginning of a command in a Python script, RStudio will treat it as a shell command rather than a Python command.

```
+ A shell command is a command that is executed in a command-line interface
(CLI) or shell, which is a text-based user interface for interacting with an
operating system or software application.
+ In a shell environment, you can type commands and execute them by pressing
the Enter key.
+ The shell interprets the command and executes it, displaying the output
in the console or terminal window.
```

```
import numpy as np

temps_list = [50, 55, 60, 65]
temps_list
```

```
## [50, 55, 60, 65]
```

```
temps_numpy = np.array([50, 55, 60, 65])
print(temps_numpy)
```

```
## [50 55 60 65]
```

To make a vector of characters, you are required to use quotation marks " " to indicate to Python that the value you are using is not an object you already created in Python.

```
animals_list = ["cat", "dog", "bird", "fish"]
animals_list
```

```
## ['cat', 'dog', 'bird', 'fish']
```

```
animals_numpy = np.array(["cat", "dog", "bird", "fish"])
print(animals_numpy)
```

```
## ['cat' 'dog' 'bird' 'fish']
```

Important features of a vector is the type of data they store. Run the following lines of code and decide what type of data the vectors contain.

```
type(temps_list)
```

```
## <class 'list'>
```

```
type(temps_numpy)
```

```
## <class 'numpy.ndarray'>
```

Remarks:

- `numpy.ndarray` is a `Python` class that represents an n-dimensional array or a multi-dimensional array. An array is a data structure that stores a collection of values of the same type.
- `list` is a `Python` class type that represents a list data structure in Python. A list is an ordered collection of objects or values, enclosed in square brackets and separated by commas. A list can contain objects of different data types, such as integers, floats, strings, or even other lists.

Exercise 2: Create a vector, named `dec`, that contains decimal valued numbers. Then check what data type that vector contains?

```
dec = np.array([1.2, 3.4, 5.6])
print(dec)
```

```
## [1.2 3.4 5.6]
```

```
print(type(dec))
```

```
## <class 'numpy.ndarray'>
```

```
# Alternatively
dec_list = [1.2, 3.4, 5.6]
dec_list
```

```
## [1.2, 3.4, 5.6]
```

```
print(type(dec_list))
```

```
## <class 'list'>
```

Another possible data type are dictionaries. In `Python`, a dictionary is an unordered collection of key-value pairs. It is represented by a pair of curly braces `{}`, with each key-value pair separated by a colon `:`. *Also known as associative arrays, maps, or hash tables in other programming languages.*

```
translate = {'Hello':'Hola', 'How are you?':'Como estas?', 'Fibula':'Perone'}
translate['Fibula']
```

```
## 'Perone'
```

So in `Python`, vectors (lists, numpy arrays) and dictionaries are data structures that allow you to store collections of values, but they have some key differences:

1.- Vectors are ordered while Dictionaries are not.

2.- Vectors are indexed by integer positions while Dictionaries are indexed by keys.

3.- All elements in a vector are of the same type, while in Dictionaries this need not be the case.

4.- You can "mutate" (change) the values contained in a vector or dictionary, BUT you cannot change the keys in a dictionary once they are assigned, i.e., they are "immutable".

```
# Creating a vector
vec = [1, 2, 3, 4]

# Accessing values in a vector by index
print(vec[0])  # Output: 1
```

```
## 1
```

```
# Modifying a value in a vector
vec[0] = 5
print(vec[0])
```

```
## 5
```

```
# Creating a dictionary
translate = {'Hello':'Hola', 'How are you?':'Como estas?', 'Fibula':'Perone'}

# Accessing values in a dictionary by key
print(translate['How are you?'])  # Output: 3
```

```
## Como estas?
```

```
# Adding a new key-value pair to a dictionary
translate['I like cheese'] = 'Me gusta el queso'
print(translate['I like cheese'])
```

```
## Me gusta el queso
```

```
# Modifying a value in a dictionary
translate['Hello'] = 'Adios'
print(translate['Hello'])
```

```
## Adios
```

```
print(translate)
```

```
## {'Hello': 'Adios', 'How are you?': 'Como estas?', 'Fibula': 'Perone', 'I like cheese': 'Me gusta el q
```

Another possible data type is a logical (Boolean) value. This type of data takes on values of `True` and `False`(*WARNING* `Python` is case sensitive so `TRUE`, `FALSE` won't work). But, we said that vectors could only be numbers or characters. If `TRUE` and `FALSE` don't have quotations around them, then they aren't characters. So, then they must be numbers. What numbers do you think they are?

```
logic = [True, False, False, True]

type(logic)
```

```
## <class 'list'>
```

Notice that the `type()` command is telling us what we already know, it's a list! But is we are interested in knowing the type of each element in a list one can perform a for loop, but if we know that all elements of a list are of the same type then we can just look at the type of any element in that list:

```
type(logic[0])
```

```
## <class 'bool'>
```

```
diff_types = [False, "Space", 2]
for i in diff_types:
  print(type(i))
```

```
## <class 'bool'>
## <class 'str'>
## <class 'int'>
```

Another instance of a data type in `Python` is called a *tuple* which is an ordered, immutable collection of elements. Like lists, tuples can contain elements of different data types, including numbers, strings, and other objects. However, unlike lists, *tuples cannot be modified once they are created.* This means that you cannot add, remove, or modify elements in a tuple after it has been defined. *Tuples are defined using parentheses*, and elements are separated by commas:

```
tuple_ex = (1, 'apple', True)
```

What do you think the output of the following code will be?

```
tuple_ex[0] = 4
```

```
## 'tuple' object does not support item assignment
```

Exercise 3: What happens when we try to mix different data types into one vector? Speculate what will happen when we run each of the following lines of code:

```
num_char = [1, 2, 3, "a"]

# for i in num_char:
#   print(type(i))

num_logic = [1, 2, 3, False]

#type(num_logic)
# for i in num_logic:
#   print(type(i))

char_logic = ["a", "b", "c", True]

guess = [1, 2, 3, "4"]
```

In each of these vectors, the two types of data were *coerced* into a single data type. This happens in a hierarchy, where some data types get preference over others. Can we draw a diagram of the hierarchy? #Not include in reviewed:

Answer:

The hierarchy of types in `Python` is as follows, using > to represent the order: `type > int > float > bool > str > list > tuple > set > dict >`···

Remarks:

In `Python` an `R` list is equivalent to a dictionary. In `R` a `Python` list is equivalent to vector.

What about a list of lists in 'Python'?

```
OS = ["Mac", "Windows", "Linux"]
fav_nums = [12, 13, 17]
logic = [True, False, False]
```

```
layered_list = [OS, fav_nums, logic]
layered_list[1]
```

```
## [12, 13, 17]
```

```
layered_list[0][1]
```

```
## 'Windows'
```

So to access the elements of list within a list we use the syntax `list[list_i][element]`.

Remarks:

- We have been outputting values with `print()` and by just running the name of the variable, why can we do this?
  - When running code in a Jupyter notebook or in an interactive Python shell (such as `RStudio`), you can simply type the name of a variable or expression to see its value printed. This is because the notebook automatically displays the output of any expression that is executed without explicitly requiring the use of `print()`.
  - When running a Python script from the command line or in an IDE, you must use print() to display output. If you don't use `print()`, the output will not be displayed.

Named Lists

To create a named list in `Python`, you can use a dictionary:

```
my_named_list = {'title': 'statistics', 'numbers': list(range(1, 11)),
'data': True}
print(my_named_list)
```

```
## {'title': 'statistics', 'numbers': [1, 2, 3, 4, 5, 6, 7, 8, 9, 10], 'data': True}
```

Importing Data

- Use the **Import Dataset** button in the **Environment** tab
- Choose the **From Text (base)** option
- Click on the **Browse** button
- Direct the computer to where you saved the `BlackfootFish.csv` data file, click **open**
- It will bring up a preview of the data
- Make sure that the box labeled "Strings as factors" is not checked
- Click on the **Import** button

Notice the code that outputs in the console (the bottom left square). This is the code that you could have typed in the code chunk below to import the data yourself. Copy and paste the code that was output in the code chunk below.

Recall the module `pandas` mentioned earlier? `pandas` is a popular `Python` library used for data manipulation and analysis. It provides data structures for efficiently storing and manipulating large, structured data sets and includes functions for data cleaning, merging, filtering, and appending.

If you haven't already, install the `pandas` module:

~~~
```{python}`python''`
~~~

```
!pip install pandas
```

```
```
```

```
#!pip install pandas
import pandas as pd
BlackfootFish = pd.read_csv('BlackfootFish.csv')
```

The path provided can also be simplified to just include the file name - if the .Rmd and data are saved in the same folder. If you have any trouble reading in the data set, here is code that allows you to read the data from our github repository:

```
BlackfootFish = pd.read_csv("https://github.com/saramannheimer/data-science-r\
-workshops/raw/master/Introduction%20to%20R/AY%202020-2021/Student%20Version/\
BlackfootFish.csv")
```

Structure of Data

The data we will use is organized into data tables. When you imported the BlackfootFish data into `RStudio` it was saved as an object. You are able to inspect the structure of the BlackfootFish object using functions built in to `Python` (no packages necessary).

Run the following code. What is output from each of the following commands?

```
print(type(BlackfootFish)) # Class of the object
```

```
## <class 'pandas.core.frame.DataFrame'>
```

```
print(BlackfootFish.shape) # Number of rows and columns
```

```
## (18352, 7)
```

```
print(BlackfootFish.columns) # Column names
```

```
## Index(['trip', 'mark', 'length', 'weight', 'year', 'section', 'species'], dtype='object')
```

```
print(BlackfootFish.dtypes) # Data types of each column and the first few rows of data
```

```
## trip          int64
## mark          int64
## length      float64
## weight      float64
## year          int64
## section      object
## species      object
## dtype: object
```

```
BlackfootFish.describe()
```

```
##                 trip          mark        length        weight          year
## count  18352.000000  18352.000000  18352.000000  16556.000000  18352.000000
## mean       1.500763      0.092851    262.330025    246.220363   1996.626744
## std        0.500013      0.290231     99.902006    272.285241      5.922414
## min        1.000000      0.000000     16.000000      0.000000   1989.000000
## 25%        1.000000      0.000000    186.000000     65.000000   1991.000000
## 50%        2.000000      0.000000    250.000000    150.000000   1996.000000
## 75%        2.000000      0.000000    330.000000    330.000000   2002.000000
## max        2.000000      1.000000    986.000000   4677.000000   2006.000000
```
```

```
type(BlackfootFish)
```

```
## <class 'pandas.core.frame.DataFrame'>
```

When we inspect dataframes, or other objects in `Python`, there are some general functions that are useful to check the content/structure of the data. Here are some (assuming you are importing data using `pandas`):

- size:
  - `datasetname.shape` : rows and columns
  - If your data set is a pandas dataframe `datasetname.shape[0]`: number of rows,
  - If your data set is a pandas dataframe `datasetname.shape[1]`: number of columns.
  - If your data set is a pandas dataframe and variable is a column in the dataframe: `len(datasetname['variable'])`: number of columns.
- content:
  - `datasetname.head()`: first 5 rows.
  - `datasetname.tail()`: last 5 rows.
- names:
  - `colnames(datasetname)`: column names.
  - `datasetname.index`: row names.
- summary of content:
  - `datasetname.info()`: structure of object and information about the columns.
  - `datasetname.describe()`: summary statistics for each column.

Dataframes

What is a dataframe? A dataframe is a two-dimensional table-like data structure, similar to a spreadsheet. It is a primary data structure provided by the pandas library. You can create a dataframe in several ways, such as loading data from a CSV, Excel file, SQL database, or by constructing it from scratch using `Python` lists or dictionaries. A dataframe is made up of columns, where each column is a series object. Each column can have a different data type, but all the values in a column must have the same data type.

Extracting Data

In `Python`, you can access a specific column of a dataframe using square bracket notation `[]` with the column name inside the brackets. What do you think the following code will output?

```
df = pd.read_csv('BlackfootFish.csv')

# Access the 'weight' column
weight_col = df['weight']

print(weight_col)
```

```
## 0        175.0
## 1        190.0
## 2        245.0
## 3        275.0
## 4        300.0
##          ...
## 18347     35.0
## 18348     60.0
## 18349     10.0
## 18350    215.0
## 18351     10.0
## Name: weight, Length: 18352, dtype: float64
```

#Remove afer review: This will print the weight column as a Pandas Series

```
years = BlackfootFish['year']
# extracts year from the dataset and saves it into a new variable named years
years.head
```

```
## <bound method NDFrame.head of 0        1989
## 1        1989
## 2        1989
## 3        1989
## 4        1989
##          ...
## 18347    1991
## 18348    1991
## 18349    1991
## 18350    1991
## 18351    1991
## Name: year, Length: 18352, dtype: int64>
```

```
years_str = str(years)
print(years_str)
```

```
## 0        1989
## 1        1989
## 2        1989
## 3        1989
## 4        1989
##          ...
## 18347    1991
## 18348    1991
## 18349    1991
## 18350    1991
## 18351    1991
## Name: year, Length: 18352, dtype: int64
```

```
## How would you determine how long the vector is?
```

Another method for accessing data in the dataset is using the `pandas` function `iloc[]`. If you look to your right in the **Environment** window, you notice that RStudio tells you the dimensions of the BlackfootFish data. You can (roughly) view the dataset as a matrix of entries, with variable names for each of the columns. I could instead use `iloc` function to perform the same task as above, using the following code,

```
# Extract the values in the fifth column and store them in a variable called "years"
years = BlackfootFish.iloc[:, 4].values
```

Practice:

The following is a preview of the dataframe `df`:

```
df = pd.DataFrame({
  'x': ["H", "N", "T", "W", "V"],
  'y': ["May", "Oct", "Mar", "Aug", "Feb"],
  'z': [2010, 2015, 2018, 2017, 2019]
})

df
```

```
##    x    y     z
## 0  H  May  2010
## 1  N  Oct  2015
## 2  T  Mar  2018
## 3  W  Aug  2017
## 4  V  Feb  2019
```

Exercise 4: What would be output if you entered: `df.iloc[2, :]`?

Exercise 5: What would you input to get an output of `2015`? Can you think of two ways to do it?

```
df.iloc[1,:]
```

```
## x       N
## y     Oct
## z    2015
## Name: 1, dtype: object
```

```
df.loc[df['y'] == 'Oct', 'z'].item()
```

```
## 2015
```

```
# a third way
df["z"][1] # select first 2nd row of "z" column
```

```
## 2015
```

Remarks:

- Notice the difference between `loc` and `iloc`. Both are indexing methods in `pandas` that allow for selection of data from a data frame, how do they differ?
  - `iloc` selects data based on the integer index of the rows and columns, with syntax `df.iloc[row_index, column_index]`.
  - `loc` selects data base on the row and column labels, with syntax `df.loc[row_label, colum_label]`.
  - *WARNING* `iloc` is exclusive of the end index, `loc` is inclusive.
  - `iloc` does not support Boolean indexing, `loc` does.

Accessing Data

When we have a data frame or a list of objects, we can extract specific items by specifying their position in the data frame or list. We saw how to do this with a single item, row, or column that we want to extract (`df.iloc[1, 5]`, `df.iloc[3,]` or `df.iloc[, 5]`). We can specify two items, rows, or columns by either using the fact that the two things we want are adjacent, or we can combine what we want into a list that we can then use for extracting. We will continue to use the indices to specify what we want to extract.

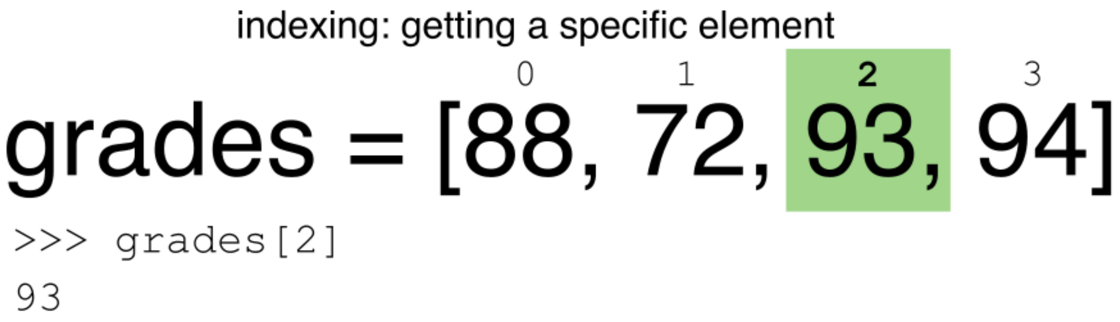
Python uses zero-based indexing, which means you have to shift your start and stop indices, they might not be exactly as you would intuitively expect. The images below came from datacarpentry.org (https://datacarpentry.org/python-ecology-lesson/03-index-slice-subset.html).

For example, `[0]` or `0:1` could identify the first object in a list, and `[0, 1]` could identify the first two objects in a list. However they are adjacent so we could use `a:b+1` to indicate that we want everything from position `a` to position `b` in the list. So, `[1,3]` would give the same items as `1:3`.

Quick Check Run the following code to see what you get. Play around with the first and last numbers to see what happens.

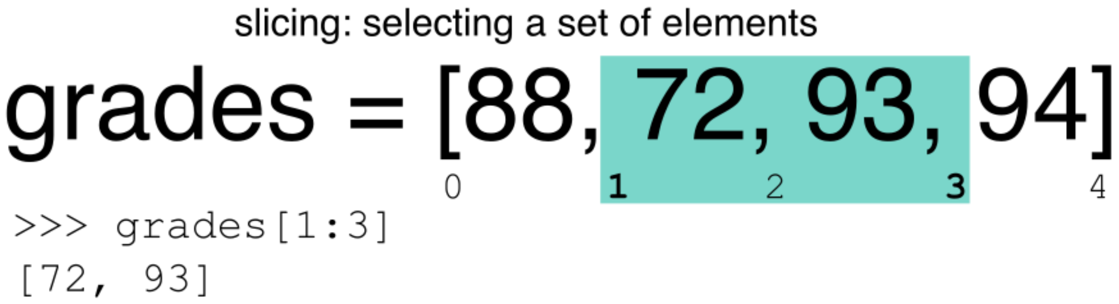
```
list([1,2,3,4,5])
```

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


indexing: getting a specific element
0
1
2
3
grades = [88, 72, 93, 94]

```
>>> grades[2]
93
```

Figure 5: Python List Indexing for a Single Element


slicing: selecting a set of elements
grades = [88, 72, 93, 94]
0
1
2
3
4

```
>>> grades[1:3]
[72, 93]
```

Figure 6: Python List Indexing for a Range of Elements

```
list(range(1,6))
```

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

```
list(range(6,1,-1))
```

```
## [6, 5, 4, 3, 2]
```

```
list(range(123,131))
```

```
## [123, 124, 125, 126, 127, 128, 129, 130]
```

```
list(range(3,-1,-1))
```

```
## [3, 2, 1, 0]
```

```
list([1,2,3,4,5])[1:3]
```

```
## [2, 3]
```

```
list(range(123,131))[3:6]
```

```
## [126, 127, 128]
```

```
list(range(6,1,-1))[2:4]
```

```
## [4, 3]
```

When you want adjacent items, using the `a:b` notation is nicer than having to type out all of the values.

What about non-adjacent items?

For non-adjacent items, you just need to fall back on listing everything out. Say you want the first, third, and 9th item in a list. Then you can use `[1, 3, 9]`.

Now that we've talked about how to create lists of the indices we want, how do we use these lists to extract items?

Using our data frame that we created above, to extract rows 1 and 2 we can use the notation `[1,2]` (or `1:3` since they are adjacent).

```
df.iloc[[1,2],]
```

```
##    x    y     z
## 1  N  Oct  2015
## 2  T  Mar  2018
```

```
df.iloc[1:3, ]
```

```
##    x    y     z
## 1  N  Oct  2015
## 2  T  Mar  2018
```

If we want to extract rows 1 and 3, we can use this list of indices: `[1, 3]`

```
df.iloc[[1,3],]
```

```
##    x    y     z
## 1  N  Oct  2015
## 3  W  Aug  2017
```

NOTE: Instead of using indices you can also do the same technique with names if the rows or columns are named.

Exercise 6: How would you pull off only columns `x` and `y`? What about pulling off only columns `x` and `z`?

```
df.iloc[:, [0,1]]
```

```
##    x    y
## 0  H  May
## 1  N  Oct
## 2  T  Mar
## 3  W  Aug
## 4  V  Feb
```

```
df.loc[:, ['x','z']]
```

```
##    x     z
## 0  H  2010
## 1  N  2015
## 2  T  2018
## 3  W  2017
## 4  V  2019
```

Exercise 7: How would you modify the script below, to get an output of `22 24`?

```
s = [22, 24, 49, 18, 1, 6]
s
```

```
## [22, 24, 49, 18, 1, 6]
```

```
s[2]
```

```
## 49
```

Exercise 8: What would be output if you entered: `s[2, ]`?

Changing Data Type

In `Python`, when building or importing a dataframe, character columns are usually represented as strings (i.e., text) by default. **Unlike in R, there is no factor data type in** `Python`. In `Python` you can use the `Pandas` library, which provides functions like `read_csv()` and `read_table()` to import data from CSV. `Pandas` does not convert string columns to any other data type, but it does infer the data type of each column.

If you want to explicitly set the data type of a column or keep a string column as a string, you can use the dtype parameter in `read_csv()` to specify the data type for each column:

```
import pandas as np
df = pd.read_csv('BlackfootFish.csv', dtype = {'column':str})
```

Remarks:

- If you are familiar with `R` note that there is no equivalent `stringAsFactors` argument in `read_csv()` from `pandas`.

If you want to determine the unique elements in a column of a dataframe in `Python`, you can use the `unique()` method of `pandas`:

```
BlackfootFish['species'].unique()
```

```
## array(['RBT', 'WCT', 'Bull', 'Brown'], dtype=object)
```

```
BlackfootFish['species'].unique
```

```
## <bound method Series.unique of 0          RBT
## 1          RBT
## 2          RBT
## 3          RBT
## 4          RBT
##          ...
## 18347    Brown
## 18348    Brown
## 18349    Brown
## 18350    Brown
## 18351    Brown
## Name: species, Length: 18352, dtype: object>
```

What are the difference in outputs? Using `unique()` the output is an array of the unique values in the `species` column of BlackfootFish. If we leave out the parenthesis, i.e., `unique` the output will be the details of the dataframe, including data type, and its length, so no unique values. The key difference is that `unique()` is a **method** from the `pandas` library, that is, some sort of function. On other hand `unique` is an **attribute** (if it exists) of the object.

Exercise 9: Year was saved as an integer data type (1989 - 2006), but we may want to consider it to be a categorical variable (a factor). Write the `Python` code to create a new variable called `yearF` and then check the unique categories for this new variable.

```
BlackfootFish['yearF'] = BlackfootFish['year'].astype('category')
### Write code to check the unique categories of yearF:
```

Alternatively,

```
BlackfootFish['yearF'] = pd.Categorical(BlackfootFish['year'])
BlackfootFish['yearF'].unique()
```

```
## [1989, 1990, 1991, 1993, 1996, 1998, 2000, 2002, 2004, 2006]
## Categories (10, int64): [1989, 1990, 1991, 1993, ..., 2000, 2002, 2004, 2006]
```

```
BlackfootFish['yearF'].unique
```

```
## <bound method Series.unique of 0        1989
## 1        1989
## 2        1989
## 3        1989
## 4        1989
##          ...
## 18347    1991
## 18348    1991
## 18349    1991
## 18350    1991
## 18351    1991
## Name: yearF, Length: 18352, dtype: category
## Categories (10, int64): [1989, 1990, 1991, 1993, ..., 2000, 2002, 2004, 2006]>
```

Exercise 10: Now, verify that `yearF` is viewed as a categorical variable, with the same levels as `year`. (hint: you have already used functions that would do this for you)

```
print(BlackfootFish.dtypes)
```

```
## trip          int64
## mark          int64
## length      float64
## weight      float64
## year          int64
## section      object
## species      object
## yearF      category
## dtype: object
```

Packages

As we mentioned previously, `Python` has many packages, which people around the world work on to provide and maintain new software and new capabilities for `Python`. We have already shown some examples like `panda`, `numpy`, and `math` and how to load them, we give a formal description now. You will slowly accumulate a number of packages that you use often for a variety of purposes. In order to use the elements (data, functions) of the packages, you have to first install the package (only once on a given computer) and then load the package (every time). If you are working with `RStudio` as an IDE for `Python` then you must make sure to have the package `reticulate` installed and loaded into `R`:

In an `R` chunk:

~~~~
```{r}
install.packages("reticulate")
library(reticulate)
```
~~~~

Now you can install any `Python` library as illustrated with the following example:

```
#Install statsmodels
#!pip install scipy
#!pip install numpy
from scipy import stats as stats
```

```
import numpy as np

# generate random numbers from a normal distribution
mu, sigma = 0, 1
samples = stats.norm.rvs(loc=mu, scale=sigma, size=1000)

# compute summary statistics
mean = np.mean(samples)
std = np.std(samples)

print(f'The mean is {mean} and the standard deviation is {std}')
```

```
## The mean is 0.03843292939644177 and the standard deviation is 1.017950882235217
```

Here we have installed the package/module `scipy.stats` which provides a wide range of probability distributions. The module includes functions for working with both continuous and discrete distributions. The general syntax is `stats.distribution`, in the above example `stats.norm.rvs(loc, scale, size)` generates a sample of size = n of random numbers from a normal distribution where `loc` (location) specifies the mean of the distribution, and `scale` specifies the standard deviation.

Moreover, notice that we made use of the `numpy` module, as it contains functions such as `mean` and `std` that can be applied to Numpy arrays. Finally we print out the output.

Additional Comments: For printing the output we used a `Python f-string` which is used to print a sentence along with a calculated value of a variable, with syntax `print(f'The result is {variable}')`.

Finding Help

`Python` has a great collection of packages and documentation, making it a popular choice for data science and scientific computing. Some of the most commonly used modules for statistical analysis, machine learning, data visualization, and much more are `NumPy`, `Pandas`, `SciPy`, `scikit-learn`, `Matplotlib`, among others. If you need a function to complete a task (say find the variance), but are not quite sure how it's spelled, what arguments it takes, or what package it lives in, don't fret! `Python` has a built-in `help()` function used to get information about `Python` functions, modules, and classes.

Another great resource for finding help is *Stack Overflow* Python's community, which is a good place to start as a beginner to learn and use `Python`.

Functions

In `Python` there are both functions that are built in (require no package to be loaded), as well as functions that are housed within specific packages. You have already used a few built in functions to inspect the structure of the BlackfootFish data (`print`, `type`, `describe`).

As you may know, a function transforms an input (potentially multiple) into an output. You have to provide `Python` with the inputs (arguments) required for the function to generate an output. The argument(s) inside a function happen after the `(` symbol. One way to identify that an object is a function when it is immediately followed by a `(` and the corresponding closing `)` comes after the arguments are complete. The output of a function does not have to be numerical and it typically is not a single number, it can be a set of things or a dataset.

Suppose we wanted to create a vector of 10 zeros. To do this, we would use the `np.array` function:

```
import numpy as np
# repeating 0 ten times
np.array([0] * 10 )
```

```
## array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0])
```

```
[0] * 10
```

```
## [0, 0, 0, 0, 0, 0, 0, 0, 0, 0]
```

```
# switching order of arguments
np.array(10 * [0])
```

```
## array([0, 0, 0, 0, 0, 0, 0, 0, 0, 0])
```

```
10 * [0]
```

```
## [0, 0, 0, 0, 0, 0, 0, 0, 0, 0]
```

Now let's look over some other functions that are often used:

```
# takes a numerical input, but there are NA's in our data
np.mean(BlackfootFish['weight'])
```

```
## 246.22036337279536
```

```
# notice Python ignores NAs automatically.
np.mean(BlackfootFish['weight'].dropna())
```

```
## 246.22036337279536
```

```
# gives an error because the input is not the correct data type
# np.median(BlackfootFish['species'])


np.corrcoef(BlackfootFish['length'], BlackfootFish['weight'])
```

```
## array([[ 1., nan],
##        [nan, nan]])
```

```
# Does corrcoef have an option to remove NA's? No, np.corrcoef does not have an option
# to remove NA's, you must deal with missing values before calling the function.
```

One way to remove the missing values and then compute the correlation coefficient is:

```
valid_mask = ~np.isnan(BlackfootFish['length']) & ~np.isnan(BlackfootFish['weight'])
length_valid = BlackfootFish['length'][valid_mask]
weight_valid = BlackfootFish['weight'][valid_mask]

corr_coeff = np.corrcoef(length_valid, weight_valid)[0,1]

print(f"The correlation coefficient is: {corr_coeff}")
```

```
## The correlation coefficient is: 0.8856327037417443
```

Let's break it down line by line:

- Line 1: `np.isnan()` finds the data points that have missing values in the data. `~` is a logical operator that inverts/negates, so `~np.isnan()` will return `True` for all data points with no NA's. Now this will create a "mask" which is a logical (boolean) array. The symbol `&` will combine the two masks into one.
- Line 2 and 3: We use the index of `valid_mask` to create `length` and `weight` variables with no missing values.
- Line 4: `np.corrcoef()` returns a correlation matrix where the (0,0) entry is the correlation coefficient between the first array with itself. The entry (1,1) is the correlation coefficient between the second array with itself. The entries (0,1)=(1,0) are the correlation coefficient between both arrays, hence the `[0,1]`.

- Line 5: We then use an `f-string` to print the output in a nice way.

As seen in the functions above, some functions have *optional* arguments. If they are not specified by the user, then they take on their default value (`True` for `dropna`). These options control the behavior of the functions, such as whether it includes/excludes NA values.

Cleaning Data

In many instances, you will deal with data that are not "clean". Based on the output we received from the `np.mean()` function, we know that there are NA's in the BlackfootFish data, possibly across a variety of variables. Before we used `dropna` as an option to remove NA's *within* a function. We can use the same command on the entire data frame before applying any functions to it. Based on the output below, how many rows in the BlackfootFish data have an NA present?

```
BlackfootFish.shape # gives the dimensions of the dataset in (row, column) format
```

```
## (18352, 8)
```

```
BlackfootFish.dropna().shape
```

```
## (16556, 8)
```

```
# .dropna() is method in Pandas which removes missing values (NaN).
```

Remark: The computer is using an algorithm to return a dataset with no NA values anywhere in it. This algorithm goes through every row of the dataset and (roughly) has the following steps,

- Inspect each row or column to check for missing values (an alternative to `dropna` is the `isnull` method).
- If a row or column contains NaN's, it is dropped (removed) from the data frame.
- Once it has stepped through every row, the function outputs the "cleaned" dataframe

If we wish to remove all of the NA's from the dataset, we can use the `dropna` command from above. We can save the new "clean" dataset under a new name (creating a new object) or under the same name as before (replacing the old object with the new object).

```
BlackfootFish_clean = BlackfootFish.dropna()
# Creates a new dataframe, where the NA's have all been removed
```

Data Visualization

There are many different genres of data graphics, with many different variations on each genre. Here are some commonly encountered kinds:

- **scatterplots**: showing relationships between two quantitative variables

- **distributions**: showing distributions of a single quantitative variable

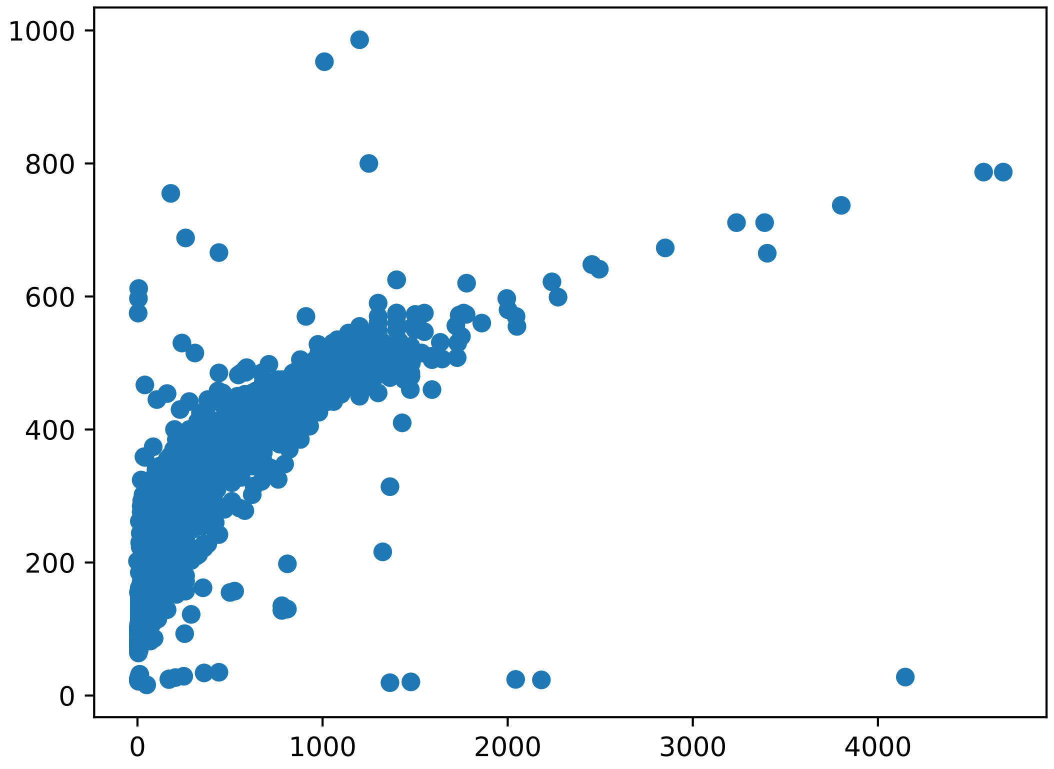
- **bar charts**: displaying frequencies or densities of a single categorical variable

Scatterplots

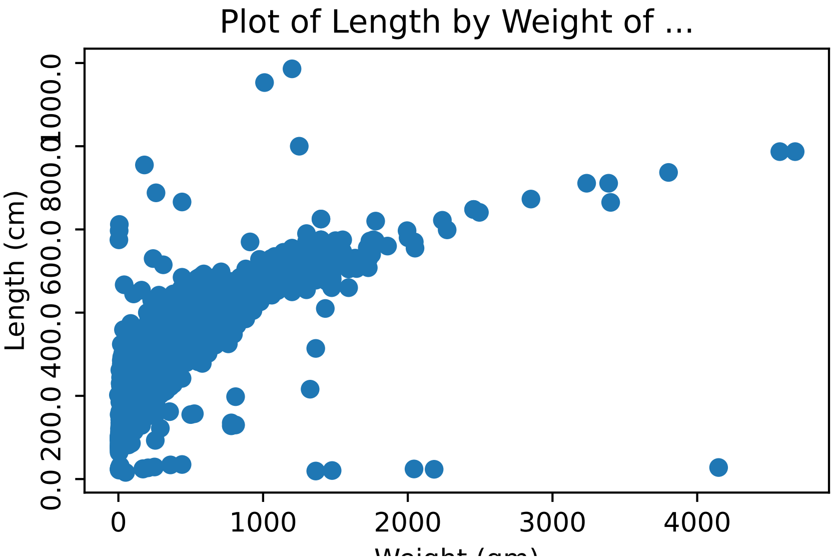
The main purpose of the scatterplot is to show the relationship between two variables across several or many cases. Most often, there is a Cartesian coordinate system in which the x-axis represents one variable and the y-axis the second variable.

```
#!pip install matplotlib
import matplotlib.pyplot as plt
```

```
plt.scatter(BlackfootFish_clean['weight'], BlackfootFish_clean['length'])
plt.show()
```



```
import matplotlib.pyplot as plt
fig, ax = plt.subplots() # creates a new figure and an axes object to plot data on
ax.scatter(BlackfootFish_clean['weight'], BlackfootFish_clean['length'])
ax.set_xlabel('Weight (gm)') # adding in axis labels
ax.set_ylabel('Length (cm)')
ax.set_yticklabels(ax.get_yticks(), rotation = 90) # changing orientation of
                                                    #y-axis labels
ax.set_title('Plot of Length by Weight of ...') # adds a title
plt.show()
```



Let's breakdown the following line `ax.set_yticklables(ax..get_yticks(), rotation = 90)`:

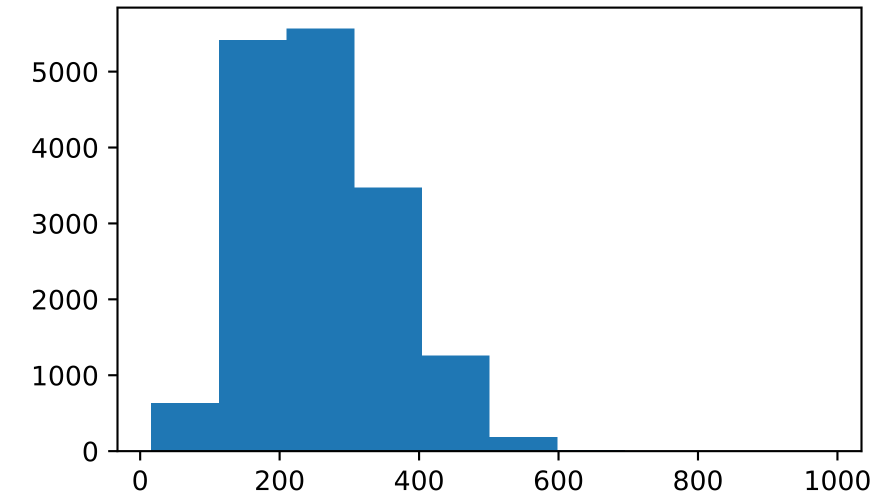
- `ax` is for `Axes` which is an object in `Matplotlib`, representing, you guessed it, the plot's axes.
- `ax.set_yticklabels()` is a method of `Axes` class, which set the labels for the y-axis "ticks".
- `ax.get_yticks()` returns the locations of the y-axis ticks.
- `rotation = 90` is self explanatory.
- `set_yticklabels()` specifies the angle (in degrees) by which the axis is rotated.

Distribution

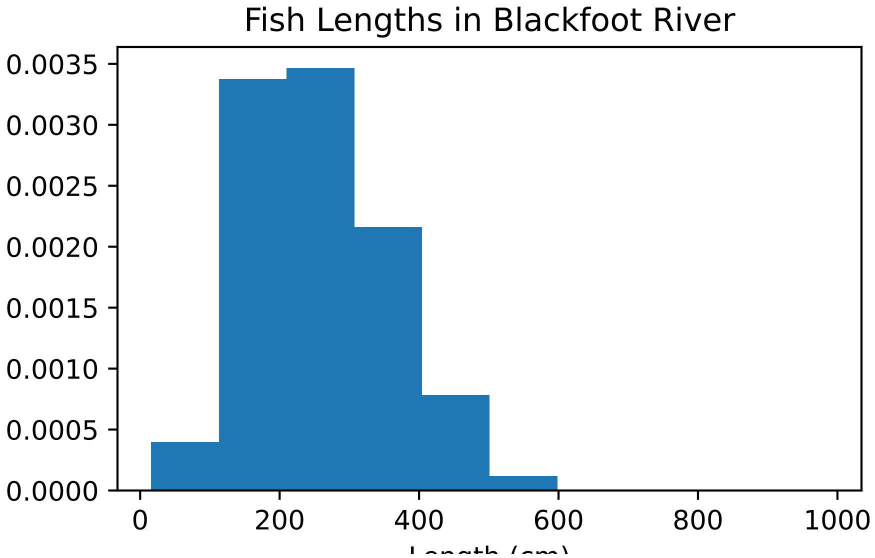
A histogram shows how many observations fall into a given range of values of a variable and can be used to visualize the distribution of a single quantitative variable.

By default, Matplotlib will use the current figure and axes to plot any new data, unless you explicitly create a new figure and axes object.

```
fig, ax_hist = plt.subplots()
ax_hist.hist(BlackfootFish_clean['length']);
plt.show()
```

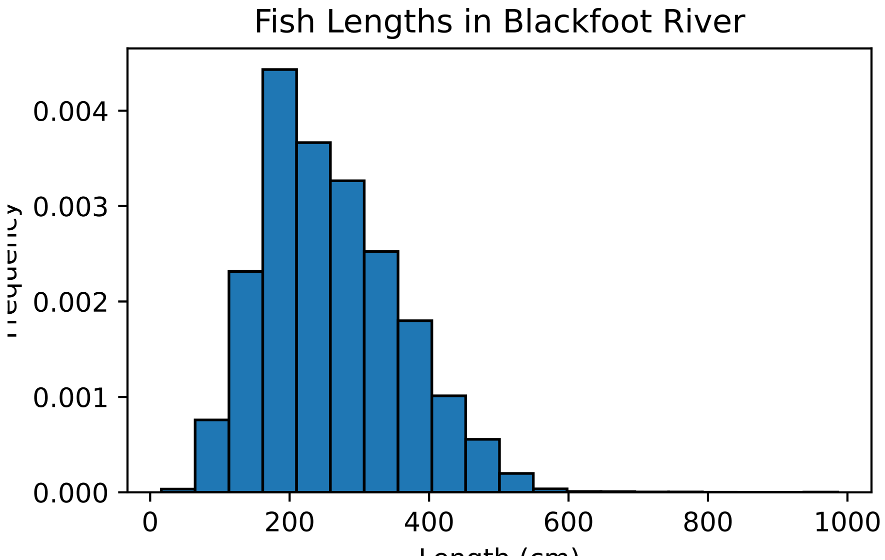


```
fig, ax_hist = plt.subplots()
# converts to a density plot (area adds to 1)
ax_hist.hist(BlackfootFish_clean['length'], density=True);
# adds x-axis label
ax_hist.set_xlabel('Length (cm)')
ax_hist.set_ylabel('Frequency')
# adds title to plot
ax_hist.set_title('Fish Lengths in Blackfoot River')
plt.show()
```



```
fig, ax_hist = plt.subplots()
# converts to a density plot (area adds to 1)
ax_hist.hist(BlackfootFish_clean['length'], density=True, edgecolor = 'black',
bins = 20);
# adds x-axis label
ax_hist.set_xlabel('Length (cm)')
ax_hist.set_ylabel('Frequency')
```

```
# adds title to plot
ax_hist.set_title('Fish Lengths in Blackfoot River')
plt.show()
```

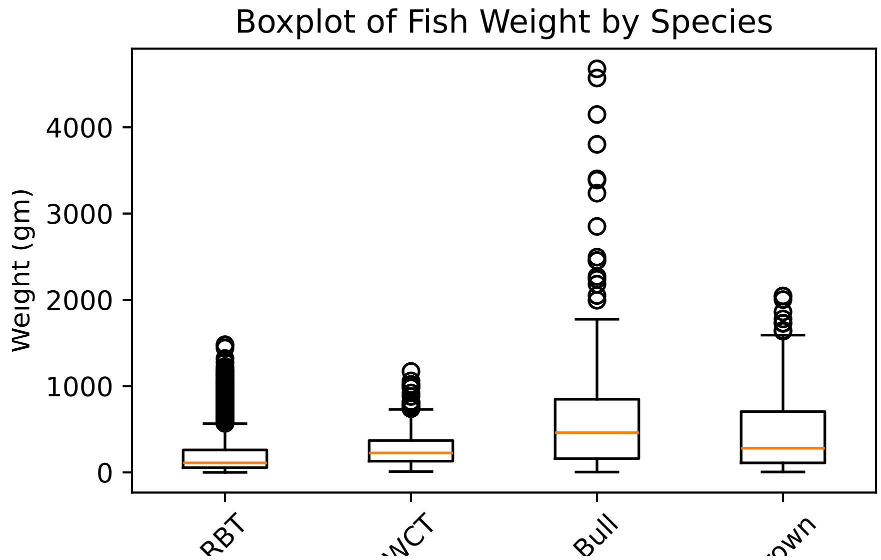


Side-by-Side Boxplots

The familiar boxplot is a simple display to use when the objective is to compare the distribution of a quantitative variable across different levels of a categorical variable.

```
# Create a list of weight data for each species
weight_data = [BlackfootFish_clean[BlackfootFish_clean['species'] == s]['weight']
for s in BlackfootFish_clean['species'].unique()];

fig, ax_box = plt.subplots()
ax_box.boxplot(weight_data);
ax_box.set_xticklabels(BlackfootFish_clean['species'].unique(), rotation=45);
ax_box.set_xlabel('Species')
ax_box.set_ylabel('Weight (gm)')
ax_box.set_title('Boxplot of Fish Weight by Species')
plt.show()
```



Let us explore the line `[BlackfootFish_clean[BlackfootFish_clean['species'] == s]['weight'] for s in BlackfootFish_clean['species'].unique()];`: The code creates a list of weight data for each unique species in the following way:

- `BlackfootFish_clean['species'] == s` selects the rows where the `species` column matches a particular (s) unique species name.
- `BlackfootFish_clean['species'].unique()` generates such s values.
- `BlackfootFish_clean[...]['weight]` selects only the `weight` column. In particular the weight data for each unique species s.

Bar Charts

Bar charts are an effective way to compare the frequencies of levels of a categorical variable.

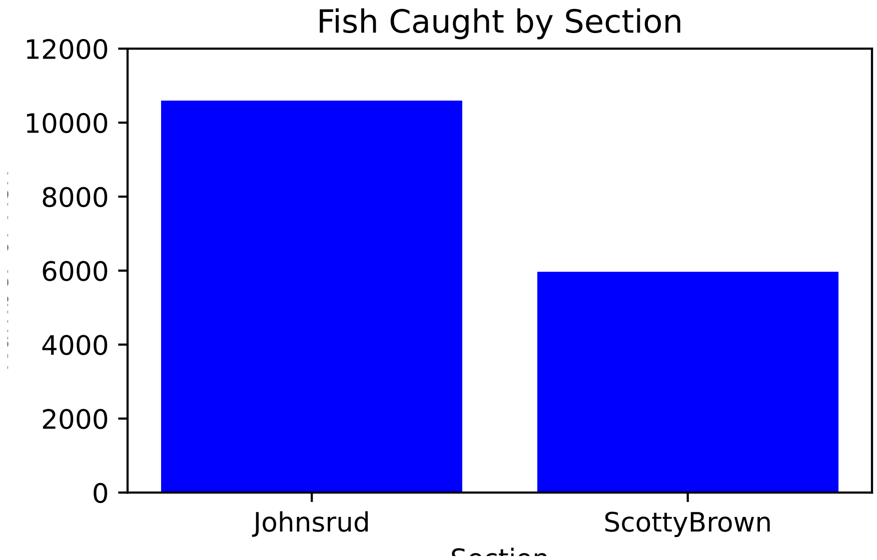
```
section = BlackfootFish_clean['section'].value_counts()

fig, ax_bar = plt.subplots()

ax_bar.bar(section.index, section.values, color='blue')
ax_bar.set_xlabel('Section')
ax_bar.set_ylabel('Number of Fish')
ax_bar.set_title('Fish Caught by Section')
ax_bar.set_ylim([0, 12000])
```

```
## (0.0, 12000.0)
```

```
plt.show()
```



Practice

Exercise 11: Using statistics or graphics, which year in our dataset had the most fish caught?

Exercise 12: Make a boxplot of the fish weights over the different years in the dataset.

Knitting/compiling

Hopefully at this point you have fixed all the code errors in the file we initially provided as you learned about the `Python` code and functions. A final (and often intermediate step) is to compile your Rmarkdown file into an HTML, Word, or PDF document. The compiling process will verify that the code you wrote works in the order that it is present in the document and is your reproducible result to share with colleagues and collaborators. The .Rmd is your archive of the code used to produce those results from the data.

The HTML format is the least nice for printing but also has the fewest dependencies on other software to compile. Compiling to Word requires a word processing software like Microsoft Word. Compiling to PDF either requires the `tinytex` package in `R` or a separate installation of `miktex`, so often requires additional steps beyond what we want to discuss today.

To attempt to knit to one of these formats, go to “Knit” and click on the triangle to select the “Knit to . . . ” version. The entire suite of code will be re-run from beginning to end and, if it works, compiled into the document type you specified.

Exiting RStudio

Finally, when you are done with your work and attempt to exit out of `RStudio`, it will ask you to save your workspace. **DO NOT DO THIS!** It will just create a cluttered workspace and could even cause you to get incorrect results. In fact, you should go into the Tools -> Global Options and then make sure that “Save workspace to .RData on exit” option on the first screen you will see is set to Never. If you save your `Python` code either as a .R or (better) an R Markdown (.Rmd) file, you can re-create any results by simply re-running that code or re-knitting the file.

Projects in `RStudio`

`RStudio` projects provide a way to organize all the code and data in one place and many consider these the best way to work in `RStudio`. We chose to avoid this step and just use a single .Rmd file to expedite your first experience using `RStudio`. A motivation for using projects is that it is important to organize your data and script files into the same or related locations and have different locations for different iterations of projects. If you don't do this:

- it is really hard to tell which version of your data is original and what versions are modified
- things get really messy because all types of files are mixed together
- it's probably hard for you to find things and relate the correct files to their respective output

Ultimately, good project organization will make your life easier! It helps ensure the integrity of your data, makes it simpler to share your code or get help with your code, allows for you know exactly what code you used on a paper, and it's easier to pick a project back up.

It is good code writing and file storage practice to keep a set of all related data, analysis, plots, documents, etc. in the same folder. `RStudio` makes this process easy with using their projects. In an `RStudio` project, all of the project's pieces are in the same folder. This allows for a clean workflow and a simple working directory for `Python`.

Whenever you start working on a new project in RStudio, go through the following steps:

1. Click on the "File" menu button, then select "New Project"
2. Click "New Directory"
3. Click "New Project"
4. Create a name for your project (make it explanatory!)
5. Select where the project should live
6. Click the "Create Project" button
7. Open the project!

After this process `R` will be searching for objects (such as data) in the <u>same</u> folder as the project. This allows for us to keep all of our files in a self-contained system.

After saving your previous work today, you can try to create a project in a new folder on your computer. After you create the project, you can create a new .Rmd file and copy and paste the text from this document into this file. And move a copy of the BlackfootFish.csv into the project folder you created. Whenever you open this project it will take you directly to the work you have done in that project folder. It may be useful to close the project before exiting RStudio to avoid confusion in later sessions.

Terminology Used in Workshop

- *Command*: A command is what `Python` executes. In an `Python` script file (script.py), commands are automatically implied, as this type of file does not accept text, only in comments. In an Rmd (Markdown) file (report.Rmd), commands are delineated between three ticks on the top (`` ```{python} ``) and three ticks (`` ``` ``) on the bottom.

  ~~~
  ```{python}`python '''`
  # Your code goes here
  ```
  ~~~

- *Comment*: Helpful text added into a script environment. Comments can be used to describe functions, processes, a train of thought, so that when you return to your code, tomorrow or next year, you are able to understand the purpose of each line of code! Comments are preceded by `#` within a code chunk.

- *Object*: A variable created in `Python`, to be used elsewhere in the code. Objects can be a variety of things, such as scalars (`x = 3`), vectors (`x = c(1, 2, 3, 4, 5)`), matrices, and dataframes, to name a few.
- *Assignment*: The assignment `=` is used to assign values on the right to the objects on the left (`x = 1`).
- *Type*: Most `Python` objects have a type attribute, a character vector giving the names of the types from which the object inherits. Examples of types are numeric, boolean, sequence types, DataFrame, tuple, list.
- *Vector*: A vector is a list of entries, all sharing the same class. A vector has only one dimension, so data extraction uses only a single entry in brackets (e.g. `x[3]`). You can create vectors of characters (`["a", "b", "c"]`), vectors of numbers (`[1, 2, 3]`), to name a few.
- *Matrix*: Similar to what you may have seen in a mathematics class, a matrix in `Python` is a two-dimensional array of numbers, symbols, or expressions arranged in rows and columns.
- *List*: A generic vector, which contains other objects. A list can contain a variety of different classes of objects, e.g., characters, vectors, data.frames, matrices, or outputs from a model! A dataframe is a special type of list where the components are vectors and they all have the same length.
- *Dataframe*: In Python, a dataframe is a two-dimensional table-like data structure that is commonly used for data analysis and manipulation, where you are able to extract elements using bracket (`[]`) notation.
- *Argument*: Input(s) into a function, so that an output is created. Most functions take named arguments (e.g., `data = BlackfootFish`) and the order of the arguments is assumed to follow the order found in the function's help file. When using a named argument in a function, the name comes first, followed by an `=` sign, then the input.
- *Logical Value*: `True` and `False` value(s) that can be used to turn off/on options in functions and plots, and also to manipulate data.

Workshop Materials & Recordings Available:

- email Sara Mannheimer (sara.mannheimer@montana.edu)
- through the MSU Library YouTube channel: https://www.youtube.com/watch?v=W6E3hpcoUkQ&feature=youtu.be
- other related information: http://www.montana.edu/datascience/

How to Learn More About `Python`

This material is intended to provide you with an introduction to using `Python` for scientific analyses of data. The best way for you to continue to learn more about `Python` is to use it in your research! This may sound daunting, but writing `Python` scripts is the best way to become familiar with the syntax. This will help you progress through more advanced operations, such as cleaning your data, using statistical methods, or creating graphics.

The best place to start is playing around with the code from today's workshop. Change parts of the code and see what happens! Better yet, use the code from the workshop to investigate your own data!

Montana State University Data Science Workshops Team

These materials were adapted from materials generated by the Data Carpentries (https://datacarpentry.org/) and were originally developed at MSU by Dr. Allison Theobold. The workshop series is co-organized by the Montana State University Library, Department of Mathematical Sciences, and Statistical Consulting and Research Services (SCRS, https://www.montana.edu/statisticalconsulting/). SCRS is supported by Montana INBRE (National Institutes of Health, Institute of General Medical Sciences Grant Number P20GM103474).

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Research related to the development of these workshops appeared in:

- Allison S. Theobold, Stacey A. Hancock & Sara Mannheimer (2021) Designing Data Science Workshops for Data-Intensive Environmental Science Research, *Journal of Statistics and Data Science Education*, 29:sup1, S83-S94, DOI: 10.1080/10691898.2020.1854636

The workshops for 2023-2024 involve modifications of materials and are being taught by:

Greta Linse

- Greta Linse is the Interim Director of Statistical Consulting and Research Services (https://www.montana.edu/statisticalconsulting/) and the Project Manager for the Human Ecology Learning and Problem Solving (HELPS) Lab (https://helpslab.montana.edu). Greta has been teaching, documenting and working with statistical software including Python, R and RStudio for over 15 years.

Sara Mannheimer

- Sara Mannheimer is an Associate Professor and Data Librarian at Montana State University, where she helps shape practices and theories for curation, publication, and preservation of data. Her research examines the social, ethical, and technical issues of a data-driven world. She is the project lead for the MSU Dataset Search, and she is working on a book about data curation to support responsible qualitative data reuse and big social research.

Devin Goodwin

- Devin Goodwin graduated with a Masters in Mathematics at Montana State University and while a GRA with Statistical Consulting and Research Services (SRCS) developed these materials thanks in part to a CLS grant. Devin has always focused in pure theoretical mathematics up until 2021, when he decided to dedicate his efforts to applied mathematics. Along with the already existing `R` Workshops developed by the team members mentioned above, Devin adapted this series to `Python`.

The materials have also been modified and improved by:

- Dr. Mark Greenwood
- Harley Clifton
- Eliot Liucci
- Dr. Allison Theobold