

## Basic Python

Content from [Getting started](#)

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### OVERVIEW

#### Questions

- Programming - why bother?
- Why Python?
- How to learn it?

#### Objectives

- Understand the concept of programming
- Understand the basics of Python language

## Programming — why bother?

Data handling and analysis in bio-research and medicine is best done using coding. In October 2017, the American technology magazine Wired published an [article](#) in which the author outlines reasons why several established bio-science researchers working in reputable institutions felt the need to learn coding — specifically in Python: “Want to Make It as a Biologist? Better Learn to Code”.

### THIS COURSE

We focus on the Python programming language throughout this course, but we discuss universal principles shared amongst many programming languages. Through a diverse range of examples, we will be training these principles by solving problems that we face in biological and medical research.

## Why Python?

Python is a general-purpose programming language. This means that it can be exploited to design any type of software, from desktop and web, to robotics and automation, to data analysis. The 2020 survey conducted by the Python Software Foundation and JetBrains® found that approximately 85% of respondents used Python as their first language [to conduct data analysis](#).

In addition, the 2021 developer survey conducted by StackOverflow found that Python is the [third most popular](#) general-purpose programming language after JavaScript and HTML/CSS. This means that it enjoys a vibrant community that support and maintain its development, and the development of the libraries associated with it. This is confirmed by the fact that the language is ranked as the [second most popular language on GitHub®](#), which is the primary code-sharing platform amongst programmers.

### HOW TO LEARN?

Learning how to code as a beginner is akin to learning how to walk as a baby. You cannot learn programming by memorising directives; no matter how well you memorise them. To learn how to code, one must learn how think algorithmically; that is, how to break different tasks down into logical procedures. The only way to learn how to “think code” is to practice, make mistakes, and how to overcome those mistakes. It is common to make the same mistake more than once, especially in different contexts, and that can become frustrating at times. However, once you get it, you have it for life.

There are lots materials on the web, both free and paid, to assist with your learning. Use them to your advantage! Great programmers are not the ones who know every technical detail by heart; rather, they are the ones who know what they are looking for, and where they can find the answer.

### KNOWN QUIRK

Unlike popular belief, the name **Python** has nothing to do with the snake. It is in fact derived from the popular British sketch comedy series [Monty Python's Flying Circus](#), of which inventor Guido van Rossum was a self-confessed fan.

## Python: The Programming Language

Python is a general-purpose, high-level programming language. It was invented by the Dutch computer programmer [Guido van Rossum](#) and was released for the first time in 1990.

A **high-level** programming language is a language that enjoys strong abstraction from computer details. This means that it is closer to the language that is spoken and understood by humans; put simply: it makes the language more enjoyable to work with.

### CATEGORIES

In terms of compilation (the conversion of code into the binary symbols understood by a computer), programming languages may be divided into two different categories:

1 - **Compiled** These are languages whose code is translated (compiled) into machine language en-masse, and in advance, using a designated compiler programme — e.g. C, Rust, Haskell.

2- **Interpreted** These languages rely on and must *always* be accompanied by an interpreter, whose job is to translate the source code into machine language one line at a time — e.g. Python, R, MATLAB®.

## KEYPOINTS

- Programming is an important skill which is highly applicable to bio-research and medicine.
- Python is one of the most popular programming language for being general-purpose and high level language.
- Python uses an interpreter for line by line code translation.

Content from [Variables, Types, and Operations](#)

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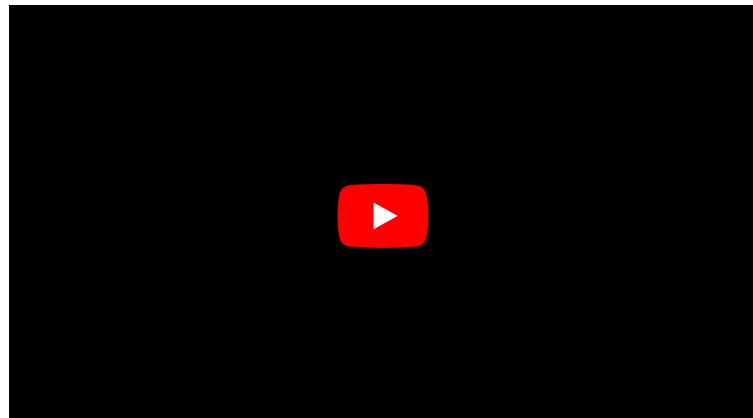
## OVERVIEW

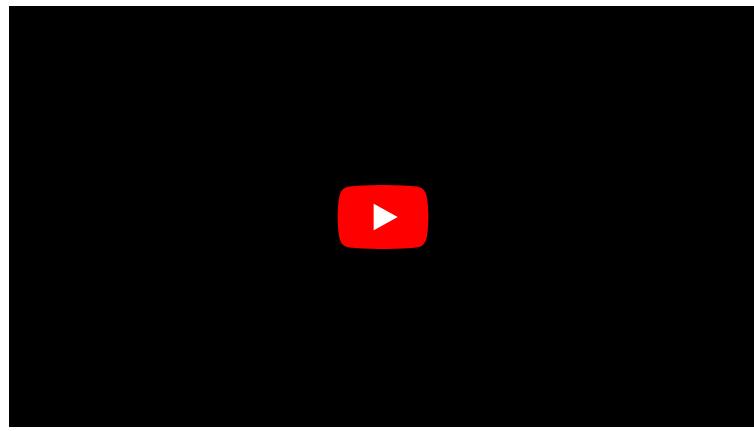
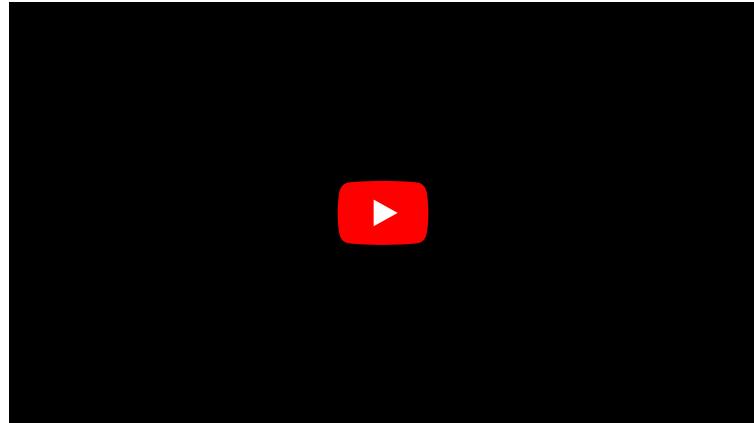
### Questions

- 
- What are I/O operations?
  - What do variables do?
  - Why types and scopes of variables are important?
  - What types of operations are used?
- 

### Objectives

- Understanding the output and input operations
- Build concepts of different types of variables
- Learning about type conversions and scope
- Understanding mathematical and logical operations





In programming, we process data and produce outputs. When data is being processed, it is stored in a memory, so that it is readily available, and can therefore be subject to the processes we want to apply.

Throughout this section, we will discuss how to handle data in Python. We start by displaying data on the screen, and see how to receive input from a user. We then use these techniques to perform different mathematical and logical operations. This chapter introduces the fundamental principles that we employ every time we code in Python. On that account, make sure you understand everything before moving on.

## I/O Operations

---

In computer science, input or output operations refer to the communication between an information processing system such as a computer, and the outside world, which may be a user or another computer. Such communications are more commonly known as *I/O operations*. In general, the outside world — especially in the context of this course, may be loosely defined as anything that falls outside of the coding environment.

## REMEMBER

Only what we define within the environment and what we store in the memory is directly controlled by our application. We may access or take control over other environments through certain mediums; however, such interactions are classified as I/O operations. An example of this is interacting with a file on our computer, which we discuss in the topic of [Strings](#). Whilst we have complete control over a file while working on it (e.g. reading from it or writing to it), the access to the file and the transmission of data is in fact controlled and managed not by the programming environment but by the operating system of the computer.

In programming, I/O operations include, but are not limited to:

- displaying the results of a calculation
- require the user to enter a value
- writing or reading data to and from a file or a database
- downloading data from the Internet
- operating a hardware (e.g. a robot)

## ADVANCED TOPIC

If you are interested in learning more about I/O systems and how they are handled at operating system level, you might benefit from chapter 13 of [\*Operating Systems Concepts, 10<sup>th</sup> ed.\*](#) by Abraham Silberschatz, Greg Gagne, and Peter Galvin.

## I/O Operations in Python

### [Input and Output](#)

In this section, we learn about two fundamental methods of I/O operations in Python. We will be using these methods throughout the course, so it is essential that you feel comfortable with them and the way they work before moving on.

## PRODUCING AN OUTPUT

### Print

The term **output** in reference to an application typically refers to data that has either been generated or manipulated by that application.

For example; we have two number and we would like to calculate their sum. The action of calculating the sum is itself a **mathematical operation** (discussed in the coming section). The result of our calculation is called an **output**. Once we obtain the result, we might want to save it in a file or display it on the screen, in which case we will be performing an **I/O operation**.

The simplest and most frequently used method for generating an output in almost every modern programming language is to display something on the screen. We recommend using JupyterLab notebooks to run our scripts and the typical method to produce an output is to display it in cell below the code. To do this, we will call a dedicated built-in function named `print()`.

### REMEMBER

In programming, a **function** is essentially an isolated piece of code. It usually takes some inputs, *does* something to or with them, and produces an **output**. The pair of (typically round) parenthesis that follow a function are there to provide the function with the *input arguments* it needs when we *call* it, so that it can do what it is supposed to do using our data. We will explore functions in more details in Lesson 4 [Functions](#).

The `print()` function can take several inputs and performs different tasks. Its primary objective, however, is to take some values as input and display them on the screen. Here is how it works:

Suppose we want to display some text in the terminal. To do so, we write:

```
print('Hello world!')
```

in a cell of our notebook (or, if not using a notebook, an editor or IDE) and save the notebook in a file. This is now a fully functioning Python programme that we can run using the Python interpreter.

If you are using an Integrated Development Environment (IDE) — e.g. Visual Studio Code, you have to save the code in a file with extension `.py` and may then execute your code using the internal tools provided by that IDE. The specifics of how you do so depend on the IDE that you are using.

`.py` Python scripts can also be executed manually. To do so, we open the terminal in MacOS or Linux or the command prompt (CMD) in Windows and navigate to the directory where we saved the script.

### NOTE

If you don't know how to navigate in the terminal, see the example in section [How to use terminal environment?](#) at the end of this chapter.

Once in the correct directory, we run a script called `script_a.py` by typing `python3 script_a.py` in our terminal as follows:

```
python3 script_a.py
```

BASH < >

```
Hello world!
```

OUTPUT < >

This will call the Python 3 interpreter to execute the code we wrote in `script_a.py`. Once executed, which in this case should be instantaneously, we should see the output.

In a JupyterLab notebook we can press the keyboard shortcut ‘shift-enter’ to execute the code in a cell. The output will be displayed below the code cell.

Congratulations you have now successfully written and executed your first programme in Python.

### REMEMBER

We know `print()` is a *function* because it ends with a pair of parenthesis, and it is written entirely in lowercase characters [PEP-8: Function Names](#). Some IDEs change color when they encounter built-in functions in the code so that we won’t accidentally overwrite them. We shall discuss *functions* in more details in Lesson 4 [Functions](#).

We can pass more than a single value to the `print()` function, provided that they are separated with a comma. For instance, if we write the code below and run the script, the results would be as shown in *output*.

```
print('Hello', 'John')
```

PYTHON < >

```
Hello John
```

OUTPUT < >

Notice that there is a space between ‘Hello’ and ‘John’ even though we did not include a space in our text. This is the default behaviour of the `print()` function when it receives more than a single value (argument).

This default behaviour may be changed:

```
print('Hello', 'John', sep='')
```

PYTHON < >

```
HelloJohn
```

OUTPUT < >

```
print('Hello', 'John', sep='--')
```

PYTHON < >

Hello--John

OUTPUT < >

```
print('Jane', 21, 'London', sep='.')
```

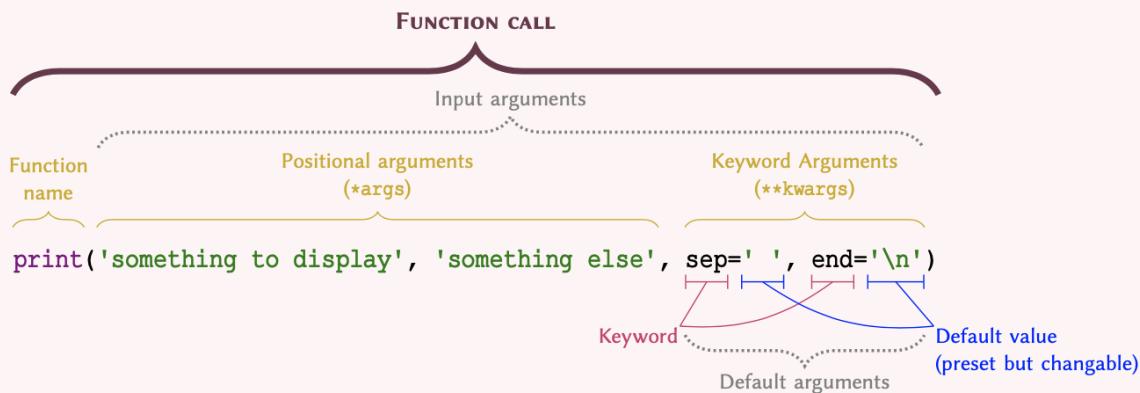
PYTHON < >

Jane.21.London

OUTPUT < >

### ! REMEMBER

In Python, values that do not require a name when passed to a function — e.g. Jane, 21, or London in the last example, are known as *positional arguments*. On the other hand, values that require their name to be specified such as `sep=...` are referred to as *keyword arguments*. Values that do not require to be specified when calling a function and have a default value — e.g. `sep=' '`, are called *default arguments*.



The *input* and *output* arguments of a function are referred to as the **function signature**.

Explanation of a function call

## DO IT YOURSELF

Write code that displays the following output:

**Protein Kinase C (Alpha subunit)**

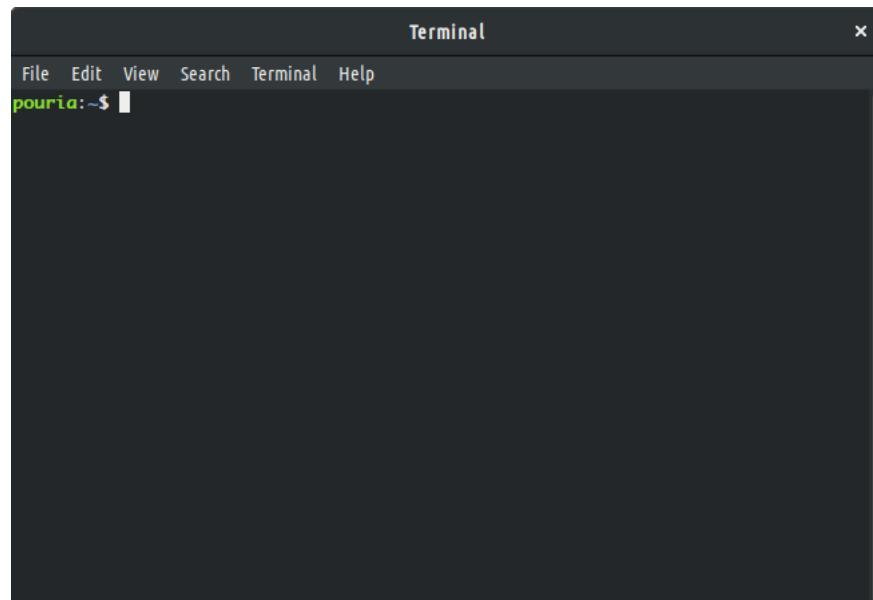
### Solution

```
print('Protein Kinase C (Alpha subunit)')
```

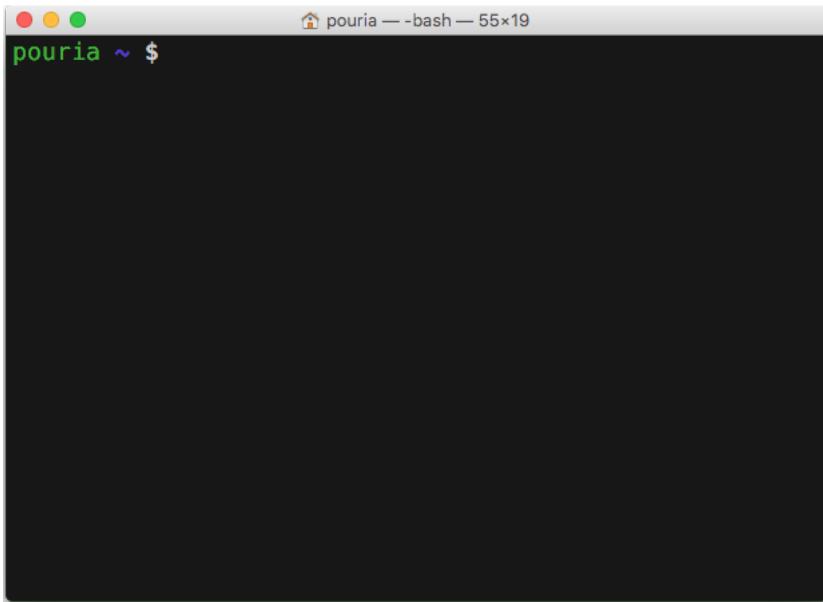
PYTHON < >

```
Protein Kinase C (Alpha subunit)
```

OUTPUT < >



Terminal window on a Linux computer



Terminal window on a Mac

## RECEIVING AN INPUT

### Input

Inputs are I/O operations that involve receiving some data from the outside world. This might include reading the contents of a file, downloading something from the Internet, or asking the user to enter a value.

The simplest way to acquire an input is to ask the user to enter a value in the terminal. To do so, we use a dedicated built-in function called `input()`.

#### NOTE

In a Unix system (Mac OS or Linux), a tilde (~) is an alias for a user's home directory.

The function takes a single *argument* called `prompt`. Prompt is the text displayed in the terminal to ask the user for an input. Figure [Terminal window on a Linux computer](#) and [Terminal window on a Mac](#), illustrates a screen shot of my personal computer's prompt, where it displays my user name (i.e. `pouria`) followed by a tilde (~). A terminal prompt may be different in each computer and operating system.

Here is how we implement the `input()` function:

```
input('Please enter your name: ')
```

which is exactly the same as:

```
input(prompt='Please enter your name: ')
```

If we save one of the above in a notebook and execute it, we will see:

```
python3 script_b.py
```

```
Please enter your name: _
```

The terminal cursor, displayed as an underscore in our example, will be in front of the prompt (i.e. `'Please enter your name: '`) waiting for a response. Once it receives a response, it will proceed to run the rest of the code (if any), or terminate the execution.

We may store the user's response in a variable. Variables are the topic of the next section, where we shall also review more examples on `input()` and how we can use it to produce results based on the responses we receive from the user.

## REMEMBER

Python is an interpreted language; that is, the code we write is executed by the Python interpreter one line at a time. The `input()` function performs a *blocking* process. This means that the execution of the code by the Python interpreter is halted upon encountering an `input()` function until the user enters a value. Once a value is entered, the interpreter then proceeds to execute the next line.

## DO IT YOURSELF

Write a script that asks the user to enter the name of a protein in the terminal.

### Solution

```
input('Please enter the name of a protein: ')
```

# Variables And Types

We use variables to store data in the memory. Each variable has 3 characteristics: *scope*, *name*, and *type*. *Scope* and *name* must be mutually unique. Starting with *name*, we will discuss each of these characteristics in more details throughout this chapter.

## Variable names

### [PEP-8 Naming Conventions](#)

Name of a variable is in fact an alias for a location in the memory. You can think of it as a postbox, which is used as a substitute for an address. Similarly, we use variable names so we wouldn't have to use the actual address to the location we want in the memory because it would look something like `0x106fb8348`.

There are some relatively simple rules to follow when defining variable names, which ultimately boil down to:

VALIDITY	EXAMPLE	NOTE
Invalid	5mins = 5 * SEC_IN_MIN	Variables cannot start with numbers — raises a <a href="#">SyntaxError</a> .
Invalid	if = 2	Attempts to overwrite an internal syntax — raises a <a href="#">SyntaxError</a> .
Worst	j = 2	Overwrites the internal identifier for complex numbers.
Worst	int = 2	Overwrites the internal definition for integer numbers.
Bad	a = 4	Meaningless name + hard to identify in code.
Okay	var1 = 0	Meaningless name + hard to distinguish.
Better	var_1 = 0	Meaningless name.
Good	current_state = 0	Good name + easy to distinguish.
Okay	five_mins_in_sec = 5 * 60	Good name, vague value.
Good	SEC_IN_MIN = 60	Good name + good value + distinguished as a constant (conventionally, names made exclusively of capital letters signify constants).
Good	five_mins2sec = 5 * SEC_IN_MIN	Good name + good value.
Good	five_mins2sec = 5 * 60 # 5 min * 60 sec	Good name + vague value clarified by a comment.
Good	current_protein = 'DNA Polymerase III'	Good name + good value.

### REMEMBER

We should never overwrite an existing, built-in definition or identifier (e.g. `int` or `print`). We will be learning many such definitions and identifiers as we progress through this course. Nonetheless, the Jupyterlab notebook as well as any good IDE highlights syntaxes and built-in identifiers in different colours. In JupyterLab the default for built-in definitions is green. The exact colouring scheme depends on the IDE and the theme.

Once a variable is defined, its value may be altered or reset:

```
total_items = 2
print(total_items)
```

PYTHON < >

2

OUTPUT < >

```
total_items = 3
print(total_items)
```

PYTHON < >

3

OUTPUT < >

```
total_values = 3.2
print(total_values)
```

PYTHON < >

```
3.2
```

OUTPUT < >

```
temperature = 16.
print(temperature)
```

PYTHON < >

```
16.0
```

OUTPUT < >

Variables can contain characters as well; but to prevent Python from confusing them with meaningful commands, we use quotation marks. So long as we remain consistent, it doesn't matter whether we use single or double quotations. These variables are known as **string** or **str**:

```
forename = 'John'
surname = "Doe"

print('Hi, ', forename, surname)
```

PYTHON < >

```
Hi, John Doe
```

OUTPUT < >

## DO IT YOURSELF

Oxidised low-density lipoprotein (LDL) receptor 1 mediates the recognition, internalisation and degradation of oxidatively modified low density lipoprotein by vascular endothelial cells. Using the [Universal Protein Resource](#) (UniProt) website, find this protein for humans, and identify:

- UniProt entry number.
- Length of the protein (right at the top).
- Gene name (right at the top).

Store the information you retrieved, including the protein name, in 4 separate variables.

Display the values of these 4 variables in *one* line, and separate the items with 3 spaces, as follows:

Name EntryNo GeneName Length

### Solution

PYTHON < >

```
name = 'Oxidised low-density lipoprotein (LDL) receptor 1'  
  
uniprot_entry = 'P78380'  
  
gene_name = 'OLR1'  
  
length = 273  
  
print(name, uniprot_entry, gene_name, length, sep='   ')
```

OUTPUT < >

```
Oxidised low-density lipoprotein (LDL) receptor 1  P78380  OLR1  273
```

## DO IT YOURSELF

1. Write a script that upon execution, asks the user to enter the name of an enzyme and then retains the response in an appropriately named variable.

2. Use the variable to display an output similar to the following:

`ENZYME_NAME` is an enzyme.

where `ENZYME_NAME` is the name of the enzyme entered in the prompt.

3. Now alter your script to ask the user to enter the number of amino acids in that enzyme. Retain the value in another appropriately named variable.

4. Alter the output of your script to display a report in the following format:

`ENZYME_NAME` is an enzyme containing a total number of `AMINO_ACIDS`} amino acids.

where `AMINO_ACIDS` is the number of amino acids.

## Solution

```
enzyme = input('Please enter the name of an enzyme: ')

print(enzyme, 'is an enzyme.')

length = input('How many amino acids does the enzyme contain? ')

print(enzyme, 'is an enzyme containing a total number of', length, 'amino acids.')
```

## Variable Types

### Built-in Types

When it comes to types, programming languages may be divided into two distinct categories:

#### TYPES

- **Statically typed** language that require the programmer to define the type for every variable (statically typed).
- **Dynamically typed** languages that define and maintain the types on the fly.

Python is a dynamically typed language. This means that, unlike statically typed languages, we rarely need to worry about the *type* definitions because in the majority of cases, Python takes care of them for us.

## REMEMBER

In a dynamically typed language, it is the value of a variable that determines the type. This is because the types are determined on the fly by the Python interpreter as and when it encounters different variables and values.

## ADVANCED TOPIC

In computer programming, type systems are syntactic methods to enforce and / or identify levels of abstraction. An entire field in computer science has been dedicated to the study of programming languages from a type-theoretic approach. This is primarily due to the implication of types and their underlying principles in such areas in software engineering as optimisation and security. To learn more about the study of type systems, refer to: Pierce B. Types and programming languages. Cambridge, Mass.: MIT Press; 2002.

## NOTE

The values determine the type of a variable in dynamically typed languages. This is in contrast with statically typed languages where a variable must be initialised using a specific type before a value — whose type is consistent with the initialised variable, can be assigned to it.

## Why learn about *types* in a dynamically typed programming language?

Python enjoys a powerful type system out of the box. Table [Built-in types in Python](#) provides a comprehensive reference for the built-in types in Python. Built-in types are the types that exist in the language and do not require any third party libraries to implement or use.

Type	Type Name	Specification	Numeric	Sequence	Iterable	Mutable	Container
<code>bool</code>	Boolean	<code>True</code> or <code>False</code>	✓				
<code>int</code>	Integer	An integer number: $x \in \mathbb{Z}$	✓				
<code>float</code>	Floating point	A rational number: $x \in \mathbb{Q}$	✓				
<code>complex</code>	Complex	A complex number: $x \in \mathbb{C}$	✓				
<code>bytes*</code>	Bytes	Single byte					
<code>bytearray*</code>	Byte Array	Array of bytes; <i>i.e.</i> binary	✓	✓	✓	✓	
<code>str</code>	String	Array of characters; <i>i.e.</i> text.	✓	✓			
<code>list</code>	List	Array of any combination	✓	✓	✓	✓	
<code>tuple</code>	Tuple	Array of any combination	✓		✓		
<code>set</code>	Set	Collection of unique members	✓			✓	✓
<code>frozenset*</code>	Frozen Set	Collection of unique members	✓				✓
<code>dict</code>	Dictionary	Mapping (associative array)	✓	✓ <sup>\$</sup>		✓	✓

A comprehensive (but non-exhaustive) reference of built-in (native) types in Python 3.

\* Not discussed in this course — included for reference only.

<sup>\$</sup>`dict` is not an iterable by default, however, it is possible to iterate through its keys.

**Mutability** is an important [concept in programming](#). A mutable object is an object whose value(s) may be altered. This will become clearer once we study [list](#) and [tuple](#). Find out more about mutability in Python from the [documentations](#).

**Complex numbers** refer to a [set of numbers](#) that have a real part, and an imaginary part; where the imaginary part is defined as  $\sqrt{-1}$ . These numbers are very useful in the study of oscillatory behaviours and flow (e.g. heat, fluid, electricity). To learn more about complex numbers, watch this [Khan Academy video tutorial](#).

Sometimes we might need want to know what is the type of a variable. To do so, we use the build-in function `type()` as follows:

```
PYTHON < >  
total_items = 2
```

```
print(type(total_items))
```

```
OUTPUT < >  
<class 'int'>
```

```
PYTHON < >  
total_values = 3.2
```

```
print(type(total_values))
```

```
OUTPUT < >  
<class 'float'>
```

```
PYTHON < >  
temperature = 16.
```

```
print(type(temperature))
```

```
OUTPUT < >  
<class 'float'>
```

```
PYTHON < >  
phase = 12.5+1.5j
```

```
print(type(phase))
```

```
OUTPUT < >  
<class 'complex'>
```

PYTHON < >

```
full_name = 'John Doe'  
  
print(type(full_name))
```

OUTPUT < >

```
<class 'str'>
```

### REMEMBER

In Python, a variable / value of a certain type may be referred to as an *instance* of that type. For instance, an integer value whose type in Python is defined as `int` is said to be an **instance of type int**.

### DO IT YOURSELF

Determine and display the type for each of these values:

- 32
- 24.3454
- 2.5 + 1.5
- "RNA Polymerase III"
- 0
- .5 - 1
- 1.3e-5
- 3e5

The result for each value should be represented in the following format:

Value X is an instance of <class 'Y'>

## Solution

```
PYTHON < >  
value = 32  
  
value_type = type(value)  
  
print('Value', value, 'is an instance of', value_type)
```

```
OUTPUT < >  
Value 32 is an instance of <class 'int'>
```

```
PYTHON < >  
value = 24.3454  
  
value_type = type(value)  
  
print('Value', value, 'is an instance of', value_type)
```

```
OUTPUT < >  
Value 24.3454 is an instance of <class 'float'>
```

```
PYTHON < >  
value = 2.5 + 1.5  
  
value_type = type(value)  
  
print('Value', value, 'is an instance of', value_type)
```

```
OUTPUT < >  
Value 4.0 is an instance of <class 'float'>
```

```
PYTHON < >  
value = "RNA Polymerase III"  
  
value_type = type(value)  
  
print('Value', value, 'is an instance of', value_type)
```

```
OUTPUT < >  
Value RNA Polymerase III is an instance of <class 'str'>
```

PYTHON < >

```
value = 0

value_type = type(value)

print('Value', value, 'is an instance of', value_type)
```

OUTPUT < >

```
Value 0 is an instance of <class 'int'>
```

PYTHON < >

```
value = .5 - 1

value_type = type(value)

print('Value', value, 'is an instance of', value_type)
```

OUTPUT < >

```
Value -0.5 is an instance of <class 'float'>
```

PYTHON < >

```
value = 1.3e-5

value_type = type(value)

print('Value', value, 'is an instance of', value_type)
```

OUTPUT < >

```
Value 1.3e-05 is an instance of <class 'float'>
```

PYTHON < >

```
value = 3e5

value_type = type(value)

print('Value', value, 'is an instance of', value_type)
```

OUTPUT < >

```
Value 300000.0 is an instance of <class 'float'>
```

## Conversion of types

### WHY CONVERT TYPES?

It is sometimes necessary to have the values returned by the `input()` function — *i.e.* the user's response, in other types. Imagine the following scenario:

"We ask our user to enter the total volume of their purified protein, so that we can work out the amount of assay they need to conduct a specific experiment. To calculate this assay volume using the volume of the purified protein, we need to perform mathematical calculations based on the response we receive from our user. It is not possible to perform mathematical operations on non-numeric values. Therefore, we ought to somehow convert the type from `str` to a numeric type."

The possibility of converting from one type to another depends entirely on the *value*, the *source type*, and the *target type*. For instance; we can convert an instance of type `str` (source type) to one of type `int` (target type) if and only if the source value consists entirely of numbers and there are *no* other characters.

### REMEMBER

To convert a variable from one type to another, we use the *Type Name* of the target type (as described in Table [Built-in types in Python](#)) and treat it as a function.

For instance, to convert a variable to integer, we:

- look up the *Type Name* for integer from Table [Built-in types in Python](#)
- then treat the *Type Name* as a function: `int()`
- use the function to convert our variable: `new_var = int(old_var)`

Here is an example of how we convert types in Python:

```
PYTHON < >  
value_a = '12'  
  
print(value_a, type(value_a))
```

```
OUTPUT < >  
12 <class 'str'>
```

```
PYTHON < >  
value_b = int(value_a)  
  
print(value_b, type(value_b))
```

OUTPUT < >

```
12 <class 'int'>
```

If we attempt to convert a variable that contains non-numeric values, a **ValueError** is raised:

PYTHON < >

```
value_a = '12y'  
  
print(value_a, type(value_a))
```

OUTPUT < >

```
12y <class 'str'>
```

PYTHON < >

```
value_b = int(value_a)
```

ERROR < >

```
Error: ValueError: invalid literal for int() with base 10: '12y'
```

## DO IT YOURSELF

In programming, we routinely face errors resulting from different mistakes. The process of finding and correcting such mistakes in the code is referred to as *debugging*.

We have been given the following snippet written in Python 3:

```
value_a = 3
value_b = '2'

result = value_a + value_b
print(value_a, '+', value_b, '=', result)
```

but when the code is executed, we encounter an error message as follows:

```
Traceback (most recent call last):
File "<stdin>", line 1, in <module>
TypeError: unsupported operand type(s) for +: 'int' and 'str'
```

Debug the snippet so that the correct result is displayed:

```
3 + 2 = 5
```

## Solution

```
PYTHON < >

value_a = 3

value_b = '2'

result = value_a + int(value_b)

print(value_a, '+', value_b, '=', result)
```

```
OUTPUT < >

3 + 2 = 5
```

## Handling input variables

### DISCUSSION

When we use `input()` to obtain a value from the user, the results are by default an instance of type `str`. An `input()` function always stores the response as a `str` value, no matter what the user enters. However, it is possible to convert the type afterwards.

### REMEMBER

The `input()` function *always* returns a value of type `str` regardless of the user's response. In other words, if a user's response to an `input()` request is numeric, Python will *not* automatically recognise it as a numeric type.

We may use *type conversion* in conjunction with the values returned by the `input()` function:

```
response = input('Please enter a numeric value: ')

response_numeric = float(response)

print('response:', response)
print('response type:', type(response))
print('response_numeric:', response_numeric)
print('response_numeric type:', type(response_numeric))
```

The output shows the results when we enter numeric values as directed.

### DO IT YOURSELF

We know that each amino acid in a protein is encoded by a triplet of mRNA nucleotides.

With that in mind, alter the script you wrote for [Do it Yourself](#) and use the number of amino acids entered by the user to calculate the number of mRNA nucleotides.

Display the results in the following format:

ENZYME\_NAME is an enzyme with AMINO\_ACIDS amino acids and NUCLEOTIDES nucleotides.

where `NUCLEOTIDES` is the total number of mRNA nucleotides that you calculated.

**Note:** Multiplication is represented using the asterisk (\*) sign.

## Solution

```
enzyme = input('Please enter the name of an enzyme: ')

length = input('How many amino acids does the enzyme contain? ')

nucleotides = 3 * int(length)

print(enzyme, 'is an enzyme with', length, 'amino acids and', nucleotides, 'nucleotides.')
```

## Variable scopes

### Resolution of names

When defining a variable, we should always consider where in our programme we intent to use it. The more localised our variables, the better. This is because local variables are easier to distinguish, and thus reduce the chance of making mistakes — e.g. unintentionally redefine or alter the value of an existing variable.

To that end, the scope of a variable defines the ability to reference a variable from different *points* in our programmes. The concept of local variables becomes clearer once we explore functions in programming in chapter [Functions](#).

As displayed in Figure [Variable scopes](#), the point *at* or *from* which a variable can be referenced depends on the location where the variable is defined.

In essence, there are three general rules to remember in relation variable scopes in Python:

- I. A variable that is defined in the outer scope, can be *accessed* or *called* in the inner scopes, but it cannot be *altered* implicitly. Note that such variables may still be altered using special techniques (not discussed).
- II. A variable that is defined in the innermost scopes (local), can only be *accessed*, *called*, or *altered* within the boundaries of the scope it is defined in.
- III. The inner scopes *from* which a variable is referenced must themselves have be contained within the defining scope — e.g. in [FuncB](#) of Figure [Variable scopes](#), we can reference `a`, `b`, and `x`; but not `f1`. This is because the scope of `f1` is `Script → FuncA`, so it can only be referenced from `Script → FuncA → ...`, but not `'Script → ...'` or `Script → FuncB → ...`.

## PYTHON SCRIPT FILE

### >\_ Script (part 1)

```
a = 2  
b = 3
```

[global]

#### FuncA

```
f1 = a * b
```

[local]

Reference a, b, f1  
Call FuncA()  
Alter f1

#### FuncB

```
x = 5
```

[local]

Reference a, b, x  
Call FuncA(), FuncB()  
Alter x

### >\_ Script (part 2)

```
result = a + b
```

Reference a, b, result  
Call FuncA(), FuncB()  
Alter a, b, result, FuncA, FuncB

#### FuncC

```
y = 10
```

[local]

Reference a, b, result  
Call FuncA(), FuncB(), FuncC()  
Alter y

Variable scopes in Python with respect to scripts and functions.

Python is an interpreted language. This means that the Python interpreter goes through the codes that we write line by line, interpreting it to machine language. It is only then that the commands are processed and executed by the computer. On that account, a variable (or a function) can be referenced only *after* its initial definition. That is why, for instance, in [Script \(part 2\)](#) of Figure [Variable scopes](#), we can reference every variable and function except for [FuncC](#), which is declared further down the code hierarchy.

Although scope and hierarchy appear at first glance as theoretical concepts in programming, their implications are entirely practical. The definition of these principles vary from one programming language to another. As such, it is essential to understand these principles and their implications in relation to any programming language we are trying to learn.

## Optional: How to use terminal environment?

### How to navigate the terminal in Mac OS X and Linux?

The Unix terminal — *i.e.* the one used by Mac OS X® and Linux; uses a command language known as [Bash](#), also referred to as the Unix Shell. This is not the topic of this book, so we won't discuss its properties and features in much detail.

Microsoft Windows®, on the other hand, relies on DOS (Microsoft Disk Operating System®) commands to navigate the terminal. The terminal environment in is sometimes referred to as the CMD or the command prompt.

The environment in which we can use Bash or DOS commands is known as the terminal. To use a terminal, we need a terminal emulator. Every operating system has a default terminal emulator, but you can always use an alternative software if you so wish.

#### CURRENT WORKING DIRECTORY

To navigate the terminal environment, we should first find out where we are. Here is how we do that:

Unix	Microsoft Windows®
pwd 	pwd 

Remember that the path to an environment is displayed (and supplied differently in Unix and Microsoft Windows®). To that end, the response (output) to these commands may slightly vary:

Unix	Microsoft Windows®
/home/UserName/Documents	C:\Documents

Notice that in Microsoft Windows®, we separate directories using a backslash (\ ), whilst in Unix, we use a forward slash (/ ) for that purpose.

#### CHANGING THE CURRENT DIRECTORY

To navigate to another directory, we do as follows:

	<b>Unix</b>	<b>Microsoft Windows®</b>
<i>Without spaces in the name</i>	cd /home/UserName/Documents/Python_Scripts	cd C:\Documents\Python_Scripts
<i>With spaces in the name</i>	cd "/home/UserName/Documents/Python Scripts"	cd "C:\Documents\Python Scripts"

Note that paths containing one or more space characters must be encapsulated by double quotation marks ("...").

If we are already in the **Documents** directory, and want to navigate onto **Python\_Scripts**, we can use the following shorthand versions of the above method:

	<b>Unix</b>	<b>Microsoft Windows®</b>
<i>Without spaces in the name</i>	cd Python_Scripts	cd Python_Scripts
<i>With spaces in the name</i>	cd "Python Scripts"	cd "Python Scripts"

#### PARENT DIRECTORY

To navigate to the parent directory — *i.e.* from **Python\_Scripts** to **Documents** in this example; we do:

	<b>Unix</b>	<b>Microsoft Windows®</b>
	cd ..	cd ..

#### HOME DIRECTORY

We can also navigate all the way back to the home directory in one go:

	<b>Unix</b>	<b>Microsoft Windows®</b>
	cd	cd \

#### CREATING A NEW DIRECTORY

We can create a new directory as follows:

	<b>Unix</b>	<b>Microsoft Windows®</b>
	mkdir new_dir_name	md new_dir_name

#### CONTENTS OF A DIRECTORY

To see the contents of a directory, we use the following commands:

	<b>Unix</b>	<b>Microsoft Windows®</b>
	ls	dir

# Operations

Through our experimentations with [variable types](#), we already know that variables may be subject to different operations.

When assessing [type conversions](#) we also established that the operations we can apply to each variable depend on the *type* of that variable. To that end, we learned that although it is sometimes possible to mix variables from different types to perform an operation — e.g. multiplying a floating point number with an integer, there are some logical restrictions in place.

Throughout this section, we will take a closer look into different types of operations in Python. This will allow us to gain a deeper insight into the concept and familiarise ourselves with the underlying logic.

To recapitulate on what we have done so far, we start off by reviewing *additions* — the most basic of all operations.

Give the variable `total_items`:

```
PYTHON < >  
total_items = 2  
  
print(total_items)
```

```
OUTPUT < >  
2
```

We can increment the value of an *existing* variable by `1` as follows:

```
PYTHON < >  
total_items = total_items + 1  
  
print(total_items)
```

```
OUTPUT < >  
3
```

Given 2 different variables, each containing a different value; we can perform an operation on these values and store the result in *another* variable without altering the original variables in any way:

```
PYTHON < >  
old_items = 4  
new_items = 3  
  
total_items = old_items + new_items  
  
print(total_items)
```

OUTPUT < >

7

We can change the value of an *existing* variable using the value stored in *another* variable:

PYTHON < >

```
new_items = 5
total_items = total_items + new_items

print(total_items)
```

12

There is also a shorthand method for applying the operation on an *existing* variable:

PYTHON < >

```
total_items = 2

print(total_items)
```

2

PYTHON < >

```
total_items += 1

print(total_items)
```

3

OUTPUT < >

```
new_items = 5
total_items += new_items

print(total_items)
```

8

OUTPUT < >

As highlighted in the [introduction](#), different operations may be applied to any variable or value. Throughout the rest of this section, we will explore the most fundamental operations in programming, and learn about their implementation in Python.

### REMEMBER

There are 2 very general categories of operations in programming: *mathematical*, and *logical*. Naturally, we use mathematical operations to perform calculations, and logical operations to perform tests.

## Mathematical Operations

Suppose `a` and `b` are 2 variables representing integer numbers as follows:

```
a = 17  
b = 5
```

Using `a` and `b` we can itemise built-in mathematical operations in Python as follows:

OPERATION	NOTATION	RESULT
Addition	<code>a + b</code>	22
Subtraction	<code>a - b</code>	12
Multiplication	<code>a * b</code>	85
Division	<code>a / b</code>	3.4
Floor quotient	<code>a // b</code>	3
Remainder	<code>a % b</code>	2
Quotient and remainder	<code>divmod(a, b)</code>	(3, 2)
Power	<code>a ** b</code>	1419857
Absolute value	<code>abs(b - a)</code>	12

Routine mathematical operations in Python

### REMEMBER

As far as mathematical operations are concerned, variables `a` and `b` may be an instance of any *numeric* type. See Table [Routine mathematical operations in Python](#) to find out more about numeric types in Python.

Values of type `int` have been chosen in our examples to facilitate the understanding of the results.

## DO IT YOURSELF

1. Calculate the following and store the results in appropriately named variables:

a.  $5.8 \times 3.3$

b.  $\frac{180}{6}$

c.  $35 - 3.0$

d.  $35 - 3$

e.  $2^{1000}$

Display the result of each calculation – including the type, in the following format:

Result: X is an instance of <class 'Y'>

2. Now using the results you obtained:

I. Can you explain why the result of  $35 - 3.0$  is an instance of type `float`, whilst that of  $35 - 3$  is of type `int`?

II. Unlike the numeric types, string values have a length. To obtain the length of a string value, we use `len()`. Convert the result for  $2^{1000}$  from `int` to `str`, then use the aforementioned function to work out the length of the number — i.e. how many digits is it made of?

If you feel adventurous, you can try this for  $2^{10000}$  or higher; but beware that you might overwhelm your computer and need a restart if you go too far (i.e. above  $2^{1000000}$ ). Just make sure you save everything beforehand, so you don't accidentally step on your own foot.}

**Hint:** We discuss `len()` in [subsection of arrays](#). However, at this point, you should be able to use the official documentations and StackOverflow to work out how it works.

## Solution

```
PYTHON < >  
q1_a = 5.8 * 3.3  
print('Result:', q1_a, 'is an instance of', type(q1_a))
```

```
OUTPUT < >  
Result: 19.139999999999997 is an instance of <class 'float'>
```

```
PYTHON < >  
q1_b = 180 / 6  
print('Result:', q1_b, 'is an instance of', type(q1_b))
```

```
OUTPUT < >  
Result: 30.0 is an instance of <class 'float'>
```

```
PYTHON < >  
q1_c = 35 - 3.0  
print('Result:', q1_c, 'is an instance of', type(q1_c))
```

```
OUTPUT < >  
Result: 32.0 is an instance of <class 'float'>
```

```
PYTHON < >  
q1_d = 35 - 3  
print('Result:', q1_d, 'is an instance of', type(q1_d))
```

```
OUTPUT < >  
Result: 32 is an instance of <class 'int'>
```

```
PYTHON < >  
q1_e = 2 ** 1000  
print('Result:', q1_e, 'is an instance of', type(q1_e))
```

```
OUTPUT < >  
Result: 107150860718626732094842504906000181056140481170553360744375038837035105112493612249319837881569
```

### Solution

In the case of `35 - 3.0` vs `35 - 3`, the former includes a floating point number. Operations involving multiple numeric types always produce the results as an instance of the type that covers all of the operands – i.e. `float` covers `int`, but not vice-versa.

### Solution

```
PYTHON < >  
big_num = 2 ** 1000  
big_num_str = str(big_num)  
big_num_len = len(big_num_str)  
  
print('Length of 2**1000:', big_num_len)
```

```
OUTPUT < >  
Length of 2**1000: 302
```

### INTERESTING FACT

As of Python 3.6, you can use an underscores (`_`) *within* large numbers as a separator to make them easier to read in your code. For instance, instead of `x = 1000000`, you can write `x = 1_000_000`.

## Shorthands

When it comes to mathematical operations in Python, there is a frequently used shorthand method that every Python programmer should be familiar with.

Suppose we have a variable defined as `total_residues = 52` and want to perform a mathematical operation on it. However, we would like to store the result of that operation in `total_residues` instead of a new variable. In such cases, we can do as follows:

```
PYTHON < >  
total_residues = 52  
  
# Addition:  
total_residues += 8  
  
print(total_residues)
```

```
OUTPUT < >  
60
```

PYTHON < >

```
# Subtraction:  
total_residues -= 10  
  
print(total_residues)
```

OUTPUT < >

50

PYTHON < >

```
# Multiplication:  
total_residues *= 2  
  
print(total_residues)
```

OUTPUT < >

100

PYTHON < >

```
# Division:  
total_residues /= 4  
  
print(total_residues)
```

OUTPUT < >

25.0

PYTHON < >

```
# Floor quotient:  
total_residues // 2  
  
print(total_residues)
```

OUTPUT < >

12.0

```
PYTHON < >  
# Remainder:  
total_residues %= 5  
  
print(total_residues)
```

```
OUTPUT < >  
2.0
```

```
PYTHON < >  
# Power:  
total_residues **= 3  
  
print(total_residues)
```

```
OUTPUT < >  
8.0
```

We can also perform such operations using multiple variables:

```
PYTHON < >  
total_residues = 52  
new_residues = 8  
number_of_proteins = 3  
  
total_residues += new_residues  
  
print(total_residues)
```

```
OUTPUT < >  
60
```

```
PYTHON < >  
total_residues += (number_of_proteins * new_residues)  
  
print(total_residues)
```

```
OUTPUT < >  
84
```

## DO IT YOURSELF

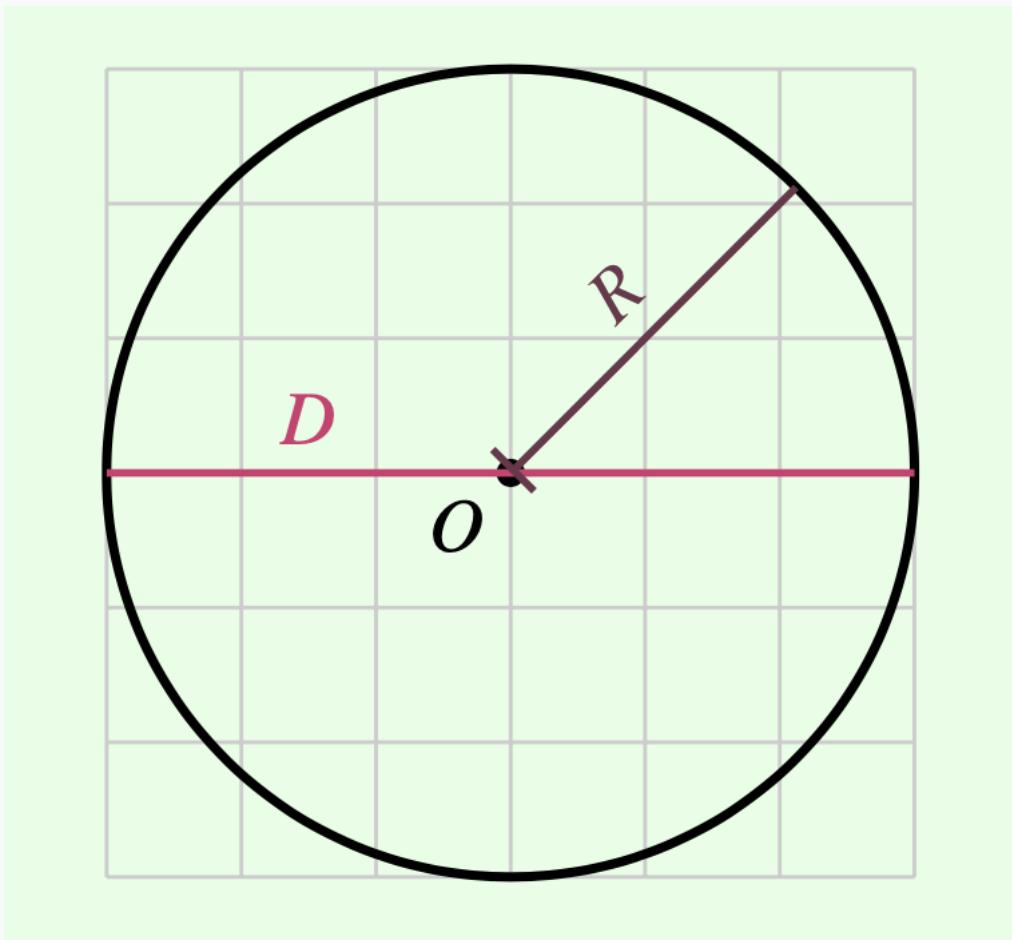
1. Given:

- Circumference:  $C = 18.84956$
- Radius:  $R = 3$

and considering that the properties of a circle are defined as follows:

$$\pi = \frac{C}{D}$$

calculate  $\pi$  using the above equation and store it in a variable named `pi`:



Then round the results to 5 decimal places and display the result in the following format:

The value of pi calculated to 5 decimal places: X.XXXXX

**Note:** To round floating point numbers in Python, we use `round()`. This is a built-in function that takes 2 input arguments: the first is the variable/value to be rounded, and the second is the number decimal places. Read more about `round()` in the [official documentation](#).

2. Now without creating a new variable, perform the following operation:

$$pi = \frac{pi}{(3 \bmod 2) - 1}$$

where the expression "3 mod 2" represents the remainder for the division of 3 by 2.

Explain the output.

### Solution

```
PYTHON < >  
c = 18.84956  
r = 3  
d = r * 2  
  
pi = c / d  
  
print('The value of pi calculated to 5 decimal places:', round(pi, 5))
```

```
OUTPUT < >  
The value of pi calculated to 5 decimal places: 3.14159
```

### Solution

```
pi /= (3 % 2) - 1
```

The calculation raises a `ZeroDivisionError`. This is because division by zero is mathematically impossible.

## Precedence

In mathematics and computer programming, there is a collection of conventional rules on the precedence of procedures to evaluate a mathematical expression. This collection of rules is referred to as the *order of operation* or *operator precedence*.

Suppose we have a mathematical expression as follows:

$$x = 2 + 3 \times 9$$

Such an expression can *only* be evaluated correctly if we do the multiplication first and then perform the addition. This means that the evaluation is done as follows:

$$\begin{aligned} \text{given : } 3 \times 9 &= 27 \\ \implies x &= 2 + 27 \\ &= 29 \end{aligned}$$

For instance, in an expression such as:

$$x = 2 \times (3 + (5 - 1)^2)$$

the evaluation workflow may be described as follows:

$$\begin{aligned} x &= 2 \times (3 + 4^2) \\ &= 2 \times (3 + 16) \\ &= 38 \end{aligned}$$

The same principle applies in Python. This means that if we use Python to evaluate the above expression, the result would be identical:

PYTHON < >

```
result = 2 * (3 + (5 - 1) ** 2)  
print(result)
```

OUTPUT < >

38

### REMEMBER

Operator precedence in mathematical operations may be described as follows:

1. Exponents and roots
2. Multiplication and division
3. Addition and subtraction

If there are any parenthesis ( ) in the expression, the expression is evaluated from the innermost parenthesis outwards.

## DO IT YOURSELF

Display the result of each item in the following format:

EXPRESSION = RESULT

For example:

2 + 3 = 5

1. Calculate each expression *without* using parentheses:

a.  $3 \times \frac{2}{4}$

b.  $5 + 3 \times \frac{2}{4}$

c.  $3 \times \frac{2}{4} + 5$

d.  $\frac{2}{4} \times 3$

2. Calculate these expressions *using* parentheses:

a.  $5 + \frac{2}{4} \times 3$

b.  $5 + \frac{2 \times 3}{4}$

c.  $5 + \frac{2}{4 \times 3}$

3. Given

a = 2

b = 5

use a and b to calculate the following expressions:

a.  $(a + b)^2$

b.  $a^2 + 2ab + b^2$

## Solution

```
PYTHON < >  
q1_a = 3 * 2 / 4  
print('3 * 2 / 4 =', q1_a)
```

```
OUTPUT < >  
3 * 2 / 4 = 1.5
```

```
PYTHON < >  
q1_b = 5 + 3 * 2 / 4  
print('5 + 3 * 2 / 4 =', q1_b)
```

```
OUTPUT < >  
5 + 3 * 2 / 4 = 6.5
```

```
PYTHON < >  
q1_c = 3 * 2 / 4 + 5  
print('3 * 2 / 4 + 5 =', q1_c)
```

```
OUTPUT < >  
3 * 2 / 4 + 5 = 6.5
```

```
PYTHON < >  
q1_d = 2 / 4 * 3  
print('2 / 4 * 3 =', q1_d)
```

```
OUTPUT < >  
2 / 4 * 3 = 1.5
```

## Solution

PYTHON < >

```
q2_a = 5 + (2 / 4) * 3  
print('5 + (2 / 4) * 3 =', q2_a)
```

OUTPUT < >

```
5 + (2 / 4) * 3 = 6.5
```

PYTHON < >

```
q2_b = 5 + (2 * 3) / 4  
print('5 + (2 * 3) / 4 =', q2_b)
```

OUTPUT < >

```
5 + (2 * 3) / 4 = 6.5
```

PYTHON < >

```
q2_c = 5 + 2 / (4 * 3)  
print('5 + 2 / (4 * 3) =', q2_c)
```

OUTPUT < >

```
5 + 2 / (4 * 3) = 5.1666666666666667
```

## Solution

```
PYTHON < >  
a = 2  
b = 5  
  
q3_a = (a + b) ** 2  
print('a + b)^2 =', q3_a)
```

```
OUTPUT < >  
(a + b)^2 = 49
```

```
PYTHON < >  
q3_b = a ** 2 + 2 * a * b + b ** 2  
print('a^2 + 2ab + b^2 =', q3_b)
```

```
OUTPUT < >  
a^2 + 2ab + b^2 = 49
```

## Non-numeric values

It sometimes makes sense to apply *some* mathematical operations to non-numeric variables too.

We can multiply strings to repeat them. There is no specific advantage to the use of multiplication instead of manually repeating characters or words, but it makes our code look cleaner, and that's always a good thing!

We can also add string values to each other. This is called *string concatenation*. It is a useful method for concatenating a few strings and / or string variables.

```
PYTHON < >  
SEPARATOR = '-' * 20  
NEW_LINE = '\n'  
SPACE = ' '  
  
forename = 'Jane'  
surname = 'Doe'  
birthday = '01/01/1990'  
  
full_name = forename + SPACE + surname  
  
data = full_name + NEW_LINE + SEPARATOR + NEW_LINE + 'DoB: ' + birthday  
  
print(data)
```

OUTPUT < >

Jane Doe

-----

DoB: 01/01/1990

### REMEMBER

New line character or '`\n`' is a universal directive to induce a line-break in Unix based operating systems (MACOS) and Linux. In WINDOWS, we usually use '`\r`' or '`\r\n`' instead. These are known as [escape sequences](#), which we explore in additional details under [string operations](#) in chapter [Strings](#)

## DO IT YOURSELF

The risk of Huntington's disease appears to increase proportional to the continuous repetition of **CAG** nucleotides (glutamine codon) once they exceed 35 near the beginning of the Huntingtin (**IT15**) gene. The **CAG** repeats are also referred to as a polyglutamine or polyQ tract.

```
glutamine_codon = 'CAG'
```

1. Create a polynucleotide chain representing 36 glutamine codons. Store the result in a variable called **polyq\_codons**.

Display the result as:

```
Polyglutamine codons with 36 repeats: XXXXXXXX...
```

2. Use **len()** to work out the length of **polyq\_codons**, and store the result in a variable called **polyq\_codons\_length**.

Display the result in the following format:

```
Number of nucleotides in a polyglutamine with 36 repeats: XXX
```

3. Use **len()** to work out the length of **glutamin\_codon**, and store the result in variable **amino\_acids\_per\_codon**.

4. Divide **polyq\_codons\_length** by **amino\_acids\_per\_codon** to prove that the chain contains the codon for exactly 36 amino acids. Store the result in variable **polyq\_peptide\_length**.

Display the result in the following format:

```
Number of amino acids in a polyglutamine with 36 repeats: XXX
```

5. Determine the types for the following variable:

- **amino\_acids\_per\_codon**
- **polyq\_codons\_length**
- **polyq\_peptide\_length**

and display the result for each item in the following format:

```
Value: XXX - Type: <class 'XXXX'>
```

6. Are all the variables in task #5 of the same type? Why?



### Solution

PYTHON < >

```
polyq_peptide_length = polyq_codons_length / amino_acids_per_codon  
  
print('Number of amino acids in a polyglutamine with 36 repeats:', polyq_peptide_length)
```

OUTPUT < >

```
Number of amino acids in a polyglutamine with 36 repeats: 36.0
```

### Solution

PYTHON < >

```
print('Value:', amino_acids_per_codon, '- Type:', type(amino_acids_per_codon))  
  
print('Value:', polyq_codons_length, '- Type:', type(polyq_codons_length))  
  
print('Value:', polyq_peptide_length, '- Type:', type(polyq_peptide_length))
```

OUTPUT < >

```
Value: 3 - Type: <class 'int'>  
Value: 108 - Type: <class 'int'>  
Value: 36.0 - Type: <class 'float'>
```

### Solution

No, `polyq_peptide_length` is an instance of type `float`. This is because we used the normal division (`/`) and not floor division (`//`) to calculate its value. The result of normal division is always presented as a floating point number.

## Solution

PYTHON < >

```
polyq_peptide_length = polyq_codons_length // amino_acids_per_codon  
  
print('Number of amino acids in a polyglutamine with 36 repeats:', polyq_peptide_length)  
  
print('Value:', amino_acids_per_codon, '- Type:', type(amino_acids_per_codon))  
  
print('Value:', polyq_codons_length, '- Type:', type(polyq_codons_length))  
  
print('Value:', polyq_peptide_length, '- Type:', type(polyq_peptide_length))
```

OUTPUT < >

```
Number of amino acids in a polyglutamine with 36 repeats: 36  
Value: 3 - Type: <class 'int'>  
Value: 108 - Type: <class 'int'>  
Value: 36 - Type: <class 'int'>
```

## INTERESTING FACT

The Boolean data type is named after the English mathematician and logician George Boole (1815–1864).

## Logical Operations

An operation may involve a comparison. The result of such operations is either **True** or **False**. This is known as the *Boolean* or **bool** data type. In reality, however, computers record **True** and **False** as **1** and **0** respectively.

Operations with Boolean results are referred to as *logical operations*. Testing the results of such operations is known as *truth value testing*.

Given the two variables **a** and **b** as follows:

```
a = 17  
b = 5
```

Boolean operations may be defined as outlined in Table [Routine logical operations in Python..](#)

LOGIC	STATEMENT	RESULT
Equivalence	<code>a == b</code>	<code>False</code>
Non-equivalence	<code>a != b</code>	<code>True</code>
Greater	<code>a &gt; b</code>	<code>True</code>
Either greater or equal	<code>a &gt;= b</code>	<code>True</code>
Smaller	<code>a &lt; b</code>	<code>False</code>
Either smaller or equal	<code>a &lt;= b</code>	<code>False</code>
Between	<code>5 &lt; a &lt; 20</code>	<code>True</code>

**TABLE 2.2** Routine logical operations in Python.

Routine logical operations in Python.

### DO IT YOURSELF

We know that in algebra, the first identity (square of a binomial) is:

$$(a + b)^2 = a^2 + 2ab + b^2$$

now given:

```
a = 15
b = 4
```

1. Calculate

$$y_1 = (a + b)^2$$

$$y_2 = a^2 + 2ab + b^2$$

Display the results in the following format:

```
y1 = XX
y2 = XX
```

2. Determine whether or not `y_1` is indeed equal to `y_2`. Store the result of your test in another variable called `equivalence`.

Display the results in the following format:

```
Where a = XX and b = XX:
y1 is equal to y2: [True/False]
```

### Solution

```
a = 15
b = 4

y_1 = (a + b) ** 2
y_2 = a ** 2 + 2 * a * b + b ** 2

print('y1 =', y_1)
print('y2 =', y_2)
```

PYTHON < >

```
y1 = 361
y2 = 361
```

OUTPUT < >

### Solution

```
equivalence = y_1 == y_2

print('Where a =', a, ' and b=', b)
print('y1 is equal to y2:', equivalence)
```

PYTHON < >

```
Where a = 15 and b= 4
y1 is equal to y2: True
```

OUTPUT < >

## Negation

We can also use negation in logical operations. Negation in Python is implemented using `not`:

LOGIC	STATEMENT	RESULT
Not equal	<code>not a == b</code>	True
Not greater	<code>not a &gt; b</code>	False
Neither greater nor equal	<code>not a &gt;= b</code>	False
Smaller	<code>not a &lt; b</code>	True
Neither smaller nor equal	<code>not a &lt;= b</code>	True

Negations in Python.

## DO IT YOURSELF

Using the information from previous [Do it Yourself](#):

- Without using `not`, determine whether or not `y_1` is *not equal* to `y_2`. Display the result of your test and store it in another variable called `inequivalent`.
- Negate `inequivalent` and display the result.

### Solution

```
PYTHON < >  
inequivalent = y_1 != y_2  
  
print(inequivalent)
```

```
OUTPUT < >  
False
```

### Solution

```
PYTHON < >  
inequivalent_negated = not inequivalent  
  
print(inequivalent_negated)
```

```
OUTPUT < >  
True
```

## Disjunctions and Conjunctions

Logical operations may be combined using conjunction with `and` and disjunction with `or` to create more complex logics:

LOGIC	STATEMENT	RESULT
Either smaller or equal	<code>a &lt; b or a == b</code>	False
Either greater or smaller	<code>a &lt; b or a &gt; b</code>	True
Either greater or equal	<code>a &gt; b or a == b</code>	True
Greater but not greater than	<code>a &gt; b and not a &gt; 18</code>	True
Either equal or not between	<code>a == b or not b &lt; a &lt; 20</code>	False
Equal and between	<code>a == b and 5 &lt;= a &lt; 20</code>	False

### DO IT YOURSELF

Given

```
a = True  
b = False  
c = True
```

Evaluate the following statements:

1. `a == b`
2. `a == c`
3. `a or b`
4. `a and b`
5. `a or b and c`
6. `(a or b) and c`
7. `not a or (b and c)`
8. `not a or not(b and c)`
9. `not a and not(b and c)`
10. `not a and not(b or c)`

Display the results in the following format:

```
1. [True/False]  
2. [True/False]  
...
```

Given that:

```
a = True  
b = False  
c = True
```

PYTHON < >

Solution

```
print('1.', a == b)
```

PYTHON < >

1. False

OUTPUT < >

Solution

```
print('2.', a == c)
```

PYTHON < >

2. True

OUTPUT < >

Solution

```
print('3.', a or b)
```

PYTHON < >

3. True

OUTPUT < >

Solution

```
print('4.', a and b)
```

PYTHON < >

4. False

OUTPUT < >

Solution

```
print('5.', a or b and c)
```

PYTHON < >

5. True

OUTPUT < >

Solution

```
print('6.', (a or b) and c)
```

PYTHON < >

6. True

OUTPUT < >

Solution

```
print('7.', not a or (b and c))
```

PYTHON < >

7. False

OUTPUT < >

Solution

```
print('8.', not a or not(b and c))
```

PYTHON < >

8. True

OUTPUT < >

### Solution

```
PYTHON < >
print('9.', not a and not(b and c))
```

9. False

OUTPUT < >

### Solution

```
PYTHON < >
print('10.', not a and not(b or c))
```

10. False

OUTPUT < >

## Complex logical operations

It may help to break down more complex operations, or use parenthesis to make them easier to both read and write:

LOGIC	STATEMENT	RESULT
Complex logic	a == b or (5 <= a or b < 20 and a < b)	True
Complex logic	a == b or (5 <= a or b < 20) and a < b	False
Complex logic	a == b or 5 <= a or (b < 20 and a < b)	True

Complex Logical Operations in Python.

Notice that in the last example, all notations are essentially the same and only vary in terms of their collective results as defined using parenthesis. Always remember that in a logical statement:

## LOGICAL STATEMENT

- The statement in parenthesis does **not** have precedence over the rest of the state (unlike mathematical statements). It merely defines an independent part of the operation whose response is evaluated separately.
- The precedence is established on a first come, first serve basis (from left to right).
- Always use parenthesis in longer statements for clarification.
- In disjunctive statements —i.e.  $a > 5$  **or**  $b > 5$ , if the first part is **True**, the second part is *not* checked. In other words, if  $a$  is greater than 5, the computer does not proceed to check whether or not  $b$  is greater than 5.
- In conjunctive statements —i.e.  $a > 5$  **and**  $b > 5$ , the statement proceeds to the seconds part if and only if the first part is **True**. In other words, the result of a conjunctive statement is only **True** if and only if both  $a$  and  $b$  are greater than 5. If  $a$  is **False**, the entire statement will inevitably be **False**.
- The longer the statement, the more difficult it would be to understand it properly, and by extension, the more likely it would be to cause problems.

PYTHON < >

```
a, b, c = 17, 5, 2 # Alternative method to define variables.
```

PYTHON < >

```
# Disjunction: false OR true.  
a < b or b > c
```

OUTPUT < >

```
True
```

PYTHON < >

```
# Disjunction: true OR true.  
a > b or b > c
```

OUTPUT < >

```
True
```

PYTHON < >

```
# Conjunction: true AND true.  
a > b and b > c
```

True

OUTPUT < >

```
# Conjunction: false and true.  
a < b and b > c
```

False

OUTPUT < >

```
# Disjunction and conjunction: true OR false AND true  
a > b or b < c and b < a
```

True

OUTPUT < >

```
# Disjunction and conjunction: false OR true AND false  
a < b or b > c and b > a
```

False

OUTPUT < >

```
# Disjunctions and conjunction: false OR true AND true  
a < b or b > c and b < a
```

True

OUTPUT < >

```
# Disjunction and negated conjunction and conjunction:  
# true AND NOT false AND false  
a < b or not b < c and b > a
```

OUTPUT < >

False

PYTHON < >

```
# Disjunction and negated conjunction - similar to the  
# previous example: true AND NOT (false AND false)  
a < b or not (b < c and b > a)
```

OUTPUT < >

True

These are only a few examples. There are endless possibilities, try them yourself and see how they work.

### REMEMBER

Some logical operations may be written in different ways. However, we should always use the notation that is most coherent in the context of our code. If in doubt, use the simplest / shortest notation.

To that end, you may want to use variables to split complex statements down to smaller portions:

PYTHON < >

```
age_a, age_b = 15, 35  
  
are_positive = age_a > 0 and age_b > 0  
  
a_is_older = are_positive and (age_a > age_b)  
b_is_older = are_positive and (age_a < age_b)  
  
a_is_teenager = are_positive and 12 < age_a < 20  
b_is_teenager = are_positive and 12 < age_b < 20  
  
a_is_teenager and b_is_older
```

OUTPUT < >

True

PYTHON < >

```
a_is_teenager and a_is_older
```

False

OUTPUT < >

```
a_is_teenager and (b_is_teenager or b_is_older)
```

PYTHON < >

True

OUTPUT < >

### DO IT YOURSELF

Given

```
a = 3  
b = 13
```

Test the following statements and display the results:

- $a^2 < b$
- $3 - a^3 < b$
- $|25 - a^2| > b$
- $25 \text{ mod } a^2 > b$
- $25 \text{ mod } a^2 > b \text{ or } 25 \text{ mod } b < a$
- $25 \text{ mod } a^2 < b \text{ and } 25 \text{ mod } b > a$
- $\frac{12}{a} \text{ and } a \times 4 < b$

where “[...]” represents the absolute value, and “ $n \text{ mod } m$ ” represents the remainder for the division of  $n$  by  $m$ .}

Display the results in the following format:

- ```
1. [True/False]  
2. [True/False]  
...
```

Solution

```
PYTHON < >  
  
#Given that:  
a = 3  
b = 13  
print('1.', a**2 < b)
```

1. True

Solution

```
PYTHON < >  
  
print('2.', (3 - a**3) < b)
```

2. True

Solution

```
PYTHON < >  
  
print('3.', abs(25 - a**2) > b)
```

3. True

Solution

```
PYTHON < >  
  
print('4.', (25 % a**2) > b)
```

4. False

Solution

```
PYTHON < >  
print('5.', (25 % a**2) > b or (25 % b) < a)
```

5. False

OUTPUT < >

Solution

```
PYTHON < >  
print('6.', (25 % a**2) < b and (25 % b) > a)
```

6. True

OUTPUT < >

Solution

```
PYTHON < >  
print('7.', (12 / a) and (a * 4) < b)
```

7. True

OUTPUT < >

## Exercises

---

---

## END OF CHAPTER EXERCISES

1. Write and execute a Python script to display your own name as an output in the terminal.
2. Write and execute a Python script that:
  - Displays the text `Please press enter to continue...`, and waits for the user to press enter.
  - Once the user pressed enter, the program should display `Welcome to my programme!` before it terminates.
3. We have an enzyme whose reaction velocity is  $v = 50 \text{ mol} \cdot L^{-1} \cdot s^{-1}$  at the substrate concentration of  $[S] = K_m = 2.5 \text{ mol} \cdot L^{-1}$ . Work out the maximum reaction velocity or  $V_{\max}$  for this enzyme using the Michaelis-Menten equation:

$$v = \frac{V_{\max}[S]}{K_m + [S]}$$

## Solution

Q1

```
PYTHON < >  
name = 'Gerold Baier'  
  
# Displaying the author's name:  
  
print(name)
```

```
OUTPUT < >  
Gerold Baier
```

Q2

```
# Blocking the execution until the user  
# presses enter:  
  
input('Please press enter to continue...')  
  
print('Welcome to my programme!')
```

Q3

```
PYTHON < >  
  
v = 50 #mol/L/s  
k_m = S = 2.5 #mol/L  
  
# Rearranged the equation to  
# solve for v_max:  
  
v_max = (v * (k_m + S)) / S  
# Unit: mol/L/s  
print('Vmax =', v_max, '[ mol / (l * sec) ]')
```

```
OUTPUT < >  
Vmax = 100.0 [ mol / (l * sec) ]
```

## KEYPOINTS

- Two key functions for I/O operations are `print()` and `input()`
- Three most commonly used variables such as `int`, `float`, and `str`.
- Variable scope can be local or global depending where they are being used.
- Mathematical operations follow conventional rules of precedence
- Logical operations provide results in Boolean (True or False)

Content from [Conditional Statements](#)

Last updated on 2023-07-11 | [Edit this page](#) 

[Download Chapter notebook \(ipynb\)](#)

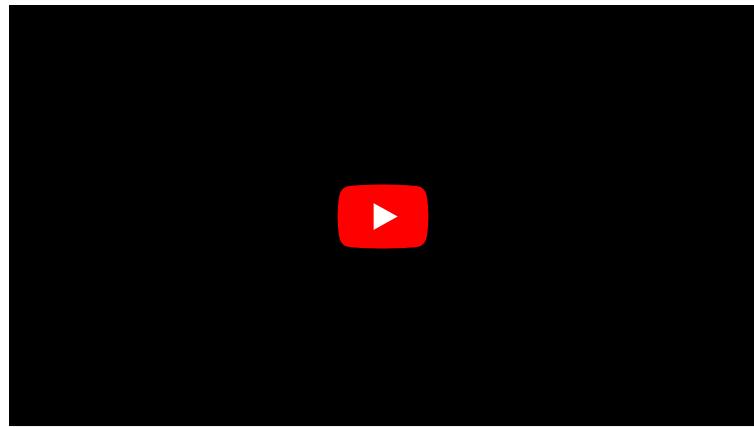
## OVERVIEW

### Questions

- 
- What are conditional statements?
  - How conditional statements are used to make decisions?
  - Why indentation is so important in Python?
  - Is there any hierarchical importance of conditional statements?
- 

### Objectives

- Understand the logic behind using conditional statements.
- Practice conditional statements.
- Learning structuring code using correct indentation.
- Understanding the hierarchy of conditional statements.



This chapter assumes that you are familiar with the following concepts in Python 3:

#### CHECKLIST

- I/O Operations
- Variables And Types
- Mathematical Operation

When we construct logical expressions, we almost always do so because we need to test something. The definition of a process through which we test our logical expressions and provide directives on how to proceed is known in computer science as a *conditional statement*. Conditional statements are a feature of programming languages. This means that although their definitions and grammar may vary slightly from one programming language to another, their principles are almost universally identical.

Being a high-level programming language, defining conditional statements is very easy in Python. Before we start, however, let us briefly review the way conditional statements actually work. To help us with that, we use [flowchart diagrams](#).

#### REMEMBER

The term *conditional statements* is often used in relation to imperative programming languages. In functional programming, however, it is more common to refer to them as *conditional expressions* or *conditional constructs*. Python supports both imperative and functional programming.

## EXAMPLE: ALGORITHMS IN DAILY LIFE

We use algorithms in our life every day without realising it.

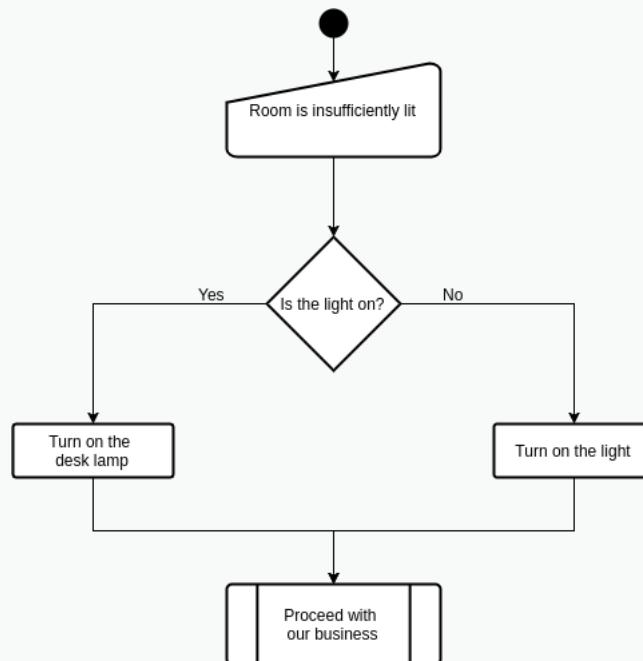
Suppose we enter a room poorly lit room to work. The first things that we notice is that the room is insufficiently lit. We check to see whether or not the light is on; *if* not, we find the switch to turn on the light. Likewise, *if* the light is on, we go ahead and turn on the desk lamp before we proceed with our business.

### PROCESSES OF ALGORITHMS

This scenario may be perceived as a set of processes. These processes include a set of procedures that may be outlined as follows:

1. **Action:** Enter the room.
2. **Input:** Determine that the room is insufficiently lit.
3. **Condition:** Is the light switched on?
  - NO: **Action:** turn on the lights,
  - YES: **Action:** turn on the desk lamp.
4. **Action:** Proceed with our business.

Now that we know what procedures are involved, we can draw a flowchart of the process:



Flowchart

Programming is not merely a hard skill. It is the door to a different way of thinking that enables one to break complex procedures down to simple, stepwise components and tasks. Flowcharts help us perceive processes as computers do — that is, one task or component at a time. As we progress in programming, our brains develop the ability to think in a procedural way. This is called *algorithmic thinking*, and is one of the most important soft-skills that a programmer can develop.

There are international competitions and comprehensive courses dedicated to this concept. At the end of the day, however, one can only acquire a skill through practice.

### ADVANCED TOPIC

If you are keen to learn more about algorithms and algorithmic thinking, or just want to try out some of the problems, you may want to look into some of the past competition papers on [Computational and Algorithmic Thinking \(CAT\)](#) published by the Australian Mathematics Trust.

[Exercise](#) is provided to give you an idea of the type of problems that may be tackled in a procedural way.

### DO IT YOURSELF

On a distant planet, the dominant carnivore, the zab, is nearing extinction. The number of zabs born in any year is one more than the (positive) difference between the number born in the previous year and the number born in the year before that.

#### Examples

- If 7 zabs were born last year and 5 the year before, 3 would be born this year.
- If 7 zabs were born last year and 10 the year before, 4 would be born this year.

If 2 zabs were born in the year 2000 and 9 zabs were born in 2001. What is the first year after 2000 when just 1 zab will be born?

- a. 2009
- b. 2011
- c. 2013
- d. 2015
- e. 2017

**Credit:** This question is taken from the 2011 Computational and Algorithmic Thinking (CAT) Competition held by the Australian Mathematics Trust.}

Solution

To obtain the answer, we may write an algorithm in a pseudo-code format as follows:

```
let a_total = 2  
  
let b_total = 9  
  
let current_total = absolute(a_total - b_total) + 1  
  
let a_total = b_total  
  
let b_total = current_total  
  
let current_year = 2002  
  
  
do {  
  
    current_total = absolute(a_total - b_total) + 1  
  
    a_total = b_total  
  
    b_total = current_total  
  
    current_year = current_year + 1  
  
} while current_total > 1  
  
  
display current_year
```

Given:

```
year = 2000; a_total = 2  
year = 2001; b_total= 9
```

the above process will repeat the section written in curly brackets for as long as `current_total > 1`:

```
current_year: 2002; a_total = 2, b_total = 9, current_total = 8
```

Is `current_total > 1` ? Yes:

```
current_year: 2003; a_total = 9, b_total = 8; current_total = 2
```

Is `current_total > 1` ? Yes:

```
current_year: 2004; a_total = 8; b_total = 2; current_total = 7
```

Is `current_total > 1` ? Yes:

```
current_year: 2005; a_total = 2; b_total = 7; current_total = 6
```

Is `current_total > 1` ? Yes:

```
current_year: 2006; a_total = 7; b_total = 6; current_total = 2
```

Is `current_total > 1` ? Yes:

```
current_year: 2007; a_total = 6; b_total = 2; current_total = 5

Is current_total > 1 ? Yes:

    current_year: 2008; a_total = 2; b_total = 5; current_total = 4

Is current_total > 1 ? Yes:

    current_year: 2009; a_total = 5; b_total = 4; current_total = 2

Is current_total > 1 ? Yes:

    current_year: 2010; a_total = 4; b_total = 2; current_total = 3

Is current_total > 1 ? Yes:

    current_year: 2011; a_total = 2; b_total = 3; current_total = 2

Is current_total > 1 ? Yes:

    current_year: 2012; a_total = 3; b_total = 2; current_total = 2

Is current_total > 1 ? Yes:

    current_year: 2013; a_total = 2; b_total = 2; current_total = 1

Is current_total > 1 ? No:
```

The correct answer is c) 2013.

If this algorithm/pseudo-code is translated to Python language, it will look like this:

```
PYTHON < >

a_total = 2
b_total = 9
current_year = 2002

current_total = abs(a_total - b_total) + 1
a_total = b_total
b_total = current_total

while (current_total > 1):
    current_total = abs(a_total - b_total) + 1
    a_total = b_total
    b_total = current_total
    current_year = current_year + 1

print(current_year)
```

2013

OUTPUT < >

## REMEMBER

There is almost always more than one answer to any algorithmic problem; some answer might even be more efficient than other. The less repetition there is, the better more efficient an algorithm is considered to be.

# Conditions in Python

## **if statements**

To implement conditional statements in Python, we use 3 syntaxes:

- To initiate the statement, we use the syntax **if** followed by the condition and a colon;

```
PYTHON < >  
students_present = 15  
  
# Conditional statement:  
if students_present > 10: # Initiation  
    # Directive (must be indented).  
    print('More than 10 students are present.')  
    
```

More than 10 students are present.

OUTPUT < >

- To create an alternative condition after the first condition has been defined, we use the syntax **elif** followed by the new condition and a colon;

```
PYTHON < >  
students_present = 5  
  
# Conditional statement:  
if students_present > 10: # Initiation  
  
    # Directive (must be indented).  
    print('More than 10 students are present.')  
  
elif 0 < students_present < 10:  
    print('Less than 10 students are present.')  
    
```

OUTPUT < >

Less than 10 students are present.

- To introduce a default — i.e. where none of the above are `True`, we use the syntax `else`.

PYTHON < >

```
students_present = 0

# Conditional statement:
if students_present > 10: # Initiation
    # Directive (must be indented).
    print('More than 10 students are present.')

elif 0 < students_present < 10: # Alternative condition
    # Alternative directive (must be indented).
    print('Less than 10 students are present.')

else: # Default (none of the conditions are met).
    # Directive (must be indented).
    print('There is no one!')
```

OUTPUT < >

There is no one!

### REMEMBER

We can use disjunctions or conjunctions, as discussed in topic [Disjunctions and Conjunctions](#), to test for more than one condition at a time.

## Indentation Rule

### [PEP-8: Indentation](#)

Always use 4 spaces for indentation. Indentations are how the Python interpreter determines the code hierarchy. A consistent hierarchy is therefore essential for the interpreter to parse and execute our code.

The indented part of the code is known as a *block*. A block represents a part of the code that always “belongs” to (is the child process of) the first *unindented* (dedented) line that precedes it. In other words, the action(s) within a conditional statement (actions that are subject to a specific condition) must always be *indented*.

```
value = 10

# Statement A:
if value > 0:

    # First dedented line before the block.
    # This is a block, and it belongs to the
    # preceding "if" (Statement A):
    print('The value is positive.')

    # We can have nested blocks too.
    # Statement B:
    if value > 9:
        # First dedented line before the block.
        # This is another block (nested).
        # This block belongs to the preceding "if" (Statement B).
        print('The value is not a single digit.')

    # Introducing a default behaviour for Statement B:
else:
    # This block belongs to the preceding "else".
    print('The value is a single digit.')

# Introducing an alternative condition for Statement A:
elif value < 0:
    # This block belongs to the preceding "elif".
    print('The value is negative.')

# Introducing a default behaviour for Statement A:
else:
    # This block belongs to the preceding "else".
    print('The value is zero.')
```

```
The value is positive.
The value is not a single digit.
```

It is not a good practice to have too many nested indentation. This would make the code more difficult to read. A rule of thumb is that you should not need more than 4 nested indentations in your code. If you do, you should reconsider the code structure to somehow simplify the process.

On that note, where possible, it is better to use conjunctions and disjunctions, or implement alternative conditions using `elif` instead of creating nested conditional statements. We can therefore restructure the previous example in a better, more coherent way as follows:

```
value = 10

if value > 9:
    print('The value is positive.')
    print('The value is not a single digit.')
elif value > 0:
    print('The value is positive.')
    print('The value is a single digit.')
elif value < 0:
    print('The value is negative.')
else:
    print('The value is zero.)
```

The value is positive.  
The value is not a single digit.

It is customary and also best practice to use 4 spaces for indentation in Python. It is also paramount that all indentations throughout the code are consistent; that is, you may not use 4 spaces here and 3 spaces somewhere else in your code. Doing so will cause an `IndentationError` to be raised. It is recommended to *not* use `Tab` to indent your code; it is regarded as a bad practice in Python.

```
value = 10

if value > 0:
    print('The value is: ') # Indented with 4 spaces.
    print('POSITIVE.') # Indented with 3 spaces.
```

```
File <STDIN>, line 5
    print('POSITIVE.') # Indented with 3 spaces.
   ^
IndentationError: unindent does not match any outer indentation level
```

## CALLOUT

`Tab` indentations represent different number of spaces on different computers and operating systems. It is therefore more than likely that they will lead to `IndentationError`. Additionally, Python 3 disallows the mixing of `tab` and `space` indentations. Some Python IDEs such as *PyCharm* automatically convert `Tab` indentations to 4 spaces. Some other IDEs (e.g. Jupyter) typically highlight `Tab` indentations to explicitly distinguish them and thereby notify the programmer of their existence. However, more often than not, IDEs and text editors tend to *ignore* this, which amounts to inconsistencies and subsequently `IndentationError`. This is a very common difficulty that new Python programmers face, and can be very confusing if not handled correctly.

## DO IT YOURSELF

In previous chapter, [Do it Yourself](#), we explored the implication of **CAG** repeats in Huntington's disease. We also created a polynucleotide chain containing 36 repetition of the **CAG** codons.

Write a conditional statement that tests the length of a polyQ tract to determine the *classification* and the *disease status* based on the following Table:

| NUMBER OF REPEATS | CLASSIFICATION     | DISEASE STATUS |
|-------------------|--------------------|----------------|
| < 26              | Normal             | Unaffected     |
| 27 – 35           | Intermediate       | Unaffected     |
| 36 – 40           | Reduced Penetrance | +/- Affected   |
| > 40              | Full Penetrance    | Affected       |

Using the technique you used in [Do it Yourself](#), create 5 polyQ tracts containing 26, 15, 39, 32, 36, and 54 codons. Use these polynucleotide chains to test your conditional statement.

Display the result for each chain in the following format:

```
PolyQ chain with XXX number of CAG codons:  
Status: XXX  
Classification: XXX
```

**Hint:** The length of a polyQ tract represents the number of nucleotides, not the number of **CAG** codons. See task 4 of [Do it Yourself](#) for additional information.

Solution

PYTHON &lt; &gt;

```
#Constructing the codons:

glutamine_codon = 'CAG'

polyq_codons = glutamine_codon * 26

#Determining the length of our codon:

signle_codon = len('CAG')

len_polyq = len(polyq_codons)

polyq = len_polyq / signle_codon

#Constructing the conditional statement:

NORMAL = 26
INTERMEDIATE = 35
REDUCED_PENETRANCE = 40

classification = str()
status = str()

if polyq < NORMAL:
    classification, status = 'Normal', 'Unaffected'
elif polyq <= INTERMEDIATE:
    classification, status = 'Intermediate', 'Unaffected'
elif polyq <= REDUCED_PENETRANCE:
    classification, status = 'Reduced Penetrance', '+/- Affected'
else:
    classification, status = 'Full Penetrance', 'Affected'

#Displaying the results:

print('PolyQ chain with', polyq, 'number of CAG codons:')
print('Classification:', classification)
print('Status:', status)

#Repeat this with 15, 39, 32, 36, and 54 codons.
```

OUTPUT &lt; &gt;

```
PolyQ chain with 26.0 number of CAG codons:
Classification: Intermediate
Status: Unaffected
```

## Hierarchy of conditional statements

The hierarchy of conditional statement is always the same. We start the statement with an `if` syntax (initiation). This is the only essential part to implement a conditional statement. Other parts include the `elif` and the `else` syntaxes. These are the non-essential part, and we implement these as and when needed. It is, however, important that we adhere to the correct order when we implement these:

- Always start with the initiation syntax `if`.
- Where needed, implement as many alternative conditions as necessary `elif`.
- Where needed, implement a default behaviour using `else`.

In an `if...elif...else` hierarchy, once one condition in the hierarchy is `True`, all *subsequent* conditions in that group are skipped and would no longer be checked.

In the following example, the first condition is `True`, therefore its corresponding block is executed and the rest of this conditional statement is skipped:

```
TATA_BOX = 'TATA'

promoter_region = 'GTAACGTGGTATAATCGT'

if TATA_BOX in promoter_region:
    # This condition is "True", so this
    # and only this block is executed.
    print('There is a "TATA" box in this promoter region.')
else:
    # The last condition was "False", so this
    # block is skipped.
    print('There is no "TATA" box in this promoter region.)
```

There is a "TATA" box in this promoter region.

## REMEMBER

We already know from subsection [Logical Operations](#) that the value of a *boolean* (`bool`) variable is either `False` or `True`.

We have also learned that in conditional statements, we use *double equals* {or `... == ...`} to test for equivalence. So naturally, one could test for the *truth value* of a `bool` variables as follows:

```
PYTHON < >  
variable = False  
  
if variable == False:  
    print('The variable is False.')  
  
OUTPUT < >
```

The variable is False.

This works, and it looks simple enough. However, this is the **wrong approach** for testing the value of `bool` variables and should *not* be used. Whilst the answer is correct in the above example, using *double equals* for testing *boolean* variables can sometimes produce incorrect results.

The correct way to test the *truth value* of a *boolean* variable is by using `is` as follows:

```
PYTHON < >  
variable = False  
  
if variable is False:  
    print('The variable is False.')  
  
OUTPUT < >
```

The variable is False.

and the negative test is:

```
PYTHON < >  
variable = True  
  
if variable is not False:  
  
    print('The variable is True.')  
  
OUTPUT < >
```

The variable is True.

In short; as far as *boolean* variables are concerned, we should always use `is` or `is not` to test for their *truth value* in a conditional statement.

Consequently, we can now write the example [algorithm](#) (room and light) as follows:

PYTHON < >

```
light_status = False

if light_status is True:

    action = 'The light is on; you may want to turn off the desk light.'

else:
    action = 'The light is off... turn it on.'

print(action)
```

OUTPUT < >

```
The light is off... turn it on.
```

There are a few very popular shorthands in Python that you should be familiar with when writing or reading conditional statements:

In an `if` statement, Python expects the result of the condition to be `True`. As result of that, we can simplify the above example as follows:

PYTHON < >

```
light_status = False

if light_status:

    action = 'The light is on; you may want to turn off the desk light.'

else:
    action = 'The light is off... turn it on.'

print(action)
```

OUTPUT < >

```
The light is off... turn it on.
```

Sometime, however, we might need to test for a `False` outcome. To do so, we can write a negated conditions as described in subsection [Negation](#) instead:

PYTHON < >

```
# Note that we have changed the order of the condition
# and added a "not" before "light_status"
if not light_status:

    action = 'The light is off... turn it on.'

else:

    action = 'The light is on; you may want to turn off the desk light.'

print(action)
```

OUTPUT < >

```
The light is off... turn it on.
```

## EXAMPLE: A FAMILIAR SCENARIO

Suppose we want to determine the classification of the final mark for a student.

The classification protocol is as follows:

- Above 70%: First class.
- Between 60% and 70%: Second class (upper division).
- Between 50% and 60%: Second class (lower division).
- Between 40% and 50%: Pass.
- Below 40%: Fail.

PYTHON < >

```
mark = 63

# Thresholds
first = 70
second_upper = 60
second_lower = 50
passed = 40 # "pass" is a syntax in Python.

if mark >= first:
    classification = 'First Class'
elif mark >= second_upper:
    classification = 'Second Class (upper division)'
elif mark >= second_lower:
    classification = 'Second Class (lower division)'
elif mark >= passed:
    classification = 'Pass'
else:
    classification = 'Fail'

print('The student obtained a', classification, 'in their studies.')
```

OUTPUT < >

```
The student obtained a Second Class (upper division) in their studies.
```

## Exercises

## END OF CHAPTER EXERCISES

1. Protein Kinases have a phosphorylation site and a consensus sequence has been determined for these sites ([Rust and Thompson, 2012](#)). All the proteins incorporate either a Serine or a Threonine residue that gets phosphorylated. Naturally, the consensus sequence for each protein varies slightly from that of other proteins.

When studying a polypeptide in the lab, a colleague realised that it has a phosphorylated Serine. So they tried to sequence the polypeptide, and managed to obtain a sequence for the protein:

```
kinase_peptide = (
    "PVWNETFVFNKPGDVERRLSVEVWDWDRTRNDFMGAMSFGVSELLK"
    "APVDGKYKLLNQEEGEYYNVPVADADNCSSLQKFEACNYPLELYERVR"
    "MGPSSPIPSPSPSPTDPKRCFFGASPGRHLHISDFSLMRRRKGSFGK"
    "VMLAERRGSDELYAIKILKKDVIVQDDDVCTLVEKRVLAALGGRGPGG"
    "RPHFLTQLHSTFQTPDRLYFVMEYVTGGDLMYHIQLGKFKEPHAAFY"
    "AAEIAIGLFLHNQGIIYRDLKLDNVMLDAEGHIKITDFGMCKENVF"
)
```

Desperate to find a match, and knowing that we are good at doing [computer stuff](#), they asked us if we can help them identify what protein kinase does the sequence correspond to?

So we extract the consensus sequence of 3 protein kinases from [the paper](#):

- PKC- $\eta$ : either [RKGSFRR](#) or [RRRSFRR](#)
- PKC- $\gamma$ : either [RRRKGSF](#) or [RRRKKSF](#)
- DMPK-E: one of [KKRRRSL](#), [RKRRRSL](#), [KKRRRSV](#), or [RKRRRSV](#).

Now all we need is to write a conditional statement in Python to identify which of the above protein kinases, if any, does our sequence correspond to. That is, which one of the consensus peptides exists in our mystery sequence?

If there is a match, our programme should display the name of the corresponding protein kinase; otherwise, it should say [No matches found](#) for good measures.

## Solution

PYTHON < >

```
peptide = (
    "PVWNETFVFNKPGDVERRLSVEVWDWDRTRSNDFMGAMSFGVSELLK"
    "APVDGKYKLLNQEEGEYYNPVADADNCSSLQKFEACNYPLEYERVR"
    "MGPSSSPIPSPSPSPTDPKRCFFGASPGRHLISDFSFLMRRRKGSFGK"
    "VMLAERRGSDELYAIKILKKDVIVQDDVDCTLVEKRVLALGGRGPGG"
    "RPHFLTQLHSTFQTPDRLYFVMEYVTGGDLMYHIQLGKFKEPHAAFY"
    "AAEIAIGLFFLHNQGIIYRDLKLDNVMLDAEGHIKITDFGMCKENVF"
)

if "RKGSFRR" in peptide or "RRRSFRR" in peptide:
    print('PKC-eta')
elif "RRRKGSF" in peptide or "RRRKKSF" in peptide:
    print('PKC-gamma')
elif ("KKRRRSL" in peptide or "RKRRRSL" in peptide or
      "KKRRRSV" in peptide or "RKRRRSV" in peptide):
    print('DMPK-E')
else:
    print('No matches found.')
```

OUTPUT < >

```
PKC-gamma
```

## KEYPOINTS

- Python used `if`, `elif` and `else` as conditional statements.
- In Python, there is an indentation rule of 4 spaces.
- The hierarchy of conditional statement is always the same.

Content from [Introduction to Arrays](#)

Last updated on 2023-07-11 | [Edit this page](#) 

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[Mandatory Lesson Feedback Survey](#)

## OVERVIEW

### Questions

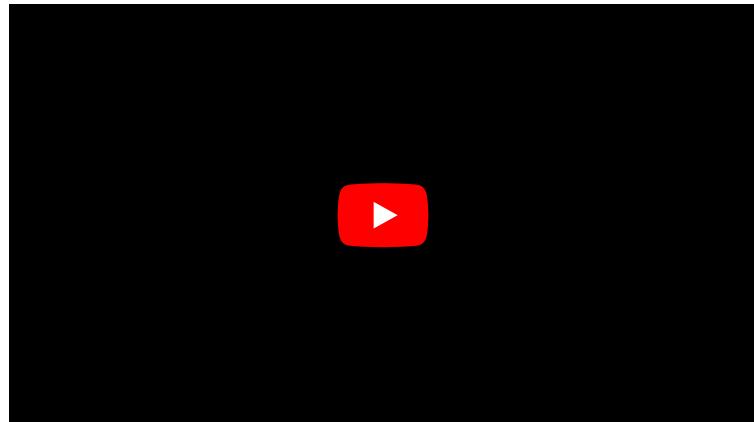
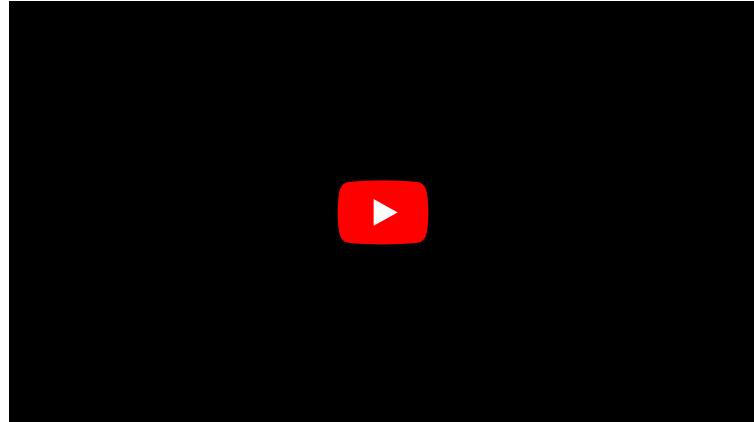
- What are different types of arrays?

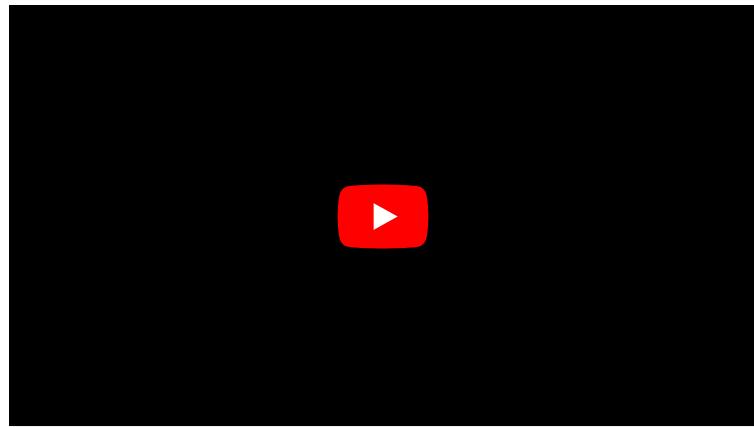
- How is data stored and retrieved from an array
  - Why nested arrays?
  - What are tuples?
- 

## Objectives

---

- Understanding difference between lists and tuples.
- Building concepts of operations on arrays.
- knowing storing multidimensional data.
- Understanding mutability and immutability.





## PREREQ

- [Variables and Types](#)
- [Logical Operations](#)
- [Conditional Statements](#)

So far, we have been using variables to store individual values. In some circumstances, we may need to access multiple values to perform operations. In such occasions, defining a variable for every single value can become very tedious. To address this, we use arrays.

Arrays are variables that hold any number of values. Python provides 3 types of built-in arrays: [list](#), [tuple](#), and [set](#). There are several common features amongst all arrays in Python; however, each type of array enjoys its own range of unique features that facilitate specific operations.

## REMEMBER

Each item inside an array may be referred to as a *member* or *item* of that array.

# Lists

## [Resource for Lists](#)

Lists are the most frequently used type of arrays in Python. It is therefore important to understand how they work, and that how can we use them and features they offer to our advantage.

The easiest way to imagine how a [list](#) works is to think of it as a table that can have any number of rows. This is akin to a spreadsheet with one column. For instance, suppose we have a table with 4 rows in a spreadsheet application as follows:

Untitled 1 - LibreOffice Calc

The screenshot shows a LibreOffice Calc spreadsheet window. The menu bar includes File, Edit, View, Insert, Format, Sheet, Data, Tools, Window, and Help. The toolbar has icons for fx, Σ, and =. The spreadsheet area has rows labeled 1 through 12 and columns labeled A through H. Row 5 contains the values 5, 21, 5, and -1. Row 6 is empty. The status bar at the bottom shows 'Sheet1 of 1', 'Default', and 'Average: Sum: 0'. The zoom level is set to 140%.

|    | A  | B | C | D | E | F | G | H |
|----|----|---|---|---|---|---|---|---|
| 1  | 5  |   |   |   |   |   |   |   |
| 2  | 21 |   |   |   |   |   |   |   |
| 3  | 5  |   |   |   |   |   |   |   |
| 4  | -1 |   |   |   |   |   |   |   |
| 5  |    |   |   |   |   |   |   |   |
| 6  |    |   |   |   |   |   |   |   |
| 7  |    |   |   |   |   |   |   |   |
| 8  |    |   |   |   |   |   |   |   |
| 9  |    |   |   |   |   |   |   |   |
| 10 |    |   |   |   |   |   |   |   |
| 11 |    |   |   |   |   |   |   |   |
| 12 |    |   |   |   |   |   |   |   |

The number of rows in an array determine the *length*. The above table has 4 rows; therefore it is said to have a *length* of 4.

## Implementation

### REMEMBER

To implement a `list` in Python, we place the values separated by commas inside square brackets [1, 2, 3, ...].

PYTHON < >

```
table = [5, 21, 5, -1]
print(table)
```

OUTPUT < >

```
[5, 21, 5, -1]
```

PYTHON < >

```
print(type(table))
```

OUTPUT < >

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

## DO IT YOURSELF

Implement a `list` array called `fibonacci`, whose members represent the first 8 numbers of the [Fibonacci sequence](#) as follows:

### FIBONACCI NUMBERS (FIRST 8)

1                  1    2    3    5    8    13    21

#### Solution

```
fibonacci = [1, 1, 2, 3, 5, 8, 13, 21]
```

PYTHON < >

## Indexing

In arrays, an index is an integer number that corresponds to a specific item.

You can think of an index as a *unique reference* or a *key* that corresponds to a specific row in a table. We don't always write the row number when we create a table. However, we always know that the 3<sup>rd</sup> row of a table means that we start from the first row (row #1), count 3 rows down and there we find the 3<sup>rd</sup> row.

The only difference in Python is that we don't take the first row as row #1; instead, we consider it to be row #0. As a consequence of starting from #0, we count rows in our table down to row #2 instead of #3 to find the 3<sup>rd</sup> row. So our table may in essence be visualised as follows:

| INDEX | VALUE |
|-------|-------|
| 0     | 5     |
| 1     | 21    |
| 2     | 5     |
| 3     | -1    |

## REMEMBER

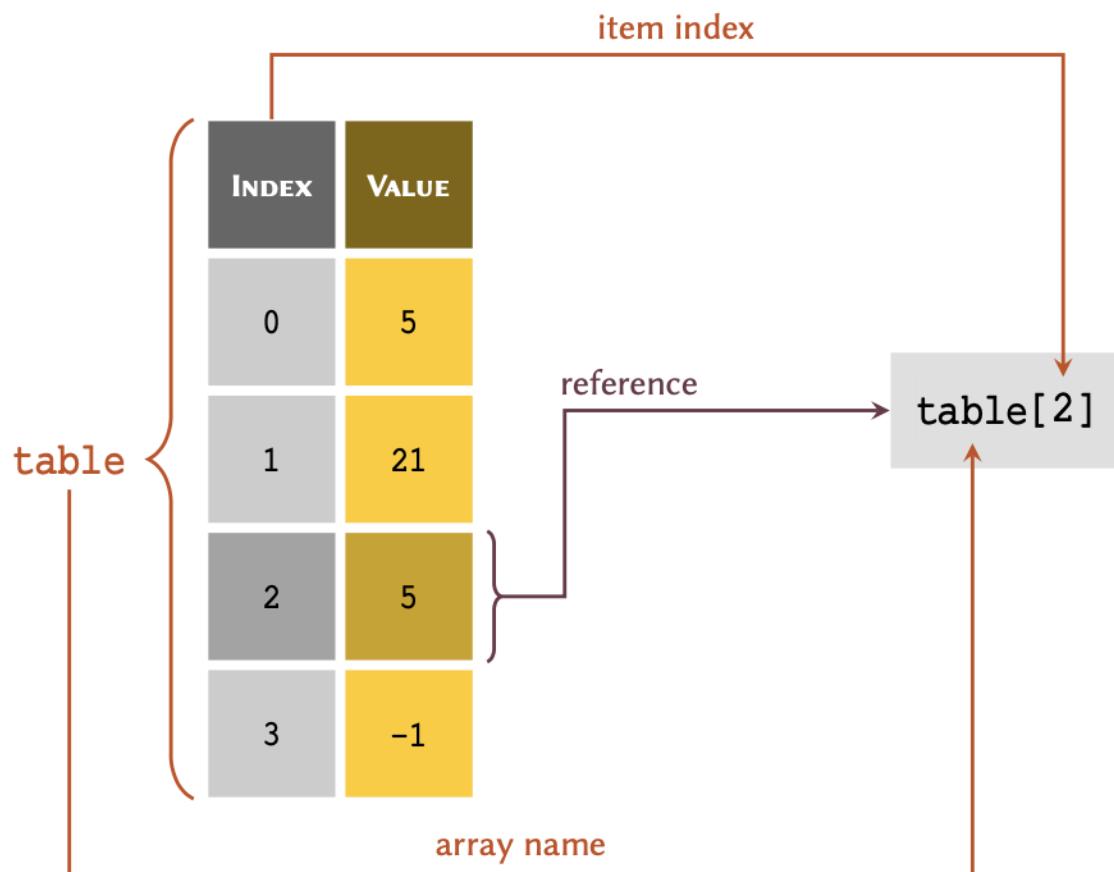
Python uses a zero-based indexing system. This means that the first row of an array, regardless of its type, is always #0.

With that in mind, we can use the index for each value to retrieve it from a `list`.

Given a `list` of 4 members stored in a variable called `table`:

```
table = [5, 21, 5, -1]
```

we can visualise the referencing protocol in Python as follows:



As demonstrated in the diagram; to retrieve a member of an array through its index, we write the name of the variable immediately followed by the index value inside a pair of square brackets — e.g. `table[2]`.

```
print(table[2])
```

PYTHON < >

5

OUTPUT < >

```
print(table[0])
```

5

OUTPUT < >

```
item = table[3]  
print(item)
```

-1

OUTPUT < >

### DO IT YOURSELF

Retrieve and display the 5<sup>th</sup> Fibonacci number from the [list](#) you created in previous [DIY](#).

#### Solution

```
print(fibonacci[4])
```

PYTHON < >

5

OUTPUT < >

It is sometimes more convenient to index an array backwards — that is, to reference the members from the bottom of the array. This is called *negative indexing* and is particularly useful when we are dealing with very lengthy arrays. The indexing system in Python supports both positive and negative indexing systems.

The table above therefore may also be represented as follows:

| Index | Value |
|-------|-------|
| -4    | 5     |
| -3    | 21    |
| -2    | 5     |
| -1    | -1    |

### REMEMBER

Unlike the normal indexing system, which starts from #0, negative indexes start from #-1 so that it will always be clear which indexing system is being used.

If the index is a negative number, the indices are counted from the end of the `list`. We can implement negative indices the same way we do positive ones:

```
print(table[-1])
```

PYTHON < >

-1

OUTPUT < >

```
print(table[-2])
```

PYTHON < >

5

OUTPUT < >

```
print(table[-3])
```

PYTHON < >

21

OUTPUT < >

We know that in `table`, index #**-3** refers the same value as index #**1**. So let us go ahead and test this:

```
equivalence = table[-3] == table[1]
print(equivalence)
```

PYTHON < >

True

OUTPUT < >

If the index requested is larger than the length of the `list` minus one, an `IndexError` will be raised:

```
print(table[4])
```

PYTHON < >

Error: IndexError: list index out of range

ERROR < >

### REMEMBER

The values stored in a `list` may be referred to as the **members** of that `list`.

### DO IT YOURSELF

Retrieve and display the *last* Fibonacci number from the `list` you created in [DIY](#).

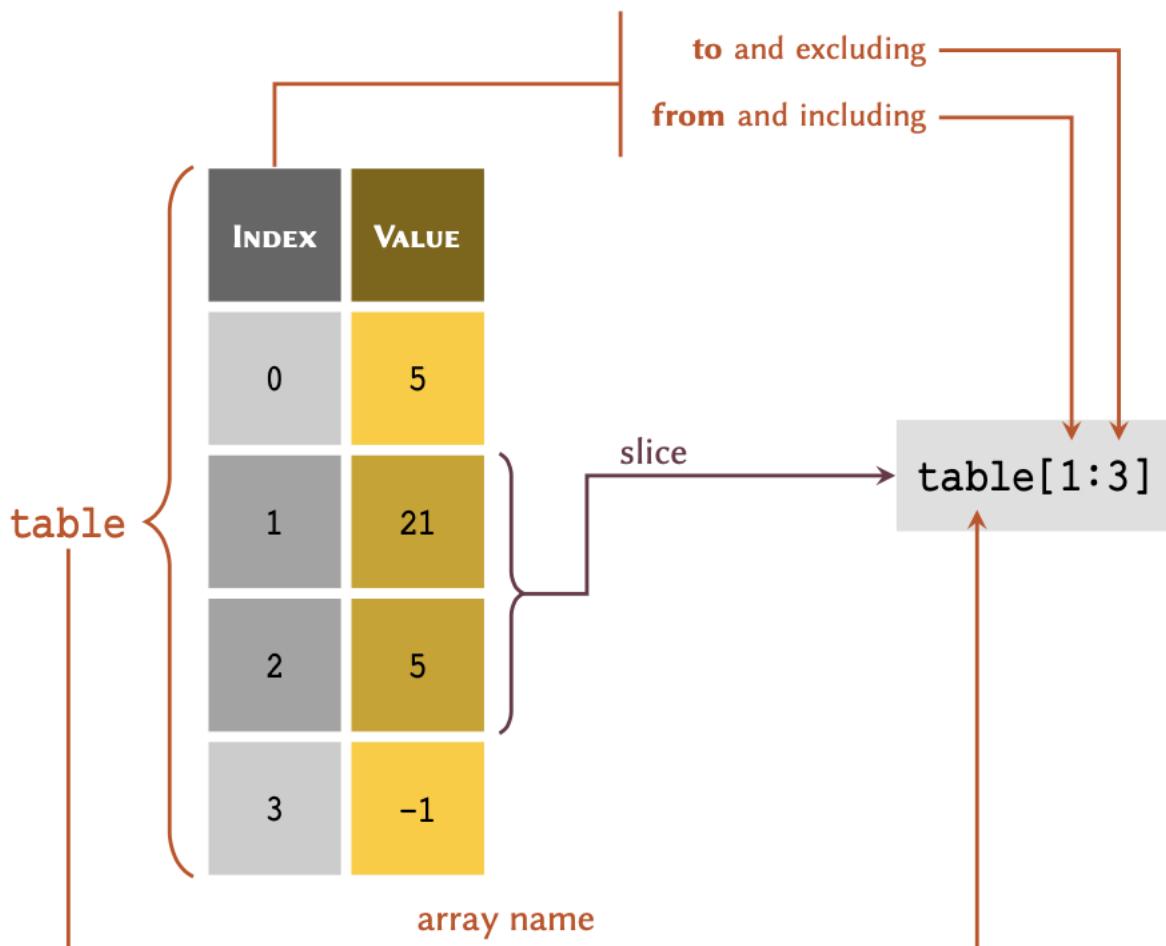
## Solution

```
PYTHON < >  
print(fibonacci[-1])
```

```
OUTPUT < >  
21
```

## Slicing

We may retrieve more than one value from a `list` at a time, as long as the values are in *consecutive* rows. This process is known as `slicing`, and may be visualised as follows:



## REMEMBER

Python is a **non-inclusive** language. This means that in `table[a:b]`, a *slice* includes all the values from, and including index `a` right down to, but *excluding*, index `b`.

Given a `list` representing the above table:

```
table = [5, 21, 5, -1]
```

we may retrieve a slice of `table` as follows:

```
PYTHON < >  
my_slice = table[1:3]  
  
print(my_slice)
```

```
OUTPUT < >  
[21, 5]
```

```
print(table[0:2])
```

If the first index of a slice is #0, the slice may also be written as:

```
PYTHON < >  
print(table[:2])
```

```
OUTPUT < >  
[5, 21]
```

Negative slicing is also possible:

```
PYTHON < >  
# Retrieves every item from the first member down  
# to, but excluding the last one:  
print(table[:-1])
```

```
[5, 21, 5]
```

OUTPUT < >

```
print(table[1:-2])
```

PYTHON < >

```
[21]
```

OUTPUT < >

If the second index of a slice represents the last index of a **list**, it be written as:

```
print(table[2:])
```

PYTHON < >

```
[5, -1]
```

OUTPUT < >

```
print(table[-3:])
```

PYTHON < >

```
[21, 5, -1]
```

OUTPUT < >

We may store indices and slices in variables:

```
start, end = 1, 3
new_table = table[start:end]

print(new_table)
```

PYTHON < >

```
[21, 5]
```

OUTPUT < >

The `slice()` function may also be used to create a slice variable:

```
my_slice = slice(1, 3)  
print(table[my_slice])
```

PYTHON < >

```
[21, 5]
```

OUTPUT < >

### DO IT YOURSELF

Retrieve and display a slice of Fibonacci numbers from the `list` you created in `DIY` that includes all the members from the 2nd number onwards — *i.e.* the slice must not include the first value in the `list`.

#### Solution

```
print(fibonacci[1:])
```

PYTHON < >

```
[1, 2, 3, 5, 8, 13, 21]
```

OUTPUT < >

### NOTE

**Methods** are features of **Object-Oriented Programming (OOP)**, a programming paradigm that we do not discuss in the context of this course. You can think of a *method* as a *function* that is associated with a specific *type*. The job of a *method* is to provide a certain functionality unique to the *type* it is associated with. In this case, `.index()` is a *method* of type `list` that given a value, finds and produces its index from the `list`.

### **From value to index**

Given a `list` entitled `table` as:

```
table = [5, 21, 5, -1]
```

PYTHON < >

we can also find out the index of a specific value. To do so, we use the `.index()` *method*:

```
print(table.index(21))
```

PYTHON < >

1

```
last_item = table.index(-1)  
print(last_item)
```

PYTHON < >

3

If a value is repeated more than once in the `list`, the index corresponding to the *first* instance of that value is returned:

```
print(table.index(5))
```

PYTHON < >

0

If a value does *not* exist in the `list`, using `.index()` will raise a `ValueError`:

```
print(table.index(9))
```

PYTHON < >

Error: ValueError: 9 is not in list

ERROR < >

## DO IT YOURSELF

Find and display the index of these values from the `list` of Fibonacci numbers that you created in [DIY](#):

- 1
- 5
- 21

### Solution

```
PYTHON < >  
print(fibonacci.index(1))  
  
print(fibonacci.index(5))  
  
print(fibonacci.index(21))
```

```
OUTPUT < >  
0  
4  
7
```

## Mutability

Arrays of type `list` are modifiable. That is, we can add new values, change the existing ones, or remove them from the array all together. Variable types that allow their contents to be modified are referred to as *mutable types* in programming.

### Addition of new members

Given a `list` called `table` as:

We can add new values to `table` using `.append()`:

```
PYTHON < >  
table.append(29)  
  
print(table)
```

```
OUTPUT < >  
[5, 21, 5, -1, 29]
```

PYTHON < >

```
table.append('a text')

print(table)
```

OUTPUT < >

```
[5, 21, 5, -1, 29, 'a text']
```

Sometimes, it may be necessary to insert a value at a specific index in a `list`. To do so, we may use `.insert()`, which takes two input arguments; the first representing the index, and the second the value to be inserted:

PYTHON < >

```
table.insert(3, 56)

print(table)
```

OUTPUT < >

```
[5, 21, 5, 56, -1, 29, 'a text']
```

### DO IT YOURSELF

Given `fibonacci` the `list` representing the first 8 numbers in the Fibonacci sequence that you created in [DIY](#):

1. The 10<sup>th</sup> number in the Fibonacci sequence is 55. Add this value to `fibonacci`.
2. Now that you have added 55 to the `list`, it no longer provides a correct representation of the Fibonacci sequence. Alter `fibonacci` and insert the missing number such that your it correctly represents the first 10 numbers in the Fibonacci sequence, as follows:

---

#### FIBONACCI NUMBERS (FIRST 8)

---

|   |   |   |   |   |   |    |    |    |    |
|---|---|---|---|---|---|----|----|----|----|
| 1 | 1 | 2 | 3 | 5 | 8 | 13 | 21 | 34 | 55 |
|---|---|---|---|---|---|----|----|----|----|

Solution

PYTHON < >

```
fibonacci.append(55)
```

## Solution

```
fibonacci.insert(8, 34)
```

PYTHON < >

## Modification of members

Given a **list** as:

```
table = [5, 21, 5, 56, -1, 29, 'a text']
```

PYTHON < >

We can also modify the existing value or values inside a **list**. This process is sometimes referred to as *item assignment*.

```
# Changing the value of the 2nd member.  
  
table[1] = 174  
  
print(table)
```

PYTHON < >

```
[5, 174, 5, 56, -1, 29, 'a text']
```

OUTPUT < >

```
table[-4] = 19  
  
print(table)
```

PYTHON < >

```
[5, 174, 5, 19, -1, 29, 'a text']
```

OUTPUT < >

It is also possible to perform *item assignment* over a *slice* containing any number of values. Note that when modifying a slice, the replacement values must be the same length as the slice we are trying to replace:

PYTHON < >

```
print('Before:', table)

replacement = [-38, 0]

print('Replacement length:', len(replacement))
print('Replacement length:', len(table[2:4]))

# The replacement process:
table[2:4] = replacement

print('After:', table)
```

OUTPUT < >

```
Before: [5, 174, 5, 19, -1, 29, 'a text']
Replacement length: 2
Replacement length: 2
After: [5, 174, -38, 0, -1, 29, 'a text']
```

PYTHON < >

```
# Using the existing value to determine the new value:
table[2] = table[2] + 50

print(table)
```

OUTPUT < >

```
[5, 174, 12, 0, -1, 29, 'a text']
```

### DO IT YOURSELF

Given a **list** containing the first 10 **prime numbers** as:

```
primes = [2, 3, 5, 11, 7, 13, 17, 19, 23, 29]
```

However, values 11 and 7 have been misplaced in the sequence. Correct the order by replacing the slice of **primes** that represents **[11, 7]** with **[7, 11]**.

## Solution

PYTHON < >

```
primes = [2, 3, 5, 11, 7, 13, 17, 19, 23, 29]  
primes[3:5] = [7, 11]
```

## Removal of members

When removing a value from a `list` array, we have two options depending on our needs: we either remove the member and retain the value in another variable, or we remove it and dispose of the value.

To remove a value from a `list` without retaining it, we use `.remove()`. The method takes one input argument, which is the value we would like to remove from our `list`:

PYTHON < >

```
table.remove(174)  
  
print(table)
```

OUTPUT < >

```
[5, 12, 0, -1, 29, 'a text']
```

Alternatively, we can use `del`; a Python syntax that we can use in this context to delete a specific member using its index:

PYTHON < >

```
del table[-1]  
  
print(table)
```

OUTPUT < >

```
[5, 12, 0, -1, 29]
```

As established above, we can also delete a member and retain its value. Of course we can do so by holding the value inside another variable before deleting it.

Whilst that is a valid approach, Python's `list` provide us with `.pop()` to simplify the process even further. The method takes one input argument for the index of the member to be removed. It removes the member from the `list` and returns its value, so that we can retain it in a variable:

PYTHON < >

```
removed_value = table.pop(2)  
  
print('Removed value:', removed_value)  
print(table)
```

OUTPUT < >

```
Removed value: 0  
[5, 12, -1, 29]
```

### DO IT YOURSELF

We know that the nucleotides of DNA include A, C, T, and G.

Given a `list` representing the nucleotides of a DNA strand as:

```
strand = ['A', 'C', 'G', 'G', 'C', 'M', 'T', 'A']
```

1. Find the index of the invalid nucleotide in `strand`.
2. Use the index you found to remove the invalid nucleotide from `strand` and retain the value in another variable. Display the result as:

```
Removed from the strand: X  
New strand: [X, X, X, ...]
```

3. What do you think happens once we run the following code, and why? What would be the final result displayed on the screen?

```
strand.remove('G')  
  
print(strand)
```

### Solution

PYTHON < >

```
strand = ['A', 'C', 'G', 'G', 'C', 'M', 'T', 'A']  
  
outlier_index = strand.index('M')
```

## Solution

```
PYTHON < >  
outlier_value = strand.pop(outlier_index)  
  
print('Removed from the strand:', outlier_value)  
print('New strand:', strand)
```

```
OUTPUT < >  
Removed from the strand: M  
New strand: ['A', 'C', 'G', 'G', 'C', 'T', 'A']
```

## Solution

One of the two **G** nucleotides, the one at index 2 of the original array, is removed. This means that the `.remove()` method removes only *first* instance of a member in an array. The output would therefore be:

```
['A', 'C', 'G', 'C', 'M', 'T', 'A']
```

## Method-mediated operations

We already know that *methods* are akin to functions that are associated with a specific type. In this subsection, we will be looking into how operations are performed using *methods*. To that end, we will not be introducing anything new, but recapitulate what we already know from different perspectives.

So far in this chapter, we have learned how to perform different operations on `list` arrays in Python. You may have noticed that some operations return a result that we can store in a variable, whilst others change the original value.

With that in mind, we can divide operations performed using *methods* into two general categories:

1. Operations that return a result *without* changing the original array:

```
PYTHON < >  
table = [1, 2, 3, 4]  
  
index = table.index(3)  
  
print(index)  
print(table)
```

```
OUTPUT < >  
2  
[1, 2, 3, 4]
```

2. Operations that use specific **methods** to *change* the original array, but do *not* necessarily return anything (in-place operations):

PYTHON < >

```
table = [1, 2, 3, 4]
table.append(5)
print(table)
```

OUTPUT < >

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

If we attempt to store the output of an operation that does not return result inside a variable, the variable will be created, but its value will be set to `None`:

PYTHON < >

```
result = table.append(6)
print(result)
print(table)
```

OUTPUT < >

```
None
[1, 2, 3, 4, 5, 6]
```

It is important to know the difference between these types of operations. So as a rule of thumb, when we use *methods* to perform an operation, we can only change the original value if it is an instance of a *mutable* type. See [Table](#) to find out which built-in types are mutable in Python.

The *methods* that are associated with *immutable* objects always return the results and do not provide the ability to alter the original value:

- In-place operation on a *mutable* object of type `list`:

PYTHON < >

```
table = [5, 6, 7]
table.remove(6)
print(table)
```

OUTPUT < >

```
[5, 7]
```

- In-place operation on an *immutable* object of type `str`:

```
string = '567'
```

```
string.remove(20)
```

PYTHON < >

```
Error: AttributeError: 'str' object has no attribute 'remove'
```

ERROR < >

```
print(string)
```

```
567
```

PYTHON < >

OUTPUT < >

- Normal operation on a *mutable* object of type `list`:

```
table = [5, 6, 7]
```

```
ind = table.index(6)
```

```
print(ind)
```

PYTHON < >

```
1
```

OUTPUT < >

- Normal operation on a *mutable* object of type `list`:

```
string = '567'
```

```
ind = string.index('6')
```

```
print(ind)
```

PYTHON < >

```
1
```

OUTPUT < >

## List members

A `list` is a collection of members that are independent of each other. Each member has its own `type`, and is therefore subject to the properties and limitation of that type:

PYTHON < >

```
table = [1, 2.1, 'abc']

print(type(table[0]))
print(type(table[1]))
print(type(table[2]))
```

OUTPUT < >

```
<class 'int'>
<class 'float'>
<class 'str'>
```

For instance, mathematical operations may be considered a feature of all numeric types demonstrated in [Table](#). However, unless in specific circumstance described in subsection [Non-numeric values](#), such operations do not apply to instances of type `str`.

PYTHON < >

```
table = [1, 2.1, 'abc']

table[0] += 1
table[-1] += 'def'

print(table)
```

OUTPUT < >

```
[2, 2.1, 'abcdef']
```

Likewise, the `list` plays the role of a container that may incorporate any number of values. Thus far, we have learned how to handle individual members of a `list`. In this subsection, we will be looking at several techniques that help us address different circumstances where we look at a `list` from a ‘wholist’ perspective; that is, a container whose members are unknown to us.

## Membership test

### [Membership test operations \[advanced\]](#)

We can check to see whether or not a specific value is a member of a `list` using the operator syntax `in`:

PYTHON < >

```
items = [1, 2.4, 'John', 5, 4]

print(2.4 in items)
```

OUTPUT < >

```
True
```

PYTHON < >

```
print(3 in items)
```

OUTPUT < >

False

The results may be stored in a variable:

PYTHON < >

```
has_five = 5 in items  
print(has_five)
```

OUTPUT < >

True

Similar to any other [logical expression](#), we can [negate](#) membership tests by using :

PYTHON < >

```
expr = 10 not in items  
print(expr)
```

OUTPUT < >

True

PYTHON < >

```
expr = 5 not in items  
print(expr)
```

OUTPUT < >

False

## REMEMBER

When testing against `str` values — *i.e.* text; don't forget that in programming, operations involving texts are *always* case-sensitive.

PYTHON < >

```
items = [1, 2.4, 'John', 5, 4]

john_capital = 'John'
john_small = 'john'

print(john_capital in items)
print(john_small in items)
```

OUTPUT < >

```
True
False
```

For *numeric* values, `int` and `float` may be used interchangeably:

PYTHON < >

```
print(4 in items)
```

OUTPUT < >

```
True
```

PYTHON < >

```
print(4.0 in items)
```

OUTPUT < >

```
True
```

Similar to other [logical expression](#), membership tests may be incorporated into conditional statements:

PYTHON < >

```
if 'John' in items:
    print('Hello John')
else:
    print('Hello')
```

OUTPUT < >

Hello John

## DO IT YOURSELF

Given a **list** of randomly generated peptide sequences as:

PYTHON < >

```
peptides = [  
    'FAEKE', 'DMSGG', 'CMGFT', 'HVEFW', 'DCYFH', 'RDFDM', 'RTYRA',  
    'PVTEQ', 'WITFR', 'SWANQ', 'PFELC', 'KSANR', 'EQKVL', 'SYALD',  
    'FPNCF', 'SCDYK', 'MFRST', 'KFMII', 'NFYQC', 'LVKVR', 'PQKTF',  
    'LTWFQ', 'EFAYE', 'GPCCQ', 'VFDYF', 'RYSAY', 'CCTCG', 'ECFMY',  
    'CPNLY', 'CSMFW', 'NNVSR', 'SLNKF', 'CGRHC', 'LCQCS', 'AVERE',  
    'MDKHQ', 'YHKQT', 'HVRWD', 'YNFQW', 'MGCLY', 'CQCCL', 'ACQCL'  
]
```

Determine whether or not each of the following sequences exist in **peptides**; and if so, what is their corresponding index:

- IVADH
- CMGFT
- DKAKL
- THGYP
- NNVSR

Display the results in the following format:

```
Sequence XXXXX was found at index XX
```

Solution

PYTHON < >

```
sequence = "IVADH"  
if sequence in peptides:  
    index = peptides.index(sequence)  
    print('Sequence', sequence, 'was found at index', index)
```

### Solution

```
PYTHON < >  
sequence = "CMGFT"  
if sequence in peptides:  
    index = peptides.index(sequence)  
    print('Sequence', sequence, 'was found at index', index)
```

```
OUTPUT < >  
Sequence CMGFT was found at index 2
```

### Solution

```
PYTHON < >  
sequence = "DKAKL"  
if sequence in peptides:  
    index = peptides.index(sequence)  
    print('Sequence', sequence, 'was found at index', index)
```

### Solution

```
PYTHON < >  
sequence = "THGYP"  
if sequence in peptides:  
    index = peptides.index(sequence)  
    print('Sequence', sequence, 'was found at index', index)
```

### Solution

```
PYTHON < >  
sequence = "NNVSR"  
if sequence in peptides:  
    index = peptides.index(sequence)  
    print('Sequence', sequence, 'was found at index', index)
```

```
OUTPUT < >  
Sequence NNVSR was found at index 30
```

## Length

Built-in functions: len

The number of members contained within a `list` defines its length. Similar to the length of `str` values as discussed in [mathematical operations DIY-I](#) and [DIY-IV](#), we use the built-in function `len()` also to determine the length of a `list`:

```
PYTHON < >  
items = [1, 2.4, 'John', 5, 4]  
  
print(len(items))
```

```
OUTPUT < >  
5
```

```
PYTHON < >  
print(len([1, 5, 9]))
```

```
OUTPUT < >  
3
```

The `len()` function *always* returns an integer value (`int`) equal to or greater than zero. We can store the length in a variable and use it in different [mathematical](#) or [logical](#) operations:

```
PYTHON < >  
table = [1, 2, 3, 4]  
items_length = len(items)  
table_length = len(table)  
  
print(items_length + table_length)
```

```
OUTPUT < >  
9
```

```
PYTHON < >  
print(len(table) > 2)
```

```
OUTPUT < >  
True
```

We can also use the length of an array in [conditional statements](#):

PYTHON < >

```
students = ['Julia', 'John', 'Jane', 'Jack']
present = ['Julia', 'John', 'Jane', 'Jack', 'Janet']

if len(present) == len(students):
    print('All the students are here.')
else:
    print('One or more students are not here yet.)
```

OUTPUT < >

One or more students are not here yet.

### REMEMBER

Both `in` and `len()` may be used in reference to any *type* of array or sequence in Python.

See [Table](#) to find out which built-in types in Python are regarded as a sequence.

### DO IT YOURSELF

Given the `list` of random peptides defined in [DIY](#):

1. Define a `list` called `overlaps` containing the sequences whose presence in `peptides` you confirmed in [DIY](#).
2. Determine the length of `peptides`.
3. Determine the length of `overlaps`.

Display yours results as follows:

```
overlaps = ['XXXXXX', 'XXXXXX', ...]
Length of peptides: XX
Length of overlaps: XX
```

### Solution

PYTHON < >

```
overlaps = list()

sequence = "IVADH"
if sequence in peptides:
    overlaps.append(sequence)

sequence = "CMGFT"
if sequence in peptides:
    overlaps.append(sequence)

sequence = "DKAKL"
if sequence in peptides:
    overlaps.append(sequence)

sequence = "THGYP"
if sequence in peptides:
    overlaps.append(sequence)

sequence = "NNVSR"
if sequence in peptides:
    overlaps.append(sequence)

print('overlaps:', overlaps)
```

OUTPUT < >

```
overlaps: ['CMGFT', 'NNVSR']
```

### Solution

PYTHON < >

```
print('Length of peptides:', len(peptides))
```

OUTPUT < >

```
Length of peptides: 42
```

## Solution

```
PYTHON < >
print('Length of overlaps:', len(overlaps))
```

```
OUTPUT < >
Length of overlaps: 2
```

## Weak References and Copies

In our discussion on [mutability](#), we also discussed some of the in-place operations such as `.remove()` and `.append()` that we use to modify an existing `list`. The use of these operations gives rise the following question: What if we need to perform an in-place operation, but also want to preserve the original array?

In such cases, we create a *deep copy* of the original array before we call the method and perform the operation.

Suppose we have:

```
PYTHON < >
table_a = [1, 2, 3, 4]
```

A weak reference for `table_a`, also referred to as an alias or a symbolic link, may be defined as follows:

```
PYTHON < >
table_b = table_a
print(table_a, table_b)
```

```
OUTPUT < >
[1, 2, 3, 4] [1, 2, 3, 4]
```

Now if we perform an in-place operation on only *one* of the two variables (the original or the alias) as follows:

```
PYTHON < >
table_a.append(5)
```

we will in effect change *both* of them:

```
PYTHON < >
print(table_a, table_b)
```

```
OUTPUT < >
[1, 2, 3, 4, 5] [1, 2, 3, 4, 5]
```

This is useful if we need to change the name of a variable under certain conditions to make our code more explicit and readable; however, it does *nothing* to preserve an actual copy of the original data.

To retain a copy of the original array, however, we must perform a *deep copy* as follows:

```
PYTHON < >  
table_c = table_b.copy()  
  
print(table_b, table_c)
```

```
OUTPUT < >  
[1, 2, 3, 4, 5] [1, 2, 3, 4, 5]
```

where `table_c` represents a *deep copy* of `table_b`.

In this instance, performing an in-place operation on one variable would *not* have any impacts on the other one:

```
PYTHON < >  
table_b.append(6)  
  
print(table_a, table_b, table_c)
```

```
OUTPUT < >  
[1, 2, 3, 4, 5, 6] [1, 2, 3, 4, 5, 6] [1, 2, 3, 4, 5]
```

where both the original array and its weak reference (`table_a` and `table_b`) changed without influencing the *deep copy* (`table_c`).

There is also a shorthand for the `.copy()` method to create a *deep copy*. As far as arrays of type `list` are concerned, writing:

```
new_table = original_table[:]
```

is exactly the same as writing:

```
new_table = original_table.copy()
```

Here is an example:

```
PYTHON < >  
table_a = ['a', 3, 'b']  
table_b = table_a  
table_c = table_a.copy()  
table_d = table_a[:]  
  
table_a[1] = 5  
  
print(table_a, table_b, table_c, table_d)
```

OUTPUT < >

```
['a', 5, 'b'] ['a', 5, 'b'] ['a', 3, 'b'] ['a', 3, 'b']
```

Whilst both the original array and its weak reference (`table_a` and `table_b`) changed in this example; the *deep copies* (`table_c` and `table_d`) have remained unchanged.

### DO IT YOURSELF

When defining a consensus sequence, it is common to include annotations to represent ambiguous amino acids. Four such annotations are as follows:

| RESIDUES                   |          | ANNOTATION |          |
|----------------------------|----------|------------|----------|
| NAMES                      | 1-LETTER | 3-LETTER   | 1-LETTER |
| Any / Unknown              | All      | Xaa        | X        |
| Asparagine / Aspartic Acid | D / B    | Asx        | B        |
| Glutamine / Glutamic Acid  | E / Q    | Glx        | Z        |
| Leucine / Isoleucine       | I / L    | Xle        | J        |

Given a `list` of amino acids as:

```
amino_acids = [  
    'A', 'R', 'N', 'D', 'C', 'E', 'Q', 'G', 'H', 'I',  
    'L', 'K', 'M', 'F', 'P', 'S', 'T', 'W', 'Y', 'V'  
]
```

PYTHON < >

1. Use `amino_acids` to create an independent `list` called `amino_acids_annotations` that contains all the standard amino acids.
2. Add to `amino_acids_annotations` the **1-letter** annotations for the ambiguous amino acids as outlined in the table.
3. Evaluate the lengths for `amino_acids` and `amino_acids_annotations` and retain the result in a new `list` called `lengths`.
4. Using **logical operations**, test the two values stored in `lengths` for equivalence and display the result as a boolean (i.e. `True` or `False`) output.

### Solution

PYTHON < >

```
amino_acid_annotations = amino_acids.copy()
```

### Solution

PYTHON < >

```
ambiguous_annotations = ['X', 'B', 'Z', 'J']
amino_acid_annotations.extend(ambiguous_annotations)
```

### Solution

PYTHON < >

```
lengths = [len(amino_acids), len(amino_acid_annotations)]
```

### Solution

PYTHON < >

```
equivalence = lengths[0] == lengths[1]
print(equivalence)
```

OUTPUT < >

```
False
```

## Conversion to list

As highlighted earlier in the section, arrays in Python can contain any value regardless of type. We can exploit this feature to extract some interesting information about the data we store in an array.

To that end, we can [convert](#) any sequence to a [list](#). See [Table](#) to find out which of the built-in types in Python are considered to be a sequence.

Suppose we have the sequence for [Protein Kinase A Gamma \(catalytic\) subunit for humans](#) as follows:

PYTHON < >

```
# Multiple lines of text may be split into
# several lines inside parenthesis:

human_pka_gamma = (
    'MAAPAAATAMGNAPAKKDTEQEESVNEFLAKARGDFLYRWGNPAQNTASSDQFERLRTLGMGSFGRVMLV'
    'RHQETGGHYAMKILNKQKVVKMKQVEHILNEKRILQAIDFPFLVKLQFSFKDNSYLYLVMEYVPGGEMFS'
    'RLQRVGRFSEPHACFYAAQVVLAVQYLHSLDLIHRDLKPENLLIDQQGYLQVTDFGFAKRVKGRTWTLCG'
    'TPEYLAPEIILSKGYNKAVIDWALGVLIYEMAVGFPPFYADQPIQIYEKIVSGRVRFPSKLSSDLKDLLR'
    'SLLQVDLTKRFGNLRNGVGDIKNHKWFATTSWIAIYEKKVEAPFIPKYTGPGDASNFDDYEEEELRISIN'
    'EKCAKEFSEF'
)

print(type(human_pka_gamma))
```

OUTPUT < >

```
<class 'str'>
```

We can now *convert* our sequence from its original type of `str` to `list` by using `list()` as a *function*. Doing so will automatically decompose the text down to individual characters:

PYTHON < >

```
# The function "list" may be used to convert string
# variables into a list of characters:
pka_list = list(human_pka_gamma)

print(pka_list)
```

OUTPUT < >

```
['M', 'A', 'A', 'P', 'A', 'A', 'A', 'T', 'A', 'M', 'G', 'N', 'A', 'P', 'A', 'K', 'K', 'D', 'T', 'E', 'Q', 'E', 'E', 'S', 'V', 'N', 'F', 'L', 'A', 'R', 'G', 'D', 'F', 'L', 'Y', 'R', 'W', 'G', 'N', 'P', 'A', 'Q', 'N', 'T', 'A', 'S', 'S', 'D', 'Q', 'F', 'E', 'R', 'L', 'R', 'T', 'L', 'G', 'M', 'G', 'S', 'F', 'G', 'R', 'V', 'M', 'L', 'V', 'R', 'M', 'E', 'Y', 'V', 'P', 'G', 'G', 'E', 'M', 'F', 'S', ' ', 'R', 'H', 'Q', 'E', 'T', 'G', 'G', 'H', 'Y', 'A', 'M', 'K', 'I', 'L', 'N', 'K', 'Q', 'K', 'V', 'V', 'K', 'M', 'K', 'Q', 'V', 'E', 'H', 'I', 'L', 'N', 'E', 'K', 'R', 'I', 'L', 'Q', 'A', 'I', 'D', 'F', 'P', 'F', 'L', 'V', 'K', 'L', 'Q', 'F', 'S', 'F', 'K', 'D', 'N', 'S', 'Y', 'L', 'Y', 'L', 'V', 'M', 'E', 'Y', 'V', 'P', 'G', 'G', 'E', 'M', 'F', 'S', ' ', 'R', 'L', 'Q', 'R', 'V', 'G', 'R', 'F', 'S', 'E', 'P', 'H', 'A', 'C', 'F', 'Y', 'A', 'A', 'Q', 'V', 'V', 'L', 'A', 'V', 'Q', 'Y', 'L', 'H', 'S', 'L', 'D', 'L', 'I', 'H', 'R', 'D', 'L', 'K', 'P', 'E', 'N', 'L', 'L', 'I', 'D', 'Q', 'Q', 'G', 'Y', 'L', 'Q', 'V', 'T', 'D', 'F', 'G', 'F', 'A', 'K', 'R', 'V', 'K', 'G', 'R', 'T', 'W', 'T', 'L', 'C', 'G', ' ', 'T', 'P', 'E', 'Y', 'L', 'A', 'P', 'E', 'I', 'I', 'L', 'S', 'K', 'G', 'Y', 'N', 'K', 'A', 'V', 'D', 'W', 'A', 'L', 'G', 'V', 'L', 'I', 'Y', 'E', 'M', 'A', 'V', 'G', 'F', 'P', 'P', 'F', 'Y', 'A', 'D', 'Q', 'P', 'I', 'Q', 'I', 'Y', 'E', 'K', 'I', 'V', 'S', 'G', 'R', 'V', 'R', 'F', 'P', 'S', 'K', 'L', 'S', 'S', 'D', 'L', 'K', 'D', 'L', 'L', 'R', ' ', 'S', 'L', 'L', 'Q', 'V', 'D', 'L', 'T', 'K', 'R', 'F', 'G', 'N', 'L', 'R', 'N', 'G', 'V', 'G', 'D', 'I', 'K', 'N', 'H', 'K', 'W', 'F', 'A', 'T', 'T', 'S', 'W', 'I', 'A', 'I', 'Y', 'E', 'K', 'K', 'V', 'E', 'A', 'P', 'F', 'I', 'P', 'K', 'Y', 'T', 'G', 'P', 'G', 'D', 'A', 'S', 'N', 'F', 'D', 'D', 'Y', 'E', 'E', 'E', 'L', 'R', 'I', 'S', 'I', 'N', ' ', 'E', 'K', 'C', 'A', 'K', 'E', 'F', 'S', 'E', 'F', ' ', ' )'
```

## DO IT YOURSELF

Ask the user to enter a sequence of single-letter amino acids in *lower case*. Convert the sequence to `list` and:

1. Count the number of serine and threonine residues and display the result in the following format:

```
Total number of serine residues: XX  
Total number of threonine residues: XX
```

2. Check whether or not the sequence contains both serine and threonine residues:

- If it does, display:

```
The sequence does contain both serine and threonine residues.
```

- if it does not, display:

```
The sequence does not contain both serine and threonine residues.
```

## Solution

```
sequence_str = input('Please enter a sequence of single-letter amino acids in lower-case: ')  
  
sequence = list(sequence_str)  
  
ser_count = sequence.count('s')  
thr_count = sequence.count('t')  
  
print('Total number of serine residues:', ser_count)  
  
print('Total number of threonine residues:', thr_count)
```

## Solution

```
if ser_count > 0 and thr_count > 0:  
    response_state = ''  
else:  
    response_state = 'not'  
  
print(  
    'The sequence does',  
    'response_state',  
    'contain both serine and threonine residues.'  
)
```

## ADVANCED TOPIC

Generators represent a specific [type](#) in Python whose results are *not* immediately evaluated. This is a technique referred to as *lazy evaluation* in [functional programming](#), and is often used in the context of a [for-loop](#). This is because they postpone the evaluation of their results for as long as possible. We do not discuss generators in the course, but you can find out more about them in the [official documentations](#).

## Useful methods

### [Data Structures: More on Lists](#)

In this subsection, we will be reviewing some of the useful and important *methods* that are associated with object of type [list](#). To that end, we shall use snippets of code that exemplify such *methods* in practice. A [cheatsheet](#) of the *methods* associated with the built-in arrays in Python can be helpful.

| Method                  | list | tuple | set |
|-------------------------|------|-------|-----|
| .append()               | +    |       |     |
| .extend()               | +    |       |     |
| .insert()               | +    |       |     |
| .index()                | +    | +     |     |
| .sort()                 | +    |       |     |
| .reverse()              | +    |       |     |
| .copy()                 | +    | +     |     |
| .clear()                | +    | +     |     |
| .pop()                  | +    | +     |     |
| .count()                | +    | +     |     |
| .remove()               | +    | +     |     |
| .add()                  |      | +     |     |
| .intersection()         |      | +     |     |
| .difference()           |      | +     |     |
| .isdisjoint()           |      | +     |     |
| .issubset()             |      | +     |     |
| .issuperset()           |      | +     |     |
| .union()                |      | +     |     |
| .symmetric_difference() |      | +     |     |
| .discard()              |      | +     |     |
| .update()               |      | +     |     |

Commons operations for list, tuple, and set arrays in Python.

The *methods* outline here are not individually described; however, at this point, you should be able to work out what they do by looking at their names and respective examples.

Count a specific value within a `list`:

```
PYTHON < >
table_a = [1, 2, 2, 2]
table_b = [15, 16]

print(table_a.count(2))
```

3

Extend a `list`:

PYTHON < >

```
table_a = [1, 2, 2, 2]
table_b = [15, 16]

table_c = table_a.copy() # deep copy.
table_c.extend(table_b)

print(table_a, table_b, table_c)
```

OUTPUT < >

```
[1, 2, 2, 2] [15, 16] [1, 2, 2, 2, 15, 16]
```

Extend a `list` by adding two lists to each other. Note that adding two lists is *not* an in-place operation:

PYTHON < >

```
table_a = [1, 2, 2, 2]
table_b = [15, 16]

table_c = table_a + table_b

print(table_a, table_b, table_c)
```

OUTPUT < >

```
[1, 2, 2, 2] [15, 16] [1, 2, 2, 2, 15, 16]
```

PYTHON < >

```
table_a = [1, 2, 2, 2]
table_b = [15, 16]

table_c = table_a.copy() # deep copy.
table_d = table_a + table_b

print(table_c == table_d)
```

OUTPUT < >

```
False
```

We can also reverse the values in a `list`. There are two methods for doing so: Being a generator means that the output of the function is not evaluated immediately; and instead, we get a generic output:

1. Through an in-place operation using `.reverse()`

```
PYTHON < >  
table = [1, 2, 2, 2, 15, 16]  
table.reverse()  
  
print("Reversed:", table)
```

```
OUTPUT < >  
Reversed: [16, 15, 2, 2, 2, 1]
```

2. Through `reversed()`, which is a build-in generator function.

```
PYTHON < >  
table = [1, 2, 2, 2, 15, 16]  
table_rev = reversed(table)  
  
print("Result:", table_rev)  
print("Type:", type(table_rev))
```

```
OUTPUT < >  
Result: <list_reverseiterator object at 0x7f1e21100f40>  
Type: <class 'list_reverseiterator'>
```

We can, however, force the evaluation process by converting the generator results onto a `list`:

```
PYTHON < >  
table_rev_evaluated = list(table_rev)  
  
print('Evaluated:', table_rev_evaluated)
```

```
OUTPUT < >  
Evaluated: [16, 15, 2, 2, 2, 1]
```

Members of a `list` may be sorted in-place as follows:

```
PYTHON < >  
table = [16, 2, 15, 1, 2, 2]  
table.sort()  
  
print("Sorted (ascending):", table)
```

```
OUTPUT < >  
Sorted (ascending): [1, 2, 2, 2, 15, 16]
```

## ADVANCED TOPIC

There is also the built-in function `sorted()` that works in a similar way to `reversed()`. Also a generator function, it offers more advanced features that are beyond the scope of this course. You can find out more about it from the [official documentations](#) and [examples](#).

The `.sort()` method takes an optional keyword argument entitled `reverse` (default: `False`). If set to `True`, the method will perform a descending sort:

PYTHON < >

```
table = [16, 2, 15, 1, 2, 2]
table.sort(reverse=True)

print("Sorted (descending):", table)
```

OUTPUT < >

```
Sorted (descending): [16, 15, 2, 2, 2, 1]
```

We can also create an empty `list`, so that we can add members to it later in our code using `.append()` or `.extend()` amongst other tools:

PYTHON < >

```
table = list()

print(table)
```

OUTPUT < >

```
[]
```

PYTHON < >

```
table.append(5)

print(table)
```

OUTPUT < >

```
[5]
```

PYTHON < >

```
another_table = ['Jane', 'Janette']
table.extend(another_table)

print(another_table)
```

OUTPUT < >

```
['Jane', 'Janette']
```

### DO IT YOURSELF

Create a `list`, and experiment with each of the methods provided in the above example. Try including members of different *types* in your `list` and see how each of these methods behave.

#### Solution

This DIY was intended to encourage you to experiment with the methods outlined.

## Nested arrays

At this point, you should be comfortable with creating, handling, and manipulating arrays of type `list` in Python. It is important to have a relatively good understanding of the principles outlined in this section so far before you start learning about *nested arrays*.

We have already established that arrays can contain any value regardless of type. This means that they also contain other arrays. An array that includes at least one member that is itself an array is referred to as a *nested arrays*. This can be thought of as a table with more than one column:

|                  |  | VALUE         |   |   |
|------------------|--|---------------|---|---|
|                  |  | INDEX<br>ROWS |   |   |
|                  |  | 0             | 1 | 2 |
|                  |  | 1             | 4 |   |
|                  |  | 2             | 7 | 8 |
| INDEX<br>columns |  | 0             | 1 | 2 |

### REMEMBER

Arrays can contain values of any *type*. This rule applies to nested arrays too. We have exclusively included `int` numbers in our table to trivialise that example.

### Implementation

The table can be written in Python as a nested array:

```
# The list has 3 members, 2 of which
# are arrays of type list:
table = [[1, 2, 3], 4, [7, 8]]

print(table)
```

PYTHON < >

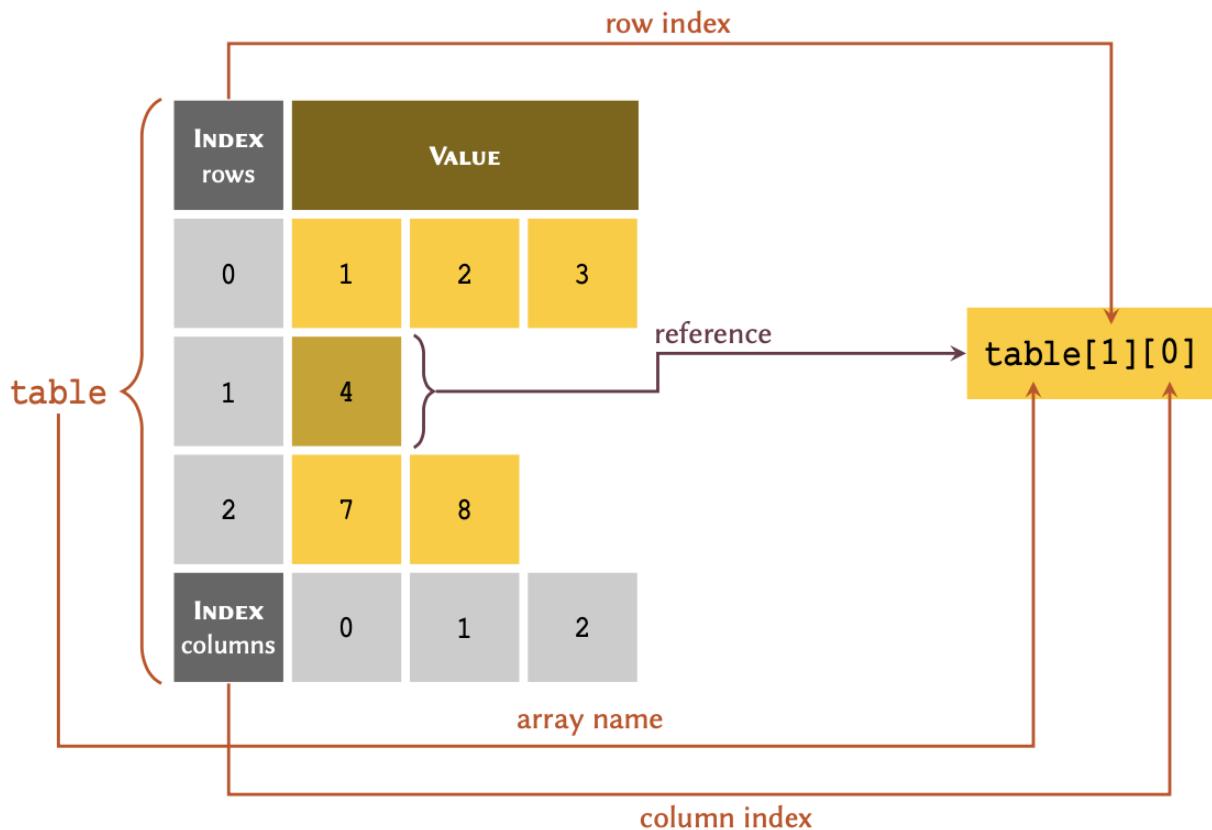
```
[[1, 2, 3], 4, [7, 8]]
```

OUTPUT < >

### Indexing

The indexing principles for nested arrays is slightly different. To retrieve an individual member in a nested `list`, we always reference the *row index*, followed by the *column index*.

We may visualise the process as follows:



To retrieve an entire row, we only need to include the reference for that row:

```
PYTHON < >
print(table[0])
```

```
OUTPUT < >
[1, 2, 3]
```

and to retrieve a specific member, we include the reference for both the row and column:

```
PYTHON < >
print(table[0][1])
```

```
OUTPUT < >
2
```

We may also extract slices from a nested array. The protocol is identical to normal arrays described in subsection [slicing](#). In nested arrays, however, we may take slices from the columns as well as the rows:

```
print(table[:2])
```

PYTHON < >

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

OUTPUT < >

```
print(table[0][:2])
```

PYTHON < >

```
[1, 2]
```

OUTPUT < >

Note that only 2 of the 3 members in `table` are arrays of type `list`:

```
print(table[0], type(table[0]))
```

PYTHON < >

```
[1, 2, 3] <class 'list'>
```

OUTPUT < >

```
print(table[2], type(table[2]))
```

PYTHON < >

```
[7, 8] <class 'list'>
```

OUTPUT < >

However, there is another member that is not an array:

```
print(table[1], type(table[1]))
```

PYTHON < >

```
4 <class 'int'>
```

OUTPUT < >

In most circumstances, we would want all the members in an array to be *homogeneous* in type — *i.e.* we want them all to have the same type. In such cases, we can implement the table as:

PYTHON < >

```
table = [[1, 2, 3], [4], [7, 8]]  
  
print(table[1], type(table[1]))
```

OUTPUT < >

```
[4] <class 'list'>
```

An array with only one member — e.g. [4], is sometimes referred to as a *singleton* array.

### DO IT YOURSELF

Give then following of pathogens and their corresponding diseases:

| PATHOGEN TYPE | GRAM     | PATHOGEN NAME                     | DISEASE                                   |
|---------------|----------|-----------------------------------|-------------------------------------------|
| Bacterium     | Negative | <i>Shigella flexneri</i>          | Bacillary dysentery                       |
| Prion         | N/A      | PrP(sc)                           | Transmissible spongiform encephalopathies |
| Bacterium     | Negative | <i>Vibrio cholerae</i>            | Cholera                                   |
| Bacterium     | Negative | <i>Listeria monocytogenes</i>     | Listeriosis                               |
| Virus         | N/A      | Hepatitis C                       | Hepatitis                                 |
| Bacterium     | Negative | <i>Helicobacter pylori</i>        | Peptic ulcers                             |
| Bacterium     | Negative | <i>Mycobacterium tuberculosis</i> | Tuberculosis                              |
| Bacterium     | Negative | <i>Chlamydia trachomatis</i>      | Chlamydial diseases                       |
| Virus         | N/A      | Human Immunodeficiency Virus      | Human Immunodeficiency                    |

1. Substituting N/A for None, create an array to represent the table in the original order. Retain the array in a variable and display the result.
2. Modify the array you created so that the members are sorted *descendingly* and display the result.

### Solution

PYTHON < >

```
disease_pathogen = [
    ["Bacterium", "Negative", "Shigella flexneri" , "Bacillary dysentery"],
    ["Prion", None, "PrP(sc)", "Transmissible spongiform encephalopathies"],
    ["Bacterium", "Negative", "Vibrio cholerae", "Cholera"],
    ["Bacterium", "Negative", "Listeria monocytogenes", "Listeriosis"],
    ["Virus", None, "Hepatitis C", "Hepatitis"],
    ["Bacterium", "Negative", "Helicobacter pylori", "Peptic ulcers"],
    ["Bacterium", "Negative", "Mycobacterium tuberculosis", "Tuberculosis"],
    ["Bacterium", "Negative", "Chlamydia trachomatis", "Chlamydial diseases"],
    ["Virus", None, "Human Immunodeficiency Virus", "Human Immunodeficiency"]
]

print(disease_pathogen)
```

OUTPUT < >

```
[['Bacterium', 'Negative', 'Shigella flexneri', 'Bacillary dysentery'], ['Prion', None, 'PrP(sc)', 'Transmissible spongiform encephalopathies'], ['Bacterium', 'Negative', 'Vibrio cholerae', 'Cholera'], ['Bacterium', 'Negative', 'Listeria monocytogenes', 'Listeriosis'], ['Virus', None, 'Hepatitis C', 'Hepatitis'], ['Bacterium', 'Negative', 'Helicobacter pylori', 'Peptic ulcers'], ['Bacterium', 'Negative', 'Mycobacterium tuberculosis', 'Tuberculosis'], ['Bacterium', 'Negative', 'Chlamydia trachomatis', 'Chlamydial diseases'], ['Virus', None, 'Human Immunodeficiency Virus', 'Human Immunodeficiency']]
```

### Solution

PYTHON < >

```
disease_pathogen.sort(reverse=True)

print(disease_pathogen)
```

OUTPUT < >

```
[['Virus', None, 'Human Immunodeficiency Virus', 'Human Immunodeficiency'], ['Virus', None, 'Hepatitis C', 'Hepatitis'], ['Bacterium', 'Negative', 'Shigella flexneri', 'Bacillary dysentery'], ['Prion', None, 'PrP(sc)', 'Transmissible spongiform encephalopathies'], ['Bacterium', 'Negative', 'Vibrio cholerae', 'Cholera'], ['Bacterium', 'Negative', 'Listeria monocytogenes', 'Listeriosis'], ['Virus', None, 'Hepatitis C', 'Hepatitis'], ['Bacterium', 'Negative', 'Helicobacter pylori', 'Peptic ulcers'], ['Bacterium', 'Negative', 'Mycobacterium tuberculosis', 'Tuberculosis'], ['Bacterium', 'Negative', 'Chlamydia trachomatis', 'Chlamydial diseases']]
```

## Dimensions

A nested array is considered *two dimensional* or *2D* when:

- *all* of the members in a nested array are arrays themselves;
- *all* of the sub-arrays have the same length — *i.e.* all the columns in the table are filled and have the same number of rows; and,
- *all* of the members of the sub-arrays are *homogeneous* in type — *i.e.* they all have the same type (e.g. `int`).

A two dimensional arrays may be visualised as follows:

| INDEX<br>rows    | VALUE |   |   |
|------------------|-------|---|---|
| 0                | 1     | 2 | 3 |
| 1                | 4     | 5 | 6 |
| 2                | 7     | 8 | 9 |
| INDEX<br>columns | 0     | 1 | 2 |

#### ADVANCED TOPIC

Nested arrays may themselves be nested. This means that, if needed, we can have 3, 4 or  $n$  dimensional arrays, too. Analysis and organisation of such arrays is an important part of a field known as [optimisation](#) in computer science and mathematics. Optimisation is itself the cornerstone of machine learning, and addresses the problem known as [curse of dimensionality](#).

Such arrays are referred to in mathematics as a [matrix](#). We can therefore represent a two-dimensional array as a mathematical matrix. To that end, the above array would translate to the annotation displayed in equation below.

$$table = \begin{bmatrix} 1 & 2 & 3 \\ 4 & 5 & 6 \\ 7 & 8 & 9 \end{bmatrix}$$

The implementation of these arrays is identical to the implementation of other nested arrays. We can therefore code our table in Python as:

```
table = [  
    [1, 2, 3],  
    [4, 5, 6],  
    [7, 8, 9]  
]  
  
print(table)
```

PYTHON < >

```
[[1, 2, 3], [4, 5, 6], [7, 8, 9]]
```

OUTPUT < >

```
print(table[2])
```

PYTHON < >

```
[7, 8, 9]
```

OUTPUT < >

```
print(table[1][0])
```

PYTHON < >

```
4
```

OUTPUT < >

```
print(table[:2])
```

PYTHON < >

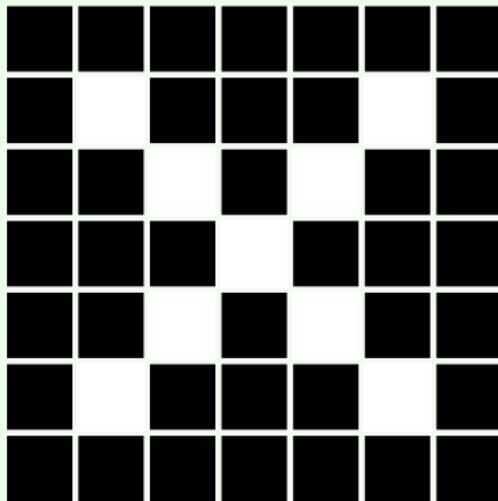
```
[[1, 2, 3], [4, 5, 6]]
```

OUTPUT < >

## DO IT YOURSELF

Computers see images as multidimensional arrays (matrices). In its simplest form, an image is a two-dimensional array containing only 2 colours.

Given the following black and white image:



1. Considering that black and white squares represent zeros and ones respectively, create a two-dimensional array to represent the above image. Display the results.
2. Create a new array, but this time use `False` and `True` to represent black and white respectively.

Display the results.

### Solution

```
cross = [
    [0, 0, 0, 0, 0, 0, 0],
    [0, 1, 0, 0, 0, 1, 0],
    [0, 0, 1, 0, 1, 0, 0],
    [0, 0, 0, 1, 0, 0, 0],
    [0, 0, 1, 0, 1, 0, 0],
    [0, 1, 0, 0, 0, 1, 0],
    [0, 0, 0, 0, 0, 0, 0]
]

print(cross)
```

PYTHON < >

```
[[0, 0, 0, 0, 0, 0, 0], [0, 1, 0, 0, 0, 1, 0], [0, 0, 1, 0, 1, 0, 0], [0, 0, 0, 1, 0, 0, 0], [0, 0, 1, 0, 1, 0, 0], [0, 1, 0, 0, 0, 1, 0], [0, 0, 0, 0, 0, 0, 0]]
```

OUTPUT < >

## Solution

PYTHON < >

```
cross_bool = [
    [False, False, False, False, False, False, False],
    [False, True, False, False, False, True, False],
    [False, False, True, False, True, False, False],
    [False, False, False, True, False, False, False],
    [False, False, True, False, True, False, False],
    [False, True, False, False, False, True, False],
    [False, False, False, False, False, False, False]
]

print(cross_bool)
```

OUTPUT < >

```
[[False, False, False, False, False, False, False], [False, True, False, False, False, True, False], [False, False, True, False, True, False, False], [False, False, False, True, False, False, False], [False, False, True, False, True, False, False], [False, True, False, False, False, True, False], [False, False, False, False, False, False, False]]
```

## Summary

At this point, you should be familiar with arrays and how they work in general. Throughout this section, we talked about `list`, which is one the most popular types of *built-in* arrays in Python. To that end, we learned:

- how to `list` from the scratch;
- how to *manipulate* `list` using different *methods*;
- how to use *indexing* and *slicing* techniques to our advantage;
- *mutability*—a concept we revisit in the forthcoming lessons;
- *in-place operations*, and the difference between *weak references* and *deep copies*;
- *nested* and *multi-dimensional* arrays; and,
- how to *convert* other sequences (e.g. `str`) to `list`.

# Tuple

## Data Structures: Tuples and Sequences

Another type of built-in arrays, `tuple` is an immutable alternative to `list`. That is, once created, the contents may not be modified in any way. One reason we use tuples is to ensure that the contents of our array does not change accidentally.

For instance, we know that in the [Wnt signaling pathway](#), there are two co-receptors. This is final, and would not change at any point in our programme.

## REMEMBER

To implement a **tuple** in Python, we place our values separated by commas inside parenthesis or (1, 2, 3, ...).

PYTHON < >

```
pathway = 'Wnt Signaling'  
coreceptors = ('Frizzled', 'LRP')  
  
print(type(coreceptors))
```

OUTPUT < >

```
<class 'tuple'>
```

PYTHON < >

```
print(coreceptors)
```

OUTPUT < >

```
('Frizzled', 'LRP')
```

PYTHON < >

```
wnt = (pathway, coreceptors)  
  
print(type(wnt))
```

OUTPUT < >

```
<class 'tuple'>
```

PYTHON < >

```
print(wnt)
```

OUTPUT < >

```
('Wnt Signaling', ('Frizzled', 'LRP'))
```

PYTHON < >

```
print(wnt[0])
```

Wnt Signaling

OUTPUT < >

Indexing and slicing principles for `tuple` is identical to `list`, which we discussed in subsection [indexing](#) and [slicing](#) respectively.

## Conversion to tuple

Similar to `list`, we can convert other sequences to `tuple`:

PYTHON < >

```
numbers_list = [1, 2, 3, 4, 5]  
  
print(type(numbers_list))
```

OUTPUT < >

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

PYTHON < >

```
numbers = tuple(numbers_list)  
  
print(numbers)
```

OUTPUT < >

```
(1, 2, 3, 4, 5)
```

PYTHON < >

```
print(type(numbers))
```

OUTPUT < >

```
<class 'tuple'>
```

PYTHON < >

```
text = 'This is a string.'  
  
print(type(text))
```

OUTPUT < >

```
<class 'str'>
```

```
characters = tuple(text)

print(characters)
```

PYTHON < >

```
('T', 'h', 'i', 's', ' ', 'i', 's', ' ', 'a', ' ', 's', 't', 'r', 'i', 'n', 'g', '.')
```

OUTPUT < >

```
print(type(characters))
```

PYTHON < >

```
<class 'tuple'>
```

OUTPUT < >

## Immutability

In contrast with `list`, however, if we attempt to change the contents of a `tuple`, a `TypeError` is raised:

```
coreceptors[1] = 'LRP5/6'
```

PYTHON < >

```
Error: TypeError: 'tuple' object does not support item assignment
```

ERROR < >

Even though `tuple` is an immutable type, it can contain both mutable and immutable objects:

```
# (immutable, immutable, immutable, mutable)
mixed_tuple = (1, 2.5, 'abc', (3, 4), [5, 6])

print(mixed_tuple)
```

PYTHON < >

```
(1, 2.5, 'abc', (3, 4), [5, 6])
```

OUTPUT < >

and mutable objects inside a `tuple` may still be changed:

```
print(mixed_tuple, type(mixed_tuple))
```

PYTHON < >

```
(1, 2.5, 'abc', (3, 4), [5, 6]) <class 'tuple'>
```

OUTPUT < >

```
print(mixed_tuple[4], type(mixed_tuple[4]))
```

PYTHON < >

```
[5, 6] <class 'list'>
```

OUTPUT < >

## ADVANCED TOPIC

**Why / how can we change mutable objects inside a tuple when it is immutable?** Members of a `tuple` are not directly stored in the memory. An immutable value (e.g. an `int`) has an existing, predefined reference in the memory. When used in a `tuple`, it is that reference that is *associated* with the `tuple`, and not the value itself. On the other hand, a mutable object does not have a predefined reference in the memory and is instead created on request somewhere in the memory (wherever there is enough free space). Whilst we can never change or redefine predefined references, we can always manipulate something we have defined ourselves. When we make such an alteration, the location of our mutable object in the memory may well change, but its reference — which is what is stored in a `tuple`, remains identical. You can find out what is the reference an object in Python using the function `id()`. If you experiment with it, you will notice that the reference to an immutable object (e.g. an `int` value) would never change, no matter how many time you define it in a different context or variable. In contrast, the reference number to a mutable object (e.g. a `list`) changes every time it is defined, even if it contains exactly the same values.

```
# Lists are mutable, so we can alter their values:  
mixed_tuple[4][1] = 15  
  
print(mixed_tuple)
```

PYTHON < >

```
(1, 2.5, 'abc', (3, 4), [5, 15])
```

OUTPUT < >

```
mixed_tuple[4].append(25)  
  
print(mixed_tuple)
```

PYTHON < >

```
(1, 2.5, 'abc', (3, 4), [5, 15, 25])
```

OUTPUT < >

PYTHON < >

```
# We cannot remove the list from the tuple,  
# but we can empty it by clearing its members:  
mixed_tuple[4].clear()  
  
print(mixed_tuple)
```

OUTPUT < >

```
(1, 2.5, 'abc', (3, 4), [])
```

Tuples may be empty or have a single value (singleton):

PYTHON < >

```
member_a = tuple()  
  
print(member_a, type(member_a), len(member_a))
```

OUTPUT < >

```
() <class 'tuple'> 0
```

PYTHON < >

```
# Empty parentheses also generate an empty tuple.  
# Remember: we cannot add values to an empty tuple later.  
member_b = ()  
  
print(member_b, type(member_b), len(member_b))
```

OUTPUT < >

```
() <class 'tuple'> 0
```

PYTHON < >

```
# Singleton - Note that it is essential to include  
# a comma after the value in a single-member tuple:  
member_c = ('John Doe',)  
  
print(member_c, type(member_c), len(member_c))
```

OUTPUT < >

```
('John Doe',) <class 'tuple'> 1
```

PYTHON < >

```
# If the comma is not included, a singleton tuple  
# is not constructed:  
member_d = ('John Doe')  
  
print(member_d, type(member_d), len(member_d))
```

OUTPUT < >

```
John Doe <class 'str'> 8
```

## Packing and unpacking

A `tuple` may be constructed without parenthesis. This is an implicit operation and is known as *packing*.

### REMEMBER

Implicit processes must be used sparingly. As always, the more coherent the code, the better it is.

PYTHON < >

```
numbers = 1, 2, 3, 5, 7, 11  
  
print(numbers, type(numbers), len(numbers))
```

OUTPUT < >

```
(1, 2, 3, 5, 7, 11) <class 'tuple'> 6
```

PYTHON < >

```
# Note that for a singleton, we still need to  
# include the comma.  
member = 'John Doe',  
  
print(member, type(member), len(member))
```

OUTPUT < >

```
('John Doe',) <class 'tuple'> 1
```

The reverse of this process is known as unpacking. Unpacking is no longer considered an implicit process because it replaces unnamed values inside an array, with named variables:

```
PYTHON < >  
dimensions = 14, 17, 12  
  
x, y, z = dimensions  
  
print(x)
```

```
OUTPUT < >  
14
```

```
PYTHON < >  
print(x, y)
```

```
OUTPUT < >  
14 17
```

```
PYTHON < >  
member = ('Jane Doe', 28, 'London', 'Student', 'Female')  
name, age, city, status, gender = member  
  
print('Name:', name, '- Age:', age)
```

```
OUTPUT < >  
Name: Jane Doe - Age: 28
```

### DO IT YOURSELF

Given:

```
PYTHON < >  
protein_info = ('GFP', 238)
```

Unpack `protein_info` into two distinct variables `protein_name` and `protein_length`.

## Solution

PYTHON < >

```
protein_name, protein_length = protein_info
```

## NOTE

There is another type of `tuple` in Python entitled `namedtuple`. It allows for the members of a `tuple` to be named independently (e.g. `member.name` or `member.age`), and thereby eliminates the need for unpacking. It was originally implemented by [Raymond Hettinger](#), one of Python's core developers, for Python 2.4 (in 2004) but was much neglected at the time. It has since gained popularity as a very useful tool. `namedtuple` is not a built-in tool, so it is not discussed here. However, it is included in the default library and is installed as a part of Python. If you are particularly adventurous, or want to learn more, feel free to have a look at the [official documentations](#) and examples. Raymond is also a regular speaker at PyCon (International Python Conferences), recordings of which are available on YouTube. He also uses his Twitter to talk about small, but important features in Python (yes, tweets!).

## Summary

In this section, we learned about `tuple`, another type of built-in arrays in Python that is *immutable*. This means that once created, the array can no longer be altered. We saw that trying to change the value of a `tuple` raises a `TypeError`. We also established that `list` and `tuple` follow an identical indexing protocol, and that they have 2 methods in common: `.index()` and `.count()`. Finally, we talked about *packing* and *unpacking* techniques, and how they improve the quality and readability of our code.

If you are interested in learning about `list` and `tuple` in more depth, have a look at the [official documentations of Sequence Types – list, tuple, range](#).

## INTERESTING FACT

Graph theory was initially developed by the renowned Swiss mathematician and logician Leonhard Euler (1707 – 1783). However, graphs in the sense discussed here were introduced by the English mathematician James Joseph Sylvester (1814 – 1897).

## Exercises

---

## END OF CHAPTER EXERCISES

1. We have

```
table = [[1, 2, 3], ['a', 'b'], [1.5, 'b', 4], [2]]
```

what is the length of `table` and why?

Store your answer in a variable and display it using `print()`.

2. Given the sequence for the Gamma (catalytic) subunit of the Protein Kinase A as:

```
human_pka_gamma = (
    'MAAPAAATAMGNAPAKKDTEQEESVNEFLAKARGDFLYRWGNPAQNTASSDQFERLRTLGMSFGRVML'
    'VRHQETGGHYAMKILNKQKVVKMKQVEHILNEKRILQAIDFPFLVKLQFSFKDNSYLYLVMEYVPGGEM'
    'FSRLQRVGRFSEPHACYAAQVVLAVQYLHSLDLIHRDLKPENLLIDQQGYLQVTDFGFAKRVKGRTWT'
    'LCGTPEYLAPEIILSKGYNKAVDWALGVLIYEMAVGFPPFYADQPIQIYEKIVSGRVRFPSKLSSDLK'
    'DLLRSLLQVDLTKRGFNLRNGVGDIKNHKWFATTSWIAIYEKKVEAPFIPKYTGPGDASNFDYEEEEEL'
    'RISINEKECAKEFSEF'
)
```

Using the sequence;

- work out and display the number of Serine (`S`) residues.
- work out and display the number of Threonine (`T`) residues.
- calculate and display the total number of Serine and Threonine residues in the following format:

```
Serine: X  
Threonine: X
```

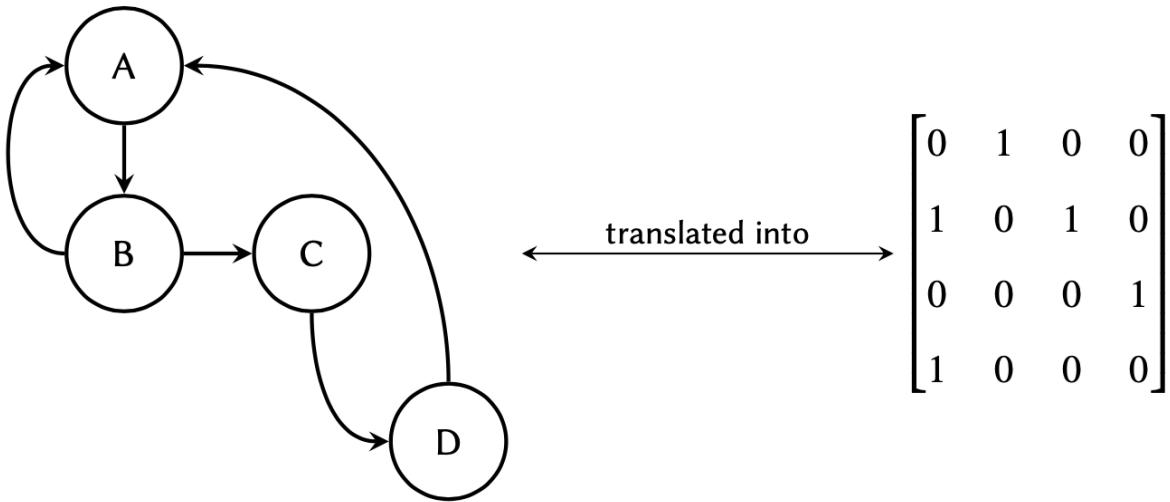
- create a nested array to represent the following table, and call it :

| Row    | Value |                               |
|--------|-------|-------------------------------|
| Column | 0     | 1                             |
| 0      | S     | <i>Number of Ser residues</i> |
| 1      | T     | <i>Number of Thr residues</i> |

3. Explain why in the previous question, we used the term *nested* instead of *two-dimensional* in reference to the array? Store your answer in a variable and display it using `print()`.

4. [Graph theory](#) is a prime object of discrete mathematics and is utilised for the non-linear analyses of data. The theory is extensively used in systems biology, and is gaining momentum in bioinformatics too. In essence, a [graph](#) is a structure that represents a set of objects (nodes) and the connections between them (edges).

The aforementioned connections are described using a special binary (zero and one) matrix known as the [adjacency matrix](#). The elements of this matrix indicate whether or not a pair of nodes in the graph are adjacent to one another.



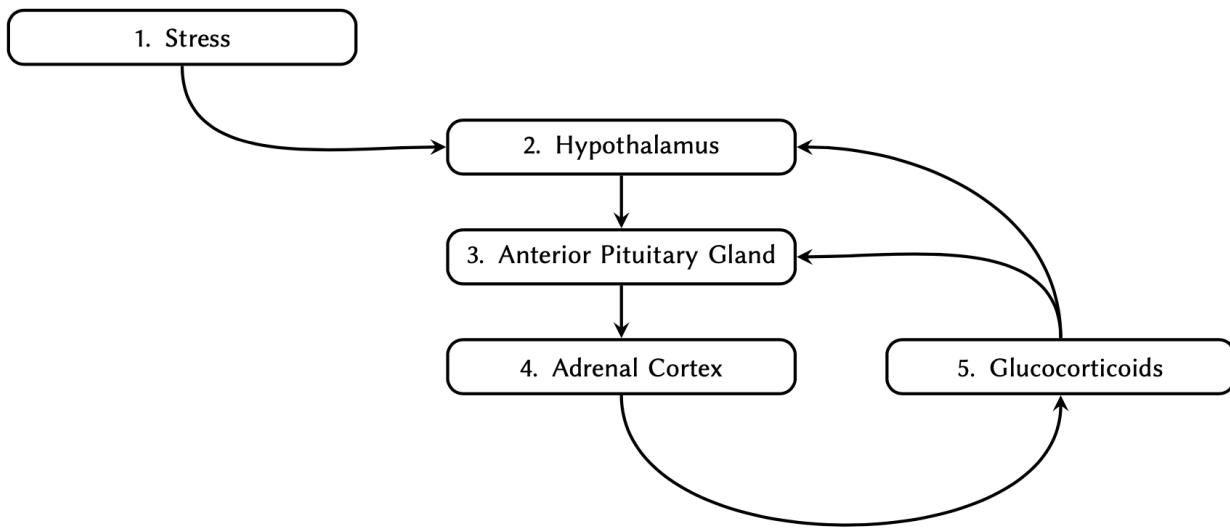
where each row in the matrix represents a node of origin in the graph, and each column a node of destination:

|          | <b>A</b> | <b>B</b> | <b>C</b> | <b>D</b> |
|----------|----------|----------|----------|----------|
| <b>A</b> | 0        | 1        | 0        | 0        |
| <b>B</b> | 1        | 0        | 1        | 0        |
| <b>C</b> | 0        | 0        | 0        | 1        |
| <b>D</b> | 1        | 0        | 0        | 0        |

If the graph maintains a connection (edge) between 2

nodes (e.g. between nodes **A** and **B** in the graph above), the corresponding value between those nodes would be #1 in the matrix, and if there are no connections, the corresponding value would #0.

Given the following graph:



Determine the adjacency matrix and implement it as a two-dimensional array in Python. Display the final array.

## Solution

### Q1

PYTHON < >

```
table = [[1, 2, 3], ['a', 'b'], [1.5, 'b', 4], [2]]  
  
table_length = len(table)  
print('length of Table:', table_length)  
  
reason = (  
    "The length of a `list` is a function of its "  
    "distinct members, regardless of their types."  
)  
  
print()  
print(reason)
```

OUTPUT < >

```
length of Table: 4  
  
The length of a `list` is a function of its distinct members, regardless of their types.
```

### Q2

PYTHON < >

```
human_pka_gamma = (  
    'MAAPAAATAMGNAPAKKDTEQEESVNEFLAKARGDFLYRWGNPAQNTASSDQFERLRTLGMGSFGRVML'  
    'VRHQETGGHYAMKILNKQKVVKMKQVEHILNEKRILQAIDFPFLVKLQFSFKDNSYLYLVMEYVPGGEM'  
    'FSRLQRVGRFSEPHACFYAAQVVLAVQYLHSLDLIHRDLKPENLLIDQQGYLQVTDFGFAKRVKGRTWT'  
    'LCGTPEYLAPEIILSKGYNKAVIDWALGVLIYEMAVGFPPFYADQPIQIYEKIVSGRVRFPSKLSSDLK'  
    'DLLRSLLQVDLTKRGFLNRNGVGDIKNHKWFATTSWIAIYEKKVEAPFIPKYTGPGDASNFDDYEEEEL'  
    'RISINEKCAKEFSEF'  
)  
  
total_serine = human_pka_gamma.count("S")  
total_threonine = human_pka_gamma.count("T")  
  
print('Serine:', total_serine)  
print('Threonine:', total_threonine)  
  
residues = [  
    ['S', total_serine],  
    ['T', total_threonine]  
]  
print(residues)
```

OUTPUT < >

```
Serine: 19  
Threonine: 13  
[['S', 19], ['T', 13]]
```

### Q3

PYTHON < >

```
answer = (
    "Members of a two-dimensional array must themselves be arrays of "
    "equal lengths containing identically typed members."
)
print(answer)
```

OUTPUT < >

```
Members of a two-dimensional array must themselves be arrays of equal lengths containing identically typed members.
```

### Q4

PYTHON < >

```
# Column initials:
#     S, H, A, A, G
adjacency_matrix = [
    [0, 1, 0, 0, 0], # Stress
    [0, 0, 1, 0, 0], # Hypothalamus
    [0, 0, 0, 1, 0], # Anterior Pituitary Gland
    [0, 0, 0, 0, 1], # Adrenal Cortex
    [0, 1, 1, 0, 0], # Glucocorticoids
]

print(adjacency_matrix)
```

OUTPUT < >

```
[[0, 1, 0, 0, 0], [0, 0, 1, 0, 0], [0, 0, 0, 1, 0], [0, 0, 0, 0, 1], [0, 1, 1, 0, 0]]
```

### KEYPOINTS

- **lists** and **tuples** are 2 types of arrays.
- An index is a unique reference to a specific value and Python uses a zero-based indexing system.
- **lists** are mutable because their contents can be modified.
- **slice()**, **.pop()**, **.index()**, **.remove()** and **.insert()** are some of the key functions used on mutable arrays.
- **tuples** are immutable which means its contents cannot be modified.

[Download Chapter notebook \(ipynb\)](#)

[Mandatory Lesson Feedback Survey](#)

## OVERVIEW

### Questions

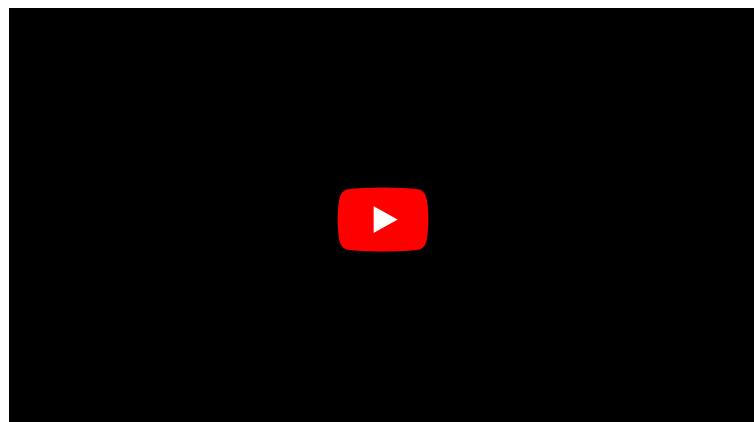
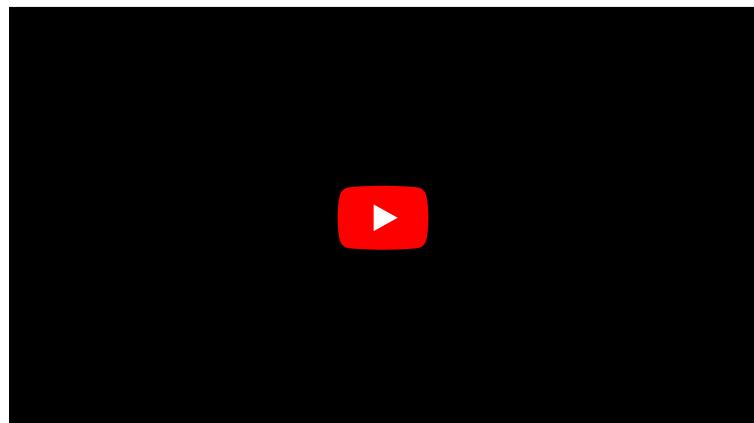
---

- What do we mean by *iterations* and *loops*?
  - How are `for`-loops implemented?
  - Can conditional statements be used in iterations?
  - When to use `while`-loops?
- 

### Objectives

---

- Understanding the concept of iterations and loops.
- Learning the processes involved in `for`-loops implementation.
- Building concept of using conditional statements in loops.
- Understanding when to use while loop.



This chapter assumes that you are familiar with the following concepts in Python 3:

## PREREQ

- [I/O Operations](#)
- [Variables and Types](#)
- [Mathematical Operation](#)
- [Logical Operations](#)
- [Indentation Rule](#)
- [Conditional Statements](#)
- [Arrays](#)

Additionally, make sure that you are comfortable with the principles of [indexing](#) in arrays before you start this section. It is very important that you have a good understanding of arrays and sequences, because the concept of iteration in programming deals *almost* exclusively with these subjects.

## NOTE

You can practice everything in this section and the subsequent ones as you have been doing so far. However, if you find it hard to grasp some of the concepts, don't worry, you are not alone. It takes practice. To help you with that, [Philip Guo](#) from UC San Diego (Calif., USA) has developed [PythonTutor.com](#), an excellent online tool for learning Python. On that website, write (or 'copy and paste') your code in the editor, then click *Visualize Execution*. In the new page, use the *forward* and *back* buttons to see a step-by-step graphical visualisation of the processes that occur during the execution of your code. Try it on the examples in this section.

# The concept

We employ iterations and loops in programming to perform repetitive operations. A repetitive operation is a reference to one or several defined operations that are repeated multiple times.

For instance, suppose we have a [list](#) of 5 numbers as follows:

```
numbers = [-3, -2, 5, 0, 12]
```

Now we would like to multiply each number by 2. Based on what we have learned thus far, this is how we would approach this problem:

PYTHON < >

```
numbers = [-3, -2, 5, 0, 12]

numbers[0] *= 2
numbers[1] *= 2
numbers[2] *= 2
numbers[3] *= 2
numbers[4] *= 2

print(numbers)
```

OUTPUT < >

```
[-6, -4, 10, 0, 24]
```

Whilst this does the job, it is clearly very tedious and repetitive. In addition to that, if we have an array of several thousand members, this approach becomes infeasible.

The process of multiplying individual members of our array with 2 is a very simple example of a repetitive operations.

#### REMEMBER

In programming, there is a universally appreciated golden principle known as the **DRY** rule; and this is what it stand for:

Don't Repeat Yourself

So if you find yourself doing something again and again, it is fair to assume that there might a better way of getting the results you're looking for ...

Some programmers (with questionable motives) have come up with a **WET** rule too. Find out more about DRY and WET from [Wikipedia](#).

There are some universal tools for iterations that exist in all programming languages — e.g. **for** and **while** loops. Some other tools such as vectorisation or generators, however, are unique to one or several specific programming languages.

Throughout this section, we will discuss iterations via **for** and **while** loops, and review some real-world examples that may only be addressed using iterative processes.

## for-loops

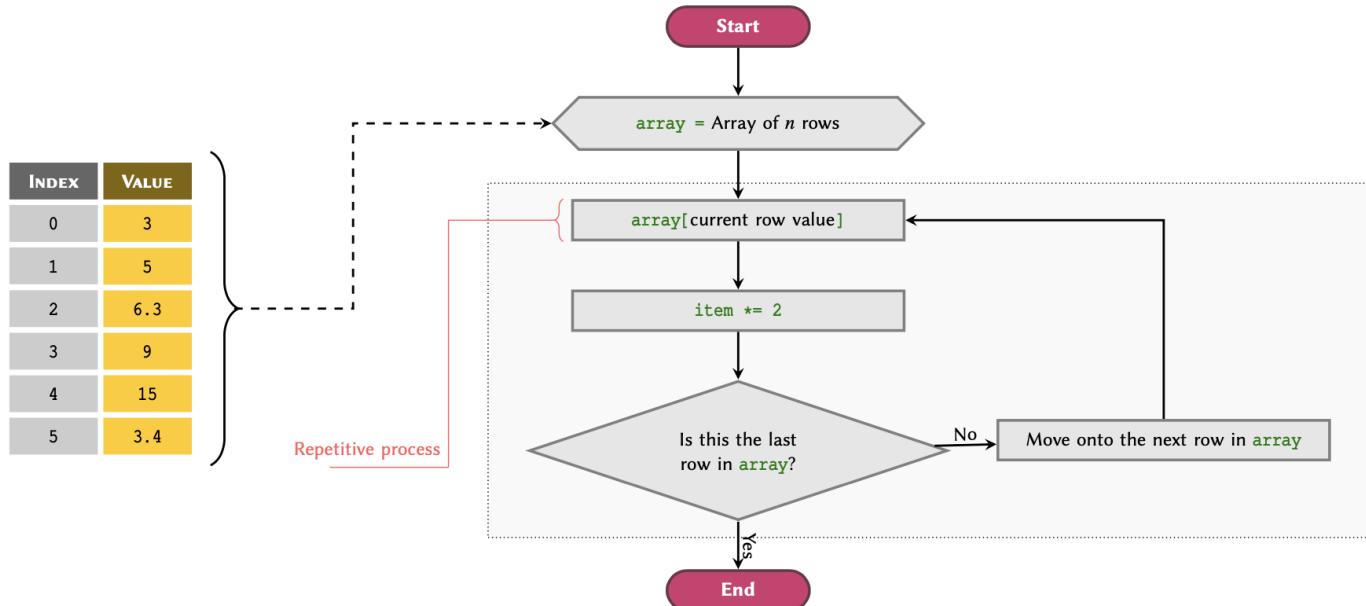
Some of the data show that up to 80% of all conventional iterations are implemented as **for** loops. Whether or not it is the best choice in all these cases is a matter of opinion. What is important, however, is to learn the difference between the 2 methods and feel comfortable with how they work.

Implementation of **for** loops in Python is simple compared to other programming languages. It essentially iterates through an existing *iterable* variable — e.g. an array, and retrieves the values from it one by one, from the beginning right down to the end.

## REMEMBER

In Python, *iterable* is a term used in reference to variables that can be iterated through. Any variable type that can be used in a `for` loop *without* any modifications is therefore considered an *iterable*.

Most arrays and sequences are iterable. See [Table](#) to find out which native types in Python are iterable. A rule of thumb is that if an array or a sequence is numerically indexed (e.g. `list`, `tuple`, or `str`), it is an iterable.



Flowchart of a `for`-loop workflow applied to a `list` array.

[Figure](#) illustrates a flowchart to visualise the workflow of an iterative process using `for` loops in Python. The process depicted in the flowchart may be described as follows:

## ADVANCED TOPIC

An iterable is a Python variable that contains the built-in method `__iter__()`. Methods starting and ending with two underscores (dunder methods) are also known as *magic methods* in Python. See [Python documentation](#)s for additional information.

## PROCESS

1. A `for`-loop is initialised using an array or a sequence and begins its process by going through the array values from the first row.
2. **Iterative Process:** The value of the *current row* is retrieved and given the alias `item`, which now represents a variable in the context of the loop.
3. **Repetitive Operation(s):** Designated operations are performed using the value of `item`:
  - `item *= 2`
4. **Loop Condition:** The `for` loop *automatically* checks whether or not it has reached the last row of the sequence:
  - **NO:** Move onto the next row and *repeat* the process from #2.
  - **YES:** Exit the loop.

We write this process in Python as:

```
PYTHON < >  
numbers = [3, 5, 6.3, 9, 15, 3.4]  
  
for item in numbers:  
    item *= 2  
    # Display the item to see the results:  
    print(item)
```

```
OUTPUT < >  
6  
10  
12.6  
18  
30  
6.8
```

where we can see that the result for each iteration is displayed in a new line. [Example](#) outlines other such applications and expands on repetitive operations that may be simplified using `for` loops.

## REMEMBER

A `for` loop is always initialised as:

```
for variable_name in an_array:  
    # An indented block of processes  
    # we would like to perform on the  
    # members of our array one by one.
```

where `an_array` is an *iterable* variable, and `variable_name` is the name of the variable we temporarily assign to a member of `an_array` that corresponds with the current loop cycle (iteration). The number of loop cycles performed by a `for` loop is equal to the length (number of members) of the array that we are iterating through, which in this case is called `an_array`.

You can think of each iteration cycle as pulling out a row from table that is our array (as exemplified in section [arrays](#)) and temporarily assigning its corresponding value to a variable until the next iteration cycle.

See subsection [List Members](#) to find the length of an array.

## DO IT YOURSELF

Given:

```
peptides = [  
    'GYSAR',  
    'HILNEKRILQAIID',  
    'DNSYLY'  
]
```

PYTHON < >

Write a `for` loop to display each item in `peptides` alongside its index and length. Display the results in the following format:

`Peptide XXXX at index X contains X amino acids.`

Solution

PYTHON < >

```
for sequence in peptides:  
    length = len(sequence)  
    index = peptides.index(sequence)  
  
    print('Peptide', sequence, 'at index', index, 'contains', length, 'amino acids.')
```

OUTPUT < >

```
Peptide GYSAR at index 0 contains 5 amino acids.  
Peptide HILNEKRILQALD at index 1 contains 13 amino acids.  
Peptide DNSYLY at index 2 contains 6 amino acids.
```

## EXTENDED EXAMPLE OF ITERATIONS USING `for` LOOPS

When using a `for` loop, we can also reference other variables that have already been defined outside of the loop block:

PYTHON < >

```
numbers = [3, 5, 6.3, 9, 15, 3.4]
counter = 0

for item in numbers:
    item *= 2

    # Display the item to see the results:
    print('Iteration number', counter, ':', item)

    counter += 1
```

OUTPUT < >

```
Iteration number 0 : 6
Iteration number 1 : 10
Iteration number 2 : 12.6
Iteration number 3 : 18
Iteration number 4 : 30
Iteration number 5 : 6.8
```

It is also possible to define new variables inside the loop, but remember that the value of any variables defined inside a loop is reset in each iteration cycle:

PYTHON < >

```
numbers = [3, 5, 6.3, 9, 15, 3.4]
counter = 0

for item in numbers:
    new_value = item * 2

    # Display the item to see the results:
    print('Iteration number', counter, ':', item, '* 2 =', new_value)

    counter += 1
```

OUTPUT < >

```
Iteration number 0 : 3 * 2 = 6
Iteration number 1 : 5 * 2 = 10
Iteration number 2 : 6.3 * 2 = 12.6
Iteration number 3 : 9 * 2 = 18
Iteration number 4 : 15 * 2 = 30
Iteration number 5 : 3.4 * 2 = 6.8
```

## DO IT YOURSELF

Write a `for` loop to display the values of a `tuple` defined as:

PYTHON < >

```
protein_kinases = ('PKA', 'PKC', 'MPAK', 'GSK3', 'CK1')
```

such that each protein is displayed on a new line and follows the phrase `Protein Kinase X:` as in

```
Protein Kinase 1: PKA  
Protein Kinase 2: PKC
```

and so on.

### Solution

PYTHON < >

```
counter = 1  
  
for protein in protein_kinases:  
    print('Protein Kinase ', counter, ': ', protein, sep='')  
    counter += 1
```

OUTPUT < >

```
Protein Kinase 1: PKA  
Protein Kinase 2: PKC  
Protein Kinase 3: MPAK  
Protein Kinase 4: GSK3  
Protein Kinase 5: CK1
```

## Retaining the new values

It is nice to be able to manipulate and display the values of an array but in the majority of cases, we need to retain the new values and use them later.

In such cases, we have two options:

- Create a new array to store our values.
- Replace the existing values with the new ones by overwriting them in the same array.

Creating a new array to store our values is very easy. All we need to do is to create a new `list` and add values to it in every iteration. In other words, We start off by creating an empty `list`; to which we then add members using the `.append()` method inside our `for` loop. The process of creating a new `list` and using the `.append()` method to values to an existing `list` are discussed in subsections [Useful Methods](#) and [mutability](#), respectively.

PYTHON < >

```
numbers = [-4, 0, 0.3, 5]
new_numbers = list()

for value in numbers:
    squared = value ** 2
    new_numbers.append(squared)

print('numbers:', numbers)
```

OUTPUT < >

```
numbers: [-4, 0, 0.3, 5]
```

PYTHON < >

```
print('new_numbers:', new_numbers)
```

OUTPUT < >

```
new_numbers: [16, 0, 0.09, 25]
```

### DO IT YOURSELF

Given:

```
peptides = [
    'GYSAR',
    'HILNEKRILQAIID',
    'DNSYLY'
]
```

PYTHON < >

write a `for` loop in which you determine the length of each sequence in `peptides`, and then store the results as a `list` of `tuple` items as follows:

```
[('SEQUENCE_1', X), ('SEQUENCE_2', X), ...]
```

## Solution

PYTHON < >

```
peptides_with_length = list()

for sequence in peptides:
    length = len(sequence)
    item = (sequence, length)

    peptides_with_length.append(item)
```

The replacement method uses a slightly different approach. Essentially what we try to achieve is:

- read the value of an item in an array;
- manipulate the value via operations;
- put the value back to the original array through *item assignment* and thereby replace the existing value.

We learned about modifying an existing value in a [list](#) in subsection [mutability](#), where we discussed the concept of *item assignment*. The process of replacing the original values of an array in a `for` loop is identical. The key to performing this process, however, is that we need to have the correct *index* for the specific member of the array that we are trying to modify. Additionally, don't forget that *item assignment* is only possible in mutable arrays such as [list](#). See [Table](#) to see which types of array are mutable in Python.

To perform *item assignment*; we can implement a variable to represent the current iteration cycle in our `for` loop. We do so by initialising the variable with a value of 0, and adding 1 to its value at the end of each cycle. We can then use that variable as an *index* in each iteration cycle:

PYTHON < >

```
numbers = [-4, 0, 0.5, 5]

# Variable representing the
# index (iteration cycle):
index = 0

for value in numbers:
    new_value = value ** 5

    # Putting it back into
    # the original array:
    numbers[index] = new_value

    # Adding one to the index for
    # the next iteration cycle:
    index += 1

print(numbers)
```

OUTPUT < >

```
[-1024, 0, 0.03125, 3125]
```

## ADVANCED TOPIC

The `enumerate()` function actually returns a *generator* of `tuple` items each time it is called in the context of a `for` loop. A generator is in principle very similar to a normal array; however, unlike an array, the values of a generator are not evaluated by the computer until the exact time at which they are going to be used. This is an important technique in functional programming known as *lazy evaluation*. It is primarily utilised to reduce the workload on the computer (both the processor and the memory) by preventing the execution of processes that may be delayed for a later time. In the case of the `enumerate()` function, the values are evaluated at the beginning of each iteration cycle in a `for` loop. Learn more about lazy evaluation in [Wikipedia](#) or read more on generators in Python in the [official documentations](#).

This is a perfectly valid approach and it is used in many programming languages. However, Python makes this process even easier by introducing the function `enumerate()`. We often use this function at the initiation of a `for` loop. The function takes an array as an input and as the name suggests, enumerates them; thereby simplifying the indexing process. The previous example may therefore be written more concisely in Python as follows:

PYTHON < >

```
numbers = [-4, 0, 0.5, 5]

for index, value in enumerate(numbers):
    # Manipulating the value:
    new_value = value ** 5
    numbers[index] = new_value

print(numbers)
```

OUTPUT < >

```
[-1024, 0, 0.03125, 3125]
```

## DO IT YOURSELF

Given:

PYTHON < >

```
characters = ['1', '2', '3', '4']
```

Display each item in `characters` as many times in one line as the index of that item in `characters`. The results should appear as follows:

```
2
33
444
```

## Solution

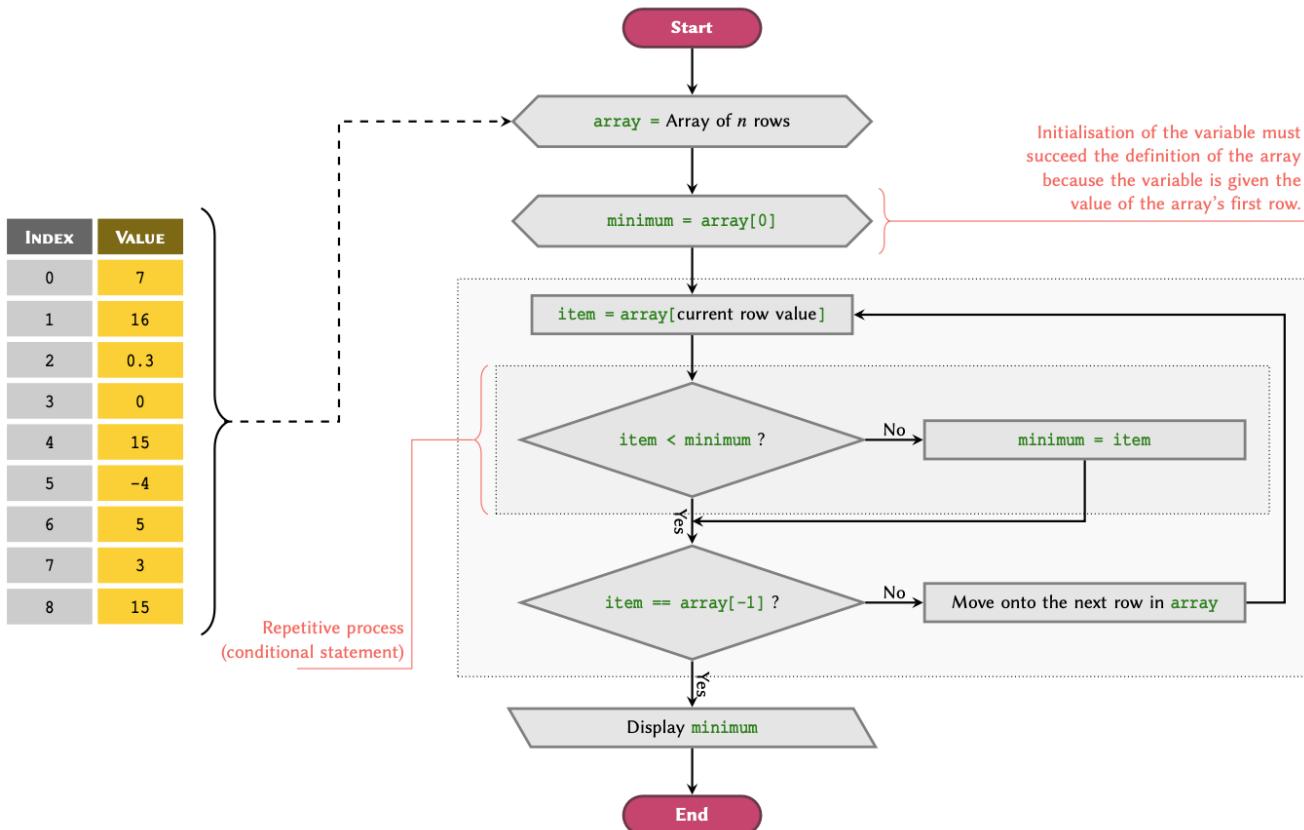
```
PYTHON < >  
for index, item in enumerate(characters):  
    print(item * index)
```

```
OUTPUT < >  
  
2  
33  
444
```

## for-loop and conditional statements

We can use conditional statements within `for` loops to account for and handle different situations.

Suppose we want to find the smallest value (the minimum) within a `list` of numbers using a `for` loop. The workflow of this process is displayed as a flowchart diagram in [figure below](#).



Given an array, we can break down the problem as follows:

1. Define the variable `minimum` outside our `for`-loop, and set its value to be equal to the value of the first row in our array.
2. A `for`-loop is initialised using an array or a sequence and begins its process by going through the array values from the first row.
3. **ITERATIVE PROCESS:** The value of the *current row* is retrieved and given the alias `item`, which now represents a variable in the context of the loop.
4. **REPETITIVE OPERATION(s):** Designated operations are performed using the value of `item`:
  - Compare the value of `minimum` with the value of every row in the array at each iteration cycle as test if `item < minimum`:
    - `True`: update the value of `minimum` to be `minimum = item`.
    - `False`: do nothing and proceed to the next step.
5. **LOOP CONDITION:** The `for`-loop *automatically* checks whether or not it has reached the last row of the sequence:
  - **NO:** Move onto the next row and *repeat* the process from #3.
  - **YES:** Exit the loop.

Finally, we can implement the process displayed in [figure](#) as follows:

```
numbers = [7, 16, 0.3, 0, 15, -4, 5, 3, 15]

minimum = numbers[0]

for value in numbers:
    if value < minimum:
        minimum = value

print('The minimum value is:', minimum)
```

PYTHON < >

The minimum value is: -4

OUTPUT < >

## DO IT YOURSELF

Given:

PYTHON < >

```
peptides = [  
    'FAEKE',  
    'CDYSK',  
    'ATAMGNAPAKKDT',  
    'YSFQW',  
    'KRFGNLR',  
    'EKKVEAPF',  
    'GMGSFGRVML',  
    'YSFQMGSFGRW',  
    'YSFQMGSFGRW'  
]
```

Using a `for` loop and a conditional statement, find and display the sequences in `peptides` that contain the amino acid serine (`S`) in the following format:

```
Found S in XXXXX.
```

## Solution

PYTHON < >

```
target = 'S'  
  
for sequence in peptides:  
    if target in sequence:  
        print('Found', target, 'in', sequence)
```

OUTPUT < >

```
Found S in CDYSK  
Found S in YSFQW  
Found S in GMGSFGRVML  
Found S in YSFQMGSFGRW  
Found S in YSFQMGSFGRW
```

## **Sequence of numbers in for-loops**

To produce a sequence of `int` numbers to use in a `for` loop, we can use the built-in `range()` function. The function takes in 3 positional arguments representing `start`, `stop`, and `step`. Note that `range()` is *only* capable of producing a sequence of integer numbers.

## REMEMBER

The `range()` function does not create the sequence of numbers immediately. Rather, it behaves in a similar way as the `enumerate()` function does (as a generator).

Displaying the output of a `range()` function is not, as one might expect, an array of numbers:

PYTHON < >

```
range_generator = range(0, 10, 2)

print(range_generator)
```

OUTPUT < >

```
range(0, 10, 2)
```

It is, however, possible to evaluate the values outside of a `for` loop. To do so, we need to convert the output of the function to `list` or a `tuple`:

PYTHON < >

```
range_sequence = list(range_generator)

print(range_sequence)
```

OUTPUT < >

```
[0, 2, 4, 6, 8]
```

## REMEMBER

The `range()` function is *non-inclusive*. That is, it creates a sequence that starts from and includes the value given as the *start* argument, up to but excluding the value of the *end* argument. For instance, `range(1, 5, 1)` creates a sequence starting from `1`, which is then incremented `1` step at a time right up to `5`, resulting in a sequence that includes the following numbers: `1, 2, 3, 4`

## EXAMPLE: SEQUENCE COMPARISON. DOT PLOTS AND `for`-LOOPS

There are different methods to evaluate the similarity of two or more polypeptide or polynucleotide sequences. The [dot matrix](#) (also known as the *dot plot*) is one such method. A *dot matrix* is in essence a [two-dimensional array](#) of binary values — *i.e.* it only contains zeros and ones, or `True` and `False`.

For instance, given the following polypeptide sequences, extracted from the **CFTR** (Cystic fibrosis transmembrane conductance regulator) protein in humans and mice:

```
In [1]: 1 cftr_human = 'GRMMMKYRDQRAGKISERLVITSEMIENIQSVKAYCWEEAMEKMIENLRQTELKLTRKAA'  
2 cftr_mouse = 'GKMMVKYRDORAAKINERLVITSEIIDNIYSVKAYCWESAMEKMIENLREVELKMTRKAA'
```

we can go ahead and construct a dot matrix by comparing each residue in `cftr_human` with every residue in `cftr_mouse`.

On this occasion,  $D$  is an  $n \times m$  matrix, where:

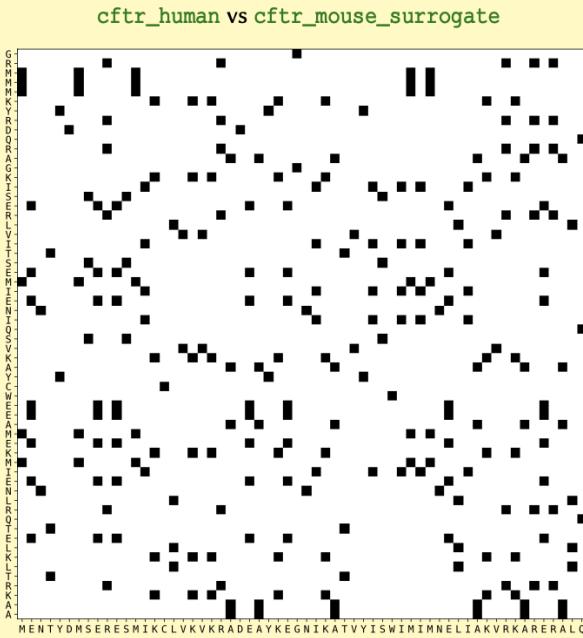
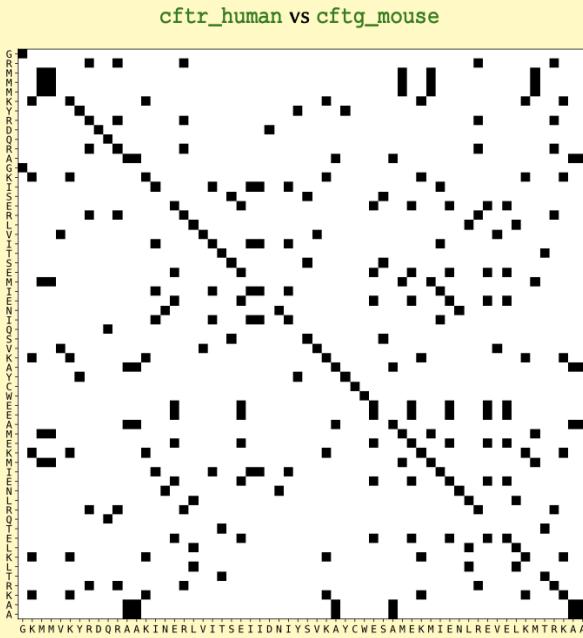
- $n$  is equal to the number of residues in `cftr_human`; and,
- $m$  is equal to that of `cftr_mouse`.

Therefore, each element in  $D$  may be referred to as  $D_{i,j}$ , where  $i$  and  $j$  represent the index of a residue in `cftr_human` and `cftr_mouse` respectively. The value of each element is either `0` or `1` depending on their similarity — *i.e.* if `cftr_human[i]` is identical to `cftr_mouse[j]`, then  $D_{i,j}$  is `1`, otherwise it is `0`.

It is beyond the scope of this book to discuss the interpretation of dot plots. However, in general, the existence of a diagonal line in the final matrix or the dot plot would imply a high degree of similarity between the two sequence. This means that if we compare `cftr_human` with a randomly shuffled version of `cftr_mouse`, we should lose the diagonal line. To test this, we will additionally create a surrogate sequence of the `cftr_mouse` sequence:

```
1 cftr_mouse_surrogate = 'MENTYDMSERESMIKCLVKVRADEAYKEGNIKATVYISWIMIMNELIAKVRKARERALQ'
```

The visualisation of the dot matrices determined for the sequences we have defined are as follows, where black dots represent a value of `1` (identical residues):



## IMPLEMENTATION

We can create the above matrix by implementing a nested `for`-loop, which we then use to construct a `nested array`, one element at a time. This might appear somewhat difficult to grasp; however, it becomes clear once you investigate the code and go through the workflow.

In [2]:

```
1 dot_matrix = list()
2
3     for residue_a in cftr_human:
4         row = list()
5
6             for residue_b in cftr_mouse:
7                 if residue_a == residue_b:
8                     | row.append(1)
9                 else:
10                     | row.append(0)
11
12     dot_matrix.append(row)
13
14 print(dot_matrix)
```

To achieve a binary matrix, we compare every character in `cftr_human` to every character in `cftr_mouse`. In other words, we iterate through `cftr_human`, and during each iteration, we also iterate through `cftr_mouse`. This allows us to compare each character in `cftr_human`, to every character in `cftr_mouse`. Given that each sequence in our example has a length of 60 characters, we will essentially complete 60 iterations for `cftr_humans` (outer loop), and  $60 \times 60 = 3600$  iterations for `cftr_mouse` (inner loop). This number is equal to the number of squares displayed in the above dot matrix.

In the context of the inner loop, depending on whether or not the two characters (or amino acid residues) are identical, we append a value of #0 or #1 to the row. Each row represents a `list` and corresponds to the `cftr_human` residue in the current iteration. This means that each column (each item added to the row) represents one residue in `cftr_mouse`.

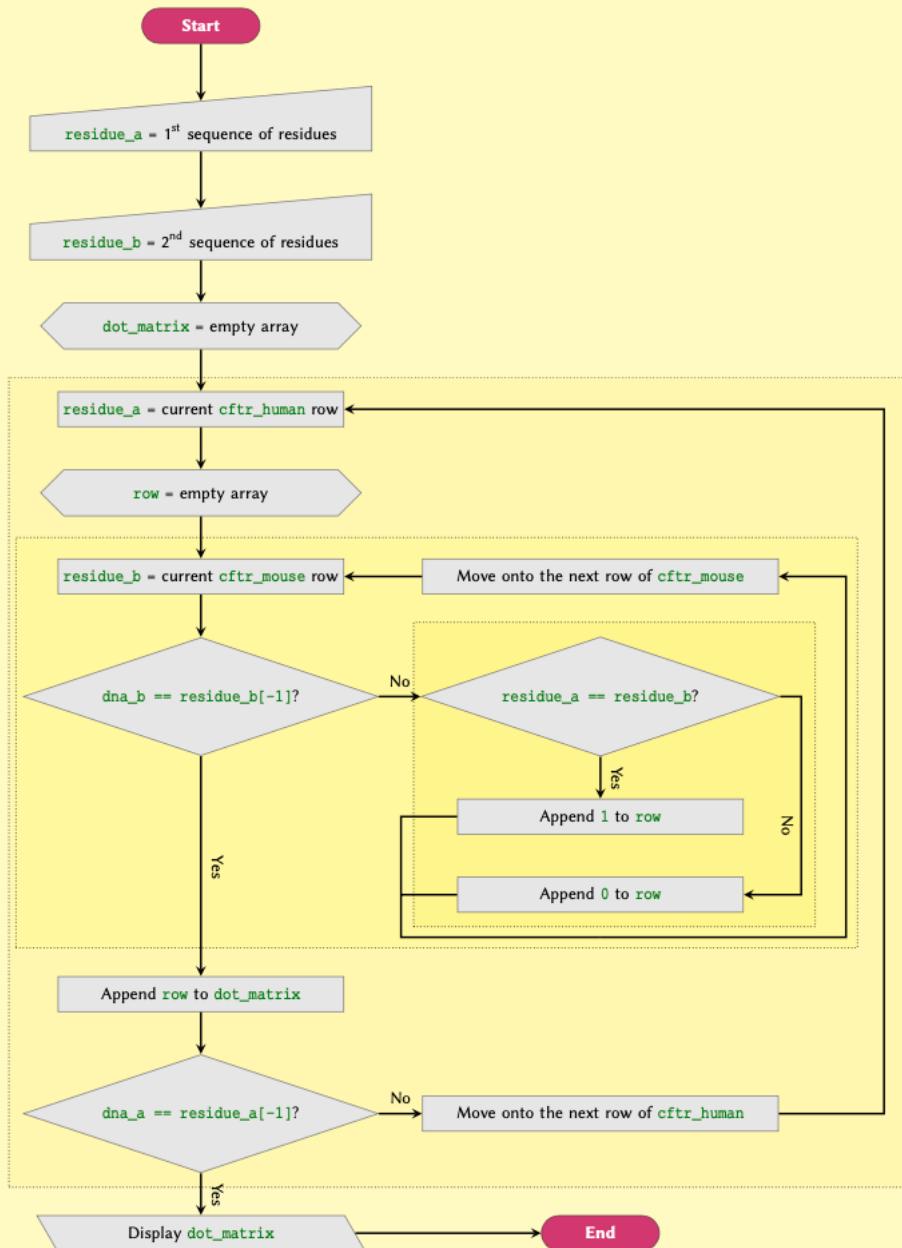
The output of the code will thus be a matrix of zeros and ones, as follows:

Out [2]:

```
[[1, 0,
 0,
 0, 0, 0, 0], [0, 0, 0, 0, 0, 0, 0, 0, 1, 0, 0, 0, 1, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0, 0,
 0,
 0, 0, 0, 0, 1, 0, 0, 0], ...]
```

## WORKFLOW

The algorithm that we implemented to create the dot matrix may appear relatively complex. However, it demonstrates the important and complementary relationship between `for`-loops and sequences in programming. The logic of the code is best described as a flowchart.



#### VISUALISATION

Dot plots are typically visualised as a heatmap. We do not investigate visualisation techniques here. Nonetheless, we shall take this opportunity to visualise the dot matrix we have created.

Visualisation and plotting in Python is done using external libraries, of which there are many varieties to choose from. For the purpose of this example, we will be using `matplotlib`, an extensive and powerful library for producing publication quality figures in Python. The library is installed automatically as a part of the Anaconda distribution. See the [official documentation](#), [examples](#), and [tutorials](#) for `matplotlib` to find out more.

Use the following code to produce a heatmap of the dot matrix:

```
In [3]:  
1  from matplotlib.pyplot import subplots, show  
2  
3  
4  # Initialising a figure and its axis:  
5  fig, ax = subplots(figsize=(10, 10))  
6  
7  # Plotting a heatmap of the matrix with  
8  # equal axes, and a reversed grayscale  
9  # colour map:  
10 ax.imshow(dot_matrix, aspect='equal', cmap='gray_r')  
11  
12 # Determining the length of each sequence:  
13 human_len, mouse_len = len(human_cftr), len(mouse_cftr)  
14  
15 # Creating a sequence of numbers to use  
16 # for tick positions in our plot:  
17 human_ticks, mouse_ticks = range(human_len), range(mouse_len)  
18  
19 # Setting tick positions:  
20 ax.set_yticks(human_ticks)  
21 ax.set_xticks(mouse_ticks)  
22  
23 # Setting tick labels:  
24 ax.set_yticklabels(human_cftr, fontsize=8)  
25 ax.set_xticklabels(mouse_cftr, fontsize=8)  
26  
27 # Display the figure:  
28 show()
```

Try this code with other polypeptide or polynucleotide sequences and experiment with the `matplotlib` options as described in its documentation.

#### LEARN MORE

To learn more about sequence comparison methods, including how to interpret dot plots, read:

- Orengo, C.A., Jones, D.T., Thornton, J.M. (2005). *Bioinformatics*. 1st ed. New York: Taylor & Francis, pp. 33-34.
- Lesk, A. (2014). *Introduction to bioinformatics*. Oxford: Oxford University Press. pp. 176-181.

## while-loops

In the previous, we explored `for`-loop mediated iterations and learned that they are *exclusively* applied to iterable objects — e.g. arrays and sequences. This is because, as demonstrated in [workflow figure](#), at the end of each iteration, the *implicit* termination condition that is inherent in the process tests whether or not it has reached the end of the sequence it is iterating through.

It may, however, be deemed necessary to apply iterative processes based on conditions other than that embedded in the `for`-loop. In such cases, we use a different class of iterations known as the `while`-loop.

## REMINDER

The termination condition of a `while`-loop is manually defined by the programmer. It is therefore paramount to ensure that the termination condition is somehow satisfied at some point in process. If the termination condition is implemented incorrectly such that the condition is never met, the iteration process would *never* end. In that case, the programme falls into what is known as the [infinite loop](#) state.

This is bound to happen to every programmer at some point. It is, however, important to know how to break out of an *infinite loop*:

**IDE** In most IDEs — e.g. PyCharm® or Jupyter, the programme may be terminated using the tools provided in the environment. Such tools often appear in the shape of a *stop* button in the shape of ■ or ⊗, and are positioned near the *start / execute* button.

**Terminal** To abort the current task and stop the execution of a programme, we send a SIGINT signal in the terminal as follows:

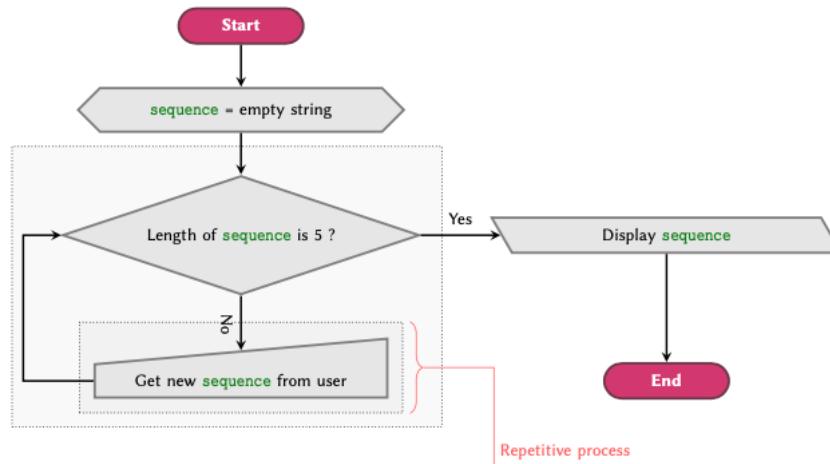
- in Linux or Microsoft Windows®, press `ctrl + c`
- in Mac OS X®, press `⌘ + c`

**Other** Try to close the window manually. This will force the termination of your programme. However, if your computer freezes, the only remaining option would be to restart the computer.

Consider the following scenario:

We want to ask the user to enter a sequence of exactly 5 amino acids in single letter code. If the provided sequence is more or less than 5 letters long, we would like to display a message and ask them to try again; otherwise, we will display the process and terminate the programme.

It is impossible to write such a process using a `for`-loop. This is because when we initialise the iteration process, the number of loops we need is unknown. In other words, we simply do not know how many times the user would need enter said sequence before they get it right.



To simplify the understanding of the concept, we can visualise the process in flowchart, as displayed in [figure](#). In the flowchart, you can see that the only way to exit the loop is to enter a sequence of exactly 5 characters. Doing anything else — i.e. entering a different number of letters — is tantamount to going back to the beginning of the loop. The process may be described verbally as follows:

1. Initialise the variable `sequence` and assign an empty string to it.
2. *While* the length of `sequence` is not equal to 5:
  - Ask the user to enter a new `sequence`.
  - Go back to #2.
3. Display the value of `sequence`.

## Implementation

We start `while`-loop using the `while` syntax, immediately followed by the loop condition.

We can now implement the process displayed in [figure](#) as follows:

```
sequence = str()

while len(sequence) != 5:
    sequence = input('Enter a sequence of exactly 5 amino acids: ')

print(sequence)
```

When executed, the above code will prompt the user to enter a value:

```
Enter a sequence of exactly 5 amino acids: GCGLLY
Enter a sequence of exactly 5 amino acids: GCGL
Enter a sequence of exactly 5 amino acids: GC
Enter a sequence of exactly 5 amino acids: GCGLL

GCGLL
```

As expected, the user is repetitively asked to enter a 5 character sequence until they supply the correct number of letters.

### DO IT YOURSELF

1. Write a script which asks the user to enter a number, then:

- if the second power of the number is smaller than [10](#), repeat the process and ask again;
- if the second power of the number is equal or greater than [10](#), display the original value and terminate the programme.

**Hint:** Don't forget to [convert](#) the value enter by the user to an appropriate numeric type *before* you perform any mathematical operations.

2. We learned in subsection [Sequence of Numbers](#) that the built-in function [range\(\)](#) may be utilised to produce a sequence of *integer* numbers. The function takes 3 input arguments in the following order: [stop](#), [start](#), [step](#).

We now need a sequence of floating point numbers with the following criteria:

```
stop = 10
start = 0
step = 0.5
```

The use of a floating point number as [step](#) means that we cannot use [range\(\)](#) to create the desired sequence. Write a script in which you use a [while](#)-loop to produce a sequence of floating point numbers with the above criteria and display the result.

The resulting sequence must be:

- presented as an instance of type [list](#);
- similar to [range\(\)](#), the sequence must be non-inclusive — *i.e.* it must include the value of [start](#), but not that of [stop](#).

Solution

```
value = 0

while value ** 2 < 10:
    response = input('Enter a number: ')
    value = float(response)

print(value)
```

Solution

```
stop = 10
start = 0
step = 0.5

number = start
sequence = list()

while number < stop:
    sequence.append(number)
    number += step

print(sequence)
```

PYTHON < >

```
[0, 0.5, 1.0, 1.5, 2.0, 2.5, 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5, 8.0, 8.5, 9.0, 9.5]
```

OUTPUT < >

## Solution

PYTHON < >

```
# A smarter solution, however, would be:  
stop = 10  
start = 0  
step = 0.5  
  
sequence = [start]  
  
while sequence[-1] < stop - step:  
    sequence.append(sequence[-1] + step)  
  
print(sequence)
```

OUTPUT < >

```
[0, 0.5, 1.0, 1.5, 2.0, 2.5, 3.0, 3.5, 4.0, 4.5, 5.0, 5.5, 6.0, 6.5, 7.0, 7.5, 8.0, 8.5, 9.0, 9.5]
```

## Breaking a while-loop

Unlike **for**-loops, it is common to *break* out of a **while**-loop mid-process. This is also known as *premature termination*.

To consider a situation that may necessitate such an approach, we shall modify our scenario as follows:

We want to ask the user to enter a sequence of exactly 5 amino acids. If the sequence the user provides is more or less than 5 letters long, we would like to display a message and ask them to try again; otherwise, we will display the sequence and terminate the programme. Additionally, the loop should be terminated: - upon 3 failed attempts; or, - if the user entered the word **exit** instead of a 5 character sequence.

In the former case, however, we would also like to display a message and inform the user that we are terminating the programme because of 3 failed attempts.

To implement the first addition to our code, we will have to make the following alterations in our code:

- Define a variable to hold the iteration cycle, then test its value at the beginning of each cycle to make sure that it is below the designated threshold. Otherwise, we manually terminate the loop using the **break** syntax.
- Create a **conjunctive** conditional statement for the **while**-loop to make so that it is also sensitive to our **exit** keyword.

```
sequence = str()
counter = 1
max_counter = 3
exit_keyword = 'exit'

while len(sequence) != 5 and sequence != exit_keyword:
    if counter == max_counter:
        sequence = "Three failed attempt - I'm done."
        break

    sequence = input('Enter a sequence of exactly 5 amino acids or [exit]: ')
    counter += 1

print(sequence)
```

## Exercises

---

## END OF CHAPTER EXERCISES

1. Can you explain the reason why in the example given in subsection [for-loop and conditional statements](#) we set `minimum` to be equal to the first value of our array instead of, for instance zero or some other number?

Store your answer in a variable and display it using `print()`.

2. Write a script that using a `for` loop, calculates the sum of all numbers in an array defined as follows:

```
numbers = [0, -2.1, 1.5, 3]
```

and display the result as:

```
Sum of the numbers in the array is 2.4
```

3. Given an array of integer values as:

```
numbers = [2, 1, 3]
```

write a script that using `for` loops, displays each number in the list as many time as the number itself. The programme must therefore display 2 twice, 1 once, and 3 three times.

4. Given a `list` of numbers defined as:

```
numbers = [7, 16, 0.3, 0, 15, -4, 5, 3, 15]
```

write a script that using at most two `for` loops, finds the *variance* of the numbers, and display the *mean*, and the *variance*. Note that you will need to calculate the *mean* as a part of your calculations to find the *variance*.

The equation for calculating the variance is:

$$\sigma^2 = \frac{\sum_{i=1}^n (x_i - \mu)^2}{n}$$

**Hint:** Breaking down the problem into smaller pieces will simplify the process of translating it into code and thereby solving it:

- a. Work out the Mean or  $\mu$  (the simple average of the numbers):

$$\mu = \frac{\sum_{i=1}^n x_i}{n}$$

- b. Calculate the sum of: each number ( $x_i$ ) subtracted by the Mean ( $\mu$ ) and square the result.

- c. Divide the resulting number by the length of `number`.

Display the results in the following format:

Mean: XXXX

Variance: XXXX

## Solution

Q1

PYTHON < >

```
answer = "Because the minimum of the array may be smaller than zero."  
print(answer)
```

OUTPUT < >

```
Because the minimum of the array may be smaller than zero.
```

Q2

PYTHON < >

```
numbers = [0, -2.1, 1.5, 3]  
  
numbers_sum = 0  
  
for value in numbers:  
    numbers_sum += value  
  
print("Sum of the numbers in the array is", numbers_sum)
```

OUTPUT < >

```
Sum of the numbers in the array is 2.4
```

Q3

PYTHON < >

```
numbers = [2, 1, 3]  
  
for value in numbers:  
    prepped_value = [value] * value  
  
    for number in prepped_value:  
        print(number)
```

OUTPUT < >

```
2  
2  
1  
3  
3  
3
```

#### Q4

PYTHON < >

```
numbers = [7, 16, 0.3, 0, 15, -4, 5, 3, 15]

numbers_length = len(numbers)

# Calculating the "sum"
# -----
numbers_sum = 0

for value in numbers:
    numbers_sum += value

# Calculating the "mean"
# -----

numbers_mean = numbers_sum / numbers_length

# Calculating the "variance"
# -----

variance_denominator = numbers_length
variance_numerator = 0

for value in numbers:
    prepped_value = (value - numbers_mean) ** 2
    variance_numerator += prepped_value

numbers_variance = variance_numerator / variance_denominator

# Results
# -----

print("Mean:", numbers_mean)
print("Variance:", numbers_variance)
```

OUTPUT < >

```
Mean: 6.366666666666666
Variance: 48.91999999999995
```

## KEYPOINTS

- Iterations and loops are used to perform repetitive operations.
- Implementation of `for`-loop involves 4 steps.
- Conditional statements are used within loops to handle different situations.
- `while`-loop is suited when exact number of conditions/iterations are unknown.

Content from [Dictionaries](#)

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## OVERVIEW

### Questions

- 
- How is a dictionary defined in Python?
  - What are the ways to interact with a dictionary?
  - Can a dictionary be nested?
- 

### Objectives

- Understanding the structure of a dictionary.
- Accessing data from a dictionary.
- Practising nested dictionaries to deal with complex data.

This chapter assumes that you are familiar with the following concepts in Python 3:

## PREREQ

- Indentation Rule
- Conditional Statements
- Arrays
- Loops and Iterations

# Dictionary

[Mapping Types – dict](#)

[Google search](#)

[StackOverflow python-3.x dictionaries](#)

[YouTube Tutorial Dictionaries](#)

One of the most useful built-in tools in Python, dictionaries associate a set of *values* with a number of *keys*.

Think of an old fashion, paperback dictionary where we have a range of words with their definitions. The words are the *keys*, and the definitions are the *values* that are associated with the keys. A Python dictionary works in the same way.

Consider the following scenario:

Suppose we have a number of protein kinases, and we would like to associate them with their descriptions for future reference.

This is an example of association in arrays. We may visualise this problem as displayed in Figure.

| KEY | ASSOCIATION | VALUE                                                            |
|-----|-------------|------------------------------------------------------------------|
| PKA |             | Involved in regulation of glycogen, sugar, and lipid metabolism. |
| PKC |             | Regulates signal transduction pathways such as the Wnt pathway.  |
| CK1 |             | Controls the function of other proteins through phosphorylation. |

One way to associate the proteins with their definitions would be to use nested arrays. However, it would make it difficult to retrieve the values at a later time. This is because to retrieve the values, we would need to know the index at which a given protein is stored.

Instead of using normal arrays, in such circumstances, we use *associative arrays*. The most popular method to create construct an associative array in Python is to create dictionaries or [dict](#).

## REMEMBER

To implement a [dict](#) in Python, we place our entries in curly bracket, separated using a comma. We separate *keys* and *values* using a colon — e.g. `{'key': 'value'}`. The combination of dictionary *key* and its associating *value* is known as a dictionary *item*.

## NOTE

When constructing a long `dict` with several *items* that span over several lines, it is not necessary to write one *item* per line or use indentations for each *item* or line. All we must is to write the as `{'key': 'value'}` in curly brackets and separate each pair with a comma. However, it is good practice to write one *item* per line and use indentations as it makes it considerably easier to read the code and understand the hierarchy.

We can therefore implement the diagram displayed in [Figure](#) in Python as follows:

PYTHON < >

```
protein_kinases = {  
    'PKA': 'Involved in regulation of glycogen, sugar, and lipid metabolism.',  
    'PKC': 'Regulates signal transduction pathways such as the Wnt pathway.',  
    'CK1': 'Controls the function of other proteins through phosphorylation.'  
}  
  
print(protein_kinases)
```

OUTPUT < >

```
{'PKA': 'Involved in regulation of glycogen, sugar, and lipid metabolism.', 'PKC': 'Regulates signal transdu
```

PYTHON < >

```
print(type(protein_kinases))
```

OUTPUT < >

```
<class 'dict'>
```

## DO IT YOURSELF

Use [Universal Protein Resource](#) (UniProt) to find the following proteins for humans: - Axin-1 - Rhodopsin

Construct a dictionary for these proteins and the number amino acids for each of them. The *keys* should represent the name of the protein. Display the result.

## Solution

```
proteins = {  
    'Axin-1': 862,  
    'Rhodopsin': 348  
}  
  
print(proteins)
```

PYTHON < >

```
{'Axin-1': 862, 'Rhodopsin': 348}
```

OUTPUT < >

Now that we have created a dictionary; we can test whether or not a specific *key* exists our dictionary:

```
'CK1' in protein_kinases
```

PYTHON < >

```
True
```

OUTPUT < >

```
'GSK3' in protein_kinases
```

PYTHON < >

```
False
```

OUTPUT < >

## DO IT YOURSELF

Using the dictionary you created in [Do it Yourself](#), test to see whether or not a protein called **ERK** exists as a *key* in your dictionary? Display the result as a Boolean value.

## Solution

```
PYTHON < >  
print('ERK' in proteins)
```

```
OUTPUT < >  
False
```

## Interacting with a dictionary

We have already learnt that in programming, the more explicit our code, the better it is. Interacting with dictionaries in Python is very easy, coherent, and explicit. This makes them a powerful tool that we can exploit for different purposes.

In arrays, specifically in `list` and `tuple`, we routinely use `indexing` techniques to retrieve *values*. In dictionaries, however, we use `keys` to do that. Because we can define the `keys` of a dictionary ourselves, we no longer have to rely exclusively on numeric indices.

As a result, we can retrieve the *values* of a dictionary using their respective *keys* as follows:

```
PYTHON < >  
print(protein_kinases['CK1'])
```

```
OUTPUT < >  
Controls the function of other proteins through phosphorylation.
```

However, if we attempt to retrieve the *value* for a *key* that does not exist in our `dict`, a `KeyError` will be raised:

```
PYTHON < >  
'GSK3' in protein_kinases
```

```
OUTPUT < >  
False
```

```
PYTHON < >  
print(protein_kinases['GSK3'])
```

```
ERROR < >  
Error: KeyError: 'GSK3'
```

## DO IT YOURSELF

Implement a `dict` to represent the following set of information:

Cystic Fibrosis:

| Full Name                                           | Gene | Type             |
|-----------------------------------------------------|------|------------------|
| Cystic fibrosis transmembrane conductance regulator | CFTR | Membrane Protein |

Using the dictionary you implemented, retrieve and display the *gene* associated with cystic fibrosis.

## Solution

```
PYTHON < >

cystic_fibrosis = {
    'full name': 'Cystic fibrosis transmembrane conductance regulator',
    'gene': 'CFTR',
    'type': 'Membrane Protein'
}

print(cystic_fibrosis['gene'])
```

```
OUTPUT < >

CFTR
```

## REMEMBER

Whilst the *values* in a `dict` can be of virtually any type supported in Python, the *keys* may only be defined using immutable types.

To find out which types are immutable, see [Table](#). Additionally, the *keys* in a dictionary must be unique.

If we attempt to construct a `dict` using a mutable value as *key*, a `TypeError` will be raised.

For instance, `list` is a mutable type and therefore cannot be used as a *key*.

```
PYTHON < >

test_dict = {
    ['a', 'b']: 'some value'
}
```

[ERROR < >](#)

```
Error: TypeError: unhashable type: 'list'
```

But we can use any immutable type as a *key*:

[PYTHON < >](#)

```
test_dict = {
    'ab': 'some value'
}

print(test_dict)
```

[OUTPUT < >](#)

```
{'ab': 'some value'}
```

[PYTHON < >](#)

```
test_dict = {
    ('a', 'b'): 'some value'
}

print(test_dict)
```

[OUTPUT < >](#)

```
{('a', 'b'): 'some value'}
```

If we define a *key* more than once, the Python interpreter constructs the entry in `dict` using the last instance.

In the following example, we repeat the *key* 'pathway' twice; and as expected, the interpreter only uses the last instance, which in this case represents the value 'Canonical':

[PYTHON < >](#)

```
signal = {
    'name': 'Wnt',
    'pathway': 'Non-Canonical', # first instance
    'pathway': 'Canonical' # second instance
}

print(signal)
```

[OUTPUT < >](#)

```
{'name': 'Wnt', 'pathway': 'Canonical'}
```

## Mutability

Dictionaries are mutable. This means that we can alter their contents. We can make any alterations to a dictionary as long as we use *immutable* values for the *keys*.

Suppose we have a dictionary stored in a variable called `protein`, holding some information about a specific protein:

```
PYTHON < >  
protein = {  
    'full name': 'Cystic fibrosis transmembrane conductance regulator',  
    'alias': 'CFTR',  
    'gene': 'CFTR',  
    'type': 'Membrane Protein',  
    'common mutations': ['Delta-F508', 'G542X', 'G551D', 'N1303K']  
}
```

We can add new *items* to our dictionary or alter the existing ones:

```
PYTHON < >  
# Adding a new item:  
protein['chromosome'] = 7  
  
print(protein)  
  
print(protein['chromosome'])
```

```
OUTPUT < >  
{'full name': 'Cystic fibrosis transmembrane conductance regulator', 'alias': 'CFTR', 'gene': 'CFTR', 'type':  
7}
```

We can also alter an existing *value* in a dictionary using its *key*. To do so, we simply access the *value* using its *key*, and treat it as a normal variable; i.e. the same way we do with members of a `list`:

```
PYTHON < >  
print(protein['common mutations'])
```

```
OUTPUT < >  
['Delta-F508', 'G542X', 'G551D', 'N1303K']
```

```
PYTHON < >  
protein['common mutations'].append('W1282X')  
print(protein)
```

```
OUTPUT < >  
{'full name': 'Cystic fibrosis transmembrane conductance regulator', 'alias': 'CFTR', 'gene': 'CFTR', 'type':
```

## DO IT YOURSELF

Implement the following dictionary:

```
signal = {'name': 'Wnt', 'pathway': 'Non-Canonical'}
```

with respect to `signal`:

- Correct the *value* of `pathway` to "Canonical";
- Add a new *item* to the dictionary to represent the *receptors* for the canonical pathway as "Frizzled" and "LRP".

Display the altered dictionary as the final result.

### Solution

PYTHON < >

```
signal = {'name': 'Wnt', 'pathway': 'Non-Canonical'}  
  
signal['pathway'] = 'Canonical'  
signal['receptors'] = ('Frizzled', 'LRP')  
  
print(signal)
```

OUTPUT < >

```
{'name': 'Wnt', 'pathway': 'Canonical', 'receptors': ('Frizzled', 'LRP')}
```

## ADVANCED TOPIC

Displaying an entire dictionary using the `print()` function can look a little messy because it is not properly structured. There is, however, an external library called `pprint` (Pretty-Print) that behaves in very similar way to the default `print()` function, but structures dictionaries and other arrays in a more presentable way before displaying them. We do not discuss ``Pretty-Print'' in this course, but it is a part of Python's default library and is therefore installed with Python automatically. To learn more it, have a read through the [official documentations](#) for the library and review the [examples](#).

Because the *keys* are immutable, they cannot be altered. However, we can get around this limitation by introducing a new *key* and assigning the *values* of the old *key* to the new one. Once we do that, we can go ahead and *remove* the old *item*. The easiest way to remove an *item* from a dictionary is to use the syntax `del`:

PYTHON < >

```
# Creating a new key and assigning to it the  
# values of the old key:  
protein['human chromosome'] = protein['chromosome']  
  
print(protein)
```

OUTPUT < >

```
{'full name': 'Cystic fibrosis transmembrane conductance regulator', 'alias': 'CFTR', 'gene': 'CFTR', 'type':
```

PYTHON < >

```
# Now we remove the old item from the dictionary:  
del protein['chromosome']  
  
print(protein)
```

OUTPUT < >

```
{'full name': 'Cystic fibrosis transmembrane conductance regulator', 'alias': 'CFTR', 'gene': 'CFTR', 'type':
```

We can simplify the above operation using the `.pop()` method, which removes the specified *key* from a dictionary and returns any *values* associated with it:

PYTHON < >

```
protein['common mutations in caucasians'] = protein.pop('common mutations')  
  
print(protein)
```

OUTPUT < >

```
{'full name': 'Cystic fibrosis transmembrane conductance regulator', 'alias': 'CFTR', 'gene': 'CFTR', 'type':
```

## DO IT YOURSELF

Implement a dictionary as:

PYTHON < >

```
signal = {'name': 'Beta-Galactosidase', 'pdb': '4V40'}
```

with respect to `signal`:

- Change the *key* name from '`pdb`' to '`pdb id`' using the `.pop()` method.
- Write a code to find out whether the dictionary:
  - contains the new *key* (i.e. '`pdb id`').
  - confirm that it no longer contains the old *key* (i.e. '`pdb`')

If both conditions are met, display:

```
Contains the new key, but not the old one.
```

Otherwise:

```
Failed to alter the dictionary.
```

## Solution

PYTHON < >

```
signal = {
    'name': 'Beta-Galactosidase',
    'pdb': '4V40'
}

signal['pdb id'] = signal.pop('pdb')

if 'pdb id' in signal and 'pdb' not in signal:
    print('Contains the new key, but not the old one.')
else:
    print('Failed to alter the dictionary.')
```

OUTPUT < >

```
Contains the new key, but not the old one.
```

## Nested dictionaries

As explained earlier the section, dictionaries are amongst the most powerful built-in tools in Python. It is possible to construct nested dictionaries to organise data in a hierarchical fashion. This useful technique is outlined extensively in [example](#).

It is very easy to implement nested dictionaries:

PYTHON < >

```
# Parent dictionary
pkc_family = {
    # Child dictionary A:
    'conventional': {
        'note': 'Require DAG, Ca2+, and phospholipid for activation.',
        'types': ['alpha', 'beta-1', 'beta-2', 'gamma']
    },
    # Child dictionary B:
    'atypical': {
        'note': (
            'Require neither Ca2+ nor DAG for'
            'activation (require phosphatidyl serine).'
        ),
        'types': ['iota', 'zeta']
    }
}
```

and we follow similar principles to access, alter, or remove the *values* stored in nested dictionaries:

PYTHON < >

```
print(pkc_family)
```

OUTPUT < >

```
{'conventional': {'note': 'Require DAG, Ca2+, and phospholipid for activation.', 'types': ['alpha', 'beta-1']}
```

PYTHON < >

```
print(pkc_family['atypical'])
```

OUTPUT < >

```
{'note': 'Require neither Ca2+ nor DAG for activation (require phosphatidyl serine).', 'types': ['iota', 'zeta']}
```

PYTHON < >

```
print(pkc_family['conventional']['note'])
```

OUTPUT < >

```
Require DAG, Ca2+, and phospholipid for activation.
```

```
print(pkc_family['conventional']['types'])
```

PYTHON < >

```
['alpha', 'beta-1', 'beta-2', 'gamma']
```

OUTPUT < >

```
print(pkc_family['conventional']['types'][2])
```

PYTHON < >

```
beta-2
```

OUTPUT < >

```
apk_types = pkc_family['conventional']['types']
print(apk_types[1])
```

PYTHON < >

```
beta-1
```

OUTPUT < >

### DO IT YOURSELF

Implement the following table of genetic disorders as a nested dictionary:

|                                | Full Name                                           | Gene | Type                               |
|--------------------------------|-----------------------------------------------------|------|------------------------------------|
| <b>Cystic fibrosis</b>         | Cystic fibrosis transmembrane conductance regulator | CFTR | Membrane Protein                   |
| <b>Xeroderma pigmentosum A</b> | DNA repair protein complementing XP-A cells         | XPA  | Nucleotide excision repair         |
| <b>Haemophilia A</b>           | Haemophilia A                                       | F8   | Factor VIII Blood-clotting protein |

Using the dictionary, display the gene for *Haemophilia A*.

Solution

PYTHON < >

```
genetic_diseases = {
    'Cystic fibrosis': {
        'name': 'Cystic fibrosis transmembrane conductance regulator',
        'gene': 'CFTR',
        'type': 'Membrane Protein'
    },
    'Xeroderma pigmentosum A': {
        'name': 'DNA repair protein complementing XP-A cells',
        'gene': 'XPA',
        'type': 'Nucleotide excision repair'
    },
    'Haemophilia A': {
        'name': 'Haemophilia A',
        'gene': 'F8',
        'type': 'Factor VIII Blood-clotting protein'
    }
}

print(genetic_diseases['Haemophilia A']['gene'])
```

OUTPUT < >

F8

## EXAMPLE: NESTED DICTIONARIES IN PRACTICE

We would like to store and analyse the structure of several proteins involved in the *Lac operon*. To do so, we create a Python `dict` to help us organise our data.

We start off by creating an empty dictionary that will store our structures:

```
structures = dict()
```

PYTHON < >

We then move onto depositing our individual entries to `structure` by adding new *items* to it.

Each *item* has a *key* that represents the name of the protein we are depositing, and a *value* that is itself a dictionary consisting of information regarding the structure of that protein:

```
structures['Beta-Galactosidase'] = {
    'pdb id': '4V40',
    'deposit date': '1994-07-18',
    'organism': 'Escherichia coli',
    'method': 'x-ray',
    'resolution': 2.5,
    'authors': (
        'Jacobson, R.H.', 'Zhang, X.',
        'Dubose, R.F.', 'Matthews, B.W.'
    )
}
```

PYTHON < >

```
structures['Lactose Permease'] = {
    'pdb id': '1PV6',
    'deposit date': '2003-06-23',
    'organism': 'Escherichia coli',
    'method': 'x-ray',
    'resolution': 3.5,
    'authors': (
        'Abramson, J.', 'Smirnova, I.', 'Kasho, V.',
        'Verner, G.', 'Kaback, H.R.', 'Iwata, S.'
    )
}
```

PYTHON < >

Dictionaries don't have to be homogeneous. In other words, there can be different *items* in each entry.

For instance, the '`LacY`' protein contains an additional *key* entitled '`note`':

PYTHON < >

```
structures['LacY'] = {  
    'pdb id': '2Y5Y',  
    'deposit date': '2011-01-19',  
    'organism': 'Escherichia coli',  
    'method': 'x-ray',  
    'resolution': 3.38,  
    'note': 'in complex with an affinity inactivator',  
    'authors': (  
        'Chaptal, V.', 'Kwon, S.', 'Sawaya, M.R.',  
        'Guan, L.', 'Kaback, H.R.', 'Abramson, J.'  
    )  
}
```

The variable `structure` which is an instance of type `dict`, is now a nested dictionary:

PYTHON < >

```
print(structures)
```

OUTPUT < >

```
{'Beta-Galactosidase': {'pdb id': '4V40', 'deposit date': '1994-07-18', 'organism': 'Escherichia coli',
```

We know that we can extract information from our nested `dict` just like we would with any other `dict`:

PYTHON < >

```
print(structures['Beta-Galactosidase'])
```

OUTPUT < >

```
{'pdb id': '4V40', 'deposit date': '1994-07-18', 'organism': 'Escherichia coli', 'method': 'x-ray', 'res
```

PYTHON < >

```
print(structures['Beta-Galactosidase']['method'])
```

OUTPUT < >

```
x-ray
```

PYTHON < >

```
print(structures['Beta-Galactosidase']['authors'])
```

OUTPUT < >

```
('Jacobson, R.H.', 'Zhang, X.', 'Dubose, R.F.', 'Matthews, B.W.')
```

PYTHON < >

```
print(structures['Beta-Galactosidase']['authors'][0])
```

OUTPUT < >

```
Jacobson, R.H.
```

Sometimes, especially when creating longer dictionaries, it might be easier to store individual entries in a variable beforehand and add them to the parent dictionary later on.

Note that our parent dictionary in this case is represented by the variable `structure`.

PYTHON < >

```
entry = {
    'Lac Repressor': {
        'pdb id': '1LBI',
        'deposit data': '1996-02-17',
        'organism': 'Escherichia coli',
        'method': 'x-ray',
        'resolution': 2.7,
        'authors': (
            'Lewis, M.', 'Chang, G.', 'Horton, N.C.',
            'Kercher, M.A.', 'Pace, H.C.', 'Lu, P.'
        )
    }
}
```

We can then use the `.update()` method to update our `structures` dictionary:

PYTHON < >

```
structures.update(entry)

print(structures['Lac Repressor'])
```

OUTPUT < >

```
{'pdb id': '1LBI', 'deposit data': '1996-02-17', 'organism': 'Escherichia coli', 'method': 'x-ray', 'res
```

We sometimes need to see what *keys* our dictionary contains. To obtain an array of *keys*, we use the method `.keys()` as follows:

PYTHON < >

```
print(structures.keys())
```

OUTPUT < >

```
dict_keys(['Beta-Galactosidase', 'Lactose Permease', 'LacY', 'Lac Repressor'])
```

Likewise, we can also obtain an array of *values* in a dictionary using the `.values()` method:

PYTHON < >

```
print(structures['LacY'].values())
```

OUTPUT < >

```
dict_values(['2Y5Y', '2011-01-19', 'Escherichia coli', 'x-ray', 3.38, 'in complex with an affinity inact
```

We can then extract specific information to conduct an analysis. Note that the `len()` function in this context returns the number of keys in the parent dictionary only.

PYTHON < >

```
sum_resolutions = 0
res = 'resolution'

sum_resolutions += structures['Beta-Galactosidase'][res]
sum_resolutions += structures['Lactose Permease'][res]
sum_resolutions += structures['Lac Repressor'][res]
sum_resolutions += structures['LacY'][res]

total_entries = len(structures)

average_resolution = sum_resolutions / total_entries

print(average_resolution)
```

OUTPUT < >

```
3.0199999999999996
```

## Useful methods for dictionary

Now we use some snippets to demonstrate some of the useful *methods* associated with `dict` in Python.

Given a dictionary as:

PYTHON < >

```
lac_repressor = {
    'pdb id': '1LBI',
    'deposit data': '1996-02-17',
    'organism': 'Escherichia coli',
    'method': 'x-ray',
    'resolution': 2.7,
}
```

We can create an array of all *items* in the dictionary using the `.items()` method:

```
PYTHON < >  
print(lac_repressor.items())
```

```
OUTPUT < >  
dict_items([('pdb id', '1LBI'), ('deposit data', '1996-02-17'), ('organism', 'Escherichia coli'), ('method',
```

Similar to the `enumerate()` function (discussed in [subsection DIY](#)), the `.items()` method also returns an array of **tuple** members. Each **tuple** itself consists of 2 members, and is structured as `('key': 'value')`. On that account, we can use its output in the context of a `for`-loop as follows:

```
PYTHON < >  
for key, value in lac_repressor.items():  
    print(key, value, sep=' : ')
```

```
OUTPUT < >  
pdb id: 1LBI  
deposit data: 1996-02-17  
organism: Escherichia coli  
method: x-ray  
resolution: 2.7
```

### DO IT YOURSELF

Try `.items()` on a nested **dict** and see how it works.

## Solution

```
nested_dict = {
    'L1-a': {
        'L2-Ka': 'L2_Va',
        'L2-Kb': 'L2_Vb',
    },
    'L1-b': {
        'L2-Kc': 'L2_Vc',
        'L2-Kd': 'L3_Vd'
    },
    'L3-c': 'L3_V'
}

print(nested_dict.items())
```

PYTHON < >

```
dict_items([('L1-a', {'L2-Ka': 'L2_Va', 'L2-Kb': 'L2_Vb'}), ('L1-b', {'L2-Kc': 'L2_Vc', 'L2-Kd': 'L3_Vd'})])
```

OUTPUT < >

We learned earlier that if we ask for a *key* that is not in the `dict`, a `KeyError` will be raised. If we anticipate this, we can handle it using the `.get()` method. The method takes in the *key* and searches the dictionary to find it. If found, the associating *value* is returned. Otherwise, the method returns `None` by default. We can also pass a second value to `.get()` to replace `None` in cases that the requested *key* does not exist:

```
print(lac_repressor['gene'])
```

PYTHON < >

```
Error: KeyError: 'gene'
```

ERROR < >

```
print(lac_repressor.get('gene'))
```

PYTHON < >

```
None
```

OUTPUT < >

```
print(lac_repressor.get('gene', 'Not found...'))
```

PYTHON < >

OUTPUT < >

Not found...

### DO IT YOURSELF

Implement the `lac_repressor` dictionary and try to extract the *values* associated with the following *keys*:

- `organism`
- `authors`
- `subunits`
- `method`

If a key does not exist in the dictionary, display `No entry` instead.

Display the results in the following format:

```
organism: XXX  
authors: XXX
```

### Solution

PYTHON < >

```
lac_repressor = {  
    'pdb id': '1LBI',  
    'deposit data': '1996-02-17',  
    'organism': 'Escherichia coli',  
    'method': 'x-ray',  
    'resolution': 2.7,  
}  
  
requested_keys = ['organism', 'authors', 'subunits', 'method']  
  
for key in requested_keys:  
    lac_repressor.get(key, 'No entry')
```

OUTPUT < >

```
'Escherichia coli'  
'No entry'  
'No entry'  
'x-ray'
```

## for-loop and dictionary

Dictionaries and `for`-loops create a powerful combination. We can leverage the accessibility of dictionary *values* through specific *keys* that we define ourselves in a loop to extract data iteratively and repeatedly.

One of the most useful tools that we can create using nothing more than a `for`-loop and a dictionary, in only a few lines of code, is a sequence converter.

Here, we are essentially iterating through a sequence of DNA nucleotides (`sequence`), extracting one character per loop cycle from our string (`nucleotide`). We then use that character as a *key* to retrieve its corresponding *value* from our a dictionary (`dna2rna`). Once we get the *value*, we add it to the variable that we initialised using an empty string outside the scope of our `for`-loop (`rna_sequence`) as discussed in [subsection](#). At the end of the process, the variable `rna_sequence` will contain a converted version of our sequence.

PYTHON < >

```
sequence = 'CCCATCTTAAGACTTCACAAGACTTGTGAAATCAGACCACTGCTCAATGCGGAACGCCCG'

dna2rna = {"A": "U", "T": "A", "C": "G", "G": "C"}

rna_sequence = str() # Creating an empty string.

for nucleotide in sequence:
    rna_sequence += dna2rna[nucleotide]

print('DNA:', sequence)
print('RNA:', rna_sequence)
```

OUTPUT < >

```
DNA: CCCATCTTAAGACTTCACAAGACTTGTGAAATCAGACCACTGCTCAATGCGGAACGCCCG
RNA: GGGUAGAAUUCUGAAGUGUUUCUGAACACUUUAGUCUGGUGACGAGUUACGCCUUGCGGGC
```

## DO IT YOURSELF

We know that in reverse transcription, RNA nucleotides are converted to their complementary DNA as shown:

| Type | Direction | Nucleotides |
|------|-----------|-------------|
| RNA  | 5'...'    | U A G C     |
| cDNA | 5'...'    | A T C G     |

with that in mind:

1. Use the table to construct a dictionary for reverse transcription, and another dictionary for the conversion of cDNA to DNA.
2. Using the appropriate dictionary, convert the following mRNA (exon) sequence for human G protein-coupled receptor to its cDNA.

PYTHON < >

```
human_gpcr = (
    'AUGGAUGUGACUUCCCAAGCCCCGGGCGUGGGCCUGGAGAUGUACCCAGGCACCGCGCAGCCUGCGGCCAACACCACUC '
    'CCCCGAGCUAACCUCCCACCGCUCCUGGGCACCGCCUGGCCAACUUGGGACAGGUGAGCUCUCGGAGCACCGAGCAGUACG '
    'UGAUCGGCCUGUUCUCUCUGGCCUACACCAUCUUCUCCUUCUCCCCAUCGGUUUGUGGGCAACAUCCUGAUCCUGGUGGUG '
    'AACAUCAUCGUUCCCGAGAAAGAUGACCAUCCCGACCUGUACUCAUCAACCUGCGGUGGGACCUCAUCCUGGUGGCCGA '
    'CUCCCUCAUUGAGGUGUUCAACCUGCACGAGCGGUACUACGACAUCGCCUCCUGUGCACCUUCAUGUGCGCUCUCCUGGUGG '
    'UCAACAUGUACAGCAGCGUUCUUCUCACCUGGAUGAGCUUCGACCGCUACAUCCGGCCUGGGCAAGGGCCAUGCGCUGCAGC '
    'CUGUCCCGCACCAGCACCACGCCGGCUGAGCUGGGCCUACUCUGGAUGGCAUCCGUGUCAGCCACGCUGGUGGCCUUCAC '
    'CGCCGUGCACCGCAGCACACCGACGAGGCCUGCUUCUGUUUCGCGGAUGUCCGGAGGUGCAGUGGCUCGAGGUACCGCUGG '
    'GCUUCAUCGUCCCCUUCGCCAUCAUCGCCUUGCUACUCCCUCAUUGUCCGGUGCUGGUCCAGGGCGCACCGGACCGUGGG '
    'CUGCGGCCCCGGCGAGAAGGCGCUCCGCAUGAUCCUCCGGUGGUCCUUCUGUCUGCUGGUCCUGGGAGAACGU '
    'CUUCAUCAGCGUGCACCUCCUGCAGCGGACGCCAGCCUUGGGCCUCCUCAAGCAGCUUUCGCCAACGCCACCCCUA '
    'CGGGCCACAUUGUCAACCUCACGCCUUCUCCAAACAGCUGCCUAACCCCUCAUCUACAGCUUUCUGGGAGGACCUUCAGG '
    'GACAAGCUGAGGCUGUACAUUGAGCAGAAAACAAAUUUGCCGGCCUAGAACCGCUUCUGUCACGCUGCCUAGAAGGCGUCAU '
    'UCCAGACAGCACCGAGCAGUCGGGAUGUGAGGUUCAGCAGUGCCGUG '
)
```

## Solution

PYTHON < >

```
mrna2cdna = {  
    'U': 'A',  
    'A': 'T',  
    'G': 'C',  
    'C': 'G'  
}  
  
cdna2dna = {  
    'A': 'T',  
    'T': 'A',  
    'C': 'G',  
    'G': 'C'  
}
```

## Q2

PYTHON < >

```
cdna = str()  
for nucleotide in human_gpcr:  
    cdna += mrna2cdna[nucleotide]  
  
print(cdna)
```

OUTPUT < >

```
TACCTACACTGAAGGGTTCGGGCCCCGCACCCGGACCTCTACATGGGTCCGTGGCGCGTCGGACGCCGGGGTTGTGGTGGAGGGGGCTCGAGTTGGACAGGGT
```

## Summary

In this section we talked about dictionaries, which are one the most powerful built-in types in Python. We learned:

- how to create dictionaries in Python,
- methods to alter or manipulate normal and nested dictionaries,
- two different techniques for changing an existing key,
- examples on how dictionaries help us organise our data and retrieve them when needed,

Finally, we also learned that we can create an *iterable* (discussed in [section](#)) from dictionary *keys* or *values* using the `.key()`, the `.values()`, or the `.items()` methods.

## Exercises

## END OF CHAPTER EXERCISES

We know that the process of protein translation starts by transcribing a gene from DNA to RNA *nucleotides*, followed by translating the RNA *codons* to protein.

Conventionally, we write a DNA sequence from the **5'**-end to the **3'**-end. The transcription process, however, starts from the **3'**-end of a gene to the **5'**-end (anti-sense strand), resulting in a sense mRNA sequence complementing the sense DNA strand. This is because RNA polymerase can only add nucleotides to the **3'**-end of the growing mRNA chain, which eliminates the need for the [Okazaki fragments](#) as seen in DNA replication.

**Example:** The DNA sequence ATGTCTAA is transcribed into AUGUCUAAA.

Given a conversion table:

| DNA  | A | T | C | G |
|------|---|---|---|---|
| cDNA | T | A | G | C |
| RNA  | A | U | C | G |

and this **5'- to 3'-end** DNA sequence of 717 nucleotides for the [Green Fluorescent Protein \(GFP\)](#) mutant 3 extracted from [Aequorea victoria](#):

PYTHON < >

```
python> dna_sequence = (  
'ATGTCTAAAGGTGAAGAATTATTCACTGGTGTGCCAATTTGGTGAATTAGATGGTATGTTAATGGT'  
'CACAAATTTCTGTCCTCCGGTGAAGGTGAAGGTGATGCTACTTACGGTAAATTGACCTTAAATTATTGCT'  
'ACTACTGGTAAATTGCCAGTTCCATGCCAACCTTAGTCACTACTTCGGTTATGGTGTCAATGTTGCT'  
'AGATACCCAGATCATATGAAACAACATGACTTTCAAGTCTGCATGCCAGAAGGTTATGTTCAAGAAAGA'  
'ACTATTTTTCAAAGATGACGTAACTACAAGACCAGAGCTGAAGTCAGTTGAAGGTGATACTTAGTT'  
'AATAGAATCGAATTAAGGTATTGATTTAAAGAAGATGGTAACTTTAGGTACAAATTGGAATACAAC'  
'TATAACTCTCACAATGTTACATCATGGCTGACAACAAAAGAATGGTATCAAAGTAACTTCAAATTAGA'  
'CACACACATTGAAGATGGTTCTGTTCAATTAGCTGACCATTATCAACAAAATCTCAATTGGTATGGTCCA'  
'GTCTTGTACCGACAACCATTACTTATCCACTCAATGCTGCCATTCAAAAGATCCAAACGAAAAGAGAGAC'  
'CACATGGTCTTGTAGAATTGTTACTGCTGGTATTACCCATGGTATGGTACAATGAAATTGTACAATCAA'  
)
```

Use the DNA sequence and the conversion table to:

1. Write a Python script to *transcribe* this sequence to mRNA as it occurs in a biological organism. That is, determine the complimentary DNA first, and use that to work out the mRNA.
2. Use the following dictionary in a Python script to obtain the translation (protein sequence) of the Green Fluorescent Protein using the mRNA sequence you obtained.

```
codon2aa = {  
    "UUU": "F", "UUC": "F", "UUA": "L", "UUG": "L", "CUU": "L",  
    "CUC": "L", "CUA": "L", "CUG": "L", "AUU": "I", "AUC": "I",  
    "AUA": "I", "GUU": "V", "GUC": "V", "GUA": "V", "GUG": "V",  
    "UCU": "S", "UCC": "S", "UCA": "S", "UCG": "S", "AGU": "S",  
    "AGC": "S", "CCU": "P", "CCC": "P", "CCA": "P", "CCG": "P",  
    "ACU": "T", "ACC": "T", "ACA": "T", "ACG": "T", "GCU": "A",  
    "GCC": "A", "GCA": "A", "GCG": "A", "UAU": "Y", "UAC": "Y",  
    "CAU": "H", "CAC": "H", "CAA": "Q", "CAG": "Q", "AAU": "N",  
    "AAC": "N", "AAA": "K", "AAG": "K", "GAU": "D", "GAC": "D",  
    "GAA": "E", "GAG": "E", "UGU": "C", "UGC": "C", "UGG": "W",  
    "CGU": "R", "CGC": "R", "CGA": "R", "CGG": "R", "AGA": "R",  
    "AGG": "R", "GGU": "G", "GGC": "G", "GGA": "G", "GGG": "G",  
    "AUG": "<Met>", "UAA": "<STOP>", "UAG": "<STOP>", "UGA": "<STOP>"  
}
```

Solution

# Q1

PYTHON < >

```
dna_sequence = (
    'ATGCTAAAGGTGAAGAATTATTCACTGGTGTGCCAATTTGGTTGAATTAGATGGTGATGTTAATGGT'
    'CACAAATTCTGTCTCCGGTGAAGGTGAAGGTGATGCTACTTACGGTAAATTGACCTTAAATTATTTGCT'
    'ACTACTGGTAAATTGCCAGTTCATGCCAACCTTAGTCACTACTTCGGTTATGGTGTCAATGTTGCT'
    'AGATACCCAGATCATATGAAACAACATGACTTTCAAGTCTGCCATGCCAGAAGGTATGTTCAAGAAAGA'
    'ACTATTTTTCAAAGATGACGTTAECTACAAGACCAGAGCTGAAGTCAAGTTGAAGGTGATACTTAGTT'
    'AATAGAATCGAATTAAAGGTATTGATTTAAAAGAGATGGTACATTTAGGTACAATTGGAATACAAC'
    'TATAACTCTCACAATGTTACATGGCTGACAAACAAAAGATGGTATCAAAGTTAACATTAGA'
    'CACAAACATTGAAGATGGTCTGTTCAATTAGCTGACCATTATCAACAAAATCTCAATTGGTATGGTCCA'
    'GTCTTGTACAGACAACCATTACTTATCCACTCAATGCCATTCCAAAGATCCAAACGAAAAGAGAGAC'
    'CACATGGTCTTGTAGAATTGTTACTGCTGGTATTACCATGGTATGGATGAATTGTACAATAA'
)
codon2aa = {
    "UUU": "F", "UUC": "F", "UUA": "L", "UUG": "L", "CUU": "L",
    "CUC": "L", "CUA": "L", "CUG": "L", "AUU": "I", "AUC": "I",
    "AUA": "I", "GUU": "V", "GUC": "V", "GUA": "V", "GUG": "V",
    "UCU": "S", "UCC": "S", "UCA": "S", "UCG": "S", "AGU": "S",
    "AGC": "S", "CCU": "P", "CCC": "P", "CCA": "P", "CCG": "P",
    "ACU": "T", "ACC": "T", "ACA": "T", "ACG": "T", "GCU": "A",
    "GCC": "A", "GCA": "A", "GCG": "A", "UAU": "Y", "UAC": "Y",
    "CAU": "H", "CAC": "H", "CAA": "Q", "CAG": "Q", "AAU": "N",
    "AAC": "N", "AAA": "K", "AAG": "K", "GAU": "D", "GAC": "D",
    "GAA": "E", "GAG": "E", "UGU": "C", "UGC": "C", "UGG": "W",
    "CGU": "R", "CGC": "R", "CGA": "R", "CGG": "R", "AGA": "R",
    "AGG": "R", "GGU": "G", "GGC": "G", "GGA": "G", "GGG": "G",
    "AUG": "<Met>", "UAA": "<STOP>", "UAG": "<STOP>", "UGA": "<STOP>"
}
dna2cdna = {
    'A': 'T',
    'C': 'G',
    'G': 'C',
    'T': 'A'
}
dna2mrna = {
    'A': 'U',
    'T': 'A',
    'G': 'C',
    'C': 'G'
}
# Transcription
# -----
m_rna = str()
for nucleotide in dna_sequence:
    # DNA to cDNA
    c_dna = dna2cdna[nucleotide]
    # cDNA to mRNA
    m_rna += dna2mrna[c_dna]
```

```
print('mRNA:', m_rna)

# Translation:
# -----
```

OUTPUT < >

```
mRNA: AUGUCUAAAGGUGAAGAAUUUAUCACUGGUGUUGUCCAAUUUUGGUUGAAUAGAUGGUGAUGGUAAUGGUACACAAAUUUUCUGUCUCGGGUAAAGC
```

```
mrna_len = len(m_rna)
codon_len = 3

protein = str()

for index in range(0, mrna_len, codon_len):
    codon = m_rna[index: index + codon_len]
    protein += codon2aa[codon]

print('Protein:', protein)

# -----
# INTERMEDIATE-LEVEL TWIST (Alternative answer):
# One can also combine the two processes.
#
# Advantages:
#   - One for-loop.
#   - No use of `range()` .
#   - Almost twice as fast (half as many iterations).
# -----
```

PYTHON < >

```
Protein: <Met>SKGEELFTGVVPILVLDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTFGYGVQCFARYPDH<Met>KQHDFFKSA
```

PYTHON < >

```
m_rna = str()
protein = str()
codon = str()

for nucleotide in dna_sequence:
    # DNA to cDNA
    c_dna = dna2cdna[nucleotide]

    # Transcription:
    transcribed_nucleotide = dna2mrna[c_dna]
    m_rna += transcribed_nucleotide

    # Translation process:
    # Retaining the residue to construct triplets.
    codon += transcribed_nucleotide

    # Check if this is a triplet (a codon):
    if len(codon) == 3:
        # Convert to amino acid and store:
        protein += codon2aa[codon]

        # Reset the codon to an empty string:
        codon = str()
print('mRNA:', m_rna)
```

OUTPUT < >

```
mRNA: AUGUCUAAAGGUGAAGAAUUUAUUCACUGGUGUUGUCCCAAUUUUGGUUGAAUAGAUGGUGAUGUUAUGGUACAAAAUUUCUGUCUCGGUGAACG
```

PYTHON < >

```
print('Protein:', protein)
```

OUTPUT < >

```
Protein: <Met>SKGEELFTGVVPILVLDGDVNGHKFSVSGEGEGDATYGKLTLKFICTTGKLPVPWPTLVTTFGYGVQCFARYPDH<Met>KQHDFFKSA
```

## KEYPOINTS

- Dictionaries associate a set of *values* with a number of *keys*.
- *keys* are used to access the values of a dictionary.
- Dictionaries are mutable.
- Nested dictionaries are constructed to organise data in a hierarchical fashion.
- Some of the useful methods to work with dictionaries are: `.items()`, `.get()`

Content from [Functions](#)

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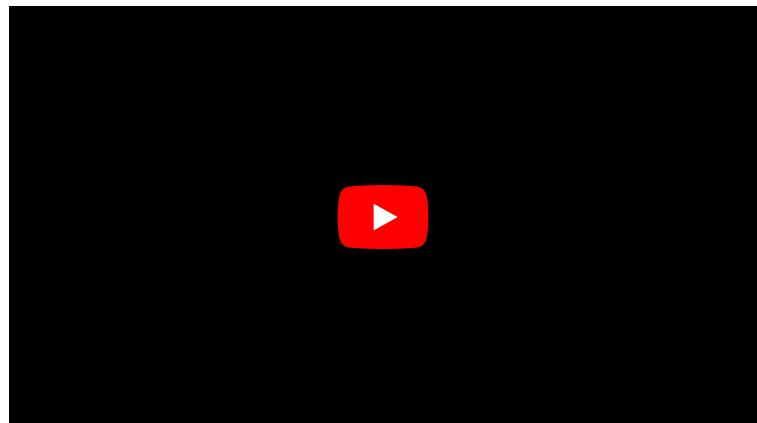
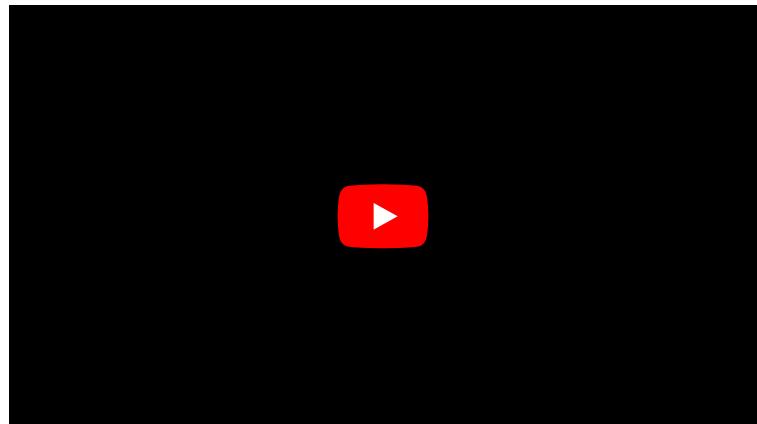
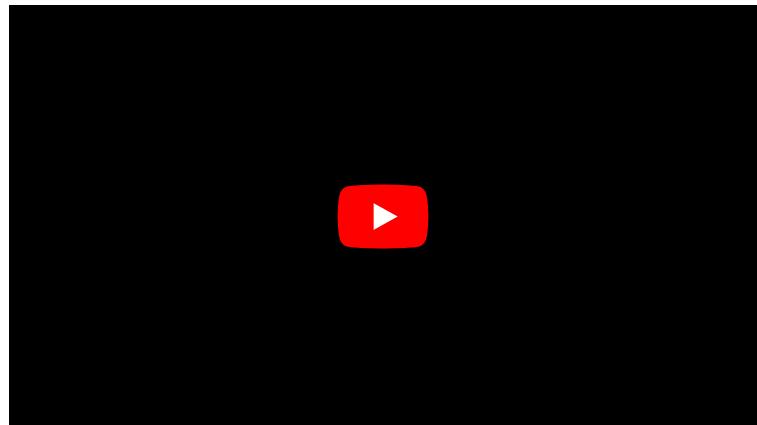
## OVERVIEW

### Questions

- 
- What are functions?
  - How are functions created?
  - What are optional arguments?
  - What makes functions powerful?
- 

### Objectives

- Develop concepts of using functions.
- Understanding different ways of creating functions.
- Explaining input arguments.
- Understanding the inter-connectivity of functions.



This chapter assumes that you are familiar with the following concepts in Python 3:

## PREREQ

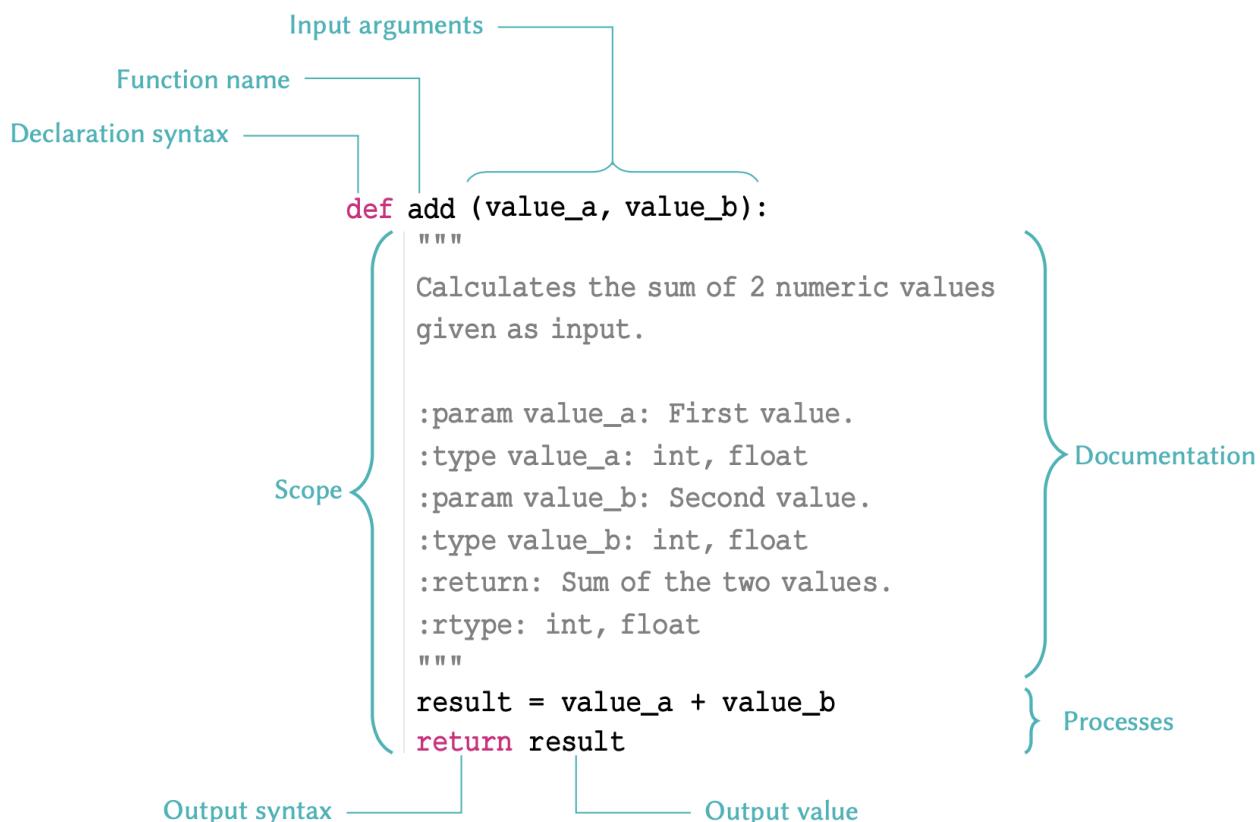
- Mathematical Operation
- Indentation Rule
- Conditional Statements
- Arrays
- Loops and Iterations

# Functions

## Defining Functions

In programming, functions are containers that incorporate some code and perform very specific tasks. As we learned in the first chapter (on [outputs](#)), a function usually takes in one or several variables or values, processes them, and produces a specific result. The variable(s) given to a function and those produced by it are referred to as *input arguments*, and *outputs* respectively.

There are different ways to create functions in Python. In this course, we will be using `def` to implement our functions. This is the easiest and by far the most common method for declaring functions. The structure of a typical function defined using `def` is as follows:



## REMEMBER

There are several points to remember in relation to functions:

- The name of a function follows same principles as that of any other variable as discussed in [variable names](#). The name must be in *lower-case* characters.
- The input arguments of a function — e.g. `value_a` and `value_b` in the above example; are essentially variables whose *scope* is the function. That is, they are *only* accessible *within* the function itself, and not from anywhere else in the code.
- Variables defined inside of a function, should *never* use the same name as variables defined outside of it; or they may override each other.
- A function declared using `def` should *always* be terminated with a `return` syntax. Any values or variables that follow `return` are regarded as the function's output.
- If we do not specify a return value, or fail to terminate a function using `return` altogether, the Python interpreter will automatically terminate that function with an implicit `return None`. Being an *implicit* process, this is generally regarded as a bad practice and should be avoided.

We implement functions to prevent repetition in our code. It is therefore important for a function to *only* perform a very specific task, so that it can be context-independent. You should therefore avoid incorporating separable tasks inside a single function.

## INTERESTING FACT

Functions are designed to perform specific tasks. That is why in the majority of cases, they are named using *verbs* — e.g. `add()` or `print()`. We use verbs to describe an action, a state, or an occurrence in everyday language. Likewise, this type of nomenclature describes the action performed by a specific function. Name your functions wisely!

Once you start creating functions for different purposes; after a while, you will have a library of ready-to-use functions to address different needs. This is the primary principle of a popular programming paradigm known as [functional programming](#).

So let us implement the example outline in the diagram:

```
def add(value_a, value_b):  
    """  
    Calculates the sum of 2 numeric values  
    given as inputs.  
  
    :param value_a: First value.  
    :type value_a: int, float  
    :param value_b: Second value.  
    :type value_b: int, float  
    :return: Sum of the two values.  
    :rtype: int, float  
    """  
  
    result = value_a + value_b  
    return result
```

PYTHON < >

Once implemented, we can go ahead use the function. We can do so in the same way as we do with the *built-in* functions such as `max()` or `print()`:

```
PYTHON < >  
res = add(2, 5)  
  
print(res)
```

```
OUTPUT < >  
7
```

### REMEMBER

When calling a function, we should always pass our *positional input arguments* in the order they are defined in the function definition, from left to right.

This is because in the case of *positional arguments*, as the name suggests, the Python interpreter relies on the *position* of each value to identify its *variable name* in the function signature. The function signature for our `add` function is as follows:

```
add(value_a, value_b)
```

So in the above example where we say `add(2, 5)`, the value `2` is identified as the *input argument* for `value_a`, and not `value_b`. This happens automatically because in our function call, the value `2` is written in the first position, where `value_a` is defined in our function declaration (signature).

Alternatively, we can use the name of each *input argument* to pass values onto them in any order. When we use the name of the *input argument* explicitly, we pass the values as *keyword arguments*. This is particularly useful in more complex functions where there are several *input arguments*.

Let us now use *keyword arguments* to pass values to our `add()` function:

```
PYTHON < >  
res = add(value_a=2, value_b=5)  
  
print(res)
```

```
OUTPUT < >  
7
```

Now even if we changed the order of our arguments, the function would still be able to associate the values correctly:

PYTHON < >

```
res = add(value_b=2, value_a=5)  
print(res)
```

OUTPUT < >

7

## REMEMBER

Choose the order of your *input argument* wisely. This is important when your function accepts multiple *input argument*.

Suppose we want to define a “division” function. It makes sense to assume that the first number passed to the function will be divided by the second number:

```
PYTHON < >  
def divide(a, b):  
    return a / b
```

It is also much less likely for someone to use *keywords* to pass arguments to this function – that is, to say:

```
PYTHON < >  
result = divide(a=2, b=4)
```

than it is for them to use positional arguments (without any keywords), that is:

```
PYTHON < >  
result = divide(2, 4)
```

But if we use an arbitrary order, then we risk running into problems:

```
PYTHON < >  
def divide_bad(denominator, numerator):  
    return numerator / denominator
```

In which case, our function would perform perfectly well if we use *keyword arguments*; however, if we rely on positional arguments and common sense, then the result of the division would be calculated incorrectly.

```
PYTHON < >  
result_a = divide_bad(numerator=2, denominator=4)  
result_b = divide_bad(2, 4)  
  
print(result_a == result_b)
```

```
OUTPUT < >  
False
```

## DO IT YOURSELF

Implement a function called `find_tata` that takes in one `str` argument called `seq` and looks for the `TATA`-box motif inside that sequence. Then:

- if found, the function should return the index for the `TATA`-box as output;
- if not found, the function should *explicitly* return `None`.

### Example:

The function should behave as follows:

```
sequence = 'GCAGTGTATAGTC'  
res = find_tata(sequence)
```

### Solution

```
PYTHON < >  
  
def find_tata(seq):  
    tata_box = 'TATA'  
    result = seq.find(tata_box)  
  
    return result
```

## Documentations

It is *essential* to write short, but proper documentation for our functions. There is no *correct* way document a code. However, a general rule, a good documentation should tell us:

- what a function does;
- the names of the input arguments, and what type each argument should be;
- the output, and its type.

The documentation string, also known as the *docstring*, is always written inside triple quotation marks. The *docstring* must be the implemented on the *very first line* following the declaration of the function to be recognised as the documentation:

PYTHON < >

```
def add(value_a, value_b):
    """
    Calculates the sum of 2 numeric values
    given as inputs.

    :param value_a: First value.
    :type value_a: int, float
    :param value_b: Second value.
    :type value_b: int, float
    :return: Sum of the two values.
    :rtype: int, float
    """

    result = value_a + value_b
    return result
```

### REMEMBER

You might feel as though you would remember what your own functions do. That, however, is scarcely the case. Functions that we implement tend to perform specialist, and at times, very complex and interconnected processes. Whilst you might remember what a specific function does for a few days after writing it, you would almost certainly have trouble remembering the details in a matter of months. And that is not even considering details regarding the type of the input argument(s) and those of the output. In addition, programmers often share their works with other fellow programmers; be it with their team, or in the context of a publication, or in public repositories as a contribution to the community. Whatever the reason, there is one golden rule: a functionality does not exist unless it is documented.

Writing the *docstring* on the first line is important because once a function is documented; we can use `help()`, which is a built-in function, to access the documentations as follows:

```
help(add)
```

PYTHON < >

```
Help on function add in module __main__:

add(value_a, value_b)
    Calculates the sum of 2 numeric values
    given as inputs.

    :param value_a: First value.
    :type value_a: int, float
    :param value_b: Second value.
    :type value_b: int, float
    :return: Sum of the two values.
    :rtype: int, float
```

OUTPUT < >

For very simple functions – e.g. the function `add()` that we implemented above, where it is fairly obvious what are the input and output arguments and their respective types; it is okay to simplify the *docstring* to something explicit and concise, such as follows:

PYTHON < >

```
def add(value_a, value_b):
    """value_a + value_b -> number"""
    result = value_a + value_b
    return result
```

PYTHON < >

```
help(add)
```

OUTPUT < >

```
Help on function add in module __main__:

add(value_a, value_b)
    value_a + value_b -> number
```

### DO IT YOURSELF

Re-implement the function you defined in the previous [Do it Yourself](#) with appropriate documentations.

### Solution

PYTHON < >

```
def find_tata(seq):
    """
    Finds the location of the TATA-box,
    if one exists, in a polynucleotide
    sequence.

    :param seq: Polynucleotide sequence.
    :type seq: str
    :return: Start of the TATA-box.
    :rtype: int
    """
    tata_box = 'TATA'
    result = seq.find(tata_box)

    return result
```

## Optional arguments

We already know that most functions take in one or more input arguments. Sometime a function does not need all of the arguments to perform a specific task.

An example we have already worked with is `print()`. We already know that this function may be utilised to display text on the screen. However, we also know that if we use the `file` argument, it will behave differently in that it will write the text inside a file instead of displaying it on the screen. Additionally, `print()` has other arguments such as `sep` or `end`, which have specific default values of '' (a single space) and \n (a linebreak) respectively.

## REMEMBER

Input arguments that are necessary to call a specific function are referred to as *non-default arguments*. Those whose definition is not mandatory for a function to be called are known as *default* or *optional arguments*.

Optional arguments may *only* be defined *after* non-default arguments (if any). If this order is not respected, a `SyntaxError` will be raised.

## ADVANCED TOPIC

The default value defined for *optional arguments* can in theory be an instance of any type in Python. However, it is better and safer to only use *immutable* types as demonstrated in [Table](#) for default values. The rationale behind this principle is beyond the scope of this course, but you can read more about it in the [official documentations](#).

To define functions with optional arguments, we need to assign to them a default value. Remember that input arguments are variables with a specific scope. As a result, we can treat our input argument as variables and assign them a value:

PYTHON < >

```
def prepare_seq(seq, name, upper=False):
    """
    Prepares a sequence to be displayed.

    :param seq: Sequence
    :type seq: str
    :param name: Name of the sequence.
    :type name: str
    :param upper: Convert sequence to uppercase characters (default: False)
    :type upper: bool
    :return: Formated string containing the sequence.
    :rtype: str
    """
    template = 'The sequence of {} is: {}'

    if not upper:
        response = template.format(name, seq)
    else:
        seq_upper = seq.upper()
        response = template.format(name, seq_upper)

    return response
```

Now if we don't explicitly define `upper` when calling `prepare_seq()`, its value is automatically considered to be `False`:

PYTHON < >

```
sequence = 'TagCtGC'

prepped = prepare_seq(sequence, 'DNA')

print(prepped)
```

OUTPUT < >

The sequence of DNA is: TagCtGC

If we change the default value of `False` for `upper` and set to `True`, our sequence should be converted to upper case characters:

PYTHON < >

```
prepped = prepare_seq(sequence, 'DNA', upper=True)

print(prepped)
```

OUTPUT < >

The sequence of DNA is: TAGCTGC

### DO IT YOURSELF

Modify the function from previous [Do it Yourself](#) to accept an *optional argument* called `upper`, with default value of `False`; thereafter:

- if `upper` is `False`, then the function should perform as it already does (similar to previous [Do it Yourself](#));
- if `upper` is `True`, then the function should convert the sequence onto uppercase characters before it looks for the `TATA`-box.

Do not forget to update the *docstring* of your function.

## Solution

PYTHON < >

```
def find_tata(seq, upper=False):
    """
    Finds the location of the TATA-box,
    if one exists, in a polynucleotide
    sequence.

    :param seq: Polynucleotide sequence.
    :type seq: str
    :param upper: Whether or not to
    homogenise the sequence
    to upper-case characters.
    :type upper: bool
    :return: Start of the TATA-box.
    :rtype: int
    """
    tata_box = 'TATA'

    if not upper:
        result = seq.find(tata_box)
    else:
        seq_prep = seq.upper()
        result = seq_prep.find(tata_box)

    return result
```

## REMEMBER

It is not necessary to implement your functions in this way. It is, however, a very common practice amongst programmers of any language. For that reason, you should be at least familiar with the technique as you are bound to encounter it sooner rather later.

It is possible to have more than one `return` in a function. This is useful when we need to account for different outcomes; such as the one we saw in the previous example with `prepare_seq()`.

This means that we can simplify the process as follows:

PYTHON < >

```
def prepare_seq(seq, name, upper=False):
    """
    Prepares a sequence to be displayed.

    :param seq: Sequence
    :type seq: str
    :param name: Name of the sequence.
    :type name: str
    :param upper: Convert sequence to uppercase characters (default: False)
    :type upper: bool
    :return: Formated string containing the sequence.
    :rtype: str
    """
    template = 'The sequence of {} is: {}'

    if not upper:
        return template.format(name, seq)

    seq_upper = seq.upper()
    return template.format(name, seq_upper)
```

Notice that we got rid of `response`. Here is a description of what happens:

- In this context, if the conditional statement holds — i.e. when `upper` is `False`, we enter the `if` block. In that case, we reach the first `return` statement. At this point, the function returns the corresponding results and terminates immediately.
- On the other hand, if the condition does not hold — i.e. where `upper` is `True`, we skip the `if` block altogether and proceed. It is only then that we arrive at the second `return` statement where the alternative set of results are prepared.

This does not alter the functionality of our function in any way. However, in complex functions that may be called repetitively (e.g. inside `for` loop), this technique may improve the performance of the function.

Now if we call our function, it will behave in exactly the same way as it did before:

```
sequence = 'TagCtGC'

prepped = prepare_seq(sequence, 'DNA')

print(prepped)
```

PYTHON < >

```
The sequence of DNA is: TagCtGC
```

OUTPUT < >

```
prepped = prepare_seq(sequence, 'DNA', upper=True)

print(prepped)
```

PYTHON < >

OUTPUT < >

The sequence of DNA is: TAGCTGC

## Interconnectivity of functions

Functions can call other functions. This is what makes them extremely powerful tools that may be utilised to address an unlimited number of problems.

This allows us to devise a network of functions that call each other to perform different tasks at different times, and collectively contribute to the production of one final answer.

### REMEMBER

Functions must have specialist functionalities. They should, as much as possible, be implemented to perform one task, and one task only.

So if you need to get more things done, do not write more code in one function. This would defy the purpose of functional programming. Instead, consider writing more functions that contain less code and perform more specialist functionalities.

## EXAMPLE: A MINI TOOLBOX FOR STATISTICS

Suppose we want to calculate the variance of an array of numbers. This is a generalisable task, which means that we could, and should write a function that is able to calculate the variance of *any* array of numbers.

We start off by breaking down the process of calculating the variance, which we know is defined as follows:

$$\sigma^2 = \frac{\sum_{i=1}^n (x_i - \mu)^2}{n}$$

which breaks down into:

1. calculating the mean or  $\mu$ ,
2. using the mean to calculate the numerator,
3. dividing the numerator by the length of the array.

At least one of these processes is not unique to the calculation of variance; and that is the process by which we work out the *mean*. To that end, we should separate this calculation from our *variance* function, and define it independently:

PYTHON < >

```
def mean(arr):
    """
    Calculates the mean of an array.

    :param arr: Array of numbers.
    :type arr: list, tuple, set
    :return: Mean of the values in the array.
    :rtype: float
    """
    summation = sum(arr)
    length = len(arr)

    result = summation / length

    return result
```

Now that we have function to calculate the *mean*, we can go ahead and write a function to calculate the variance, which itself relies on *mean*.

PYTHON < >

```
def variance(arr):
    """
    Calculates the variance of an array.

    :param arr: Array of numbers.
    :type arr: list, tuple, set
    :return: Variance of the values in the array.
    :rtype: float
    """
    arr_mean = mean(arr)
    denominator = len(arr)

    numerator = 0

    for num in arr:
        numerator += (num - arr_mean) ** 2

    result = numerator / denominator

    return result
```

Now we have two functions, which we can use to calculate the *variance* or the *mean* for any array of numbers.

Remember that testing a function a crucial part of its design. So let us go ahead and test our functions:

PYTHON < >

```
numbers = [1, 5, 0, 14.2, -23.344, 945.23, 3.5e-2]
```

PYTHON < >

```
numbers_mean = mean(numbers)

print(numbers_mean)
```

OUTPUT < >

```
134.58871428571427
```

PYTHON < >

```
numbers_variance = variance(numbers)

print(numbers_variance)
```

OUTPUT < >

```
109633.35462420408
```

Now that we have a function to calculate the *variance*, we could easily go on to calculate the *standard deviation*, too.

The standard deviation is calculated from the square root of variance. We can easily implement this in a new function as follows:

PYTHON < >

```
def stan_dev(arr):
    """
    Calculates the standard deviation of an array.

    :param arr: Array of numbers.
    :type arr: list, tuple, set
    :return: Standard deviation of the values in the array.
    :rtype: float
    """
    from math import sqrt

    var = variance(arr)

    result = sqrt(var)

    return result
```

Now let's see how it works in practice:

PYTHON < >

```
numbers_std = stan_dev(numbers)

print(numbers_std)
```

OUTPUT < >

```
331.1092789762982
```

## DO IT YOURSELF

Write a function that given an array of any values, produces a dictionary containing the value of that array as *keys*, and the count of the values in the original array (their frequencies) as *values*.

**Example:**

For the following array:

PYTHON < >

```
values = [1, 1.3, 1, 1, 5, 5, 1.3, 'text', 'text', 'something']
```

the function should return the above dictionary:

**Suggestion:** You can add this as a new tool to the statistics mini toolbox.

## Solution

PYTHON < >

```
def count_values(arr):
    """
    Converts an array into a dictionary of
    the unique members (as keys) and their
    counts (as values).

    :param arr: Array containing repeated
               members.
    :type arr: list, tuple
    :return: Dictionary of unique members
             with counts.
    :rtype: dict
    """
    unique = set(arr)
    arr_list = list(arr)

    result = dict()

    for num in unique:
        result[num] = arr_list.count(num)

    return result
```

## Exercises

---

## END OF CHAPTER EXERCISES

Write a function with the following features:

- Call the function `get_basic_stats()` and let it take one input argument which, however, may contain any number of input arrays, *e.g.* a tuple of arrays.
- Using a for loop, for each of the arrays calculate the mean and the variance using the functions 'mean' and 'variance' given above, *i.e.* call those functions from within the function `get_basic_stats()`.
- Calculate the standard deviation for each array as the square root of the variance. You will have to import the function `sqrt` from module `math`.
- Return a single array containing (in that order) the mean, the variance, and the standard deviation for each array.

To test the function, combine three arrays in a tuple as follows:

PYTHON < >

```
my_arrays = (
    [1, 2, 3, 4, 5],
    [7, 7, 7, 7],
    [1.0, 0.9, 1.2, 1.12, 0.95, 0.76],
)
```

Call the function `get_basic_stats()` with this tuple as argument and write the output to a variable. Display the results in the following form:

```
STD of array' index, ':' STD
```

The result for the above arrays should be:

```
STD of array 0 : 1.4142135623730951
STD of array 1 : 0.0
STD of array 2 : 0.14357537702854514
```

Solution

```
def mean(arr):
    """
    Calculates the mean of an array.
    :param arr: Array of numbers.
    :type arr: list, tuple, set
    :return: Mean of the values in the array. :rtype: float
    """

    summation = sum(arr)

    length = len(arr)

    result = summation / length

    return result


def variance(arr):
    """
    Calculates the variance of an array.
    :param arr: Array of numbers.
    :type arr: list, tuple, set
    :return: Variance of the values in the array.
    :rtype: float
    """

    arr_mean = mean(arr)

    denominator = len(arr)

    numerator = 0

    for num in arr:

        numerator += (num - arr_mean) ** 2

    result = numerator / denominator

    return result


def get_basic_stats(arrays):
    """
    Calculates the mean, variance and standard deviation for
    a set of arrays.
    :param arrays: An array contain any number of arrays of numbers.
    :type arrays: list, tuple
    :return: A list of arrays containing the mean, variance and
    standard deviation for each item in arrays
    :rtype: list
    """

    from math import sqrt

    results = list()

    for array in arrays:
```

```

arr_mean = mean(array)
arr_var = variance(array)
arr_std = sqrt(arr_var)

results.append((arr_mean, arr_var, arr_std))

return results

my_arrays = ([1, 2, 3, 4, 5],
             [7, 7, 7, 7],
             [1.0, 0.9, 1.2, 1.12, 0.95, 0.76],
             )

```

my\_results = get\_basic\_stats(my\_arrays)

```

for index, result in enumerate(my_results):
    print('STD of array', index, ': ', result[2])

```

OUTPUT < >

```

STD of array 0 : 1.4142135623730951
STD of array 1 : 0.0
STD of array 2 : 0.14357537702854514

```

## KEYPOINTS

- Functions make repetitive tasks efficient.
- Keyword **def** is used to create a function.
- Optional arguments does not require prior definition.
- Inter-connectivity of functions make them very powerful.