

# Scientific Programming

## Practical 2

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### Introduction

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# Modules and Objects

Modules are text files with .py extension

```
python3 exercisel.py
```

Import modules to use them

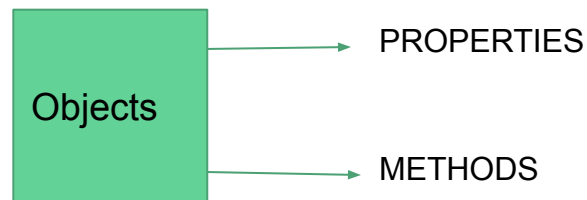
```
import math  
  
A = math.sqrt(4)  
print(A)
```

```
2.0
```

## Objects

“**Objects** are Python’s abstraction for data. All data in a Python program is represented by **objects** or by **relations between objects**.”

**More on this later on in the course**

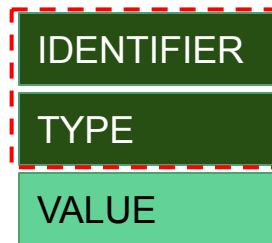


# Modules and Objects

## Objects

“**Objects** are Python’s abstraction for data. All data in a Python program is represented by **objects** or by **relations between objects**.”

**When an object is created...**



These never  
change

MUTABLE

IMMUTABLE

# Built-in data types

Type	Meaning	Domain	Mutable?
bool	Condition	True, False	No
int	Integer	$\mathbb{Z}$	No
float	Rational	$\mathbb{Q}$ (more or less)	No
str	Text	Text	No
list	Sequence	Collections of things	Yes
tuple	Sequence	Collections of things	No
dict	Map	Maps between things	Yes

# Variable assignment

What happens when we...

```
>>> sides = 4
```

A new object is created and the name 'sides' points to it (i.e. it is a reference in the Namespace)

ID:10915392

type: INT

value: 4

```
sides = 4
print( type(sides) )
print( id(sides) )
```

```
<class 'int'>
10915392
```

INT is **immutable**, therefore:

```
sides = 4 #a square
print ("value:", sides, " type:", type(sides), " id:", id(sides))
sides = 5 #a pentagon
print ("value:", sides, " type:", type(sides), " id:", id(sides))
```

```
value: 4  type: <class 'int'>  id: 10915392
value: 5  type: <class 'int'>  id: 10915424
```

# Name of variables

**You can choose the name you like but:**

1. Can only contain A-Z, a-z, 0-9 or \_  
i.e. no +, -, ; etc. allowed
2. Cannot start with a number
3. Cannot be one of the reserved words

and	as	assert	break	class	continue
def	del	elif	else	except	exec
finally	for	from	global	if	import
in	is	lambda	nonlocal	not	or
pass	raise	return	try	while	with
yield	True	False	None		

# Integers

As one would expect...

```
a = 7
b = 4

a + b # 11
a - b # 3
a // b # integer division: 1
a * b # 28
a ** b # power: 2401
a / b # division 0.8333333333333334
type(a / b)
```

float

a

ID:10914688

type: INT

value: 7

REMEMBER: **Immutable**

Their range is limited ONLY by the  
AVAILABLE memory

# Variable assignment: question for you

**What happens when we execute the following code...**

```
>>> value = 10
>>> print(id(value))
>>> print(type(value))
>>> print(value)
```

```
>>> value = value + 1
>>> print(id(value))
>>> print(type(value))
>>> print(value)
```



# Variable assignment: question for you

What happens when we execute the following code...

```
>>> value = 10
>>> print(id(value))
>>> print(type(value))
>>> print(value)
```

ID:10914784

type: INT

value: 10

```
>>> value = value + 1
>>> print(id(value))
>>> print(type(value))
>>> print(value)
```

ID:10914816

type: INT

value: 11

← id(11)

# Booleans

Assume only values True and False

```
a = bool(1)
b = bool(0)
c = bool(72)
d = bool(-5)
t = int(True)
f = int(False)

print("a: ", a, " b: ", b, " c: ", c, " d: ", d, " t: ", t, " f: ", f)
```

a: True b: False c: True d: True t: 1 f: 0

Boolean algebra rules...

```
T = True
F = False

print ("T: ", T, " F:", F)

print ("T and F: ", T and F) #False
print ("T and T: ", T and T) #True
print ("F and F: ", F and F) #False
print ("not T: ", not T) # False
print ("not F: ", not F) # True
print ("T or F: ", T or F) # True
print ("T or T: ", T or T) # True
print ("F or F: ", F or F) # False
```

All numbers evaluate to **True**, except **0**.

# Reals

In python they are floating points (**floats**). **64 bits** of information divided in **sign**, **exponent (11bits)** and **mantissa (52 bits)**.  $N : \text{mantissa} * 2^{\text{Exponent}}$

**Example:** Let's calculate the area of the center circle of a football pitch (radius = 9.15m) recalling that  $\text{area} = \text{Pi} * R^2$ :

```
R = 9.15
Pi = 3.141592653589793
Area = Pi*(R**2)
print (Area)
```

263.02199094017146

```
import math
R = 9.15
Pi = math.pi
Area = Pi*(R**2)
print (Area)
```

263.02199094017146

Use parenthesis or remember  
precedence of operators...

**	Power ( <b>Highest precedence</b> )
+, -	Unary plus and minus
* / // %	Multiply, divide, floor division, modulo
+ -	Addition and subtraction
<= < > >=	Comparison operators
== !=	Equality operators
not or and	Logical operators ( <b>Lowest precedence</b> )

# Strings

In python they are **immutable objects** that are used to represent and work with text .

They contain unicode characters (that can also represent formatting like newline `\n`, tab `\t` ...)

```
S = "my first string, in double quotes"
S1 = 'my second string, in single quotes'
S2 = '''my third string is
in triple quotes
therefore it can span several lines'''
S3 = """my fourth string, in triple double-quotes
can also span
several lines"""

print(S, '\n') #let's add a new line at the end of the string with \n
print(S1, '\n')
print(S2, '\n')
print(S3, '\n')
```

my first string, in double quotes

my second string, in single quotes

my third string is  
in triple quotes  
therefore it can span several lines

my fourth string, in triple double-quotes  
can also span  
several lines

# Strings

## Escape special characters

\\	Backslash
\n	ASCII linefeed (also known as newline)
\t	ASCII tab character
\'	Single quote
\"	Double quote
\xxxx	Unicode character xxxx (hexadecimal)

```
myString = "This is how I \'quote\' and \"double quote\" things in strings"  
print(myString)
```

This is how I 'quote' and "double quote" things in strings

```
print("Greek omega is: \u03C9")
```

Greek omega is: ω

# Strings

## Functions and operators

Result	Operator	Meaning
int	<code>len(str)</code>	Return the length of the string
str	<code>str + str</code>	Concatenate two strings
str	<code>str * int</code>	Replicate the string
bool	<code>str in str</code>	Check if a string is present in another string
str	<code>str[int]</code>	Read the character at specified index
str	<code>str[int:int]</code>	Extract a sub-string



read only!

# Strings

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**Example** A tandem repeat is a short sequence of DNA that is repeated several times in a row. Let's create a string representing the tandem repeat of the motif "ATTCG" repeated 5 times. What is the length of the whole repetitive region? Is the motif "TCGAT" (m1) present in the region? The motif "TCCT" (m2)? Let's give an orientation to the tandem repeat by adding the string "5'" (5' end) on the left and "-3'" (3' end) to the right.

```
motif = "ATTCG"

tandem_repeat = motif * 5

print(motif)
print(tandem_repeat, " has length", len(tandem_repeat))
m1 = "TCGAT"
m2 = "TCCT"

print("Is ", m1, " in ", tandem_repeat, " ? ", m1 in tandem_repeat )
print("Is ", m2, " in ", tandem_repeat, " ? ", m2 in tandem_repeat )
oriented_tr = "5\'-" + tandem_repeat + "-3\'"
print(oriented_tr)
```

```
ATTCG
ATTCGATTCGATTCGATTCGATTCG has length 25
Is TCGAT in ATTCGATTCGATTCGATTCGATTCG ? True
Is TCCT in ATTCGATTCGATTCGATTCGATTCG ? False
5'-ATTCGATTCGATTCGATTCGATTCG-3'
```

# Strings

## Indexing and Slicing

### Indexing starts from 0

str[i] : i+1-th character

str[S:E:step] slice string

**Remember:**

**S** inclusive, **E** exclusive, step is optional

0	1	2	3	4	5	6	7	8	9	10	11	12	13
L	u	t	h	e	r		C	o	l	l	e	g	e
-14	-13	-12	-11	-10	-9	-8	-7	-6	-5	-4	-3	-2	-1

```
S = "Luther College"
```

```
print(S) #print the whole string
print(S == S[:]) #a fancy way of making a copy of the original string
print(S[0]) #first character
print(S[3]) #fourth character
print(S[-1]) #last character
print(S[0:6]) #first six characters
print(S[-7:]) #final seven characters
print(S[0:len(S):2]) #every other character starting from the first
print(S[1:len(S):2]) #every other character starting from the second
```

```
Luther College
```

```
True
```

```
L
```

```
h
```

```
e
```

```
Luther
```

```
College
```

```
Lte olg
```

```
uhrClee
```



# Strings

## Methods

Result	Method	Meaning
str	<code>str.upper()</code>	Return the string in upper case
str	<code>str.lower()</code>	Return the string in lower case
str	<code>str.strip(str)</code>	Remove strings from the sides
str	<code>str.lstrip(str)</code>	Remove strings from the left
str	<code>str.rstrip(str)</code>	Remove strings from the right
str	<code>str.replace(str, str)</code>	Replace substrings
bool	<code>str.startswith(str)</code>	Check if the string starts with another
bool	<code>str.endswith(str)</code>	Check if the string ends with another
int	<code>str.find(str)</code>	Return the first position of a substring starting from the left
int	<code>str.rfind(str)</code>	Return the position of a substring starting from the right
int	<code>str.count(str)</code>	Count the number of occurrences of a substring

**OBJ . method :**  
**“apply method to OBJ”**

**IMPORTANT NOTE** Since Strings are immutable, every operation that changes the string actually produces a new *str* object having the modified string as value.

# Strings

**IMPORTANT NOTE** Since Strings are immutable, every operation that changes the string actually produces a new *str* object having the modified string as value.

Example:

```
t = """this is my text on tw  
wo lines"""
```

```
print("t:", t)  
print("")  
print("UPPER:", t.upper())  
print("")  
print("t:", t)
```

```
t: "this is my text on tw  
wo lines"
```

```
UPPER: "THIS IS MY TEXT ON TW  
WO LINES"
```

```
t: "this is my text on tw  
wo lines"
```

# Strings

**Example:** Given the DNA sequence `S = " aTATGCCCATatcgctAAATTGCTGCCATTACA "`. Print its length (removing any blank spaces at either sides), the number of adenines, cytosines, guanines and thymines present. Is the sequence "ATCG" present in `S`? Print how many times the substring "TGCC" appears in `S` and all the corresponding indexes.

```
S = " aTATGCCCATatcgctAAATTGCTGCCATTACA "

print(S)
S = S.strip(" ")
print(S)

print(len(S))
tmpS = S.upper() #for simplicity to count only 4 different nucleotides
print("A count: ", tmpS.count("A"))
print("C count: ", tmpS.count("C"))
print("T count: ", tmpS.count("T"))
print("G count: ", tmpS.count("G"))
print("Is ATCG in ", tmpS, "? ", tmpS.find("ATCG") != -1) #or tmpS.count("ATCG") > 0
print("TGCC is present ", tmpS.count("TGCC"), " times in ", tmpS)
print("TGCC is present at pos ", tmpS.find("TGCC"))
print("TGCC is present at pos ", tmpS.rfind("TGCC")) #or tmpS.find("TGCC",4)
```

```
    aTATGCCCATatcgctAAATTGCTGCCATTACA
aTATGCCCATatcgctAAATTGCTGCCATTACA
33
A count:  10
C count:  9
T count:  10
G count:  4
Is ATCG in  ATATGCCCATATCGCTAAATTGCTGCCATTACA ?  True
TGCC is present 2 times in  ATATGCCCATATCGCTAAATTGCTGCCATTACA
TGCC is present at pos  3
TGCC is present at pos  23
```

# Strings

Remember:

strings are  
immutable  
and do not  
support item  
assignment

**Example:** Since the genetic code is degenerate, there are many codons encoding for the same aminoacid. Consider Proline, it can be encoded by the following codons: CCU, CCA, CCG, CCC. Let's create a string proline and assign it to its possible codons one after the other.

```
"""  
Wrong solution. We cannot directly replace the value of a string  
"""  
  
proline = "CCU"  
print("Proline can be encoded by: ", proline)  
proline[2]="A"  
print(".. or by: ", proline)
```

# Strings

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```
"""
Wrong solution. We cannot directly replace the value of a string
"""

proline = "CCU"
print("Proline can be encoded by: ", proline)
proline[2]="A"
print(".. or by: ", proline)
```

Proline can be encoded by: CCU

```
-----
TypeError                                Traceback (most recent call last)
<ipython-input-17-9750dcfalcdb> in <module>()
      5 proline = "CCU"
      6 print("Proline can be encoded by: ", proline)
----> 7 proline[2]="A"
      8 print(".. or by: ", proline)
      9
```

TypeError: 'str' object does not support item assignment



# Strings

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```
"""  
Correct solution. Using str.replace  
"""  
proline = "CCU"  
print("Proline can be encoded by: ", proline)  
proline = proline.replace("U", "A")  
print(".. or by: ", proline)  
proline = proline.replace("A", "G")  
print(".. or by: ", proline)  
proline = proline.replace("G", "C")  
print(".. or by: ", proline)
```

```
Proline can be encoded by:  CCU  
.. or by:  CCA  
.. or by:  CCG  
.. or by:  CCC
```

# Strings

**Example:** Since the genetic code is degenerate, there are many codons encoding for the same aminoacid. Consider Proline, it can be encoded by the following codons: CCU, CCA, CCG, CCC. Let's create a string proline and assign it to its possible codons one after the other.

Remember:

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```
"""
Another correct solution. Using string slicing and catenation.
"""
proline = "CCU"
print("Proline can be encoded by: ", proline)
proline = proline[:-1]+"A" #equal to proline[0:-1] or proline[0:2]
print(".. or by: ", proline)
proline = proline[:-1]+"G"
print(".. or by: ", proline)
proline = proline[:-1]+"C"
print(".. or by: ", proline)
```

```
Proline can be encoded by:  CCU
.. or by:  CCA
.. or by:  CCG
.. or by:  CCC
```

Questions ?





# <https://qcbsciprolab2020.readthedocs.io/en/latest/practical2.html>

Go quickly  
through the  
text and do  
the exercises  
at the end

## Exercises

1. Given the following string on two lines:

```
text = """Nobody said it was easy  
No one ever said it would be this hard"""
```

write some python code that a) prints the whole string; b) prints the first and last character; c) prints the first 10 characters; d) prints from the 19th character to the 31st; e) prints the string all in capital letters.

Show/Hide Solution

2. An exon of a gene starts from position 12030 on a genome and ends at position 12174. Does an A/T SNP present at position 12111 affect this exon (i.e. is it inside the exon)? And what about a SNP present at position 12188? *Hint: create a suitable boolean expression to check if the positions are within the interval of the exon.*

Show/Hide Solution

3. SNP FB\_AFFY\_0000024 of the Apple 480K SNP chip has 5' flanking region (i.e. the forward probe) CATTATTTTCACTTGGGTCGAGGCCAGATTCCATC and 3' flanking region (i.e. the reverse probe) GGATTGCCCGAAATCAGAGAAAAGTCG. The SNP is a G/A transversion. Answer the following questions:

1. What is the length of the 5' flanking region? And that of the 3' flanking region?
2. The IUPAC code of the G/A transversion is R. What is the sequence of the whole region using the "[G/A]" notation for the SNP (hint: concatenate it in a new string called *region*) and the iupac notation R (region\_iupac)?
3. Retrieve and print only the SNP from *region* and *iupac\_region*

Show/Hide Solution

4. Compute the melting temperature  $T_m$  of the primer with sequence "TTAGCACCGTGAGCCAATGGAGCAAACGGGAATT". The melting temperature  $T_m$  (in degrees Celsius) can be computed as:  $T_m = 64.9 + 41(GC - 16.4)/N$ , where  $GC$  is the total number of G and C in the primer and  $N$  is its length.

Show/Hide Solution

5. The spike protein of the Sars-CoV-2 virus has the following aminoacidic sequence:

```
S = """  
MFVFLVLLPLVSSQCVNLTTRQLPPAYTNGSETRVYYPDKVERSSVLSHTQDLFLPFFS  
NVTWFHAIHYSGTNGTKRFDPVLFPNDGYFASTEKSNIIIRGIFGTTLSQTKQLLIV  
NNATNVVIVKVCFFQFCNDPFLGVYYHKNKMSMESEFRVYSSANNCTFEYVSQFLMDLE  
GKQGNFKNLREFVEKNIDGYFKIYSKHTPINLVBDLPQGSALPLVDLPIGINITRFQT  
LLALHRSYLTPOGSSSGWTAGAAAYVGYLQRTFLKLYNENGTIDAVDCLDPLSEK
```