

Introduction to Python

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BaRC Hot Topics

Bioinformatics and Research Computing

Whitehead Institute

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http://barc.wi.mit.edu/hot_topics/



WHITEHEAD INSTITUTE



JupyterLab

1. Login to notebook.wi.mit.edu

2. Download the exercises to your home folder:

Click on “New” -> Terminal -> Type

“`setup_Intro_Python_talk`” command

This will create a folder named as “Intro_to_Python”

3. Go to the Intro_to_Python folder, and click on `Introduction_to_Python.ipynb`

About Python

- Object oriented language; easy to read
- Scripting language; quick to write
- Massive community support
 - Biopython
- Whitespaces are important. Python uses indentation, no braces are needed
- We will learn Python 3 in this class. Many libraries in Python 2 are not compatible with Python 3.



Objectives

- Go over the basics of Python 3 to get you started on writing your own code
- Covered in this workshop:
 - Introduce variables
 - Read/Write files
 - Create Function and modules
 - Flow Control: if-else and loops
 - Create a single script



Data types

- Single variable:
 - Number: integer, float
 - String: characters
- Ordered:
 - strings: immutable; surrounded by quotation marks

```
>>> my_class = "Introduction to Python"
```
 - lists: mutable; surrounded by square brackets

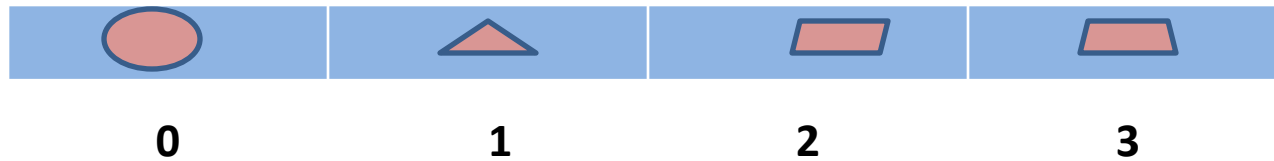
```
>>> my_list = [ 1, 4, 6 ]
```
 - tuples: immutable; surrounded by parentheses

```
>>> my_tuple = ( 1, 4, 6 )
```
- dictionary:
 - mutable; surrounded by curly brackets
 - Key is immutable
 - ```
>>> codon = { 'CUU': 'leu', 'UCU': 'ser', 'AAA': 'lys' }
```
- Use function “type” to find out a variable type



# Common Properties for Sequences strings, lists, tuples

- seq=



- Index
- Slice
- Conditional tests
- Concatenation
- Length, maximum, minimum, etc.

```
>>> len(seq)
```

```
>>> 4
```



# Index for strings, lists, tuples

– begin with 0

```
>>> seq = "ATGCT"
```

```
>>> seq[0] # A
```

```
>>> tuple1 = (5,6,7)
```

```
>>> tuple1[0] # 5
```

```
>>> list1 = ["Tgfb1", "Bmp4", "Cdh1"]
```

```
>>> list1[1] # Bmp4
```

– Access from right with negative number

```
>>> seq[-1] # T
```

```
>>> tuple1[-2] # 6
```

```
>>> list1[-1] # Cdh1
```



# slice for strings, lists, tuples

- slicing: [start:stop:step]
    - Stopping value not included
    - Omit start: start from first position
    - Omit stop: go to the last position
    - step default is 1, negative number counting backward
- ```
>>> seq = "BaRCHotTopics"  
>>> len(seq) # 13  
>>> seq[0:4] # BaRC  
>>> seq[:4] # BaRC  
>>> seq[7:] # Topics  
>>> seq[0:4:2] # BR  
>>> seq[::-1] # scipoTtoHCRaB
```



Conditional tests for strings, lists, tuples

```
>>> expr = (20, 45, 60)
```

```
>>> 55 in expr
```

```
False
```

```
>>> 60 in expr
```

```
True
```

```
>>> sum(expr) > 100
```

```
True
```

```
>>> myseq = "ACTTA"
```

```
>>> "G" in myseq
```

```
False
```

```
>>> myseq.lower() == "actta"
```

```
True
```

Conditional tests commonly used inside if/else work flow



Concatenation for strings, lists, tuples

Concatenate sequences from **same type** with “+” sign

```
>>> expr1 = (10, 20, 30)
>>> expr2 = (15, 25, 35)
>>> expr1and2 = expr1 + expr2
>>> expr1and2
(10, 20, 30, 15, 25, 35)
```

```
>>> seq1 = "ACT"
>>> seq2 = "TGC"
>>> seq1and2 = seq1+seq2
>>> seq1and2
'ACTTGC'
```



Other functions for strings, lists, tuples

- len(): amount of elements

```
>>> List1 = [ "A", "C", "T", "G" ]
```

```
>>> print (len(List1))
```

```
4
```

- max() and min():

```
>>> expr = (5, 10, 200)
```

```
>>> max(expr)
```

```
200
```



Dictionaries

- Dictionaries are lookup tables
- It includes key:value pair, and surrounded by curly brackets {}

```
>>> codon = {'CUU': 'leu', 'UCU': 'ser', 'AAA': 'lys'}
```

- Mutable; unordered data types
- Keys:
 - Unique
 - Immutable
 - Strings, tuples, numbers
- Values:
 - Duplication is allowed



type	string	list	tuple	dictionary
example	"AACTGC"	[1, 21, 48]	(1, "ATG", 4, 8)	{ 'CUU': 'leu', 'UCU': 'ser' }
mutable	No	Yes	No	Yes*
Ordered**	Yes	Yes	Yes	No

*Key is not mutable

** index and slice are applicable



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3. Go to the Intro_to_Python folder, and click
on Introduction_to_Python.ipynb
4. Do exercises: 1 to 8

Code Sharing and Reuse

Advantages:

Re-usability and readability, easy debug, improve performance

Includes:

- a. Functions
- b. Modules
- c. Packages
- d. Classes
- e. Objects



Functions:



- Create function

```
def functionName(arg1, arg2, ...):  
    """ your description (optional) """  
    function Code ...  
    return DATA
```

- Return types:
 - Single (None, string, etc.)
 - Multiple

```
def calculate_GC_percentage(seq):  
    """Calculate GC percentage of a nucleotide sequence. """  
    # count the number of C  
    C = seq.upper().count("C")  
  
    # count the number of G  
    G = seq.upper().count("G")  
  
    # calculate gc%  
    # use len to get the total number of nts  
    gc_per = 100*(C+G)/len(seq)  
  
    # only keep two digits after decimal  
    gc_per = round (gc_per, 2)  
  
    # return gc percentage  
    return(gc_per)
```

```
# call a function:  
calculate_GC_percentage("actgtgg")
```



Modules/Packages

- Module is a file with functions, constants and objects.
- packages is group of modules
 - Should include `__init__.py`

```
>>> import math
```

```
>>> math.pi
```

```
3.141592653589793
```

```
>>> from math import pi
```

```
>>> pi
```

```
3.141592653589793
```

```
>>> import os
```

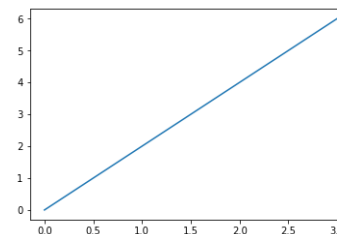
```
>>> os.getcwd()
```

```
/nfs/BaRC_training/Python/Python_Part1
```

```
>>> import matplotlib.pyplot as plt
```

```
>>> plt.plot([0,2,4,6])
```

```
>>> plt.show()
```



Open/Write files

Function: open

1. Open file:

– Two parameters:

- 1) File name
- 2) Opening mode:
 - r : read (default)
 - w : write
 - a: append

2. Read the file:

- 1) read() : read file
- 2) readline(): read one line
- 3) readlines(): return a list with lines

1) and 3): not for large files

3. Close the file with close()

Examples:

```
>>> fh = open("foo.txt")
>>> print (fh.readline())
>>> fh.close()
```

- Write to file

```
>>> fh = open("out.txt", "w")
>>> fh.write("Python is fun!")
>>> fh.close()
```

- Another way with “with open”
 - No need to close the file

```
>>> with open("foo.txt") as fh:
>>>     lines=fh.readlines()
```



Flow Control: If-Else

- *if* expression1:

Block1

- *elif* expression2:

block2

- *else*:

block3

```
>>> WT = 100
>>> KO = 56
>>> if WT > KO:
>>>     print("WT is greater than KO")
>>> elif WT == KO:
>>>     print("WT and KO are equal")
>>> else:
>>>     print("KO is greater than WT")
```

- Comparisons:

- logical conditions:

$x < y$ $x > y$ $x == y$ $x != y$

- Use **and** or **or** combine conditional statements

if $x > y$ *and* $x > z$:

if $x > y$ *or* $x > z$:



Loops

for loop

```
for VAR in ITERABLE:  
    BLOCK
```

ITERABLE:

lists, tuples, strings,
dictionaries, files

```
>>> seq = "ACTG"  
>>> for base in seq:  
>>>     print (base)
```

while loop

```
while EXPRESSION:  
    BLOCK
```

```
>>> a = 10  
>>> while a < 30:  
>>>     print (a+1)  
>>>     a = a+10
```

Avoid infinite loop



Create a script

Python file name: ends with .py

The file name for this script is
get_GC_percentage.py

Run the script:

The script asks for an input fasta file, and prints out gc% of the sequence inside the input file.

```
$ ./get_GC_percentage.py
```

```
What is your input sequence file?sample_seq.fa  
52.68
```

```
#!/usr/bin/python
```

```
input_file = input ( "What is your input sequence file?" )
```

```
def calculate_GC_percentage(seq):
```

```
    """Calculate GC percentage of a nucleotide sequence. """
```

```
    # count the number of C
```

```
    C = seq.upper().count("C")
```

```
    # count the number of G
```

```
    G = seq.upper().count("G")
```

```
    # calculate gc%
```

```
    # use len to get the total number of nts
```

```
    # only keep two digits after decimal
```

```
    return(round(100*(C+G)/len(seq), 2))
```

```
# set an empty string to hold sequences
```

```
seq = ""
```

```
# read a sequence file
```

```
with open(input_file) as fh:
```

```
    content = fh.readlines()
```

```
    # concatenate the sequences
```

```
    seq = "".join(content[1:])
```

```
    # delete end of line character
```

```
    seq = seq.replace("\n", "")
```

```
# calculate the GC percentage
```

```
print ( calculate_GC_percentage(seq) )
```



References

- Python Official website:
 - <https://www.python.org/>
- Python Tutorials from programiz website
 - <https://www.programiz.com/python-programming/#tutorial>
- GeeksforGeeks
 - <https://www.geeksforgeeks.org/>
- Software Carpentry:
 - <https://swcarpentry.github.io/python-novice-gapminder/>
- Cheat sheets:
 - <https://www.docsity.com/it/beginners-python-cheat-sheet-pcc-all/653739/>
 - <https://tmont.es/images/sheet-of-python-v1.pdf>



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Introduction_to_Python.ipynb:

Do exercises: 9 to 12

Coming up next:

Introduction to Python part 2: Python for Analysis

Thur. Nov. 18, 2021