



Puerto Rico - IDeA Networks of Biomedical Research Excellence



Python3 Part 1 – Crash Course in Python3 for Future STEM Coders

Judith S. Rodriguez-Martinez, M.S.

Ph.D. Candidate
Penn State University – University Park Campus
jzr5814@psu.edu











- The following material is the result of PR-INBRE research and curriculum development effort to provide a set of educational materials for research training and curriculum changes in biology programs across the island to support PR-INBRE efforts to establish a Community of Practice in Bioinformatics that offers a fruitful environment to increase computational and bioinformatics skills among traditional researchers and students (undergraduate and graduate) in the island. They have been developed as a part of the NIH funded project "Puerto Rico IDeA Network Biomedical Research Excellence (PRINBRE)" (Award Number 5P20GM103475).
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Competencies

June 5, 2023 - Record and write simple and common **Python scripts to deal with Bioinformatic needs for biological data analyses** using a Jupyter Notebook

Today – Exploit datatypes that can record objects, as well as, reason logical statements







Objectives

- Continue to use Google Colab as an environment to practice and learn common Python lines of code.
- Formulate logical statements through **Booleans** and **Conditions**
- Create and manage Python lists and dictionaries
- Analyze Python Lists and Dictionaries using Python For Loops and While Loops





Target Audience

• This training is addressed to beginners, highly motivated (eager to learn what is needed in order to be competitive without the tendency to self-limit when learning computational skills by saying that is difficult) wanting to become familiar with the **Python** programming language and become the Script Master of their bioinformatic analysis.







The importance of Python

- R is great however... eventually, you'll have to use Python language
- No matter your field, python will be a necessity (chemistry, biology, engineering, ecology, mathematics, etc)
- Knowing Python gives you an edge when job searching and navigating graduate research
- The majority bioinformatic tools are python-based and will lead you to understand under the hood code in order to successfully execute said program's purpose.





Lesson 2.0.0 Booleans and Conditions



Operator	Definition	Statement Example
==	Equal-to	2 + 2 == 5
!=	Not equal-to	2 + 2 != 5
>	Greater-than	2 > 5
<	Less-than	2 < 5
>=	Greater or equal-to	2 >= 2 3 >= 2
<=	Lesser or equal-to	2 <= 2 1 <= 2



Operator	Definition	Statement Example
==	Equal-to	2 + 2 == 5
!=	Not equal-to	2 + 2 != 5
>	Greater-than	2 > 5
<	Less-than	2 < 5
>=	Greater or equal-to	2 >= 2 3 >= 2
<=	Lesser or equal-to	2 <= 2 1 <= 2



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==	Equal-to	2 + 2 == 5
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Operator	Definition	Statement Example
==	Equal-to	2 + 2 == 5
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<=	Lesser or equal-to	2 <= 2 1 <= 2

[3]	2 + 2 == 5
	False
[4]	2 + 2 != 5



Operator	Definition	Statement Example
==	Equal-to	2 + 2 == 5
!=	Not equal-to	2 + 2 != 5
>	Greater-than	2 > 5
<	Less-than	2 < 5
>=	Greater or equal-to	2 >= 2 3 >= 2
<=	Lesser or equal-to	2 <= 2 1 <= 2

[3]	2 + 2 == 5
	False
[4]	2 + 2 != 5
	True



Operator	Definition	Statement Example
==	Equal-to	2 + 2 == 5
!=	Not equal-to	2 + 2 != 5
>	Greater-than	2 > 5
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>=	Greater or equal-to	2 >= 2 3 >= 2
<=	Lesser or equal-to	2 <= 2 1 <= 2

[3]	2 + 2 == 5
	False
[4]	2 + 2 != 5
	True
[45]	2 < 5



Operator	Definition	Statement Example
==	Equal-to	2 + 2 == 5
!=	Not equal-to	2 + 2 != 5
>	Greater-than	2 > 5
<	Less-than	2 < 5
>=	Greater or equal-to	2 >= 2 3 >= 2
<=	Lesser or equal-to	2 <= 2 1 <= 2

[3]	2 + 2 =	== 5
	False	
[4]	2 + 2	!= 5
	True	
[45]	2 < 5	
	True	



Conditions

Conditions in Python facilitate decision making in your code

Operator	Decision
if	When the condition is true
else	When the if condition is false
elif	When another option is true



Using an if statement

```
[48] if 2 < 5:
    print(f'Statement is {True}')

Answer</pre>
```

Using an if not statement

```
[49] if not 2 > 5:
    print(f'Statement is {False}')
```

Answer



Using an if statement

```
[48] if 2 < 5:
    print(f'Statement is {True}')

Statement is True</pre>
```

Using an if not statement

```
[49] if not 2 > 5:
    print(f'Statement is {False}')
```

Answer



Using an if statement

```
[48] if 2 < 5:
    print(f'Statement is {True}')

Statement is True</pre>
```

Using an if not statement

```
[49] if not 2 > 5:
    print(f'Statement is {False}')

□→ Statement is False
```



Is ATG in the sequence?

```
else can be used
without a
statement so when
nothing there is no
other option use
else

[53] sequence = 'ATGTGGTGGAGA'
if 'ATG' in sequence:
print(f'ATG is in {sequence}')
else:
print(f'ATG is not in {sequence}')

Answer

Answer
```



Is ATG in the sequence?

else can be used
without a
statement so when
nothing there is no
other option use
else

```
[53] sequence = 'ATGTGGTGGAGA'
    if 'ATG' in sequence:
        print(f'ATG is in {sequence}')
    else:
        print(f'ATG is not in {sequence}')

ATG is in ATGTGGTGGAGA
```



Is ATG in the sequence?

```
[53] sequence = 'ATGTGGTGGAGA'
   if 'ATG' in sequence:
      print(f'ATG is in {sequence}')
   else:
      print(f'ATG is not in {sequence}')

ATG is in ATGTGGTGGAGA
```

Is ATG in this sequence?

```
[54] sequence = 'TGGTGGAGA'
    if 'ATG' in sequence:
        print(f'ATG is in {sequence}')
    else:
        print(f'ATG is not in {sequence}')
```



Answer

Is ATG in the sequence?

```
[53] sequence = 'ATGTGGTGGAGA'
   if 'ATG' in sequence:
      print(f'ATG is in {sequence}')
   else:
      print(f'ATG is not in {sequence}')

ATG is in ATGTGGTGGAGA
```

Is ATG in this sequence?

```
[54] sequence = 'TGGTGGAGA'
   if 'ATG' in sequence:
     print(f'ATG is in {sequence}')
   else:
     print(f'ATG is not in {sequence}')

ATG is not in TGGTGGAGA
```



```
[39] sequence = 'ATGTGGTGGAGATAG'
    if 'TAA' in sequence:
        print(f'TAA in {sequence}')

elif can be
    used when
    there are
    multiple
    options

elif 'TGA' in sequence:
    print(f'TGA in {sequence}')
    elif 'TGA' in sequence:
    print(f'TGA in {sequence}')
    else:
        print(f'A stop codon does not exist in {sequence}')
```

Answer



```
[39] sequence = 'ATGTGGTGGAGATAG'
    if 'TAA' in sequence:
        print(f'TAA in {sequence}')

elif can be
    used when
    there are
    multiple
    options

Fig. 1

and 2

elif 'TAG' in sequence:
    print(f'TAG in {sequence}')
    elif 'TGA' in sequence:
        print(f'TGA in {sequence}')
    else:
        print(f'A stop codon does not exist in {sequence}')

TAG in ATGTGGTGGAGATAG
```



```
[41] sequence = 'ATGTGGTGGAGATAA'
    if 'TAA' in sequence:
        print(f'TAA in {sequence}')
    elif 'TAG' in sequence:
        print(f'TAG in {sequence}')
    elif 'TGA' in sequence:
        print(f'TGA in {sequence}')
    else:
        print(f'A stop codon does not exist in {sequence}')
```

Answer



```
sequence = 'ATGTGGTGGAGATAA'
[41]
     if 'TAA' in sequence:
       print(f'TAA in {sequence}')
    elif 'TAG' in sequence:
       print(f'TAG in {sequence}')
    elif 'TGA' in sequence:
       print(f'TGA in {sequence}')
    else:
       print(f'A stop codon does not exist in {sequence}')
    TAA in ATGTGGTGGAGATAA
```



```
[32] sequence = 'ATGTGGTGGAGA'
    if 'TAA' in sequence:
        print(f'TAA not in {sequence}')
    elif 'TAG' in sequence:
        print(f'TAA not in {sequence}')
    elif 'TGA' in sequence:
        print(f'TAA not in {sequence}')
    else:
        print(f'A stop codon does not exist in {sequence}')
```

Answer



```
[32] sequence = 'ATGTGGTGGAGA'
   if 'TAA' in sequence:
      print(f'TAA not in {sequence}')
   elif 'TAG' in sequence:
      print(f'TAA not in {sequence}')
   elif 'TGA' in sequence:
      print(f'TAA not in {sequence}')
   else:
      print(f'A stop codon does not exist in {sequence}')
```

A stop codon does not exist in ATGTGGTGGAGA







Lesson 2.1.0 More Python datatypes









Lesson 2.1.1 Lists



Method 1: Create a list with items

```
[5] stop_codons = ['TAG','TGA','ATG']
stop_codons
```

Answer

Store multiple items using brackets.



Method 1: Create a list with items

```
[5] stop_codons = ['TAG', 'TGA', 'ATG']
stop_codons

['TAG', 'TGA', 'ATG']
```

Store multiple items using brackets.



Method 2: Start an empty list

```
[18] empty_list = []
empty_list

Answer

[19] empty_list.append('TAG')
empty_list.append('TAA')
empty_list.append('TGA')
empty_list
Answer
```

The
append(object)
function will
add new
objects to an
existing list.



Method 2: Start an empty list

```
[18] empty_list = []
    empty_list

[19] empty_list.append('TAG')
    empty_list.append('TAA')
    empty_list.append('TGA')
    empty_list
Answer
```

The
append(object)
function will
add new
objects to an
existing list.



Method 2: Start an empty list

```
[18] empty_list = []
empty_list

[19] empty_list.append('TAG')
empty_list.append('TAA')
empty_list.append('TGA')
empty_list
['TAG', 'ATG', 'TGA']
```

The
append(object)
function will
add new
objects to an
existing list.



Functions you can use to evaluate and manipulate lists

Note: These functions are used similarly to string objects!

len(list)
list.count("")
list.remove(object)
list.append(object)
list.sort()
list.reverse()



What is wrong with the stop_codons list?

```
[5] stop_codons = ['TAG', 'TGA', 'ATG']
stop_codons

['TAG', 'TGA', 'ATG']
```



What is wrong with the stop_codons list?



How should we fix this?

```
[5] stop_codons = ['TAG', 'TGA', 'ATG']
stop_codons

['TAG', 'TGA', 'ATG']
```

Answer



How should we fix this?

```
[5] stop_codons = ['TAG', 'TGA', 'ATG']
stop_codons

['TAG', 'TGA', 'ATG']
```

```
[6] stop_codons.remove('ATG')
    stop_codons

['TAG', 'TGA']

[7] stop_codons.append('TAA')
    stop_codons

['TAG', 'TGA', 'TAA']
```







Lesson 2.1.2 Dictionaries

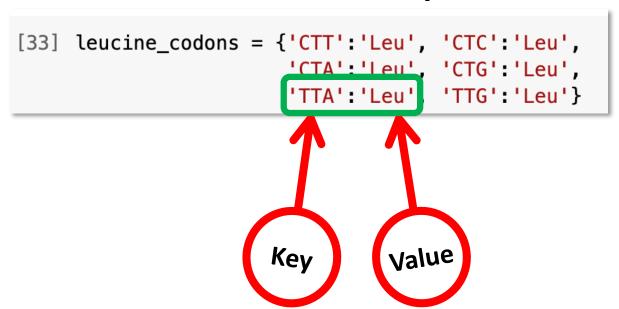


Method 1: Create a dictionary with items

```
[33] leucine_codons = {'CTT':'Leu', 'CTC':'Leu', 'CTA':'Leu', 'CTG':'Leu', 'TTA':'Leu', 'TTG':'Leu'}
```



Method 1: Create a dictionary with items





Method 1: Create a dictionary with items

Answer



Method 1: Create a dictionary with items

```
[33] leucine_codons = {'CTT':'Leu', 'CTC':'Leu', 'CTA':'Leu', 'CTG':'Leu', 'TTA':'Leu', 'TTG':'Leu'} leucine_codons

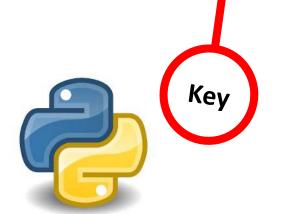
{'CTT': 'Leu', 'CTC': 'Leu', 'CTC': 'Leu', 'CTA': 'Leu', 'CTG': 'Leu', 'TTA': 'Leu', 'TTG': 'Leu', 'TTG': 'Leu'}
```



Method 1: Create a dictionary with items

```
[33] leucine_codons = {'CTT':'Leu', 'CTC':'Leu', 'CTA':'Leu', 'CTG':'Leu', 'TTA':'Leu', 'TTG':'Leu'} leucine_codons

{'CTT': 'Leu', 'CTC': 'Leu', 'CTC': 'Leu', 'CTG': 'Leu', 'CTG': 'Leu', 'TTA': 'Leu', 'TTG': 'Le
```



Method 2: Add elements to an empty/existing the dictionary

```
[36] empty_dictionary = {}
    empty_dictionary
```

Answer



Method 2: Add elements to an empty/existing the dictionary

```
[36] empty_dictionary = {}
empty_dictionary

{}

Empty
dictionary
```



Method 2: Add elements to an empty/existing the dictionary

```
[36] empty_dictionary = {}
    empty_dictionary

{}

[37] empty_dictionary['CTT'] = 'Leu'
    empty_dictionary['CTC'] = 'Leu'
    empty_dictionary['CTA'] = 'Leu'
    empty_dictionary['CTG'] = 'Leu'
    empty_dictionary['TTA'] = 'Leu'
    empty_dictionary['TTG'] = 'Leu'
```

Note: the value of a key can be any data type which include strings, integers, floats, lists, or nested dictionaries



Method 2: Add elements to an empty/existing the dictionary

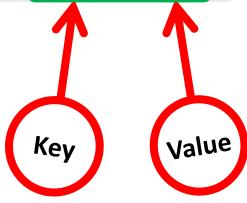
```
[36] empty_dictionary = {}
    empty_dictionary

{}

[37] empty_dictionary['CTT'] = 'Leu'
    empty_dictionary['CTC'] = 'Leu'
    empty_dictionary['CTA'] = 'Leu'
    empty_dictionary['CTG'] = 'Leu'
    empty_dictionary['TTA'] = 'Leu'
    empty_dictionary['TTG'] = 'Leu'
```

Note: the value of a key can be any data type which include strings, integers, floats, lists, or nested dictionaries





Method 2. Start an empty dictionary using curly brackets

```
[36] empty_dictionary = {}
    empty_dictionary

{}

[37] empty_dictionary['CTT'] = 'Leu'
    empty_dictionary['CTC'] = 'Leu'
    empty_dictionary['CTA'] = 'Leu'
    empty_dictionary['CTG'] = 'Leu'
    empty_dictionary['TTA'] = 'Leu'
    empty_dictionary['TTG'] = 'Leu'
```

Note: the value of a key can be any data type which include strings, integers, floats, lists, or nested dictionaries

So what data type are these keys storing?



Method 2. Start an empty dictionary using curly brackets

```
[36] empty_dictionary = {}
    empty_dictionary
{}

[37] empty_dictionary['CTT'] = 'Leu'
    empty_dictionary['CTC'] = 'Leu'
    empty_dictionary['CTA'] = 'Leu'
    empty_dictionary['CTG'] = 'Leu'
    empty_dictionary['TTA'] = 'Leu'
    empty_dictionary['TTG'] = 'Leu'
    empty_dictionary
```

Note: the value of a key can be any data type which include strings, integers, floats, lists, or nested dictionaries

Answer



Method 2. Start an empty dictionary using curly brackets

```
[36] empty_dictionary = {}
    empty_dictionary
    {}
[37] empty dictionary['CTT'] = 'Leu'
    empty_dictionary['CTC'] = 'Leu'
    empty_dictionary['CTA'] = 'Leu'
    empty_dictionary['CTG'] = 'Leu'
    empty_dictionary['TTA'] = 'Leu'
    empty_dictionary['TTG'] = 'Leu'
    empty_dictionary
             'Leu'
             'Leu'.
      'TTG': 'Leu'}
                      Value
```

Note: the value of a key can be any data type which include strings, integers, floats, lists, or nested dictionaries

```
[8] leucine_codons

{'CTT': 'Leu',
    'CTC': 'Leu',
    'CTA': 'Leu',
    'CTG': 'Leu',
    'TTA': 'Leu',
    'TTG': 'Leu'}
```

Note: Calling a key returns its value

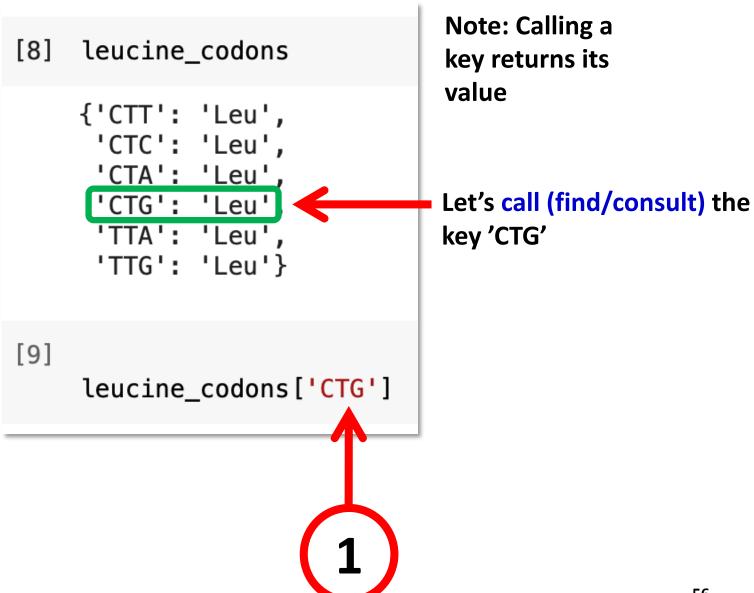


```
[8] leucine_codons key returns its value

{'CTT': 'Leu', 'CTC': 'Leu', 'CTA': 'Leu', 'CTG': 'Leu', 'CTG': 'Leu', 'Leu', 'CTG': 'Leu'}

Let's call (find/consult) the key 'CTG' 'TTG': 'Leu'}
```







```
[8]
    leucine_codons
    {'CTT': 'Leu',
     'CTC': 'Leu',
            'Leu',
     'TTG': 'Leu'}
[9]
    leucine_codons['CTG']
        Answer
```

Note: Calling a key returns (produces/result) its value



```
leucine_codons
[8]
    {'CTT': 'Leu',
     'CTC': 'Leu',
      'TTG': 'Leu'}
[9]
    leucine_codons['CTG']
    'Leu'
```

Note: Calling a key returns (produces/result) its value



A dictionary with all codons and their associated amino acid can be used to translate a protein-coding sequence

```
[3] codon_table = {
        'TCA': 'S', 'TCC': 'S', 'TCG': 'S', 'TCT': 'S', 'AGC': 'S', 'AGT': 'S',
                                                                                    # Serine
        'TTC': 'F', 'TTT': 'F',
                                                                                    # Phenilalanine
        'TTA': 'L', 'TTG': 'L', 'CTA': 'L', 'CTC': 'L', 'CTG': 'L', 'CTT': 'L',
                                                                                    # Leucine
        'TAC': 'Y', 'TAT': 'Y',
                                                                                    # Tirosine
        'TAA': '*', 'TAG': '*', 'TGA': '*',
                                                                                    # Stop
        'TGC': 'C', 'TGT': 'C',
                                                                                    # Cisteine
        'TGG': 'W'.
                                                                                    # Tryptophane
        'CCA': 'P', 'CCC': 'P', 'CCG': 'P', 'CCT': 'P',
                                                                                    # Proline
        'CAC': 'H', 'CAT': 'H',
                                                                                    # Histidine
        'CAA': 'Q', 'CAG': 'Q',
                                                                                    # Glutamine
        'CGA': 'R', 'CGC': 'R', 'CGG': 'R', 'CGT': 'R',
                                                                                    # Arginine
        'ATA': 'I', 'ATC': 'I', 'ATT': 'I',
                                                                                    # Isoleucine
        'ATG': 'M'.
                                                                                    # Methionine
        'ACA': 'T', 'ACC': 'T', 'ACG': 'T', 'ACT': 'T',
                                                                                    # Threonine
        'AAC': 'N', 'AAT': 'N',
                                                                                    # Asparagine
        'AAA': 'K', 'AAG': 'K',
                                                                                    # Lysine
        'AGA': 'R', 'AGG': 'R',
                                                                                    # Arginine
        'GTA': 'V', 'GTC': 'V', 'GTG': 'V', 'GTT': 'V',
                                                                                    # Valine
        'GCA': 'A', 'GCC': 'A', 'GCG': 'A', 'GCT': 'A',
                                                                                    # Alanine
        'GAC': 'D', 'GAT': 'D',
                                                                                    # Aspartic Acid
        'GAA': 'E', 'GAG': 'E',
                                                                                    # Glutamic Acid
        'GGA': 'G', 'GGC': 'G', 'GGG': 'G', 'GGT': 'G'
                                                                                    # Glycine
```





Lesson 2.2.0 Automating repetitive tasks using Python







Lesson 2.2.1a For Loops



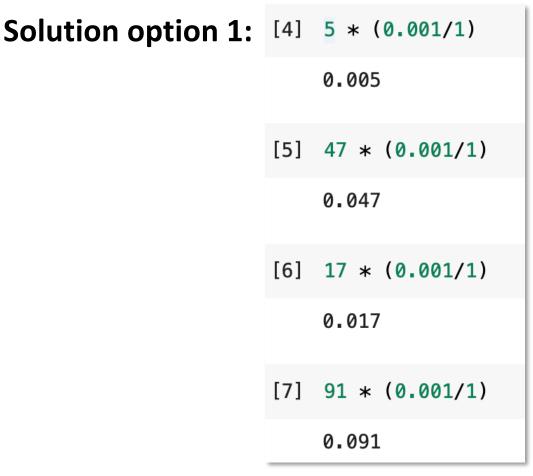
Let's say I have a list of µL measurements that I want to convert to mL

measurement	μL	mL
0	5	?
1	47	?
2	17	?
3	91	?



Let's say I have a list of µL measurements that I want to convert to mL

measurement	μL	mL
0	5	?
1	47	?
2	17	?
3	91	?





Let's say I have a list of µL measurements that I want to convert to mL

measurement	μL	mL
0	5	?
1	47	?
2	17	?
3	91	?

Solution option 2:

Create a variable x and substitute for each value

```
[1] x=5
    x * (0.001/1)
    0.005
[2] x=47
    x * (0.001/1)
    0.047
[3] x=17
    x * (0.001/1)
    0.017
[4] x=91
    x * (0.001/1)
    0.091
```



What if we have a hundred μL measurements that we converted to mL?

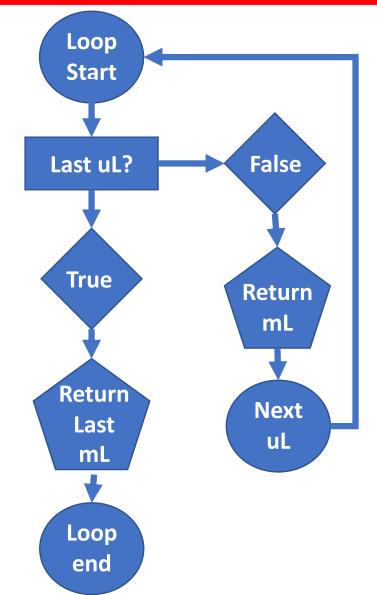
measurement	μL	mL
0	5	?
1	47	?
2	17	?
3	91	?
•	•	?
	•	?
•	•	?
99	77	?



What if we have a hundred μL measurements that we converted to mL?

measurement	μL	mL
0	5	?
1	47	?
2	17	?
3	91	?
•	•	?
•	•	?
•	•	?
99	77	?





Let's say I have a list of µL measurements that I want to convert to mL

measurement	μL	mL
0	5	?
1	47	?
2	17	?
3	91	?

Solution option 3:

```
[9] measurements=[5,27,17,91]

for x in measurements:
    print(f'iteration for {x}')
    result = x * (0.001/1)
    print(f'Measurement (microliter): {x}')
    print(f'Measurement (milliliter): {result}')
```





Let's say I have a list of µL measurements that I want to convert to mL

measurement	μL	mL
0	5	?
1	47	?
2	17	?
3	91	?

Solution option 3:

```
[9] measurements=[5,27,17,91]
    for x in measurements:
      print(f'iteration for {x}')
      result = x * (0.001/1)
      print(f'Measurement (microliter): {x}')
      print(f'Measurement (milliliter): {result}')
    iteration for 5
    Measurement (microliter): 5
    Measurement (milliliter): 0.005
    iteration for 27
    Measurement (microliter): 27
    Measurement (milliliter): 0.027
    iteration for 17
    Measurement (microliter): 17
    Measurement (milliliter): 0.017
    iteration for 91
    Measurement (microliter): 91
    Measurement (milliliter): 0.091
```







Lesson 2.2.1b Exploit information from sequences using For loops



Can we For loop through a string that is a sequence?

```
[4] sequence="ATGTGGTGG" sequence
```

'ATGTGGTGG' 012345678



Can we For loop through a string that is a sequence?

```
[4]
     sequence="ATGTGGTGG"
     sequence
      'ATGTGGTGG'
      012345678
[11] for nucleotide in sequence:
    print(nucleotide)
          Answer
```



Can we For loop through a string that is a sequence?

```
[4]
     sequence="ATGTGGTGG"
     sequence
      'ATGTGGTGG'
      012345678
[11] for nucleotide in sequence:
    print(nucleotide)
```



For looping through a string that is a sequence?

```
[4] sequence="ATGTGGTGG" sequence
```

'ATGTGGTGG' 012345678

```
[11] for nucleotide in sequence:
    print(nucleotide)
```

A T G T G What if we need to use the indexes of this sequence?





How would you produce indexes?

[4] sequence="ATGTGGTGG" sequence

'ATGTGGTGG' 012345678





Using indexes to slice a String

Index a range of the sequence

'ATGTGGTGG 012345678

[9] sequence[2:8]

Index is included and starts new string



Index is not included in new string



How would you produce indexes?

[4] sequence="ATGTGGTGG" sequence

'ATGTGGTGG' 012345678



Hint: a combination between range() and len()



How would you produce indexes?

[4] sequence="ATGTGGTGG" sequence

'ATGTGGTGG' 012345678



Hint: a combination between range()

and len()

```
[12] for nucleotide_position in range(len(sequence)):
    print(nucleotide_position)
    print(sequence[nucleotide_position])
```

Answer



How would you produce indexes?

[4] sequence="ATGTGGTGG" sequence

'ATGTGGTGG' 012345678



Hint: a combination between range() and len()

```
[12] for nucleotide_position in range(len(sequence)):
       print(nucleotide_position)
       print(sequence[nucleotide_position])
```



Do we remember how to index a range of a string?











```
INPUT

'ATGTGGTGG'

O12345678

['AUG', 'UGG', 'UGG']

O12345678

[12] sequence="ATGTGGTGG"

Identify your input sequence
```





```
[12] sequence="ATGTGGTGG"

RNA_sequence=sequence.replace("T","U")

Replace T for U in the sequence
```





```
[12] sequence="ATGTGGTGG"

RNA_sequence=sequence.replace("T","U")

coding_sequence=[] 
Initiate an empty list
```





```
[12] sequence="ATGTGGTGG"

RNA_sequence=sequence.replace("T","U")

coding_sequence=[]
temp=0 Initiate your counter at 0
```





```
| INPUT | OUTPUT | OUTPUT | ATGTGGTGG | → ['AUG', 'UGG', 'UGG'] | O12345678 | O 1 2
```









```
| INPUT | OUTPUT | OUTPUT | ATGTGGTGG | → ['AUG', 'UGG', 'UGG'] | O12345678 | O 1 2
```



```
[12] sequence="ATGTGGTGG"

RNA_sequence=sequence.replace("T","U")

coding_sequence=[]
temp=0
for x in RNA_sequence:
   if RNA_sequence[temp:temp+3] != '':
      coding_sequence.append(RNA_sequence[temp:temp+3])
      temp=temp+3
print(coding_sequence)

['AUG', 'UGG', 'UGG']
```









Lesson 2.2.2a While Loops



```
[66] # Return the index position of the gap in the following sequence
sequence = 'ATGTGG-TGGAGA'
```



```
[66] # Return the index position of the gap in the following sequence
sequence = 'ATGTGG-TGGAGA'
position = None
```



```
[66] # Return the index position of the gap in the following sequence
sequence = 'ATGTGG-TGGAGA'
position = None
temp = 0
```



```
[66] # Return the index position of the gap in the following sequence
    sequence = 'ATGTGG-TGGAGA'
    position = None
    temp = 0
    while position == None:
```



```
[66] # Return the index position of the gap in the following sequence
    sequence = 'ATGTGG-TGGAGA'
    position = None
    temp = 0
    while position == None:
        nucleotide = sequence[temp]
```



```
[66] # Return the index position of the gap in the following sequence
    sequence = 'ATGTGG-TGGAGA'
    position = None
    temp = 0
    while position == None:
        nucleotide = sequence[temp]
        if nucleotide == '-':
```



```
[66] # Return the index position of the gap in the following sequence
    sequence = 'ATGTGG-TGGAGA'
    position = None
    temp = 0
    while position == None:
        nucleotide = sequence[temp]
    if nucleotide == '-':
        position = temp
```



```
[66] # Return the index position of the gap in the following sequence
    sequence = 'ATGTGG-TGGAGA'
    position = None
    temp = 0
    while position == None:
        nucleotide = sequence[temp]
    if nucleotide == '-':
        position = temp
    print(position, temp, nucleotide)
```



```
[66] # Return the index position of the gap in the following sequence
    sequence = 'ATGTGG-TGGAGA'
    position = None
    temp = 0
    while position == None:
        nucleotide = sequence[temp]
        if nucleotide == '-':
            position = temp
        print(position, temp, nucleotide)
        temp+=1
```



```
[66] # Return the index position of the gap in the following sequence
    sequence = 'ATGTGG-TGGAGA'
    position = None
    temp = 0
    while position == None:
        nucleotide = sequence[temp]
    if nucleotide == '-':
        position = temp
    print(position, temp, nucleotide)
    temp+=1
```

Answer









Proficiency Assessment

Exercise 1: Return the total number of guanines Sequence A.

You can use the count() function in python to check your work!



Start with a variable called counter equal to 0

For loop through each nucleotide of the sequence

Use a condition statement to identify a guanine in the sequence

Record by tallying the guanines found

Exercise 2: How many differences are between Sequence A and Sequence B Refer to Exercise 1 for ideas

Exercise 3: You will be given a list of protein-coding sequences and other resources (i.e. dictionary). Find the following for each sequence:

Length of the DNA sequence

Transcript of the DNA sequence (RNA sequence)

Coding sequence as a list

Amino acid sequence

Bonus: add something yourself! ☺

