### An Introduction to Python

Day 3
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#### Combining what we've learnt

Yesterday we learnt a lot of different bits of Python. Let's summarize that knowledge by writing a **module** of functions to do various analysis on values in a list.

\* In a text editor:

```
#Functions to analyse values in a list

#print the numbers in the list
def printNums(numbers):
    for num in numbers:
        print num
```

\* Comment your code well so you remember what it does when you look at it again.

\* A function to sum values:

\* A function to average numbers:

```
#returns the mean average of a list of numbers
               def averageNums(numbers):
                        sumOfNums = sumNums(numbers)
* A function
                        average = float(sumOfNums) / len(numbers)
                        return average
  to calculate
  the
               #returns the variance of a list of numbers
               def varianceNums(numbers):
  variance:
                       variance = [0]*len(numbers)
                        average = averageNums(numbers)
                        for num in numbers:
                                variance[numbers.index(num)]=(num-average)**2
                        return averageNums(variance)
```

>>> myList = [0]

[0, 0, 0, 0, 0]

>>> myList

```
def varianceNums(numbers):
                        variance = [0]*len(numbers)
                        average = averageNums(numbers)
                        for num in numbers:
                                variance[numbers.index(num)]=(num-average)**2
* A function to
                        return averageNums(variance)
  calculate the
  population
                def stdDevNums(numbers):
                        variance = varianceNums(numbers)
  standard
                        try:
  deviation
                                return variance ** .5
  using the
                        except (TypeError):
                                print("wrong data type received")
  variance
```

#returns the variance of a list of numbers

\* Test it

```
>>> import myStats
>>> myStats.stdDevNums([3.14,5.32,1.34,5.67])
1.7518757804136684
>>> myStats.varianceNums([3.14,5.32,1.34,5.67])**0.5
1.7518757804136684
```

#### Quiz Time:

What Is the average and standard deviation of: [3.14, 5.32, 1.34, 5.67]

## More Dictionary Methods

```
* .items() returns key value pairs* .keys() returns just the keys* .values() returns just the value
```

```
>>> myDictionary={'name':'harry','hair':'brown','eyes':'brown'}
>>> print myDictionary.items()
[('hair', 'brown'), ('eyes', 'brown'), ('name', 'harry')]
>>> print myDictionary.keys()
['hair', 'eyes', 'name']
>>> print myDictionary.values()
['brown', 'brown', 'harry']
```

\* This is useful so we can iterate over dictionaries more easily...

#### Iterating over dictionaries

The comma means "on the same line":

```
>>> for key in myDictionary:
...    print key, myDictionary[key]
...
hair brown
eyes brown
name harry
>>> for key in myDictionary:
...    print key, myDictionary[key],
...
hair brown eyes brown name harry
```

If we want to create a list that is a modified version of an existing list we usually do something like this:

Python offers an easy alternative!

```
>>> squares = [x**2 for x in range(10)]
>>> squares
[0, 1, 4, 9, 16, 25, 36, 49, 64, 81]
```

```
>>> squares = [x**2 for x in range(10)]
>>> squares
[0, 1, 4, 9, 16, 25, 36, 49, 64, 81]
```

```
To create a list this way:
newList = [expression for value in oldList]
```

```
>>> compDict={'A':'T','T':'A','C':'G','G':'C'}
>>> seq = 'AAATCGAT'
>>> revComp = [compDict[x] for x in seq.upper() if x in 'ACGT']
>>> revComp
['T', 'T', 'T', 'A', 'G', 'C', 'T', 'A']
>>> revComp.reverse()
>>> ''.join(revComp)
'ATCGATTT'
```

Reverse complement function we wrote previous in much less code!

Have to reverse() the list and then use a string method (join) to turn the list of characters into a string.

# Slicing Up a List (with Stride)

#### listName[start:end:stride]

From 1<sup>st</sup> value to 6<sup>th</sup>, choosing every 3<sup>rd</sup> value.

From 2<sup>nd</sup> value to 9<sup>th</sup> value, choosing every 4<sup>th</sup>

Entire list, every value, in reverse

2<sup>nd</sup> value to 1<sup>st</sup>, don't skip any

From beginning of list to 4<sup>th</sup> value, in reverse >>> myList[:4:-1]

```
>>> myList = range(11)
                         >>> myList
                          [0, 1, 2, 3, 4, 5, 6, 7, 8, 9, 10]
                         >>> myList[:6:3]
                          [0, 3]
                         >>> myList[2:9:4]
                          [2, 6]
                         >>> myList[::2]
   Entire list, every other value [0, 2, 4, 6, 8, 10]
                         >>> myList[::-1]
                          [10, 9, 8, 7, 6, 5, 4, 3, 2, 1, 0]
                         >>> myList[2::-1]
                          [2, 1, 0]
                         >>> myList[9::-1]
9<sup>th</sup> value to end of list, in reverse [9, 8, 7, 6, 5, 4, 3, 2, 1, 0]
                          [10, 9, 8, 7, 6, 5]
```

#### Lambda functions

An alternative way to define a function.

```
>>> def byThree(x):
...     return x % 3 == 0
...
>>> byThree(9)
True
>>> lambda x:x%3==0
<function <lambda> at 0x10a51e398>
```

Not useful on its own but for use in conjunction with other functions!

#### Filters (use lambda functions!)

#### filter(function, list)

```
>>> def byThree(x):
... return x % 3 == 0
...
>>> myList = range(16)
>>> print filter(byThree, myList)
[0, 3, 6, 9, 12, 15]
```

```
>>> print filter(lambda x:x%3==0,myList)
[0, 3, 6, 9, 12, 15]
```

#### Filters (use lambda functions!)

filter(function, list)

```
>>> names = ["john", "simon", "jane", "jenny"]
>>> print filter(lambda x:x == 'simon', names)
['simon']
>>> myList = range(50)
>>> print filter(lambda x:x%3==0 and x%4==0, myList)
[0, 12, 24, 36, 48]
```

## File Input.

Reading from a file is the main way of getting biological data into Python.

```
fileVariable = open("fileName.txt", "w")
```

fileVariable.read(size)
size is optional and specifies how many bytes to read

fileVariable.readLine()
reads and returns a single line of the file

## File Output

Writing results to a file is useful for large data sets and for exporting to other programs to create graphs etc.

fileVariable.write(string)

writes the contents of string to the file.

fileVariable.tell()

returns an integer value representing how far through the file you currently are, in bytes.

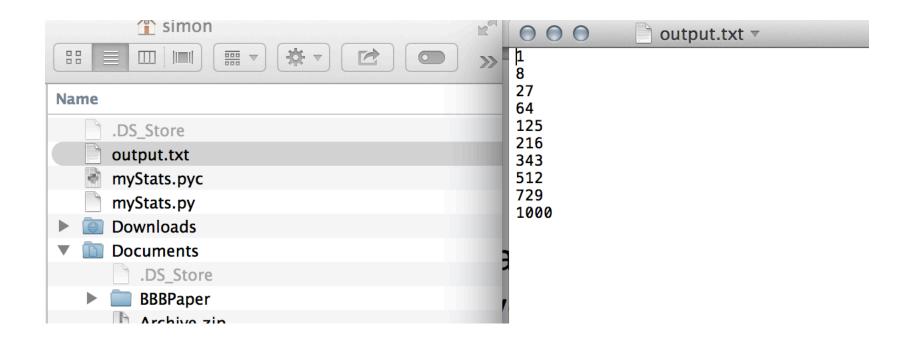
fileVariable.seek(offset,o)

change current position in file to offset bytes from the beginning. To offset from current position or end do seek(offset,1) or seek(offset,2) respectively.

### File Input/Output Example.

```
>>> myList = [x**3 for x in range(1,11)]
>>> file = open("output.txt","w")
>>> for item in myList:
... file.write(str(item) + "\n")
...
>>> file.close()
>>> ■
```

# File Output.



#### Always close() Files

It's important to close() a file when you have finished writing or reading from it.

```
>>> with open("text.txt","w") as fileVariable:
... fileVariable.write("Great Success")

>>> fileVariable
<closed file 'text.txt', mode 'w' at 0x10a4e9780>
>>> fileVariable.closed
True
>>> []
```

Alternatively use with open() as variable: to automatically close the file after the code is executed.

#### File Mode

What does the "w" do in: Open("fileName.txt", "w")

mode can be 'r' when the file will only be read, 'w' for only writing (an existing file with the same name will be erased), and 'a' opens the file for appending; any data written to the file is automatically added to the end. 'r+' opens the file for both reading and writing. The mode argument is optional; 'r' will be assumed if it's omitted.

#### File Mode

```
>>> myFile = open("output.txt","r")
>>> print myFile.readline()
>>> print myFile.readline()
>>> print myFile.readline()
27
>>> print myFile.readline()
64
>>> print myFile.read()
125
216
343
512
729
1000
>>> myFile.close
<built-in method close of file object at 0x10a4e98a0>
>>> myFile.close()
```

#### fastQ file

#### Contain reads for sequencing analysis.

A FASTQ file normally uses four lines per sequence.

- Line 1 begins with a '@' character and is followed by a sequence identifier and an optional description (like a FASTA title line).
- Line 2 is the raw sequence letters.
- Line 3 begins with a '+' character and is optionally followed by the same sequence identifier (and any description) again.
- Line 4 encodes the quality values for the sequence in Line 2, and must contain the same number of symbols as letters in the sequence.

A FASTQ file containing a single sequence might look like this:

```
@SEQ_ID
GATTTGGGGTTCAAAGCAGTATCGATCAAATAGTAAATCCATTTGTTCAACTCACAGTTT
+
!''*((((***+))%%%++)(%%%%).1***-+*''))**55CCF>>>>>CCCCCCC65
```

#### fastQ file

www.signalingsystems.ucla.edu/users/Simon/example.fastq

#### fastQ Example

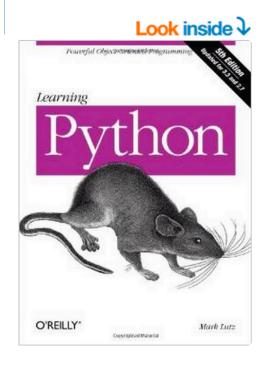
#### Code to find which reads contain an adapter sequence

#### fastQ Example

#### Let's test it!

```
SiMac:~ simon$ python fastQAdapter.py
Total Lines:25
Count of adapter:9
Percentage of reads containing the adapter:36.00
```

#### Continued learning



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