

# An Introduction to Python

Day 3

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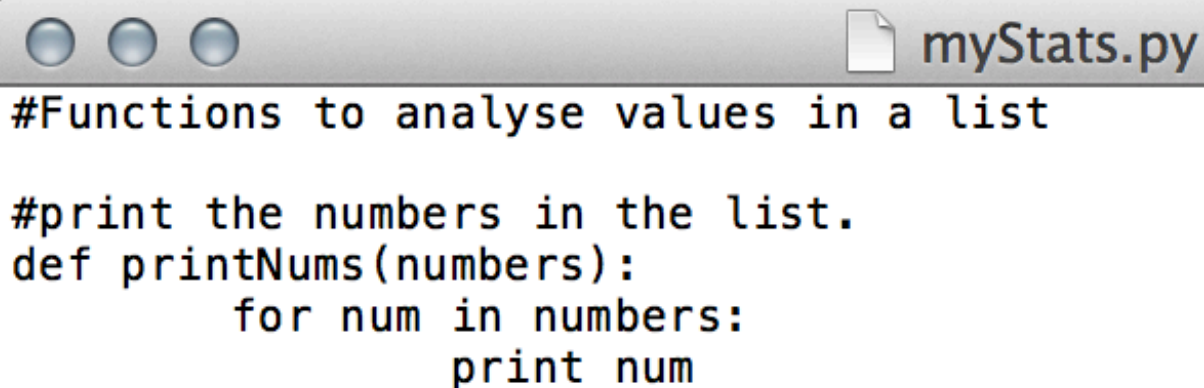
# Combining what we've learnt



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

# myStats.py

\* 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.

# myStats.py

\* A function to sum values:

```
#sum the values in the list
def sumNums(numbers):
    total = 0
    for num in numbers:
        total += num
    return total
```

# myStats.py

\* A function to average numbers:

```
#returns a mean average of the numbers in the list
def averageNums(numbers):
    sumOfNums = sumNums(numbers)
    average = float(sumOfNums) / len(numbers)
    return average
```

# myStats.py

\* A function to calculate the variance:

```
#returns the variance of a list of numbers
def varianceNums(numbers):
    variance = 0
    average = averageNums(numbers)
    for num in numbers:
        variance += (average-num) **2
    return float(variance)/len(numbers)
```

# myStats.py

- \* A function to calculate the standard deviation, given the variance:

```
#returns the standard deviation given the variance:
def stdDevNums(variance):
    try:
        return variance ** .5
    except TypeError:
        print "Variance was not a numer"
```

# myStats.py

\* Test it

```
>>> myList=[4,7,5,2,8,5,8,3]
>>> import myStats
>>> myStats.stdDevNums(myStats.varianceNums(myList))
```

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
```

# List Comprehension

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

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

Python offers an easy alternative!

# List Comprehension

```
>>> squares = []
>>> for x in range(10):
...     squares.append(x**2)
...
>>> 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]
```

# List Comprehension

```
>>> 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]`

# List Comprehension

```
>>> 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 other value

Entire list, every value, in reverse

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

9<sup>th</sup> value to end of list, in reverse

From beginning of list to 4<sup>th</sup> value, in reverse

```
>>> 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]
[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, 8, 7, 6, 5, 4, 3, 2, 1, 0]
>>> myList[:4:-1]
[10, 9, 8, 7, 6, 5]
```

# Slicing Up a List (with Stride)

`listName[start:end:stride]`

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>>> 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]
[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, 8, 7, 6, 5, 4, 3, 2, 1, 0]
>>> myList[:4:-1]
[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.

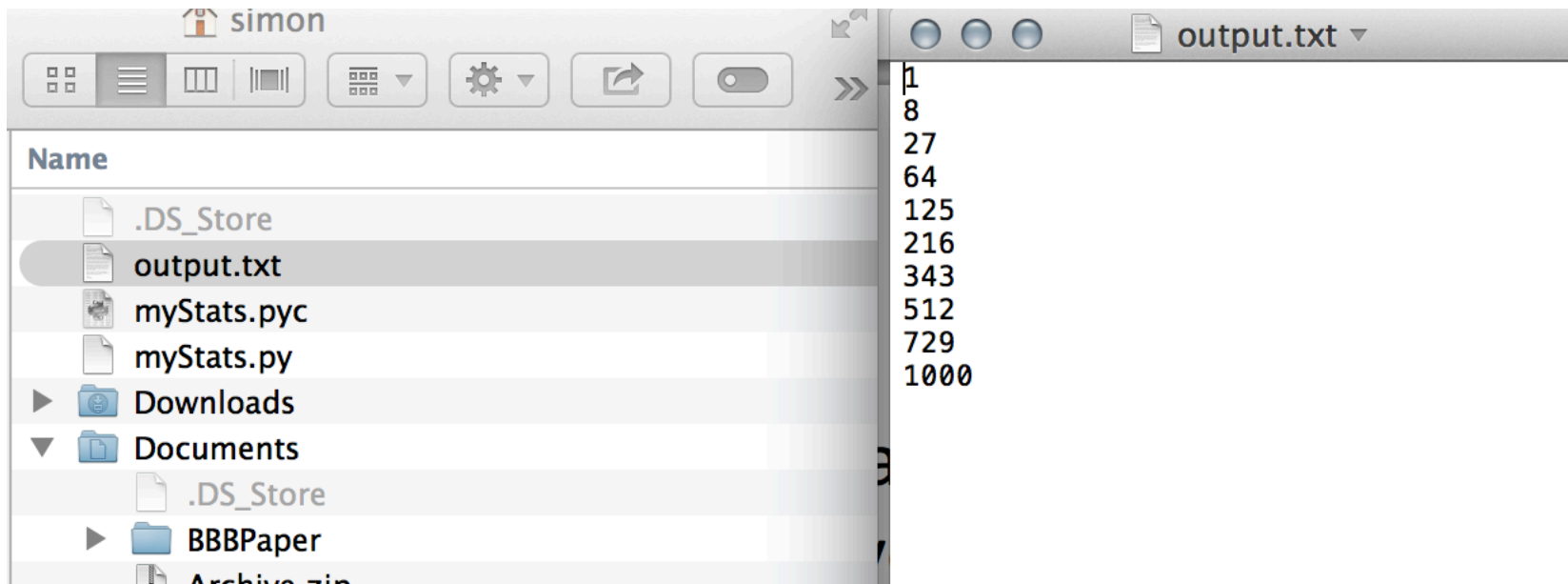
*fileVariable.seek(offset,0)*

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()
>>> █
```

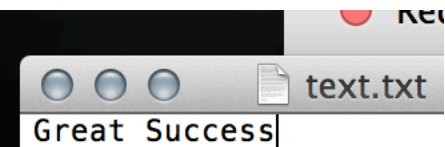
# File Output.



# 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()
1

>>> print myFile.readline()
8

>>> 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>>>>>>CCCCCCCC65
```

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```

# fastQ Example

Code to find which reads contain an adapter sequence

```
>>> myFile=open("example.fastq","r")
>>> adapterSequence='GCCAAT'
>>> totalLines=0
>>> countOfAdapter=0
>>> for line in myFile:
...     if line[0] == 'N':
...         if adapterSequence in line:
...             countOfAdapter+=1
...             totalLines+=1
...
>>> totalLines
25
>>> countOfAdapter
9
>>> percentage=(float(countOfAdapter)/totalLines)*100
>>> print "%d percent of reads contain the adapter sequence" % percentage
36 percent of reads contain the adapter sequence
```

# Thanks!



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