Programming for Biologists

Streams

- A stream is a temporally ordered sequence of indefinite length
 - Keyboard entries are a stream of characters that Python is processing
 - o Data residing in files is also accessed as a stream
 - We think of files as data on some media, but in programming it can be abstract to include anything from an external source
- Python allows you to read files in many different modes
- To create a file object, simply use the open command:f = open(path, mode)

Different modes

Value	Mode	Interpretation
t	Text (default)	Characters or Strings
b	Binary	bytes

Value	Initial Position	Read	Write
r	Beginning	Y	N
W	Beginning	N	Y
а	End	N	Υ
r+	Beginning	Υ	Υ
W+	Beginning	Υ	Υ
a+	End	Y	Υ

File operations

	Operation	Interpretation
	output = open(r'C:\spam', 'w')	Create output file ('w' means write)
ns	input = open('data', 'r')	Create input file ('r' means read)
	input = open('data')	Same as prior line ('r' is the default)
	aString = input.read()	Read entire file into a single string
	aString = input.read(N)	Read up to next N characters (or bytes) into a string
	aString = input.readline()	Read next line (including \n newline) into a string
	aList = input.readlines()	Read entire file into list of line strings (with \n)
	anyFile.seek(N)	Change file position to offset N for next operation
	for line in open('data'):	use line File iterators read line by line
	open('f.txt', encoding='latin-1')	Python 3.0 Unicode text files (str strings)
	open('f.bin', 'rb')	Python 3.0 binary bytes files (bytes strings)

File operations

Operation	Interpretation	
output.writelines(aList)	Write all line strings in a list into file	
output.close()	Manual close (done for you when file is collected)	
output.flush()	Flush output buffer to disk without closing	
output.write(aString)	Write a string of characters (or bytes) into file	

Learning Python, Table 9-2, p. 232

Input/Output: working with files

You can create a file object to work with by assigning the open function to a name:

```
input = open('sequences.fa','r')  # open a fasta file for reading
input = open('./sequences.fa')  # same as above
output = open('processed_data.txt','w') # open outfile for writing
```

Bioinformatics Programming using Python

The with statement

This statement is used to open and name a file, then automatically close the file (regardless of any errors that may occur during execution of its statements).

You can also open a list of files, e.g. to read from one file and write to another

```
with open(path, mode) as name:
    statements-using-name
```

with open(path1,mode1) as name1, open(path2,mode2) as name2, ... :
 statements-using-name

Bioinformatics Programming using Python

File data are interpreted as strings!

- Whenever you read or write a line in a file from Python, all file text takes the form of strings.
- Therefore, if you want to work with numbers in a data file, you have to convert string data to numbers.
- Similarly, you have to send output as formatted strings.
- String conversion can be done using e.g. int, float, str, and string formatting expressions.