Introduction to Python programming for biologists

MARC: Developing Bioinformatics Programs
July 2009

Alex Ropelewski
PSC-NRBSC

Bienvenido Vélez
UPR Mayaguez

Reference: How to Think Like a Computer Scientist: Learning with Python

- The following material is the result of a curriculum development effort to provide a set of courses to support bioinformatics efforts involving students from the biological sciences, computer science, and mathematics departments. They have been developed as a part of the NIH funded project "Assisting Bioinformatics Efforts at Minority Schools" (2T36 GM008789). The people involved with the curriculum development effort include:

- Dr. Hugh B. Nicholas, Dr. Troy Wymore, Mr. Alexander Ropelewski and Dr. David Deerfield II, National Resource for Biomedical Supercomputing, Pittsburgh Supercomputing Center, Carnegie Mellon University.
- Dr. Ricardo González Méndez, University of Puerto Rico Medical Sciences Campus.
- Dr. Alade Tokuta, North Carolina Central University.
- Dr. Jaime Seguel and Dr. Bienvenido Vélez, University of Puerto Rico at Mayagüez.
- Dr. Satish Bhalla, Johnson C. Smith University.

Outline

- Introduction to Programming (Today)
  - Why learn to Program?
  - The Python Interpreter
  - Software Development Process
  - Numbers, Strings, Operators, Expressions
- Control structures, decisions, iteration and recursion

Why Learn to Program?

US Department of Labor, Bureau of Labor Statistics

Engineers, Life and Physical Scientists and Related Occupations. Occupational Outlook Handbook, 2008-09 Edition.

Biological scientists "…usually study allied disciplines such as mathematics, physics, engineering and computer science. Computer courses are beneficial for modeling and simulating biological processes, operating some laboratory equipment and performing research in the emerging field of bioinformatics"

Why Learn to Program?

- Need to compare output from a new run with an old run. (new hits in database search)
- Need to compare results of runs using different parameters. (Pam120 vs Blosum62)
- Need to compare results of different programs (Fasta, Blast, Smith-Waterman)
- Need to modify existing scripts to work with new/updated programs and web sites.
- Need to use an existing program's output as input to a different program, not designed for that program:
    - Database search -> Multiple Alignment
    - Multiple Alignment -> Pattern search
    - Need to Organize your data

Why Learn to Program?

Bioinformatics Assembly Analyst

Responsibilities:

- Assembling genome sequence data using a variety of tools and parameters and performing the experiments needed to evaluate sequencing strategies
- Using existing software and databases to analyze genomic data and correlating assemblies and sequences with a variety of genetic and physical maps and other biological information
- Identifying problems and serving as point of contact for various groups to propose and implement solutions
- Proposing and implementing upgrades to existing tools and processes to enhance analysis techniques and quality of results
- Developing and implementing scripts to manipulate, format, parse, analyze, and display genome sequence data; and developing new strategies for analysis and presentation of results.

Requirements:

- A bachelor's degree in biology or related field
- At least three years of experience in DNA sequencing and sequence analysis.
- Must possess solid knowledge of sequencing software and public sequencing databases.
- Knowledge of bioinformatics tools helpful.

Good Languages to Learn
In no particular order….

- C/C++
  - Language of choice for most large development projects
- FORTRAN
  - Excellent language for math, not used much anymore
- Java
  - Popular modern object oriented language
- PERL
  - Excellent language for text-processing (bioperl.org)
- PHP
  - Popular language used to program web interfaces
- Python
  - Language easy to pick up and learn (biopython.org)
- SQL
  - Language used to communicate with a relational database

Python is Object Oriented

- "Object Oriented" is simply a convenient way to organize your data and the functions that operate on that data
- A biological example of organizing data:
  - Human.CytochromeC.protein.sequence
  - Human.CytochromeC.RNA.sequence
  - Human.CytochromeC.DNA.sequence
- Some things only make sense in the context that they are used:
  - Human,CytochromeC.DNA.intron
  - Human.CytochromeC.DNA.exon
  - Human.CytochromeC.DNA.sequence
  - Human.CytochromeC.protein.sequence
  - Human.CytochromeC.protein.intron
  - Human.CytochromeC.protein.exon

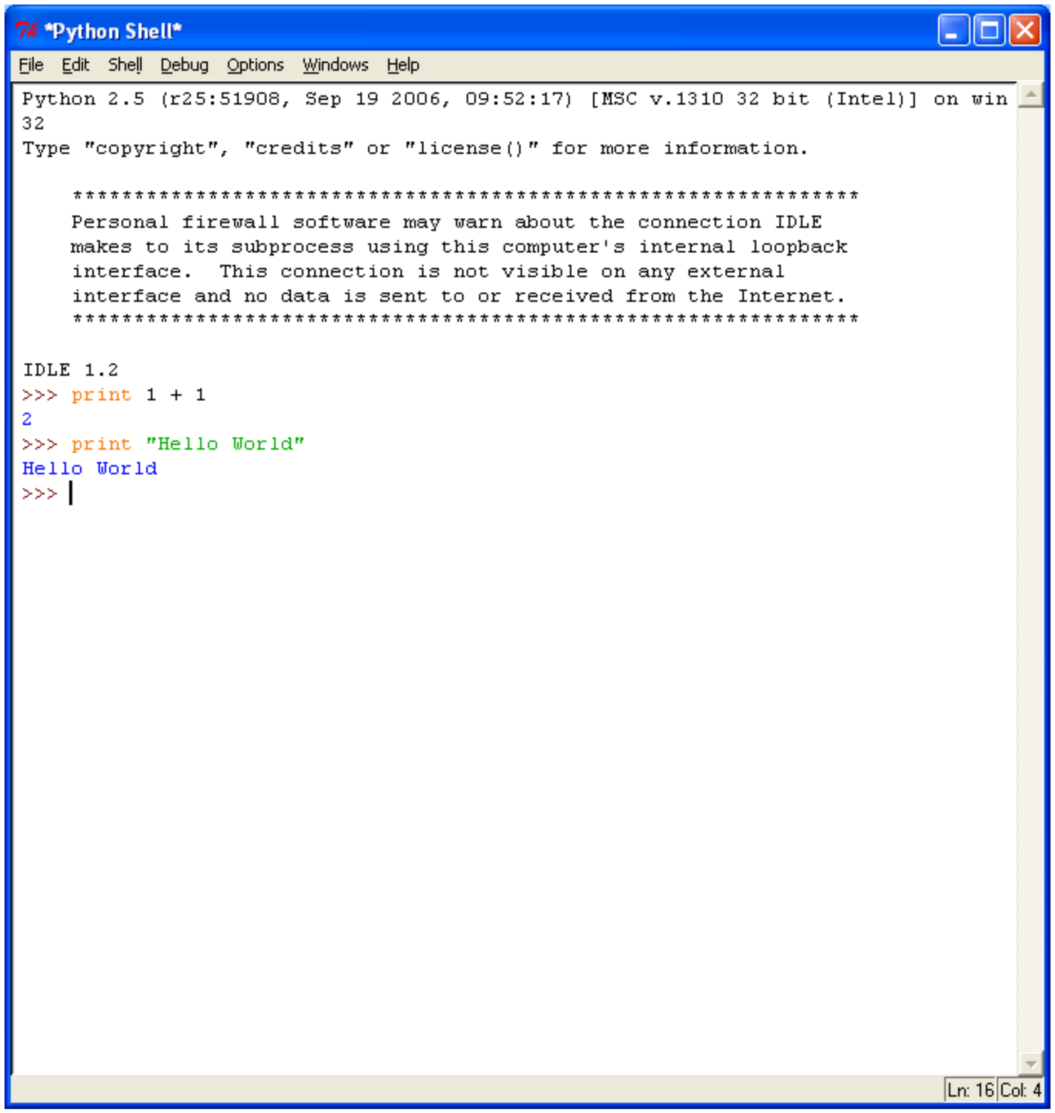
Meaningful

Meaningless

Downloading and Installing Python

- Go to www.python.org
- Go to DOWNLOAD section
- Click on Python 2.6.2 Windows installer
- Save ~10MB file into your hard drive
- Double click on file to install
- Follow instructions
- Start -> All Programs -> Python 2.6 -> Idle

Idle: The Python Shell



```
Python 2.5 (r25:51908, Sep 19 2006, 09:52:17) [MSC v.1310 32 bit (Intel)] on win
32
Type "copyright", "credits" or "license()" for more information.

    ****************************************************************
    Personal firewall software may warn about the connection IDLE
    makes to its subprocess using this computer's internal loopback
    interface.  This connection is not visible on any external
    interface and no data is sent to or received from the Internet.
    ****************************************************************

IDLE 1.2
>>> print 1 + 1
2
>>> print "Hello World"
Hello World
>>> 
```

Python as a Number Cruncher

```
>>> print 1 + 3
4
>>> print 6 * 7
42
>>> print 6 * 7 + 2
44
>>> print 2 + 6 * 7
44
>>> print 6 - 2 - 3
1
>>> print 6 - ( 2 - 3)
7
>>> print 1 / 3
0
>>>
```

/ and * higher precedence than + and -

Operators are left associative

Parenthesis can override precedence

integer division truncates fractional part

Floating Point Expressions

```
>>> print 1.0 / 3.0
0.333333333333
>>> print 1.0 + 2
3.0
>>> print 3.3 * 4.23
13.959
>>> print 3.3e23 * 2
6.6e+023
>>> print float(1) /3
0.333333333333
>>>
```

12 decimal digits default precision

Mixed operations converted to float

Scientific notation allowed

Explicit conversion

String Expressions

```
>>> print "aaa"
aaa
>>> print "aaa" + "ccc"
aaaccc
>>> len("aaa")
3
>>> len ("aaa" + "ccc")
6
>>> print "aaa" * 4
aaaaaaaaaaaa
>>> "aaa"
'aaa'
>>> "c" in "atc"
True
>>> "g" in "atc"
False
>>>
```

+ concatenates string

len is a function that returns the length of its argument string

any expression can be an argument

* replicates strings

a value is an expression that yields itself

in operator finds a string inside another
And returns a boolean result

Values Can Have (MEANINGFUL) Names

```
>>> numAminoAcids = 20
>>> eValue = 6.022e23
>>> prompt = "Enter a sequence ->"
>>> print numAminoAcids
20
>>> print eValue
6.022e+023
>>> print prompt
Enter a sequence ->
>>> print "prompt"
prompt
>>>
>>> prompt = 5
>>> print prompt
5
>>>
```

= binds a name to a value

use Camel case for compound names

prints the value bound to a name

= can change the value associated with a name even to a different type

Values Have Types

```
>>> type("hello")
<type 'str'>
>>> type(3)
<type 'int'>
>>> type(3.0)
<type 'float'>
>>> type(eValue)
<type 'float'>
>>> type (prompt)
<type 'int'>
>>> type(numAminoAcids)
<type 'float'>
>>>
```

$\rightarrow$ type is another function

$\rightarrow$ the “type” is itself a value

$\rightarrow$ the type of a name is the type of the value bound to it

In Bioinformatics Words …

```
>>> codon=“atg”
>>> codon * 3
’atgatgatg’
>>> seq1 =“agcgccttgaattcggcaccaggcaaatctcaaggagaagttccggggagaaggtgaaga”
>>> seq2 = “cggggagtggggagttgagtcgcaagatgagcgagcggatgtccactatgagcgataata”
>>> seq = seq1 + seq2
>>> seq
'agcgccttgaattcggcaccaggcaaatctcaaggagaagttccggggagaaggtgaagacggggagtggggagttgagtc
gcaagatgagcgagcggatgtccactatgagcgataata‘
>>> seq[1]
'g'
>>> seq[0]
'a'
>>> “a” in seq
True
>>> len(seq1)
60
>>> len(seq)
120
```

First nucleotide starts at 0

More Bioinformatics
Extracting Information from Sequences

```
>>> seq[0] + seq[1] + seq[2]
'agc'
>>> seq[0:3]
'agc'
>>> seq[3:6]
'gcc'
>>> seq.count('a')
35
>>> seq.count('c')
21
>>> seq.count('g')
44
>>> seq.count('t')
12
>>> long = len(seq)
>>> pctA = seq.count('a')
>>> float(pctA) / long * 100
29.166666666666668
```

Find the first codon from the sequence

get 'slices' from strings:

How many of each base does this sequence contain?

Count the percentage of each base on the sequence.

Additional Note About Python Strings

```
>>> seq="ACGT"
>>> print seq
ACGT

>>> seq="TATATA"
>>> print seq
TATATA
```

Can replace one whole string with another whole string

```
>>> seq[0] = seq[1]
Traceback (most recent call last):
  File "<pyshell#33>", line 1, in <module>
    seq[0]=seq[1]
TypeError: 'str' object does not support item assignment
```

Can NOT simply replace a sequence character with another sequence character, but…

```
seq = seq[1] + seq[1:]
```

Can replace a whole string using substrings

Commenting Your Code!

- How?
  - Precede comment with # sign
  - Interpreter ignores rest of the line
- Why?
  - Make code more readable by others AND yourself?
- When?
  - When code by itself is not evident

    ```
    # compute the percentage of the hour that has elapsed
    percentage = (minute * 100) / 60
    ```

  - Need to say something but Python cannot express it, such as documenting code changes

    ```
    percentage = (minute * 100) / 60 # FIX: handle float division
    ```

Please <u>do not</u> over do it $\longrightarrow$ $\boxed{\text{X = 5 # Assign 5 to x}}$

Software Development Cycle

- Problem Identification
  - What is the problem that we are solving
- Algorithm Development
  - How can we solve the problem in a step-by-step manner?
- Coding
  - Place algorithm into a computer language
- Testing/Debugging
  - Make sure the code works on data that you already know the answer to
- Run Program
  - Use program with data that you do not already know the answer to.

Lets Try It With Some Examples!

- First, lets learn to SAVE our programs in a file:
  - From Python Shell: File -> New Window
  - From New Window: File->Save
- Then, To run the program in the new window:
  - From New Window: Run->Run Module

Problem Identification

- What is the percentage composition of a nucleic acid sequence
  - DNA sequences have four residues, A, C, G, and T
  - Percentage composition means the percentage of the residues that make up of the sequence

Algorithm Development

- Print the sequence
- Count characters to determine how many A, C, G and T’s make up the sequence
- Divide the individual counts by the length of the sequence and take this result and multiply it by 100 to get the percentage
- Print the results

Coding

```
seq="ACTGTCGTAT"
print seq
Acount= seq.count('A')
Ccount= seq.count('C')
Gcount= seq.count('G')
Tcount= seq.count('T')
Total = len(seq)
APct = int((Acount/Total) * 100)
print 'A percent = %d ' % APct
CPct = int((Ccount/Total) * 100)
print 'C percent = %d ' % CPct
GPct = int((Gcount/Total) * 100)
print 'G percent = %d ' % GPct
TPct = int((Tcount/Total) * 100)
print 'T percent = %d ' % TPct
```

Let’s Test The Program

- First SAVE the program:
    - From New Window: File->Save

Testing / Debugging

- Six Common Python Coding Errors:
  - Delimiter mismatch: check for matches and proper use.
    - Single and double quotes: ‘ ’   “ ”
    - Parenthesis and brackets: { }   [ ]   ( )
  - Spelling errors:
    - Among keywords
    - Among variables
    - Among function names
  - Improper indentation
  - Import statement missing
  - Function calling parameters are mismatched
  - Math errors:
    - Automatic type conversion: Integer vs floating point
    - Incorrect order of operations – always use parenthesis.

Testing / Debugging

```
seq='ACTGTCGTAT"
print seq;
Acount= seq.count('A')
Ccount= seq.count('C')
Gcount= seq.count('G')
Tcount= seq,count('T')
Total = Len(seq)
APct = int((Acount/Total) * 100)
print 'A percent = %d ' % APct
CPct = int((Ccount/Total) * 100)
print 'C percent = %d ' % Cpct
GPct = int(Gcount/Total) * 100)
primt 'G percent = %d ' % GPct
TPct = int((Tcount/Total) * 100)
print 'T percent = %d ' % TPct
```

Let’s Test The Program

- First, re-SAVE the program:
  - File->Save
- Then RUN the program:
  - Run->Run Module
- Then LOOK at the Python Shell Window:
  - If successful, the results are displayed
  - If unsuccessful, error messages will be displayed

Testing/Debugging

- The program says that the composition is:
  - 0%A,   0%C, 0%G, 0%T
- The real answer should be:
  - 20%A, 20%C, 20%G, 40%T
- The problem is in the coding step:
  - Integer math is causing undesired rounding!

Testing/Debugging

```
seq="ACTGTCGTAT"
print seq
Acount= seq.count('A')
Ccount= seq.count('C')
Gcount= seq.count('G')
Tcount= seq.count('T')
Total = float(len(seq))
APct = int((Acount/Total) * 100)
print 'A percent = %d ' % APct
CPct = int((Ccount/Total) * 100)
print 'C percent = %d ' % CPct
GPct = int((Gcount/Total) * 100)
print 'G percent = %d ' % GPct
TPct = int((Tcount/Total) * 100)
print 'T percent = %d ' % TPct
```

Let’s change the nucleic acid sequence from DNA to RNA…

- If the first line was changed to:
  - seq = “ACUGCUGUAU”
- Would we get the desired result?

Testing/Debugging

- The program says that the composition is:
    - 20%A,   20%C, 20%G, 0%T
- The real answer should be:
    - 20%A, 20%C, 20%G, 40%U
- The problem is that we have not defined the problem correctly!
    - We designed our code assuming input would be DNA sequences
    - We fed the program RNA sequences

Problem Identification

- What is the percentage composition of a nucleic acid sequence
  - DNA sequences have four residues, A, C, G, and T
  - In RNA sequences “U” is used in place of “T”
  - Percentage composition means the percentage of the residues that make up of the sequence

Algorithm Development

- Print the sequence
- Count characters to determine how many A, C, G, T and U's make up the sequence
- Divide the individual A,C,G counts and the sum of T's and U's by the length of the sequence and take this result and multiply it by 100 to get the percentage
- Print the results

Testing/Debugging

```
seq="ACUGUCGUAU"
print seq
Acount= seq.count('A')
Ccount= seq.count('C')
Gcount= seq.count('G')
TUcount= seq.count('T') + seq.count('U')
Total = float(len(seq))
APct = int((Acount/Total) * 100)
print 'A percent = %d ' % APct
CPct = int((Ccount/Total) * 100)
print 'C percent = %d ' % CPct
GPct = int((Gcount/Total) * 100)
print 'G percent = %d ' % GPct
TUPct = int((TUcount/Total) * 100)
print 'T/U percent = %d ' % TUPct
```

What's Next

- Extend your code to handle the nucleic acid ambiguous sequence characters "N" and "X"
- Extend your code to handle protein sequences