Practical Bioinformatics

Mark Voorhies

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Course website:

• http://histo.ucsf.edu/BMS270/

Resources on the course website:

- Syllabus
 - Papers and code (for downloading before class)
 - Slides and transcripts (available after class)
- On-line textbooks (Dive into Python, Numerical Recipes, ...)
- Programs for this course (Canopy, Cluster3, JavaTreeView, ...)

Homework

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- E-mail Mark any homework code/results before tomorrow's class

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- If you get stuck, try working things out on paper first.

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- Writing standalone scripts.

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- Shepherding data between analysis tools.

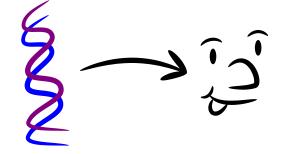
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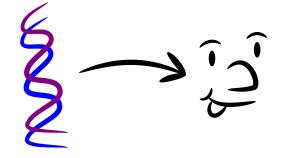
This is also good preparation for communicating with computational collaborators.

Course problems: expression and sequence analysis



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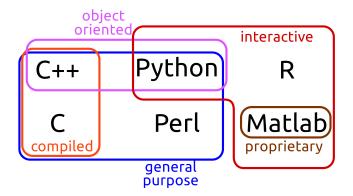
Course problems: expression and sequence analysis



Part 2: Genotype (Sequence analysis)

Part 1: Phenotype (Expression profiling)

Course tool: Python



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Python distribution: Enthought Canopy

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Python distribution: Enthought Canopy



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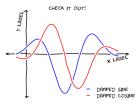
Python distribution: Enthought Canopy

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Python shell: ipython (jupyter) notebook

```
In [3]: np.random.seed(0)
ax = pylab.axes()
x = np.lanpace(0, 10, 100)
x.plot(x, np.sin(x) * np.exp(-0.1 * (x - 5) ** 2), 'b', lw=1, label='damped sine')
ax.plot(x, .np.cs(x) * np.exp(-0.1 * (x - 5) ** 2), 'r', lw=1, label='damped cosine')
ax.set_tile('check it out!')
ax.
```

Out[5]: <matplotlib.axes.AxesSubplot at 0x2fecbd0>



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Anatomy of a Programming Language



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Anatomy of a Programming Language

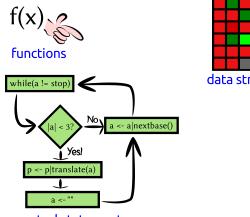




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Anatomy of a Programming Language

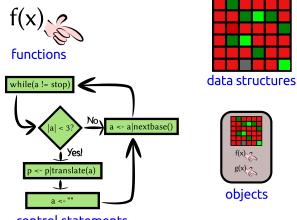


control statements

data structures

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Anatomy of a Programming Language



control statements

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Talking to Python: Nouns

```
# This is a comment
# This is an int (integer)
42
# This is a float (rational number)
4.2
# These are all strings (sequences of characters)
'ATGC'
```

"Mendel's Laws"

""">CAA36839.1 Calmodulin MADQLTEEQIAEFKEAFSLFDKDGDGTITTKELGTVMRSLGQNPTEAEL QDMINEVDADDLPGNGTIDFPEFLTMMARKMKDTDSEEEIREAFRVFDK DGNGYISAAELRHVMTNLGEKLTDEEVDEMIREADIDGDGQVNYEEFVQ MMTAK"""

Python as a Calculator

```
# Addition
1 + 1
# Subtraction
2 - 3
# Multiplication
3*5
# Division (gotcha: be sure to use floats)
5/3.0
# Exponentiation
2**3
# Order of operations
2*3-(3+4)**2
```

Remembering objects

```
# Use a single = for assignment:
TLC = "GATACA"
YFG = "CTATGT"
MFG = "CTATGT"
```

```
# A name can occur on both sides of an assignment:
codon_position = 1857
codon_position = codon_position + 3
```

```
# Short-hand for common updates:
codon += 3
weight -= 10
expression *= 2
CFU /= 10.0
```

Python as a Calculator

• Calculate the molarity of a 70mer oligonucleotide with $A_{260} = .03$ using the formula from Maniatis:

$$C = \frac{.02A_{260}}{330L} \tag{1}$$

Calculate the T_m of a QuickChange mutagenesis primer with length 25bp (L = 25), 13 GC bases ($n_{GC} = 13$), and 2 mismatches to the template ($n_{MM} = 2$) using the formula from Stratagene:

$$T_m = 81.5 + \frac{41n_{GC} - 100n_{MM} - 675}{L}$$
(2)

Displaying values with print

```
# Use print to show the value of an object
message = "Hello, world"
print(message)
# Or several objects:
print(1,2,3,4)
# Older versions of Python use a
# different print syntax
print "Hello, world"
```

Comparing objects

```
# Use double == for comparison:
YFG == MFG
```

```
# Other comparison operators:
# Not equal:
TLC != MFG
# Less than:
3 < 5
# Greater than, or equal to:
7 >= 6
```

Making decisions

```
if (YFG == MFG):
    print "Synonyms!"

if (protein_length < 60):
    print "Probably too short to fold."
elif (protein_length > 10000):
    print "What is this, titin?"
else:
    print "Okay, this looks reasonable."
```

Collections of objects

```
# A list is a mutable sequence of objects
mylist = [1, 3.1415926535, "GATACA", 4, 5]
# Indexing
mylist[0] == 1
mylist[-1] == 5
\# Assigning by index
mylist[0] = "ATG"
# Slicing
mylist [1:3] == [3.1415926535, "GATACA"]
mylist[:2] = [1, 3.1415926535]
mylist[3:] = [4,5]
# Assigning a second name to a list
also_mylist = mylist
# Assigning to a copy of a list
my_other_list = mylist [:]
```

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Repeating yourself: iteration

```
# A for loop iterates through a list one element
\# at a time:
for i in [1,2,3,4,5]:
    print i, i**2
# A while loop iterates for as long as a condition
\# is true:
population = 1
while (population < 1e5):
    print population
    population *= 2
```

Verb that noun!

```
return_value = function(parameter, ...)
"Python, do function to parameter"
```

```
# Built-in functions
# Generate a list from 0 to n-1
a = range(5)
# Sum over an iterable object
sum(a)
# Find the length of an object
len(a)
```

Verb that noun!

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```
# Importing functions from modules
import numpy
numpy.sqrt(9)
```

```
import matplotlib.pyplot as plt
fig = plt.figure()
plt.plot([1,2,3,4,5],
                          [0,1,0,1,0])
```

from IPython.core.display import display
display(fig)

New verbs

def function(parameter1, parameter2): """Do this!""" # Code to do this return return_value



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- Likewise, we can use modules and scripts to document our computer "protocols".
- Most of these statements are applicable to any programming language (Perl, R, Bash, Java, C/C++, FORTRAN, ...)

Homework: Make your own Fun

Write functions for these calculations, and test them on random data:

Mean:

$$\bar{x} = \frac{\sum_{i}^{N} x_{i}}{N}$$

Standard deviation:

$$\sigma_{x} = \sqrt{\frac{\sum_{i}^{N} (x_{i} - \bar{x})^{2}}{N - 1}}$$

Sorrelation coefficient (Pearson's r):

$$r(x,y) = \frac{\sum_{i} (x_{i} - \bar{x})(y_{i} - \bar{y})}{\sqrt{\sum_{i} (x_{i} - \bar{x})^{2}} \sqrt{\sum_{i} (y_{i} - \bar{y})^{2}}}$$