

Practical Bioinformatics

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4/2/2018

Resources

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

- E-mail Mark your python sessions (.ipynb files) after class
- E-mail Mark any homework code/results before tomorrow's class

Goals

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- Implementing new methods from the literature.

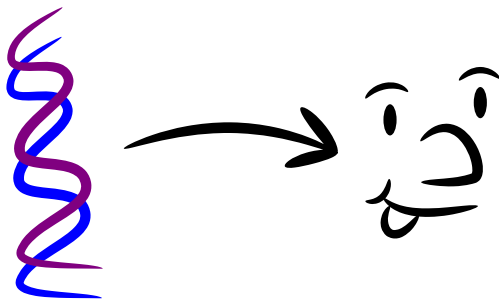
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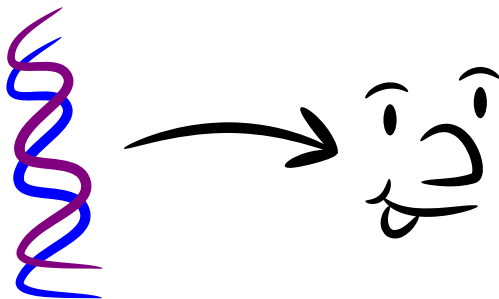
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This is also good preparation for communicating with computational collaborators.

Course problems: expression and sequence analysis



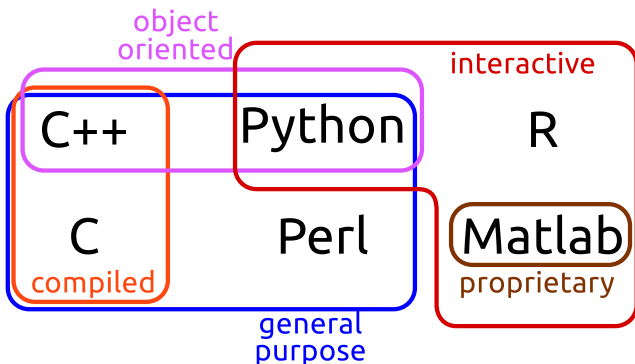
Course problems: expression and sequence analysis



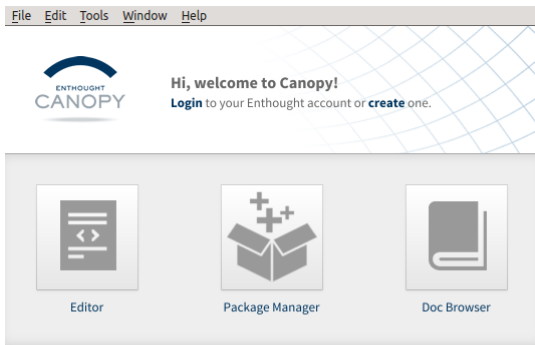
Part 2: Genotype
(Sequence analysis)

Part 1: Phenotype
(Expression profiling)

Course tool: Python



Python distribution: Enthought Canopy



Python shell: ipython (jupyter) notebook

```
In [5]: np.random.seed(0)

ax = pylab.axes()

x = np.linspace(0, 10, 100)
ax.plot(x, np.sin(x) * np.exp(-0.1 * (x - 5) ** 2), 'b', lw=1, label='damped sine')
ax.plot(x, -np.cos(x) * np.exp(-0.1 * (x - 5) ** 2), 'r', lw=1, label='damped cosine')

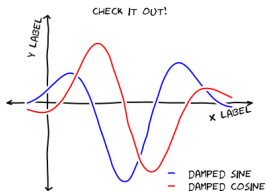
ax.set_title('check it out!')
ax.set_xlabel('x label')
ax.set_ylabel('y label')

ax.legend(loc='lower right')


ax.set_xlim(0, 10)
ax.set_ylim(-1.0, 1.0)

#XXCDify the axes -- this operates in-place
XXCDify(ax, xaxis loc=0.0, yaxis loc=1.0,
        xaxis arrow='+-', yaxis_arrow='+-',
        expand_axes=True)
```


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

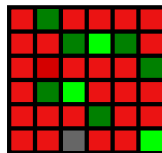


Anatomy of a Programming Language

$f(x)$ 
functions

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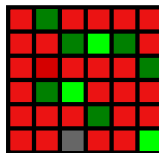


data structures

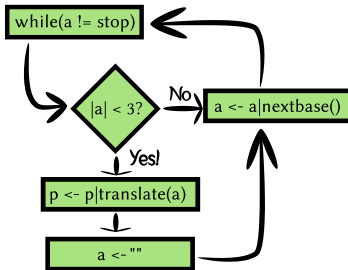
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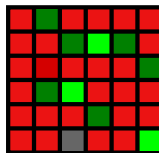


control statements

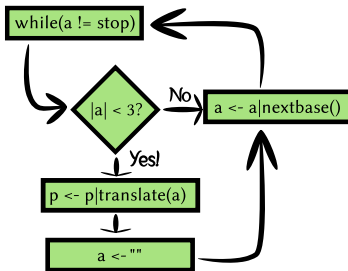
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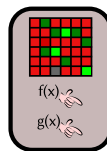
functions



data structures



control statements



objects

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
MADQLTEEQIAEFKEAFSLFDKDGDTITTKELGTVMRSLGQNPTEAEL
QDMINEVDADDLPGNGTIDFPEFLTMMARKMKD TDSEEEIREAFRVFDK
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

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

$$C = \frac{.02A_{260}}{330L} \quad (1)$$

- 2 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:

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

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"
```


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[:]
```

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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```

“Python, do *function* to *parameter*”

```
# 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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- Saving interactive sessions is a good way to document our computer "experiments".
- 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:

- 1 Mean:

$$\bar{x} = \frac{\sum_i^N x_i}{N}$$

- 2 Standard deviation:

$$\sigma_x = \sqrt{\frac{\sum_i^N (x_i - \bar{x})^2}{N - 1}}$$

- 3 Correlation coefficient (Pearson's r):

$$r(x, y) = \frac{\sum_i (x_i - \bar{x})(y_i - \bar{y})}{\sqrt{\sum_i (x_i - \bar{x})^2} \sqrt{\sum_i (y_i - \bar{y})^2}}$$