582670 Algorithms for Bioinformatics

Lecture 0: Primer to algorithms and molecular biology

1.9.2015

These slides are based on previous years' slides of
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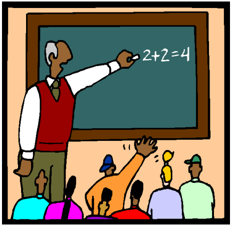
Course format

Thursday 12-14



Tuesday 10-12

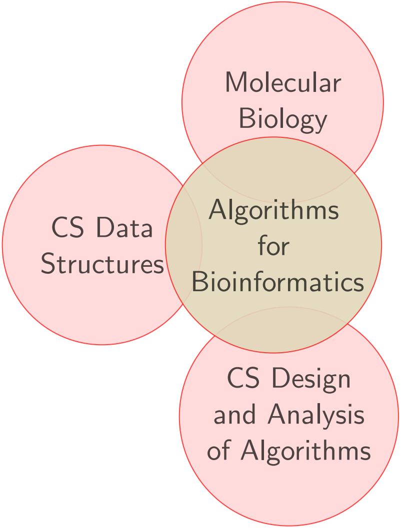
Tuesday 12-14

Grading

- Exam 48 points
- Exercises 12 points
  - 30% $\implies$ 1
  - 85% $\implies$ 12
- Grading $\sim 30 \implies 1$, $\sim 50 \implies 5$ (depending on difficulty of exam)
- Tuesday study group is mandatory!
  (Inform beforehand if you cannot attend)

Course overview

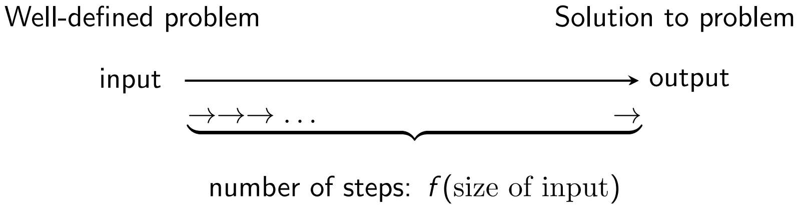
- Introduction to algorithms in the context of molecular biology
- Targeted for
  - biology and medicine students
  - first year bioinformatics students
  - CS / Math / Statistics students thinking of specializing in bioinformatics
- Some programming skills required
  - We will use Python in this course
- Not as systematic as other CS algorithm courses, emphasis on learning some design principles and techniques with the biological realm as motivation



Algorithms *for* Bioinformatics

- State-of-the-art algorithms in bioinformatics are rather involved
- Instead, we study toy problems motivated by biology (but not too far from reality) that have clean and introductory level algorithmic solutions
- The goal is to arouse interest to study the real advanced algorithms in bioinformatics!
- We avoid statistical notions to give algorithmic concepts the priority
- Continue to further bioinformatics course to learn the practical realm

Algorithm



Homework:
Find out what the following algorithm running time notions mean:

$$f(n) \in O(g(n)) \qquad g(n) \in \Omega(f(n))$$

$$f(n) \in o(g(n)) \qquad g(n) \in \omega(f(n))$$

$$f(n) \in \Theta(g(n))$$

Algorithms in Bioinformatics

Weakly defined problem   Solution to problem

input $\longrightarrow$ output=input‘ $\longrightarrow$ output‘=input“ $\longrightarrow$ output“

- Reasons:
  - Biological problems usually too complex to admit a simple algorithmic formulation
  - Problem modeling sometimes leads to statistical notions
- Problematic for CS theory:
  - optimal solutions to subproblems do not necessarily lead to best global solution

Algorithms in Bioinformatics

Plenty of important subproblems where algorithmic techniques have been vital:

- Fragment assembly $\Longrightarrow$ human genome
- Design of microarrays $\Longrightarrow$ gene expression measurements
- Sequence comparison $\Longrightarrow$ comparative genomics
- Phylogenetic tree construction $\Longrightarrow$ evolution modeling
- Genome rearrangements $\Longrightarrow$ comparative genomics, evolution
- Motif finding $\Longrightarrow$ gene regulatory mechanism
- Biomolecular secondary structure prediction $\Longrightarrow$ function
- Analysis of high-throughput sequencing data $\Longrightarrow$ genomic variations in populations

Course prerequisites

- Programming skills
- High-school level biology++

Assignments

- Next Tuesday: exercises (10-12) and study group (12-14)
- The exercise problems and the first part of study group assignments are available on the course home page
- The second part of study group assignments becomes available before the lecture on Thursday

Outline

Programming on this course

- We will use Python in this course
- What we need:
  - Built-in data types
  - Syntax for control flow statements
  - Function definitions
- What we can omit (i.e. software engineering):
  - Standard library, OOP, exceptions, I/O, etc.

Assignment

Pseudocode

$b \leftarrow 2$

$a \leftarrow b$

Python

```
b = 2
a = b
print a
```

Arithmetic

Pseudocode

DIST (x_1, y_1, x_2, y_2)

1. $dx \leftarrow (x_2 - x_1)^2$
2. $dy \leftarrow (y_2 - y_1)^2$
3. return $\sqrt{dx + dy}$

Python

```
from math import sqrt


def dist(x1, y1, x2, y2):
    dx = pow(x2-x1, 2)
    dy = pow(y2-y1, 2)
    return sqrt(dx+dy)


print dist(0, 0, 3, 4)
```

Conditional

Pseudocode

MAX (a, b)

if $(a < b)$

    return b

else

    return a

Python

```
def MAX(a, b):
    if a < b:
        return b
    else:
        return a

print MAX(1,99)
```

for loops

Pseudocode

SumIntegers (n)

$sum \leftarrow 0$
for $i \leftarrow 1$ to n
    $sum \leftarrow sum + i$
return sum

Python

```
def SUMINTEGERS(n):
    sum = 0
    for i in range(1,n+1):
        sum = sum + i
    return sum

print SUMINTEGERS(10)
```

while loops

Pseudocode

AddUntil (b)

$i \leftarrow 1$

$total \leftarrow i$

while $total \leq b$

    $i \leftarrow i + 1$

    $total \leftarrow total + i$

return i

Python

```
def ADDUNTIL(b):
    i = 1
    total = i
    while total <= b:
        i = i + 1
        total = total + i
    return i

print ADDUNTIL(25)
```

Recursion

Pseudocode

$$F(n) = \begin{cases} 0, & \text{when } n = 0 \\ 1, & \text{when } n = 1 \\ F(n-1) + F(n-2), & \text{otherwise} \end{cases}$$

Python

```
def RECURSIVEFIBONACCI(n):
    if n == 0:
        return 0
    elif n == 1:
        return 1
    else:
        a = RECURSIVEFIBONACCI(n-1)
        b = RECURSIVEFIBONACCI(n-2)
        return a+b

print RECURSIVEFIBONACCI(8)
```

Lists

Python

```
l = [0] * 3

l[0] = 1     # list is mutable

l = range(1,4)

l.append('four')

l = [2**i for i in range(6)]

l2 = l[2:4]
```

Output

```
[0,0,0]

[1,0,0]

[1,2,3]

[1,2,3,'four']

[1,2,4,8,16,32]

[4,8]
```

List access

Pseudocode

FIBONACCI (n)

1 $F_0 \leftarrow 0$

2 $F_1 \leftarrow 1$

3 for $i \leftarrow 2$ to n

4 $\quad F_i \leftarrow F_{i-1} + F_{i-2}$

5 return F_n

Python

```
def FIBONACCI(n):
    F = [0]*(n+1)
    F[0] = 0
    F[1] = 1
    for i in range(2,n+1):
        F[i] = F[i-1] + F[i-2]
    return F[n]

print FIBONACCI(8)
```

Strings

Python

```
s='Hello'

s[0] = 'C'     # error: str
s.append('!') # is immutable

s = s + '!'

s = s[:5]

s = s.upper()
```

Output

```
Hello



Hello!

Hello

HELLO
```

Immutable vs Mutable

Immutable (int, str, ...)

```
a = 2
b = a
b = b + 1     # does not change a

s = 'Hello'
t = s
t = t + '!'   # does not change s
```

Mutable (list, set, dict, ...)

```
l = [0]
m = l          # shallow copy of l
m.append(1)    # changes also l

l = [0]
m = l
m = [0, 1]     # does not change l

l = [0]
m = l[:]       # deep copy of l
m.append[1]    # does not change l
```

Pass arguments by reference? - No.

Immutable (int, str, ...)

```
def ADDONE(x,y):
    x = x + 1    # x and y
    y = y + 1    # are local

# return a tuple instead
def ADDONE(x,y):
    return x+1, y+1

x,y = ADDONE(x,y)
```

Mutable (list, set, dict, ...)

```
def CLEAR(l):
    l = []    # l is local

# any mutable can still be
# changed in place, e.g.:
def CLEAR(l):
    l[:] = []

def ADDONE(l,i):
    l[i] = l[i] + 1
```

Multidimensional lists

Python

```
l = [[0] * 2] * 3  # Caution!
                   # You probably
                   # don't want
                   # to do this!
l[0][0] = 1


# This is safe:
l = [[0]*2 for i in range(3)]

l[0][0] = 1
```

Output (print l)

```
[[0, 0], [0, 0], [0, 0]]


[[1, 0], [1, 0], [1, 0]]



[[0, 0], [0, 0], [0, 0]]

[[1, 0], [0, 0], [0, 0]]
```

Sets and Dictionaries

Python

```
l = [0, 2, 1]
s = set(l)
s = {0, 1, 2}
s = s | {3, 4}
s = set('hello')
'e' in s

d = {'apple':2, 'orange':5}
d['apple']
d['orange'] = 8
```

Output

```
[0, 2, 1]
set([0, 1, 2])
set([0, 1, 2])
set([0, 1, 2, 3, 4])
set(['h', 'e', 'l', 'o'])
True

{'orange': 5, 'apple': 2}
2
{'orange': 8, 'apple': 2}
```

Large(r) data sets

- For mutable strings, use e.g.
  - `array.array('c', 'Hello')`
  - `bytearray('Hello')`
- `list` uses a lot of memory ($\sim$ 16 bytes per `int`). For homogeneous data, use e.g.
  - `array.array('l', [1,2,3,4])`
  - `numpy.array([1,2,3,4])`
- `list` is slow for operations at both ends. E.g. for a queue use
  - `collections.deque([1,2,3,4])`

Helpful links

- http://openbookproject.net/thinkcs/python/english2e/ (Programming tutorial for those who have no programming experience)
- http://docs.python.org/tutorial/
- http://docs.python.org/library/
- http://wiki.python.org/moin/BeginnersGuide/
- http://wiki.python.org/moin/TimeComplexity/
- http://docs.scipy.org/doc/ (NumPy documentation)
- http://biopython.org/