Genome 540 Discussion

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Outline

Homework 1 wrap-up

C/C++/Python programming tips

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C/C++/Python programming tips

- AAACCGTACACTGGGTTCAAGAGATTTCCC **p**₁₀
- AACCGTACACTGGGTTCAAGAGATTTCCC **p**₁₁
- AAGAGATTTCCC p₂₈
- ACACTGGGTTCAAGAGATTTCCC **p**₁₇
- ACCGTACACTGGGTTCAAGAGATTTCCC **p**₁₂
- p_1 GCACTAAACCGTACACTGGGTTCAAGAGATTTCCC
- AAACCGTACACTGGGTTCAAGAGATTTCCC \mathbf{p}_7
- ACTGGGTTCAAGAGATTTCCC **p**₁₉
- AGAGATTTCCC **p**₂₉
- AGATTTCCC **p**₃₁
- ATTTCCC **p**₃₃ **p**₂₇
 - CAAGAGATTTCCC
 - Common bugs

Homework #1 Wrap-up

Common debug scenarios

- Too much memory usage
 - Storing substrings (silent caching in python)
- Sort step is too slow
 - Slow comparison function
 - Many comparisons!

- Hist values slightly off •
 - Sorting logic, sorted array processing logic
- Genomic coordinate 1-index •



- p₁₀ AAACCGTACACTGGGTTCAAGAGATTTCCC
- **p**₁₁AACCGTACACTGGGTTCAAGAGATTTCCC
- p₂₈ AAGAGATTTCCC
- p₁₇ ACACTGGGTTCAAGAGATTTCCC
- **p**₁₂ ACCGTACACTGGGTTCAAGAGATTTCCC
- **p**₁ ACCTGCACTAAACCGTACACTGGGTTCAAGAGATTTCCC
- **p**₇ ACTAAACCGTACACTGGGTTCAAGAGATTTCCC
- p₁₉ ACTGGGTTCAAGAGATTTCCC
- p₂₉ AGAGATTTCCC
- p₃₁ AGATTTCCC
- p₃₃ ATTTCCC

p₂₇

CAAGAGATTTCCC

Homework #1 Wrap-up

Variant algorithm(s)

- Sort phases take log N because 2^k
- Each phase can be linear
- Limited benefit if not rate-limiting (i.e. cache misses)



http://web.stanford.edu/class/cs97si/suffix-array.pdf https://www.youtube.com/watch?v=f8S05ZS-8KY&t=703s 11:40 - end



Homework 1 wrap-up

C/C++/Python programming tips

Vectorized array operations in python with numpy

import numpy as np	<pre># compute x^2 x ** 2 # make a binary mask for x == 7 (x == 7).astype(int)</pre>
<pre># generate random data x = np.random.randint(0, 10, size=(10, 3)) print(x) [[9 1 8]</pre>	array([[81, 1, 64]], [0, 9, 49]], [0, 0, 1], [16, 49, 16], [0, 1, 0], [0, 0, 0]. [0, 0]. [0, 0]. [0, 0,
[0 3 7] [4 7 4] [1 8 4] [2 7 2] [3 0 1] [7 5 7] [0 5 3]	$\begin{bmatrix} 4, 49, 4], \\ [0, 1, 0], \\ [0, 0, 1], \\ [49, 25, 49], \\ [0, 25, 9], \\ [0, 64, 1], \\ [25, 36, 25]] \end{bmatrix} \begin{bmatrix} 0, 0, 0 \\ [0, 0, 0], \\ [0, 0, 0]] \end{bmatrix}$
[0 8 1] [5 6 5]]	
# sum down columns np.sum(x, axis=0)	<pre># transpose x x.T</pre>
<pre>array([31, 50, 42]) # sum across rows np.sum(x, axis=1)</pre>	array([[9, 0, 4, 1, 2, 3, 7, 0, 0, 5], [1, 3, 7, 8, 7, 0, 5, 5, 8, 6],
array([18, 10, 15, 13, 11, 4, 19, 8, 9, 16])	[8, 7, 4, 4, 2, 1, 7, 3, 1, 5]])

https://numpy.org/install/

Random number generation

C# System.Random



php rand()



Vectorized array operations in python with numpy

```
import numpy as np
```

```
def vector_mult(x, c):
    '''Multiply all values in the input vector x by constant c.'''
    for i in range(len(x)):
        x[i] *= c
    return x
```

```
def vector_mult_np(x, c):
    '''Vectorized version of vector_mult using numpy.'''
    return x * c
```

```
# create a vector with some data
n = 10000 # length of vector to be multiplied
c = 25  # constant used in multiplication
x = list(range(n))
x_np = np.array(x)
# benchmark python list with iteration
```

```
%timeit vector_mult(list(x), 10)
```

```
# benchmark numpy vectorized calc
%timeit vector_mult_np(x_np.copy(), 10)
```

```
947 μs ± 272 ns per loop (mean ± std. dev. of 7 runs, 1000 loops each)
10.4 μs ± 175 ns per loop (mean ± std. dev. of 7 runs, 100000 loops each)
```

1.5
<pre># example data x = [0, 2, 4, 6, 8] x_np = np.array([0, 2, 4, 6, 8]) vector_mult(list(x), 10)</pre>
[0, 20, 40, 60, 80]
<pre>vector_mult(list(x), 100)</pre>
[0, 200, 400, 600, 800]
<pre>vector_mult_np(x_np.copy(), 10)</pre>
array([0, 20, 40, 60, 80])
<pre>vector_mult_np(x_np.copy(), 100)</pre>
array([0, 200, 400, 600, 800])

https://numpy.org/install/

Random number generation in python



import numpy as np
<pre>x = np.random.randint(0, 10, size=5) x</pre>
array([8, 8, 1, 0, 3])
<pre>seq = np.random.choice(['A', 'C', 'G', 'T'], size=10) seq</pre>
array(['T', 'G', 'G', 'A', 'T', 'A', 'A', 'C', 'A', 'G'], dtype=' <u1')< td=""></u1')<>
<pre>seqs = np.random.choice(['A', 'C', 'G', 'T'], size=(5, 10)) seqs</pre>
array([['T', 'C', 'A', 'C', 'G', 'T', 'C', 'A', 'T', 'C'], ['C', 'A', 'A', 'T', 'A', 'T', 'A', 'G', 'C'], ['T', 'T', 'T', 'A', 'A', 'A', 'A', 'T', 'T

Random number generation in C++



rand() will return a random number between 0 and RNAD_MAX

RAND_MAX:21 16807 282475249 1622650073 984943658 1144108930	47483647 RAND_MAX:21 16807 282475249 1622650073 984943658 1144108930	47483647 RAND_MAX:2147483647 16807 282475249 1622650073 984943658
		984943658 1144108930

Pseudo random number

Random number generation in C++



-cout << rand()/double(RAND_MAX) << endl; [0, 1]</pre>

cout << (*rand*() % (b-a+1))+a << endl; [a, b]

Random number generation in C++

Using random() instead of rand()

rand() is typically a low quality pRNG. <random> provides a variety of engines with different characteristics suitable for many different use cases.

% generally biases the data and floating point division still produces non-uniform distributions. <random> distributions are higher quality as well as more readable.

srand() only permits a limited range of seeds. Engines in <random> can be initialized using seed sequences which permit the maximum possible seed data.

Outline

Homework 1 wrap-up

C/C++/Python programming tips

Homework 2 Overview

Part one: write a new program

- read in a file in FASTA format
- determine the frequencies of the nucleotides and dinucleotides (based on the forward strand) and the length of the sequence
- produce three simulated sequences based on the length and nucleotide or dinucleotide frequency of the original sequence
 - 'Equal frequency' model
 - Order 0 Markov model
 - Order 1 Markov model
- output three files in FASTA format containing the simulated sequence

Homework 2 Overview

order-0 Markov

"Equal frequency" model

Nucleotide Frequencies:

A=0.2500

C=0.2500

G=0.2500

T=0.2500

Fasta 1: CP003913.fna
>gi 440453185 gb CP003913.1 Mycoplasma pneumoniae M129-B7, complete genome
*=816373
A=249201
C=162924
G=163697
T=240551
N=0
Nucleotide Frequencies:
A=0.3053
C=0.1996
G=0.2005
T=0.2947

order-1 Markov



Dinucleotide Frequency Matrix: A=0.1207 0.0622 0.0587 0.0637 C=0.0650 0.0449 0.0328 0.0569 G=0.0501 0.0455 0.0450 0.0599 T=0.0695 0.0470 0.0640 0.1141	=
Conditional Frequency Matrix:	
A=0.3953 0.2037 0.1923 0.2087	= 1
C=0.3256 0.2251 0.1642 0.2851	= 1
G=0.2497 0.2269 0.2246 0.2988	= 1
T=0.2360 0.1594 0.2173 0.3873	= 1

Homework 2 Overview

Part two: run your HW1 program on three simulated genomes

- Run your HW1 program three times, using as input:
 - Human 10-Mb segment + simulated 'equal frequency' genome
 - Human 10-Mb segment + simulated Mouse Markov-0
 - Human 10-Mb segment + simulated Mouse Markov-1
- Given observed matches between the Human and simulated genomes, what can you conclude about the statistical significance of matches between the orthologous mouse and human regions in homework 1?

Reminders

- Homework 2 due this Sunday Jan. 22, 11:59 pm
 - Single text file, compressed with gzip
 - name in the file: camplisson_hw2.txt.gz

• Homework 3 will be posted tomorrow (Jan. 18)