String Algorithms and Data Structures String Graph Assembly

CS 199-225 Brad Solomon April 18, 2022



Department of Computer Science

Assignment 11: a_edist due April 18 11:59 PM!

Last assignment!



READING THE BOOK OF LIFE: THE OVERVIEW

READING THE BOOK OF LIFE: THE OVERVIEW; Genetic Code of Human Life Is Cracked by Scientists

By NICHOLAS WADE Published: June 27, 2000

Human Genome Project: 1990-2003

The New Hork Times http://nyti.ms/1tcvLXq

SCIENCE

Man's Genome From 45,000 Years Ago Is Reconstructed

OCT. 22, 2014

Carl Zimmer

Team of Rival Scientists Comes Together to Fight Zika

By AMY HARMON MARCH 30, 2016

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A visualization of the recently sequenced Aedes aegypti genome. Each of the 3,752 colored lines is a fragment of its three chromosomes that could not be fit together without the additional information that the Aedes Genome Working Group hopes to produce. A 2007 genome map for Aedes aegypti is fragmented into about 10 times as many pieces. Mark Kunitomi



Whole-genome "shotgun" sequencing first copies the input DNA:

Input: GGCGTCTATATCTCGGCTCTAGGCCCTCATTTTT

Copy: GGCGTCTATATCTCGGCTCTAGGCCCTCATTTTT GGCGTCTATATCTCGGCTCTAGGCCCTCATTTTTT GGCGTCTATATCTCGGCTCTAGGCCCTCATTTTTT GGCGTCTATATCTCGGCTCTAGGCCCTCATTTTTT

Then fragments it:

Fragment: GGCGTCTA TATCTCGG CTCTAGGCCCTC ATTTTTT GGC GTCTATAT CTCGGCTCTAGGCCCTCA TTTTTT GGCGTC TATATCT CGGCTCTAGGCCCT CATTTTTT GGCGTCTAT ATCTCGGCTCTAG GCCCTCA TTTTT

"Shotgun" refers to the random fragmentation of the whole genome; like it was fired from a shotgun

CTAGGCCCTCAATTTT CTCTAGGCCCTCAATTTT GGCTCTAGGCCCTCATTTTT CTCGGCTCTAGCCCCTCATTTT TATCTCGACTCTAGGCCCTCA **Reconstruct this** TATCTCGACTCTAGGCC TCTATATCTCGGCTCTAGG **GGCGTCTATATCTCG** GGCGTCGATATCT GGCGTCTATATCT GGCGTCTATATCTCGGCTCTAGGCCCTCATTTTT

From these

Reconstruct this

CTAGGCCCTCAATTTTT GGCGTCTATATCT CTCTAGGCCCTCAATTTTT TCTATATCTCGGCTCTAGG GGCTCTAGGCCCTCATTTTT CTCGGCTCTAGCCCCTCATTT TATCTCGACTCTAGGCCCTCA GGCGTCGATATCT TATCTCGACTCTAGGCC GGCGTCTATATCTCG

From these





ATGGTTAGAATTAAACCTGGATCTGCTAATAAACCUAGTGATGATGCG ATAGCACAGGTAGATCCAGTTACGTAGAGGTCATTAGCCGTATTGCTA ATAAACCTAGTGATGATGATTCGATAGCGTAGAGGTCATTAGCCTTGTGCT AATAACAGGTAGATCCGTATACGTAGAGGTCATTACCAGAGGTCATTA GTTGTGCTAATAAACCTAGTGTAGATGAAGAGGTCATTAGATCTGCTAA





Input: A set of strings $S = \{s_1, s_2, ..., s_n\}$ assumed to be substrings of some underlying text *T*

Output: The 'best' approximation of T

1) Identify all possible overlaps

2) "Assemble" the best possible layout

3) Reconstruct *T* based on consensus

Identify Overlaps

Length-*l* Overlap: Suffix of *X* of length $\geq l$ matches prefix of *Y*

Naive: look in *X* for occurrences of *Y*'s length-*l* prefix. Extend matches to the right to confirm if the suffix of *X* matches.



Identify Overlaps

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For three strings, how many overlaps must be calculated?



In bulk, there are better ways to do this...

To build a suffix tree from two strings **X** and **Y**, make a new string $X\$_0Y\$_1$ where $\$_0$, $\$_1$ are both terminal symbols. Build a suffix tree for $X\$_0Y\$_1$.

Generalized suffix tree for { "GACATA", "ATAGAC" } GACATA\$₀ATAGAC\$₁



Generalized suffix tree for { "GACATA", "ATAGAC" } GACATA\$₀ATAGAC\$₁



Let query = GACATA (first string). From root, follow path labeled with query.

Green edge implies length-3 suffix of second string equals length-3 prefix of query

ATAGAC ||| GACATA

TA

\$₀

3

GAC^{\$}1

7

\$₀

 $ATA\$_0 |\$_1$

11

5

1

ΓА

\$₀

ATAGAC

GAC\$₁

7

\$₀

 $ATA\$_0$ $\$_1$

11

GACATA

5

1

Generalized suffix tree for { "GACATA", "ATAGAC" } GACATA\$₀ATAGAC\$₁



Let query = ATAGAC (second string). From root, follow path labeled with query.

Green edge implies length-3 suffix of first string equals length-3 prefix of query

Generalized suffix tree for { "GACATA", "ATAGAC" } GACATA\$₀ATAGAC\$₁



(1) Build tree

5

1

11

3

7

(2) For each string: Walk down from root and report any outgoing edge labeled with a separator. Each corresponds to a prefix/suffix match involving prefix of query string and suffix of string ending in the separator.



Assume for given string pair we report only the longest suffix/prefix match

Time to build generalized suffix tree:O(N)... to walk down red paths:O(N)... to find & report overlaps (green):O(a)Overall:O(N + a)

Identify Overlaps: Dynamic Programming

What about *approximate* suffix/prefix matches?

Use *approximate matching* recurrence relationship

$$D[i, j] = \min \begin{cases} D[i - 1, j] + 1\\ D[i, j - 1] + 1\\ D[i - 1, j - 1] + \delta(x[i - 1], y[j - 1]) \end{cases}$$

How do we search for prefix / suffix matches between X and Y?

Identify Overlaps: Dynamic Programming

How to adjust our matrix so suffix of *X* aligns to prefix of *Y*?

First column gets 0s

First row gets ∞s

Backtrace from last row



Y

Identify Overlaps: Dynamic Programming



Say there are d strings of length n, total length N = dn, and a is total number of pairs with an overlap

# overlaps to try:	O(<i>d</i> ²)
Size of each DP matrix:	O(<i>n</i> ²)
Overall:	$O(d^2n^2)$, or $O(N^2)$

Contrast O(N²) with suffix tree: O(N + a), but where a is worst-case O(d²)

Real-world overlappers mix the two; index filters out vast majority of non-overlapping pairs, dynamic programming used for remaining pairs

There are other approaches too!

Wajid, Bilal, and Erchin Serpedin. "Review of general algorithmic features for genome assemblers for next generation sequencers." *Genomics, proteomics & bioinformatics* 10.2 (2012): 58-73.

Sohn, Jang-il, and Jin-Wu Nam. "The present and future of de novo whole-genome assembly." *Briefings in bioinformatics* 19.1 (2018): 23-40.

Input: A set of strings $S = \{s_1, s_2, ..., s_n\}$ assumed to be substrings of some underlying text *T*

Output: The 'best' approximation of *T*

1) Identify all possible overlaps How do we store them?

2) "Assemble" the best possible layout

3) Reconstruct *T* based on consensus

Each node is a string

CTCGGCTCTAGCCCCTCATTT

Draw edge A -> B when *suffix* of A overlaps *prefix* of B



TCTATATCTCGGCTCTAGG

GGCGTCTATATCT GGCGTCTATATCTCG GGCGTCGATATCTAGG CTAGGCCCTCAATTTTT TATCTCGACTCTAGGCC CTCTAGGCCCTCAATTTTT TCTATATCTCGGCTCTAGG B GGCTCTAGGCCCTCATTTTT CTCGGCTCTAGCCCCTCATTT TATCTCGACTCTAGGCCCTCA

Which direction is this edge?

TCTATATCTCGGCTCTAGG |||||||||||||| TATCTCGACTCTAGGCC

GGCGTCTATATCT GGCGTCTATATCTCG GGCGTCGATATCTAGG CTAGGCCCTCAATTTTT TATCTCGACTCTAGGCC CTCTAGGCCCTCAATTTTT TCTATATCTCGGCTCTAGG B GGCTCTAGGCCCTCATTTTT CTCGGCTCTAGCCCCTCATTT TATCTCGACTCTAGGCCCTCA

Which direction is this edge?



Not every overlap is 'meaningful'

Nodes: all 6-mers from GTACGTACGAT

Edges: overlaps of length $l \ge 4$



Input: A set of strings $S = \{s_1, s_2, ..., s_n\}$ assumed to be substrings of some underlying text *T*

Output: The 'best' approximation of *T*

Identify all possible overlaps
 Build an overlap graph

2) "Assemble" the best possible layout

3) Reconstruct *T* based on consensus

CTAGGCCCTCAATTTTT GGCGTCTATATCT CTCTAGGCCCTCAATTTTT TCTATATCTCGGCTCTAGG GGCTCTAGGCCCTCATTTTTT CTCGGCTCTAGCCCCTCATTTT TATCTCGACTCTAGGCCCTCA GGCGTCGATATCT TATCTCGACTCTAGGCC GGCGTCTATATCTCG

CTAGGCCCTCAATTTTT CTCTAGGCCCTCAATTTTT GGCTCTAGGCCCTCATTTTTT CTCGGCTCTAGGCCCTCATTTTT TATCTCGACTCTAGGCCCTCA TATCTCGACTCTAGGCC TCTATATCTCGGCTCTAGG GGCGTCTATATCTCG GGCGTCGATATCT GGCGTCTATATCT

Nodes: all 6-mers from GTACGTACGAT



GTACGT

Nodes: all 6-mers from GTACGTACGAT

Edges: overlaps of length $l \ge 4$



GTACGT

TACGTA

Our layout is a path through our graph that touches all nodes

Given overlap graph, how can we find the "best" path through this graph?



One reasonable idea: *shortest common superstring* (SCS)

Given set of strings *S*, find *SCS*(*S*): shortest string containing the strings in *S* as substrings



>>> scs(['GTACGT', 'TACGTA', 'ACGTAC', 'GTACGA', 'TACGAT']) 'GTACGTACGAT'

How can we solve SCS using graphs?



How can we solve SCS using graphs?

Imagine a modified overlap graph with edge weight = - (overlap)

The SCS is a path that visits every node once, minimizing total cost

That's the *Traveling Salesman Problem*. **NP-Hard!**



Pick order for strings in *S* and construct superstring

order 1: AAA AAB ABA ABB BAA BAB BBA BBB AAA

Pick order for strings in *S* and construct superstring

order 1: AAA AAB ABA ABB BAA BAB BBA BBB AAAB Take into account overlap whenever possible

Pick order for strings in *S* and construct superstring

order 1: AAA <u>AAB ABA</u> ABB BAA BAB BBA BBB AAABA

Pick order for strings in *S* and construct superstring

order 1: AAA AAB <u>ABA ABB</u> BAA BAB BBA BBB AAABABB

Pick order for strings in *S* and construct superstring

order 1: AAA AAB ABA ABB BAA BAB BBA BBB AAABABBBAA

Pick order for strings in *S* and construct superstring

order 1: AAA AAB ABA ABB BAA BAB BBA BBB AAABABBBAABAB

Concatenate full string when no overlap

Pick order for strings in *S* and construct superstring

order 1: AAA AAB ABA ABB BAA BAB BBA BBB AAABABBBAABABBBBB ← superstring 1

Pick order for strings in *S* and construct superstring

order 1: AAA AAB ABA ABB BAA BAB BBA BBB
 AAABABBBAABBABBBB ← superstring 1
 order 2: AAA AAB ABA BAB ABB BBB BAA BBA
 AAABABBBBAABBA ← superstring 2

Try all possible orderings and pick shortest superstring

If *S* contains *n* strings, how many orderings are are possible?

n! (n factorial) orderings possible

We want the "best" path through our graph:

SCS is not viable (NP-Hard)



Maybe we don't need the optimal path...



Greedy-SCS: in each round, merge pair of strings with maximal overlap. Stop when there's 1 string left. l = minimum overlap.

Algorithm in action (l = 1): Input strings —— AAA AAB ABB BBB BBA



Greedy-SCS: in each round, merge pair of strings with maximal overlap. Stop when there's 1 string left. l = minimum overlap.

Algorithm in action (l = 1):

► Input strings – Input strin

Pick the highest weight overlap



Greedy-SCS: in each round, merge pair of strings with maximal overlap. Stop when there's 1 string left. l = minimum overlap.

Algorithm in action (l = 1):

Input strings
 AAA AAB ABB BBB BBA
 AAA AAB ABB BBB BBA
 AAAB ABB BBB BBA
 Merge to create a
 new node



Greedy-SCS: in each round, merge pair of strings with maximal overlap. Stop when there's 1 string left. l = minimum overlap.

Algorithm in action (l = 1):

Input strings — Input strings ~ Input strings

Pick the highest weight overlap



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Greedy-SCS: in each round, merge pair of strings with maximal overlap. Stop when there's 1 string left. l = minimum overlap.

Algorithm in action (l = 1):

Input strings
 AAA AAB ABB BBB BBA
 AAA AAB ABB BBB BBA
 AAAB ABB BBB BBA
 AAAB BBBA ABB
 AAAB BBBA



Greedy-SCS: in each round, merge pair of strings with maximal overlap. Stop when there's 1 string left. l = minimum overlap.

Algorithm in action (l = 1):

Input strings
 AAA AAB ABB BBB BBA
 AAA AAB ABB BBB BBA
 AAAB ABB BBB BBA
 AAAB BBBA ABB
 AAABB BBBA
 AAABB BBBA

AAABBBA

That's the SCS

Is Greedy-SCS optimal?

AAA AAB ABB BBA BBB \checkmark \checkmark AAAB ABB BBA BBB

AAA AAB ABB BBA BBB ↓ ↓ AAAB ABB BBA BBB ↓ ↓ AAAB ABBA BBB

```
AAA AAB ABB BBA BBB

\checkmark \checkmark

AAAB ABB BBA BBB

\checkmark \checkmark

AAAB ABBA BBB

\checkmark \checkmark

AAABBA BBB
```

AAABBBA ← superstring, length=7

Greedy answer isn't necessarily optimal

Greedy-SCS assembling all substrings of length k = 6 from: a_long_long_time. l = 3.

ng_lon _long_ a_long long_l ong_ti ong_lo long_t g_long g_time ng_tim ng_time ng_lon _long_ a_long long_l ong_ti ong_lo long_t g_long ng_time g_long_ ng_lon a_long long_l ong_lo long_t ng_time long_ti g_long_ ng_lon a_long long_l ong_lo ng_time ong_lon long_ti g_long_ a_long long_l ong_lon long_time g_long_ a_long long_l long_lon long_time g_long_ a_long long_lon g_long_time a_long long_long_time a_long a_long_long_time a_long a_long_long_time

What happened?

Greedy-SCS assembling all substrings of length k = 6 from: a_long_long_time. l = 3.

ng_lon _long_ a_long long_l ong_ti ong_lo long_t g_long g_time ng_tim ng_time ng_lon _long_ a_long long_l ong_ti ong_lo long_t g_long ng_time g_long_ ng_lon a_long long_l ong_lo long_t ng_time ong_lon long_ti g_long_ a_long long_l ong_lon long_time g_long_ a_long long_l long_lon long_time g_long_ a_long long_lon g_long_time a_long long_long_time a_long a_long_long_time a_long a_long_long_time

Foiled by repeat!

Same example, but increased the substring length, k, from 6 to 8

long_lon ng_long__long_lo g_long_t ong_long g_long_l ong_time a_long_l _long_ti long_tim long_time long_lon ng_long__long_lo g_long_t ong_long g_long_l a_long_l _long_ti _long_time a_long_lo long_lon ng_long_ g_long_t ong_long g_long_l _long_time ong_long_ a_long_lo long_lon g_long_t g_long_l g_long_time ong_long_ a_long_lo long_lon g_long_l g_long_time ong_long_ a_long_lon g_long_l g_long_time ong_long_l a_long_lon g_long_l a_long_time a_long_long_l a_long_long_time a_long_long_l a_long_long_time a long_long_time

```
Got the whole thing: a_long_long_long_time
```

Why are substrings of length 8 long enough for Greedy-SCS to figure out there are 3 copies of long?

```
a_long_long_time
g_long_l
```

One length-8 substring spans all three longs

String Repeats

Basic principle: repeats foil assembly

SCS can't handle repeats at all (the 'shortest' is not the best)!

More generally, algorithms that aren't very careful about repeats may *collapse* them

Fun trivia: This is particularly bad for genomics. The human genome is ~50% repetitive!

String Repeats

Basic principle: repeats foil assembly

Another example using Greedy-SCS:

Input: swinging_and_the_ringing_of_the_bells_bells_bells

- *l, k* Output:
- 3,7 swinging_and_the_ringing_of_the_bells_bells
- 3,13 swinging_and_the_ringing_of_the_bells_bells_bells
- 3,19 swinging_and_the_ringing_of_the_bells_bells_b
- 3,25 swinging_and_the_ringing_of_the_bells_bells_bells_bells

Original example courtesy of Ben Langmead

longer and longer substrings 'reach' further into repeat



Even if we avoid collapsing copies of *A*, we can't know which paths *in* correspond to which paths *out*

Real-world Assembly

Alternative 1: Overlap-Layout-Consensus (OLC) assembly Alternative 2: De Bruijn graph (DBG) assembly

