

Exact Matching & CS Fundamentals

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Bioinformatics Lecture I
Quantitative Biology 2010

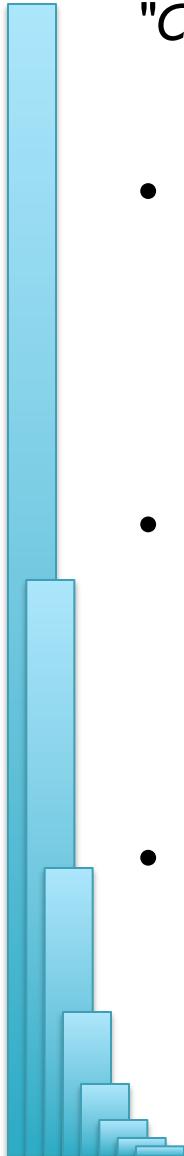


Computer Science & Computational Biology

"Computer science is no more about computers than astronomy is about telescopes."

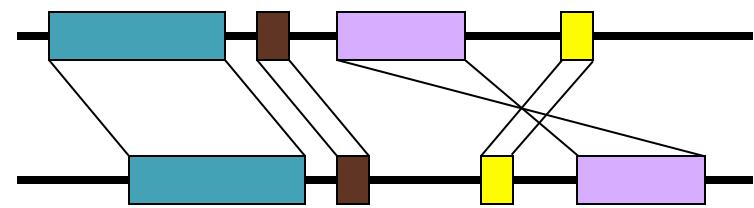
Edsger Dijkstra

- Computer Science = Science of Computation
 - Solving problems, designing & building systems
 - Thinking recursively about data, across levels of abstraction
 - Reasoning that your methods are fast & correct
- Computer Science >> Computer Programming
 - Computers are very, very dumb, but we can instruct them
 - Build complex systems out of simple components
 - They will perfectly & repeatedly execute instructions forever
- CompBio = Thinking Computationally about Biology
 - Processing: Make more powerful instruments, analyze results
 - Designing & Understanding: protocols, procedures, systems



Sequence Alignment Applications

- A very common problem in computational biology is to find occurrences of one sequence in another sequence
 - Genome Assembly
 - Gene Finding
 - Comparative Genomics
 - Functional analysis of proteins
 - Motif discovery
 - SNP analysis
 - Phylogenetic analysis
 - Primer Design
 - Personal Genomics
 - ...



Exact Matching Overview

Where is GATTACA in the human genome?

Brute Force
(3 GB)

BANANA
BAN
ANA
NAN
ANA

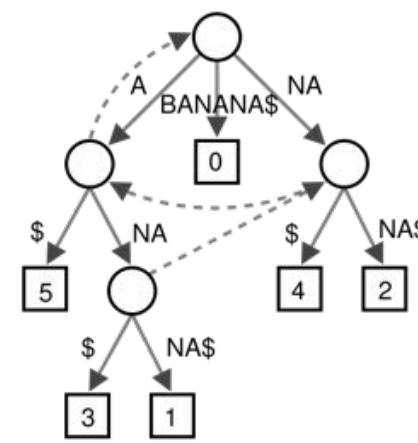
Naive
Slow & Easy

Suffix Array
(>15 GB)

6	\$
5	A\$
3	ANA\$
1	ANANA\$
0	BANANA\$
4	NA\$
2	NANA\$

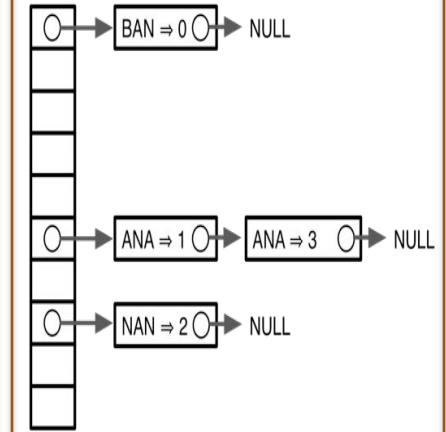
Vmatch, PacBio Aligner
Binary Search

Suffix Tree
(>51 GB)



MUMmer, MUMmerGPU
Tree Searching

Hash Table
(>15 GB)



BLAST, MAQ, ZOOM,
RMAP, CloudBurst
Seed-and-extend

Searching for GATTACA

- Where is GATTACA in the human genome?
- Strategy I: Brute Force

I	2	3	4	5	6	7	8	9	10	11	12	13	14	15	...
T	G	A	T	T	A	C	A	G	A	T	T	A	C	C	...
G	A	T	T	A	C	A									

No match at offset 1

Searching for GATTACA

- Where is GATTACA in the human genome?
- Strategy I: Brute Force

I	2	3	4	5	6	7	8	9	10	11	12	13	14	15	...
T	G	A	T	T	A	C	A	G	A	T	T	A	C	C	...
	G	A	T	T	A	C	A								

Match at offset 2

Searching for GATTACA

- Where is GATTACA in the human genome?
- Strategy I: Brute Force

I	2	3	4	5	6	7	8	9	10	11	12	13	14	15	...
T	G	A	T	T	A	C	A	G	A	T	T	A	C	C	...
		G	A	T	T	A	C	A	...						

No match at offset 3...

Searching for GATTACA

- Where is GATTACA in the human genome?
- Strategy I: Brute Force

I	2	3	4	5	6	7	8	9	10	11	12	13	14	15	...
T	G	A	T	T	A	C	A	G	A	T	T	A	C	C	...
								G	A	T	T	A	C	A	

No match at offset 9 <- Checking each possible position takes time

Brute Force Analysis



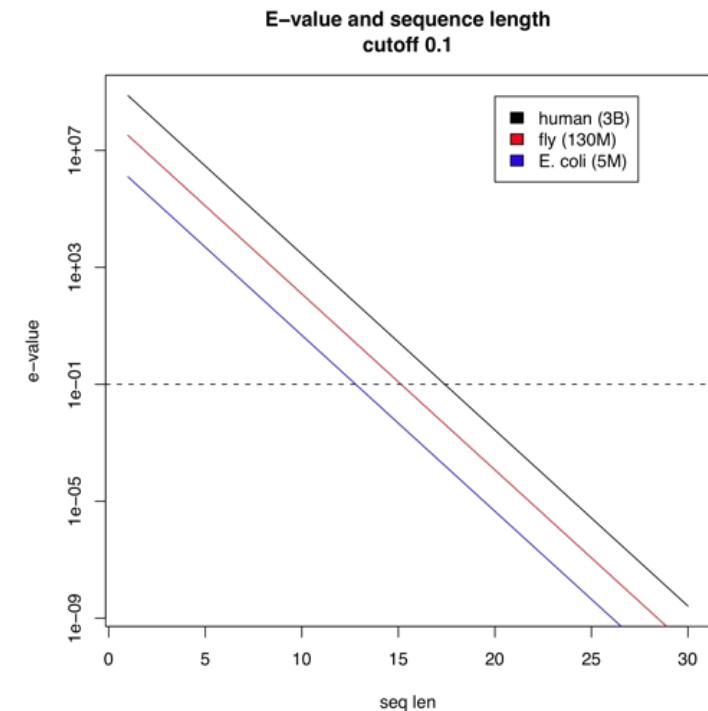
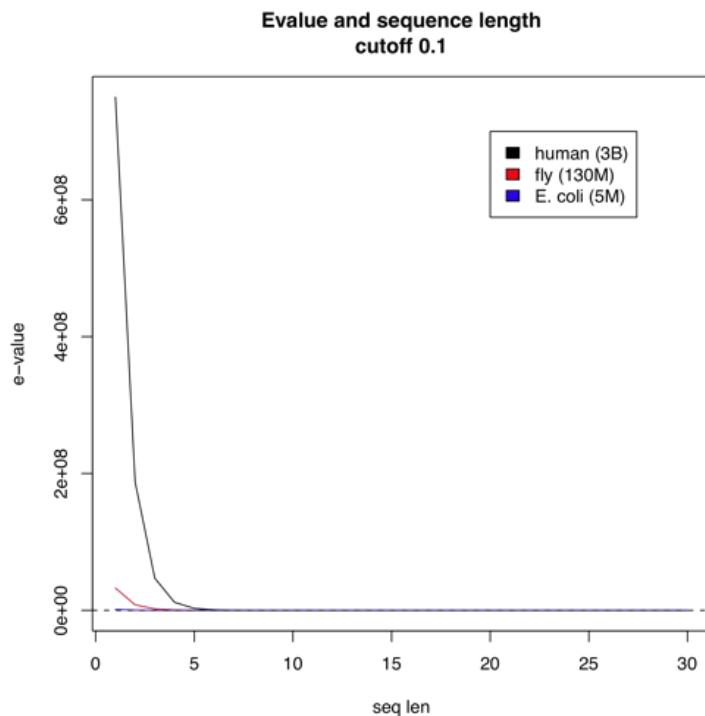
- Brute Force:
 - At every possible offset in the genome:
 - Do all of the characters of the query match?
- Analysis
 - Simple, easy to understand
 - Genome length = n [3B]
 - Query length = m [7]
 - Comparisons: $(n-m+1) * m$ [2IB]
- Overall runtime: $O(nm)$
 - If we double genome or query size, takes twice as long
 - If we double both, takes 4 times as long

Expected Occurrences

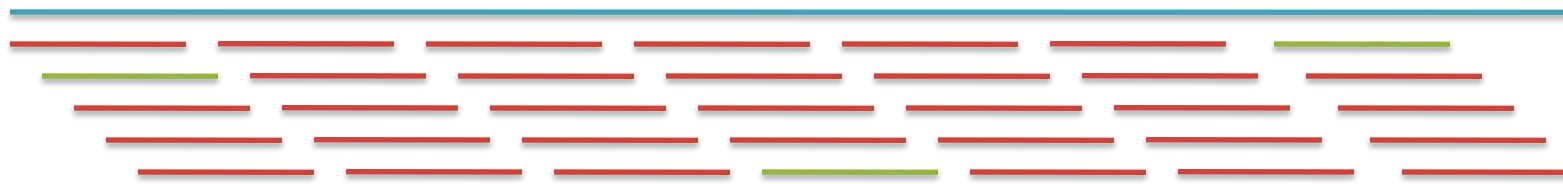
The expected number of occurrences (e-value) of a given sequence in a genome depends on the length of the genome and inversely on the length of the sequence

- 1 in 4 bases are G, 1 in 16 positions are GA, 1 in 64 positions are GAT
- 1 in 16,384 should be GATTACA
- $E=(n-m+1)/(4^m)$

[183,105 expected occurrences]



Brute Force in Matlab



```
query = 'GATTACA';
genome = 'TGATTACAGATTACC';

nummatches=0;

% At every possible offset
for offset=1:length(genome)-length(query)+1
    % Do all of the characters match?
    if (genome(offset:offset+length(query)-1) == query)
        disp(['Match at offset ', num2str(offset)])
        nummatches = nummatches+1;
    else
        %Uncomment to see every non-match
        %disp(['No match at offset ', num2str(offset)])
    end
end

disp(['Found ', num2str(nummatches), ' matches of ', query, ' in genome of length ',
      num2str(length(genome))])

disp(['Expected number of occurrences: ', num2str((length(genome)-length(query)+1)/
(4^length(query)))])
```

Brute Force Reflections

Why check every position?

- GATTACA can't start at position 15

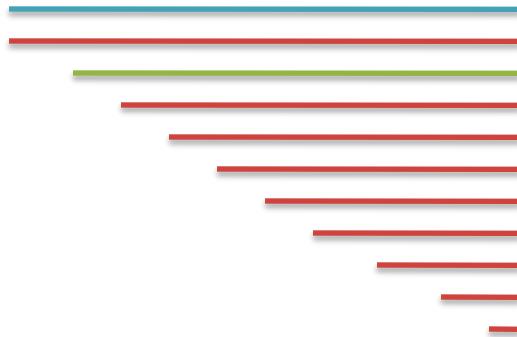
[WHY?]

I	2	3	4	5	6	7	8	9	10	11	12	13	14	15	...
T	G	A	T	T	A	C	A	G	A	T	T	A	C	C	...
								G	A	T	T	A	C	A	

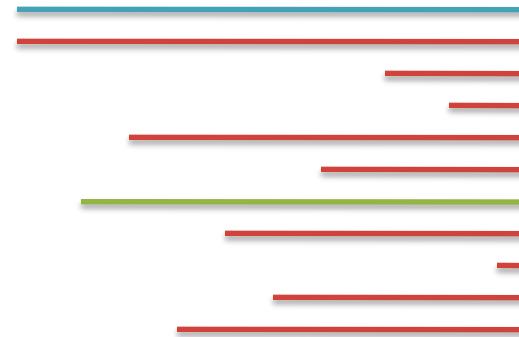
- Improve runtime to $O(n + m)$
 - If we double both, it just takes twice as long
 - Knuth-Morris-Pratt, 1977
 - Boyer-Moyer, 1977, 1991
- For one-off scans, this is the best we can do (optimal performance)
 - We have to read every character of the genome, and every character of the query
 - For short queries, runtime is dominated by the length of the genome

2. Suffix Arrays

- What if we need to check many queries?
 - We don't need to check every page of the phone book to find 'Schatz'
 - Sorting alphabetically lets us immediately skip 96% (25/26) of the book *without any loss in accuracy*
- Sorting the genome: Suffix Array (Manber & Myers, 1991)
 - Sort every suffix of the genome



Split into n suffixes



Sort suffixes alphabetically

[Challenge Question: How else could we split the genome?]

Searching the Index

- Strategy 2: Binary search
 - Compare to the middle, refine as higher or lower
- Searching for GATTACA
 - Lo = 1; Hi = 15;

#	Sequence	Pos
1	ACAGATTACC...	6
2	ACC...	13
3	AGATTACC...	8
4	ATTACAGATTACC...	3
5	ATTACC...	10
6	C...	15
7	CAGATTACC...	7
8	CC...	14
9	GATTACAGATTACC...	2
10	GATTACC...	9
11	TACAGATTACC...	5
12	TACC...	12
13	TGATTACAGATTACC...	1
14	TTACAGATTACC...	4
15	TTACC...	11

Searching the Index

- Strategy 2: Binary search
 - Compare to the middle, refine as higher or lower
- Searching for GATTACA
 - $Lo = 1; Hi = 15; Mid = (1+15)/2 = 8$
 - Middle = Suffix[8] = CC

#	Sequence	Pos
1	ACAGATTACC...	6
2	ACC...	13
3	AGATTACC...	8
4	ATTACAGATTACC...	3
5	ATTACC...	10
6	C...	15
7	CAGATTACC...	7
8	CC...	14
9	GATTACAGATTACC...	2
10	GATTACC...	9
11	TACAGATTACC...	5
12	TACC...	12
13	TGATTACAGATTACC...	1
14	TTACAGATTACC...	4
15	TTACC...	11

Searching the Index

- Strategy 2: Binary search
 - Compare to the middle, refine as higher or lower
- Searching for GATTACA
 - $Lo = 1; Hi = 15; Mid = (1+15)/2 = 8$
 - Middle = Suffix[8] = CC
=> Higher: Lo = Mid + 1

#	Sequence	Pos
1	ACAGATTACC...	6
2	ACC...	13
3	AGATTACC...	8
4	ATTACAGATTACC...	3
5	ATTACC...	10
6	C...	15
7	CAGATTACC...	7
8	CC...	14
9	GATTACAGATTACC...	2
10	GATTACC...	9
11	TACAGATTACC...	5
12	TACC...	12
13	TGATTACAGATTACC...	1
14	TTACAGATTACC...	4
15	TTACC...	11

Searching the Index

- Strategy 2: Binary search
 - Compare to the middle, refine as higher or lower
- Searching for GATTACA
 - $Lo = 1; Hi = 15; Mid = (1+15)/2 = 8$
 - Middle = Suffix[8] = CC
=> Higher: $Lo = Mid + 1$
 - $Lo = 9; Hi = 15;$

#	Sequence	Pos
1	ACAGATTACC...	6
2	ACC...	13
3	AGATTACC...	8
4	ATTACAGATTACC...	3
5	ATTACC...	10
6	C...	15
7	CAGATTACC...	7
8	CC...	14
9	GATTACAGATTACC...	2
10	GATTACC...	9
11	TACAGATTACC...	5
12	TACC...	12
13	TGATTACAGATTACC...	1
14	TTACAGATTACC...	4
15	TTACC...	11

Lo
→

Hi
→

Searching the Index

- Strategy 2: Binary search
 - Compare to the middle, refine as higher or lower
- Searching for GATTACA
 - Lo = 1; Hi = 15; Mid = $(1+15)/2 = 8$
 - Middle = Suffix[8] = CC
=> Higher: Lo = Mid + 1
 - Lo = 9; Hi = 15; Mid = $(9+15)/2 = 12$
 - Middle = Suffix[12] = TACC

#	Sequence	Pos
1	ACAGATTACC...	6
2	ACC...	13
3	AGATTACC...	8
4	ATTACAGATTACC...	3
5	ATTACC...	10
6	C...	15
7	CAGATTACC...	7
8	CC...	14
9	GATTACAGATTACC...	2
10	GATTACC...	9
11	TACAGATTACC...	5
12	TACC...	12
13	TGATTACAGATTACC...	1
14	TTACAGATTACC...	4
15	TTACC...	11

Lo

Hi

Searching the Index

- **Strategy 2: Binary search**
 - Compare to the middle, refine as higher or lower
- Searching for GATTACA
 - $Lo = 1; Hi = 15; Mid = (1+15)/2 = 8$
 - Middle = Suffix[8] = CC
=> Higher: Lo = Mid + 1
 - $Lo = 9; Hi = 15; Mid = (9+15)/2 = 12$
 - Middle = Suffix[12] = TACC
=> Lower: Hi = Mid - 1
 - $Lo = 9; Hi = 11;$

#	Sequence	Pos
1	ACAGATTACC...	6
2	ACC...	13
3	AGATTACC...	8
4	ATTACAGATTACC...	3
5	ATTACC...	10
6	C...	15
7	CAGATTACC...	7
8	CC...	14
9	GATTACAGATTACC...	2
10	GATTACC...	9
11	TACAGATTACC...	5
12	TACC...	12
13	TGATTACAGATTACC...	1
14	TTACAGATTACC...	4
15	TTACC...	11

Lo

Hi

Searching the Index

- **Strategy 2: Binary search**
 - Compare to the middle, refine as higher or lower
- Searching for GATTACA
 - Lo = 1; Hi = 15; Mid = $(1+15)/2 = 8$
 - Middle = Suffix[8] = CC
=> Higher: Lo = Mid + 1
 - Lo = 9; Hi = 15; Mid = $(9+15)/2 = 12$
 - Middle = Suffix[12] = TACC
=> Lower: Hi = Mid - 1
 - Lo = 9; Hi = 11; Mid = $(9+11)/2 = 10$
 - Middle = Suffix[10] = GATTACC

#	Sequence	Pos
1	ACAGATTACC...	6
2	ACC...	13
3	AGATTACC...	8
4	ATTACAGATTACC...	3
5	ATTACC...	10
6	C...	15
7	CAGATTACC...	7
8	CC...	14
9	GATTACAGATTACC...	2
10	GATTACC...	9
11	TACAGATTACC...	5
12	TACC...	12
13	TGATTACAGATTACC...	1
14	TTACAGATTACC...	4
15	TTACC...	11

Lo

Hi

Searching the Index

- **Strategy 2: Binary search**
 - Compare to the middle, refine as higher or lower
- Searching for GATTACA
 - Lo = 1; Hi = 15; Mid = $(1+15)/2 = 8$
 - Middle = Suffix[8] = CC
=> Higher: Lo = Mid + 1
 - Lo = 9; Hi = 15; Mid = $(9+15)/2 = 12$
 - Middle = Suffix[12] = TACC
=> Lower: Hi = Mid - 1
 - Lo = 9; Hi = 11; Mid = $(9+11)/2 = 10$
 - Middle = Suffix[10] = GATTACC
=> Lower: Hi = Mid - 1
 - Lo = 9; Hi = 9;

#	Sequence	Pos
1	ACAGATTACC...	6
2	ACC...	13
3	AGATTACC...	8
4	ATTACAGATTACC...	3
5	ATTACC...	10
6	C...	15
7	CAGATTACC...	7
8	CC...	14
9	GATTACAGATTACC...	2
10	GATTACC...	9
11	TACAGATTACC...	5
12	TACC...	12
13	TGATTACAGATTACC...	1
14	TTACAGATTACC...	4
15	TTACC...	11

Lo
Hi



Searching the Index

- Strategy 2: Binary search
 - Compare to the middle, refine as higher or lower
- Searching for GATTACA
 - Lo = 1; Hi = 15; Mid = $(1+15)/2 = 8$
 - Middle = Suffix[8] = CC
=> Higher: Lo = Mid + 1
 - Lo = 9; Hi = 15; Mid = $(9+15)/2 = 12$
 - Middle = Suffix[12] = TACC
=> Lower: Hi = Mid - 1
 - Lo = 9; Hi = 11; Mid = $(9+11)/2 = 10$
 - Middle = Suffix[10] = GATTACC
=> Lower: Hi = Mid - 1
 - Lo = 9; Hi = 9; Mid = $(9+9)/2 = 9$
 - Middle = Suffix[9] = GATTACA...
=> Match at position 2!



#	Sequence	Pos
1	ACAGATTACC...	6
2	ACC...	13
3	AGATTACC...	8
4	ATTACAGATTACC...	3
5	ATTACC...	10
6	C...	15
7	CAGATTACC...	7
8	CC...	14
9	GATTACA GATTACC...	2
10	GATTACC...	9
11	TACAGATTACC...	5
12	TACC...	12
13	TGATTACAGATTACC...	1
14	TTACAGATTACC...	4
15	TTACC...	11

Binary Search Analysis

- Binary Search

 Initialize search range to entire list

$\text{mid} = (\text{hi}+\text{lo})/2$; $\text{middle} = \text{suffix}[\text{mid}]$

 if query matches middle: done

 else if query < middle: pick low range

 else if query > middle: pick hi range

 Repeat until done or empty range

[WHEN?]

- Analysis

- More complicated method

- How many times do we repeat?

- How many times can it cut the range in half?

- Find smallest x such that: $n/(2^x) \leq 1$; $x = \lg_2(n)$

[32]

- Total Runtime: $O(m \lg n)$

- More complicated, but **much** faster!

- Looking up a query loops 32 times instead of 3B

[How long does it take to search 6B nucleotides?]

Binary Search in Matlab

```
%% create our sorted list of 100 numbers
seq=1:100;
%% seq=sort(floor(rand(100)*100));
query=33;

%% initialize search range
lo=1;
hi=length(seq);
steps=0;

%% search
while (lo<=hi)
    steps = steps+1;
    mid=floor((lo+hi)/2);
    middle=seq(mid);
    disp(['Step ', num2str(steps), ' checking seq[', num2str(mid), ']=' , num2str(middle)])
    if (query == middle)
        disp(['Found at ', num2str(mid), ' in ', num2str(steps), ' steps'])
        break
    elseif (query < middle)
        disp(['less than ', num2str(middle)])
        hi=mid-1;
    else
        disp(['greater than ', num2str(middle)])
        lo=mid+1;
    end
end
```

Suffix Array Construction

- Searching the array is very fast, but it takes time to construct
 - This time will be amortized over many, many searches
 - Run it once "overnight" and save it away for all future queries
- How do we store the suffix array?
 - Explicitly storing all n strings is not feasible

$$S = 1 + 2 + 3 + \dots + n = \sum_{i=1}^n i = \frac{n(n+1)}{2} = O(n^2)$$

For human genome $S = 9$ billion billion characters

- Instead use implicit representation
 - Keep 1 copy of the genome, and a list of sorted offsets
 - Storing 3 billion offsets requires a big server (12GB)
 - Build a separate index for each chromosome

Pos
6
13
8
3
10
15
7
14
2
9
5
12
1
4
11

TGATTACAGATTACC

Sorting

Sort these numbers into ascending order:

14, 29, 6, 31, 39, 64, 78, 50, 13, 63, 61, 19

[How do you do it?]

6, 13, 14, 29, 31, 39, 64, 78, 50, 63, 61, 19

6, 13, 14, 29, 31, 39, 64, 78, 50, 63, 61, 19

6, 13, 14, 19, 29, 31, 39, 64, 78, 50, 63, 61

6, 13, 14, 19, 29, 31, 39, 64, 78, 50, 63, 61

6, 13, 14, 19, 29, 31, 39, 64, 78, 50, 63, 61

6, 13, 14, 19, 29, 31, 39, 50, 64, 78, 63, 61

6, 13, 14, 19, 29, 31, 39, 50, 61, 64, 78, 63

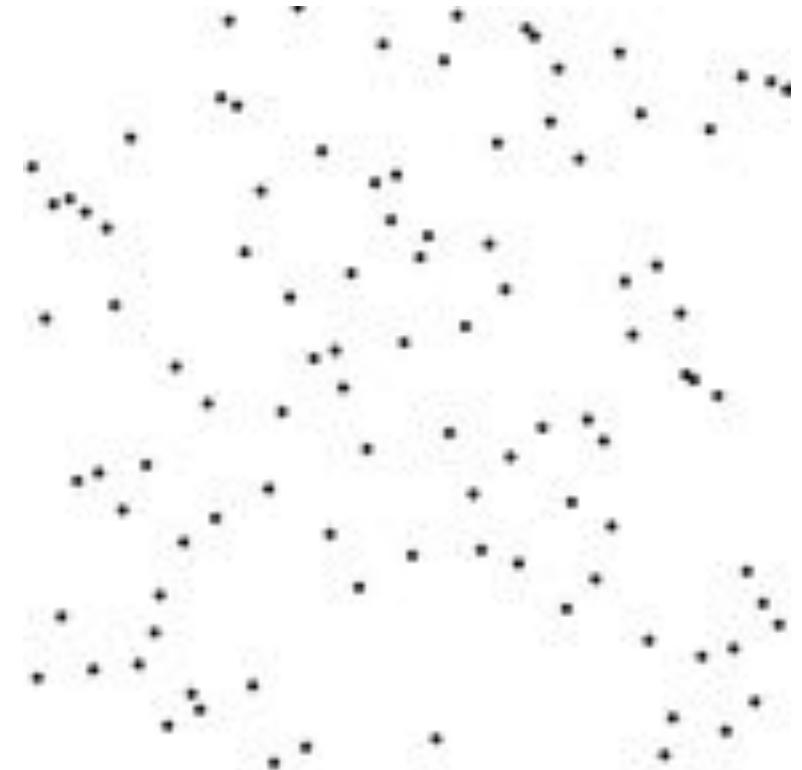
6, 13, 14, 19, 29, 31, 39, 50, 61, 63, 64, 78

6, 13, 14, 19, 29, 31, 39, 50, 61, 63, 64, 78

6, 13, 14, 19, 29, 31, 39, 50, 61, 63, 64, 78

6, 13, 14, 19, 29, 31, 39, 50, 61, 63, 64, 78

6, 13, 14, 19, 29, 31, 39, 50, 61, 63, 64, 78



Selection Sort Analysis

- Selection Sort (Input: list of n numbers)

```
for pos = 1 to n
```

```
    // find the smallest element in [pos, n]
```

```
    smallest = pos
```

```
    for check = pos+1 to n
```

```
        if (list[check] < list[smallest]): smallest = check
```

```
    // move the smallest element to the front
```

```
    tmp = list[smallest]
```

```
    list[pos] = list[smallest]
```

```
    list[smallest] = tmp
```

- Analysis

$$T = n + (n - 1) + (n - 2) + \dots + 3 + 2 + 1 = \sum_{i=1}^n i = \frac{n(n + 1)}{2} = O(n^2)$$

- Outer loop: pos = 1 to n

- Inner loop: check = pos to n

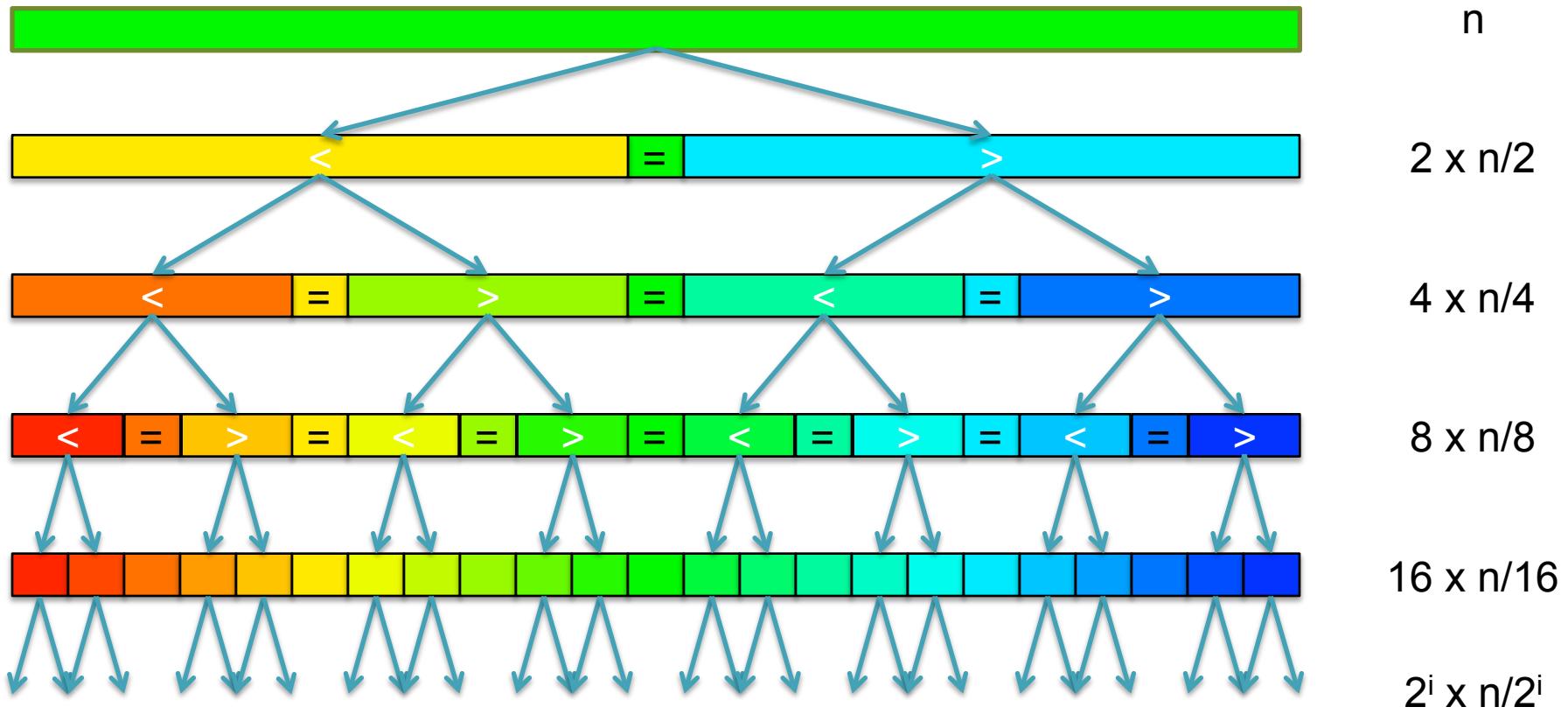
- Running time: Outer * Inner = $O(n^2)$

[9 Billion Billion]

[Challenge Questions: Why is this slow? / Can we sort any faster?]

Divide and Conquer

- Selection sort is slow because it rescans the entire list for each element
 - How can we split up the unsorted list into independent ranges?
 - Hint 1: Binary search splits up the problem into 2 independent ranges (hi/lo)
 - Hint 2: Assume we know the median value of a list



[How many times can we split a list in half?]

QuickSort Analysis

- QuickSort(Input: list of n numbers)
// see if we can quit
if (length(list)) <= 1): return list

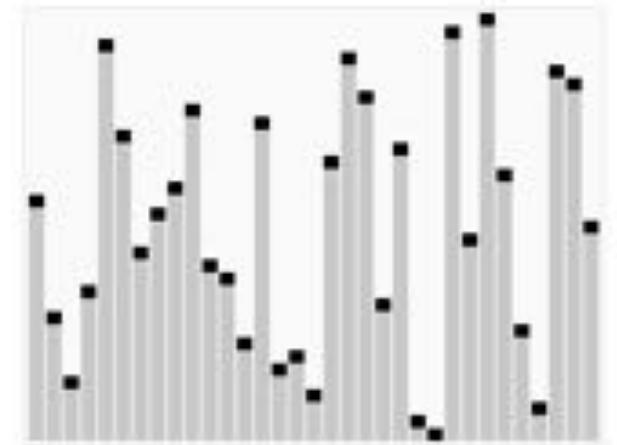
// split list into lo & hi
pivot = median(list)
lo = {}; hi = {};
for (i = 1 to length(list))
 if (list[i] < pivot): append(lo, list[i])
 else: append(hi, list[i])

// recurse on sublists
return (append(QuickSort(lo), QuickSort(hi)))

- Analysis (Assume we can find the median in $O(n)$)

$$T(n) = \begin{cases} O(1) & \text{if } n \leq 1 \\ O(n) + 2T(n/2) & \text{else} \end{cases}$$

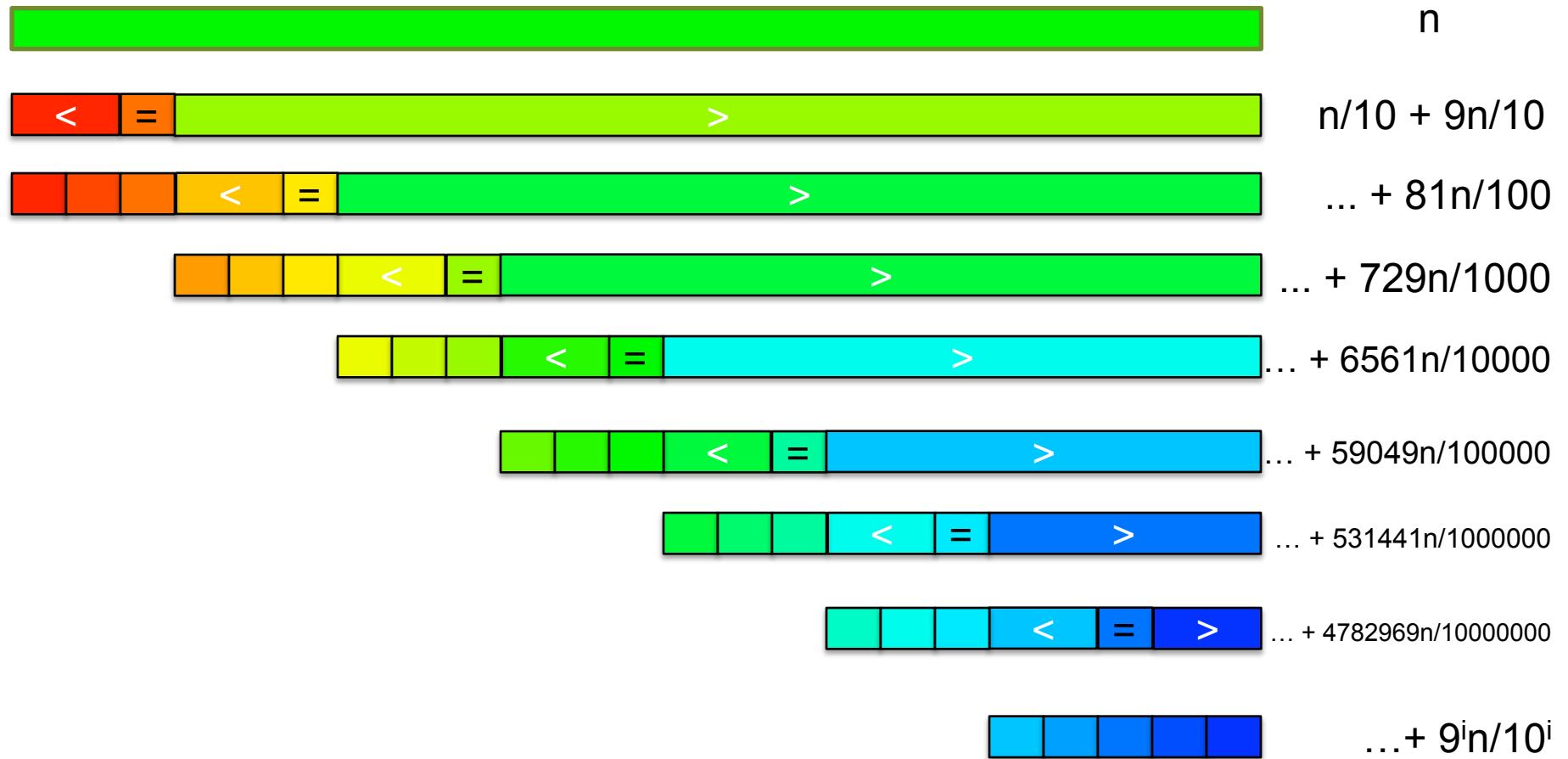
$$T(n) = n + 2\left(\frac{n}{2}\right) + 4\left(\frac{n}{4}\right) + \cdots + n\left(\frac{n}{n}\right) = \sum_{i=0}^{\lg(n)} \frac{2^i n}{2^i} = \sum_{i=0}^{\lg(n)} n = O(n \lg n) \quad [\sim 94B]$$



<http://en.wikipedia.org/wiki/Quicksort>

Picking the Median

- What if we miss the median and do a 90/10 split instead?



[How many times can we cut 10% off a list?]

Randomized Quicksort

- 90/10 split runtime analysis

Find smallest x s.t.

$$T(n) = n + T\left(\frac{n}{10}\right) + T\left(\frac{9n}{10}\right) \quad (9/10)^x n \leq 1$$

$$T(n) = n + \frac{n}{10} + T\left(\frac{n}{100}\right) + T\left(\frac{9n}{100}\right) + \frac{9n}{10} + T\left(\frac{9n}{100}\right) + T\left(\frac{81n}{100}\right) \quad (10/9)^x \geq n$$

$$T(n) = n + n + T\left(\frac{n}{100}\right) + 2T\left(\frac{9n}{100}\right) + T\left(\frac{81n}{100}\right) \quad x \geq \log_{10/9} n$$

$$T(n) = \sum_{i=0}^{\log_{10/9}(n)} n = O(n \lg n)$$

- If we randomly pick a pivot, we will get at least a 90/10 split with very high probability
 - Everything is okay as long as we always slice off a fraction of the list

[Challenge Question: What happens if we slice 1 element]

QuickSort in Matlab

`sort(seq)`

- The goal of software engineering is to build libraries of correct reusable functions that implement higher level ideas
 - Build complex software out of simple components
 - Software tends to be 90% plumbing, 10% research
 - You still need to know how they work
 - Matlab requires an explicit representation of the strings

Break

Sorting in Linear Time

- Can we sort faster than $O(n \lg n)$?
 - No – Not if we have to compare elements to each other
 - Yes – But we have to 'cheat' and know the structure of the data

Sort these numbers into ascending order:

14, 29, 6, 31, 39, 64, 78, 50, 13, 63, 61, 19

1,2,3,4,5,6,7,8,9,10,11,12,13,14,15,16,17,18,19,20,21,22,23,24,25,
26,27,28,29,30,31,32,33,34,35,36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,
51,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75,
76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100

Sorting in Linear Time

- Can we sort faster than $O(n \lg n)$?
 - No – Not if we have to compare elements to each other
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Sort these numbers into ascending order:

14, 29, 6, 31, 39, 64, 78, 50, 13, 63, 61, 19

1,2,3,4,5,**6**,7,8,9,10,11,12,**13**,**14**,15,16,17,18,**19**,20,21,22,23,24,25,
26,27,28,**29**,30,**31**,32,33,34,35,36,37,38,**39**,40,41,42,43,44,45,46,47,48,49,**50**,
51,52,53,54,55,56,57,58,59,60,**61**,62,**63**,**64**,65,66,67,68,69,70,71,72,73,74,75,
76,77,**78**,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100

Sorting in Linear Time

- Can we sort faster than $O(n \lg n)$?
 - No – Not if we have to compare elements to each other
 - Yes – But we have to 'cheat' and know the structure of the data

Sort these numbers into ascending order:

14, 29, 6, 31, 39, 64, 78, 50, 13, 63, 61, 19

1,2,3,4,5,**6**,7,8,9,10,11,12,**13**,**14**,15,16,17,18,**19**,20,21,22,23,24,25,
26,27,28,**29**,30,**31**,32,33,34,35,36,37,38,**39**,40,41,42,43,44,45,46,47,48,49,**50**,
51,52,53,54,55,56,57,58,59,60,**61**,62,**63**,**64**,65,66,67,68,69,70,71,72,73,74,75,
76,77,**78**,79,80,81,82,83,84,85,86,87,88,89,90,91,92,93,94,95,96,97,98,99,100

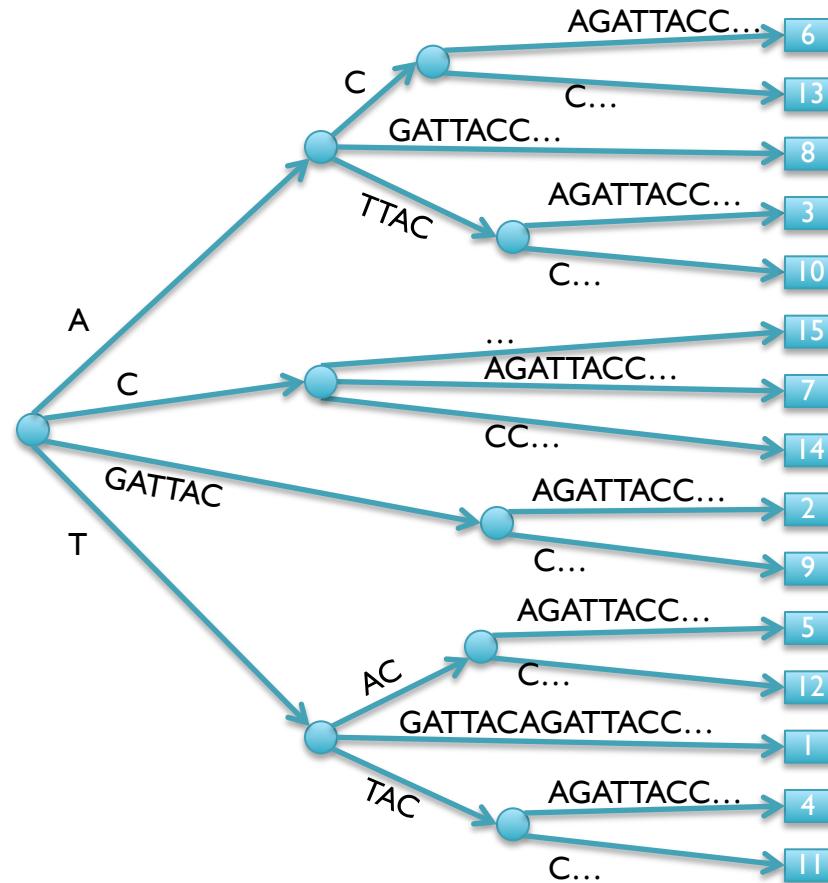
6,13,14,19,29,31,39,50,61,63,64,78

```
for(i = 1 to 100) { range[i] = 0; }
for(i = 1 to n) { range[list[i]] = 1; }
for(i = 1 to 100) { if (range[i] == 1){print i}}
```

[3B instead of 94B]

3. Suffix Trees

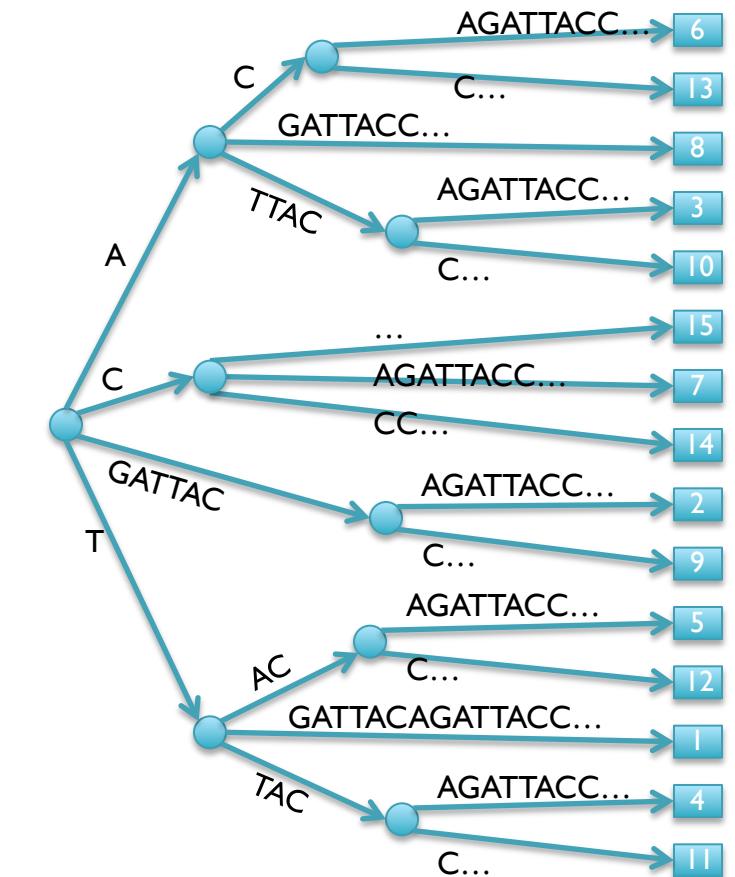
#	Sequence	Pos
1	ACAGATTACC...	6
2	ACC...	13
3	AGATTACC...	8
4	ATTACAGATTACC...	3
5	ATTACC...	10
6	C...	15
7	CAGATTACC...	7
8	CC...	14
9	GATTACAGATTACC...	2
10	GATTACC...	9
11	TACAGATTACC...	5
12	TACC...	12
13	TGATTACAGATTACC...	1
14	TTACAGATTACC...	4
15	TTACC...	11



- Suffix Tree = Tree of suffixes (indexes **all** substrings of a sequence)
 - 1 Leaf (\$) for each suffix, path-label to leaf spells the suffix
 - Nodes have at least 2 and at most 5 children (A,C,G,T,\$)

Suffix Trees Searching

- Look up a query by "walking" along the edges of the tree
 - GATTACA

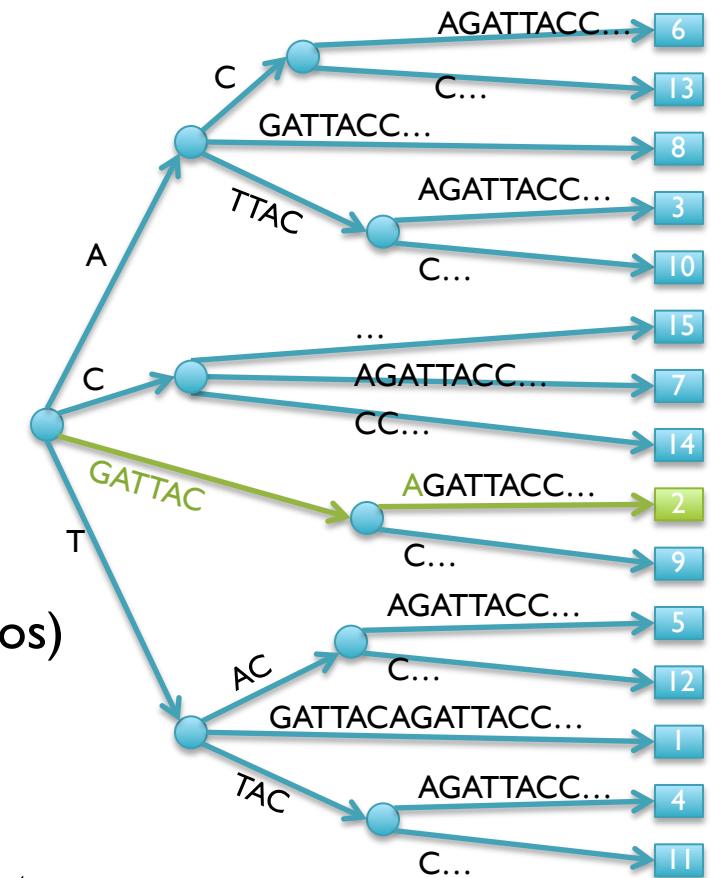


Suffix Trees Searching

- Look up a query by "walking" along the edges of the tree
 - GATTACA
 - Matches at position 2

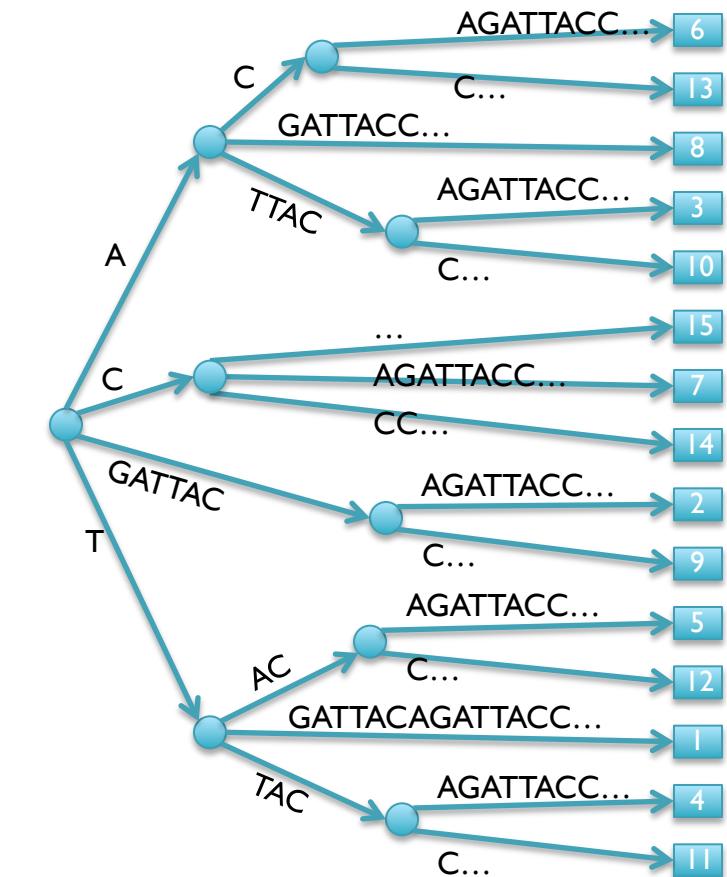
WalkTree

```
cur = ST.Root; qrypos = 0;
while (cur)
    // check for partial matches
    ...
    // walk the tree
    edge = cur.getEdge(q[qrypos]); edgepos=0
    dist = matchstrings(edge, edgepos, qry, qrypos)
    if (qrypos+dist == length(qry))
        print "end-to-end match"
    else if (dist == length(edge))
        cur=cur.getNode(edge[0]); qrypos+=dist
    else
        print "no match"
```



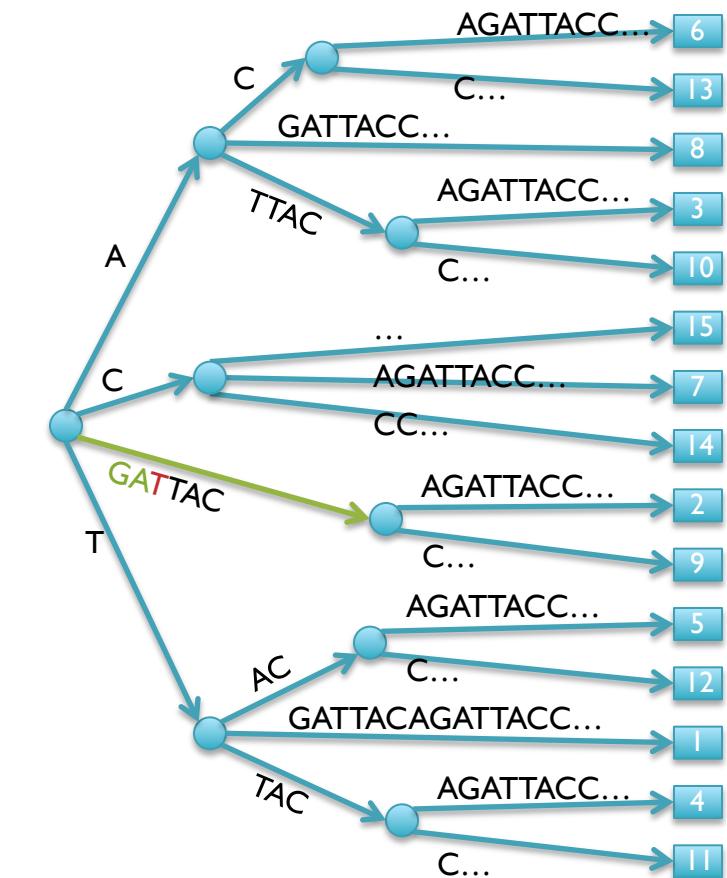
Suffix Trees Searching

- Look up a query by "walking" along the edges of the tree
 - GACTACA



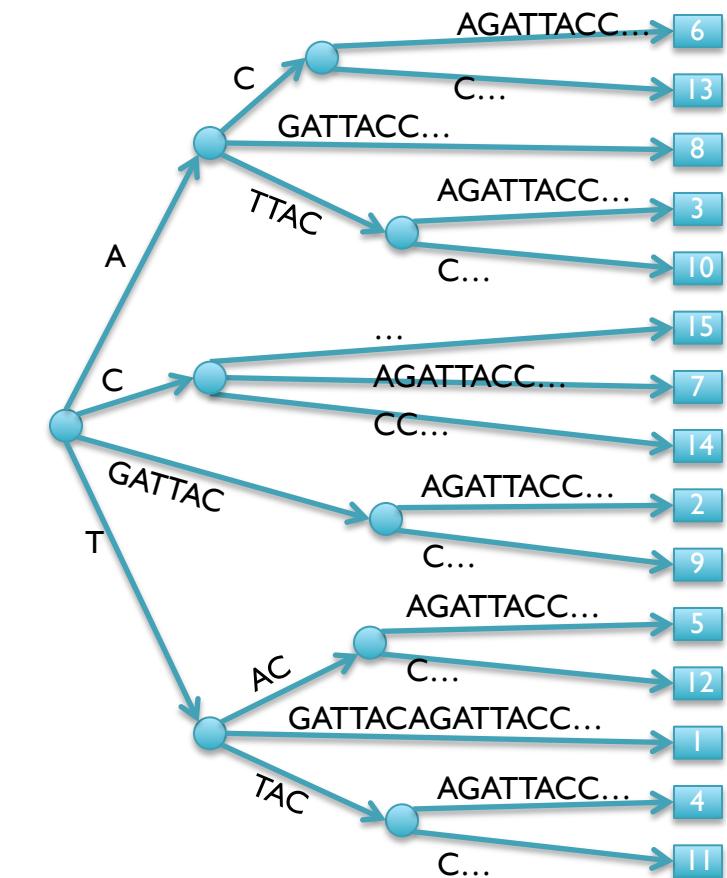
Suffix Trees Searching

- Look up a query by "walking" along the edges of the tree
 - GACTACA
 - Fell off tree – no match



Suffix Trees Searching

- Look up a query by "walking" along the edges of the tree
 - ATTAC



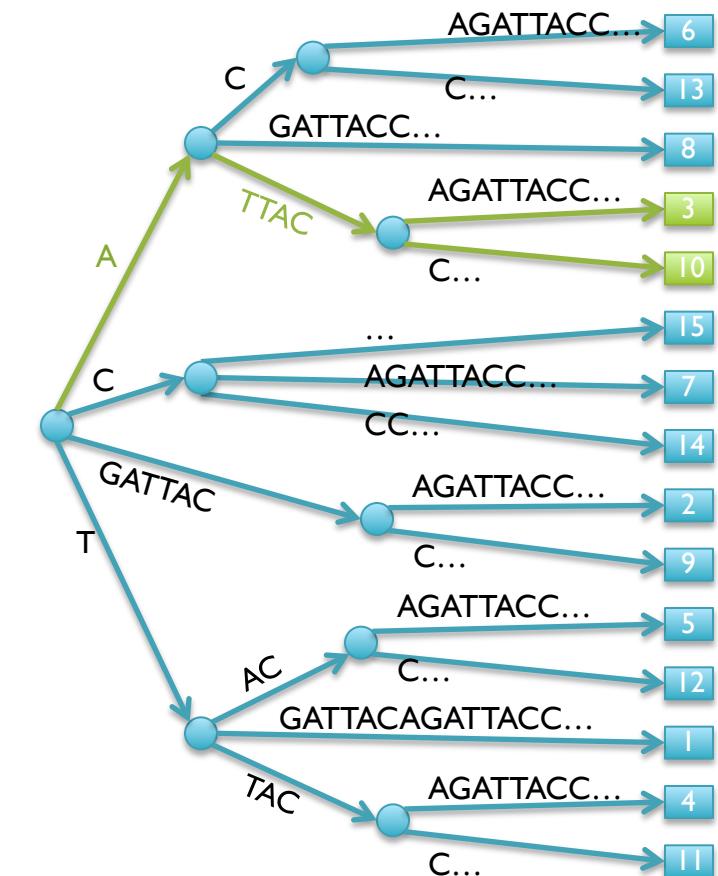
Suffix Trees Searching

- Look up a query by "walking" along the edges of the tree

- ATTAC
 - Matches at 3 and 10

- Query Lookup in 2 phases:
 - I. Walk along edges to find matches
 2. Walk subtree to find positions

```
DepthFirstPrint(Node cur)
if cur.isLeaf
    print cur.pos
else
    foreach child in cur.children
        DepthFirstPrint(child)
```



[What is the running time of DFP
=> How many nodes does the tree have?]

Suffix Tree Properties & Applications

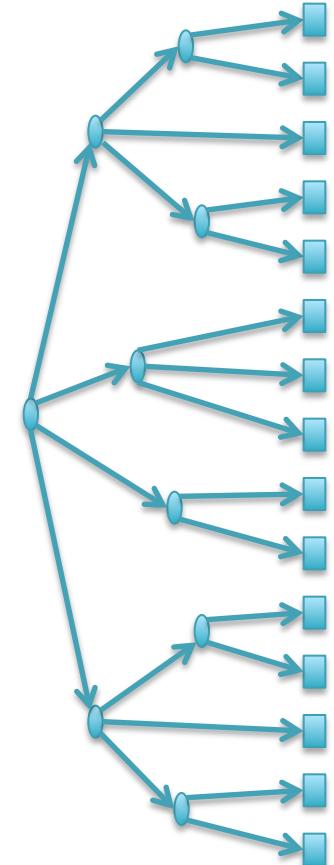
Properties

- Number of Nodes/Edges: $O(n)$
- Tree Size: $O(n)$
- Max Depth: $O(n)$
- Construction Time: $O(n)$
 - Uses suffix links to jump between nodes without rechecking
 - Tricky to implement, prove efficiency

Applications

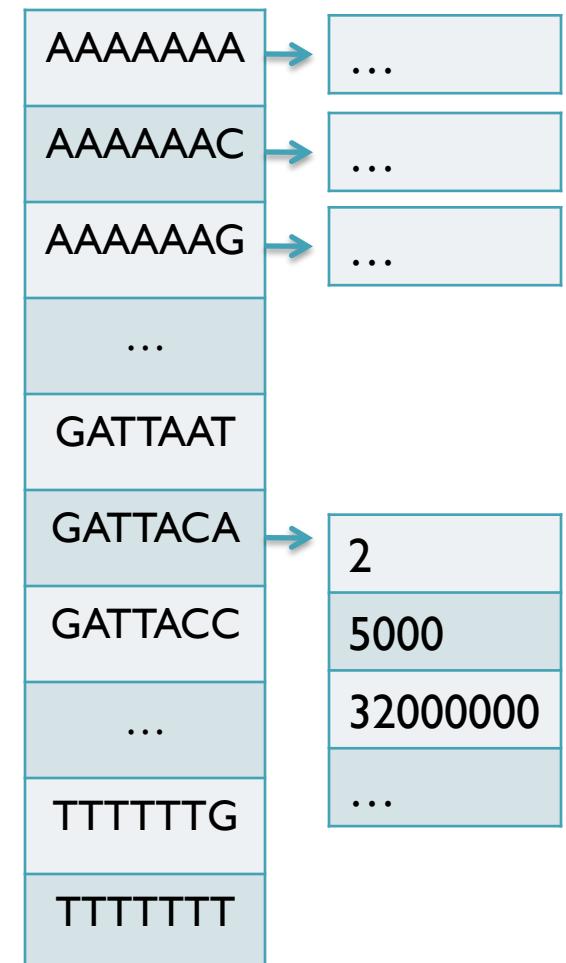
- Sorting all suffixes: $O(n)$
- Check for query: $O(m)$
- Find all z occurrences of a query $O(m + z)$
- Find maximal exact matches $O(m)$
- Longest common substring $O(m)$
- Used for many string algorithms in linear time
 - Many can be implemented on suffix arrays using a little extra work

[HOW?]



4. Hashing

- Where is GATTACA in the human genome?
 - Build an inverted index (table) of every kmer in the genome
- How do we access the table?
 - We can only use numbers to index
 - `table[GATTACA] <- error, does not compute`
 - Encode sequences as numbers
 - Easy: $A = 1_{10}, C = 2_{10}, G = 3_{10}, T = 4_{10}$
 - $GATTACA = 3144121_{10}$
 - Smart: $A = 00_2, C = 01_2, G = 10_2, T = 11_2$
 - $GATTACA = 1000111000100_2 = 9156_{10}$
 - Running time
 - Construction: $O(n)$
 - Lookup: $O(1) + O(z)$
 - Sorts the genome mers in linear time

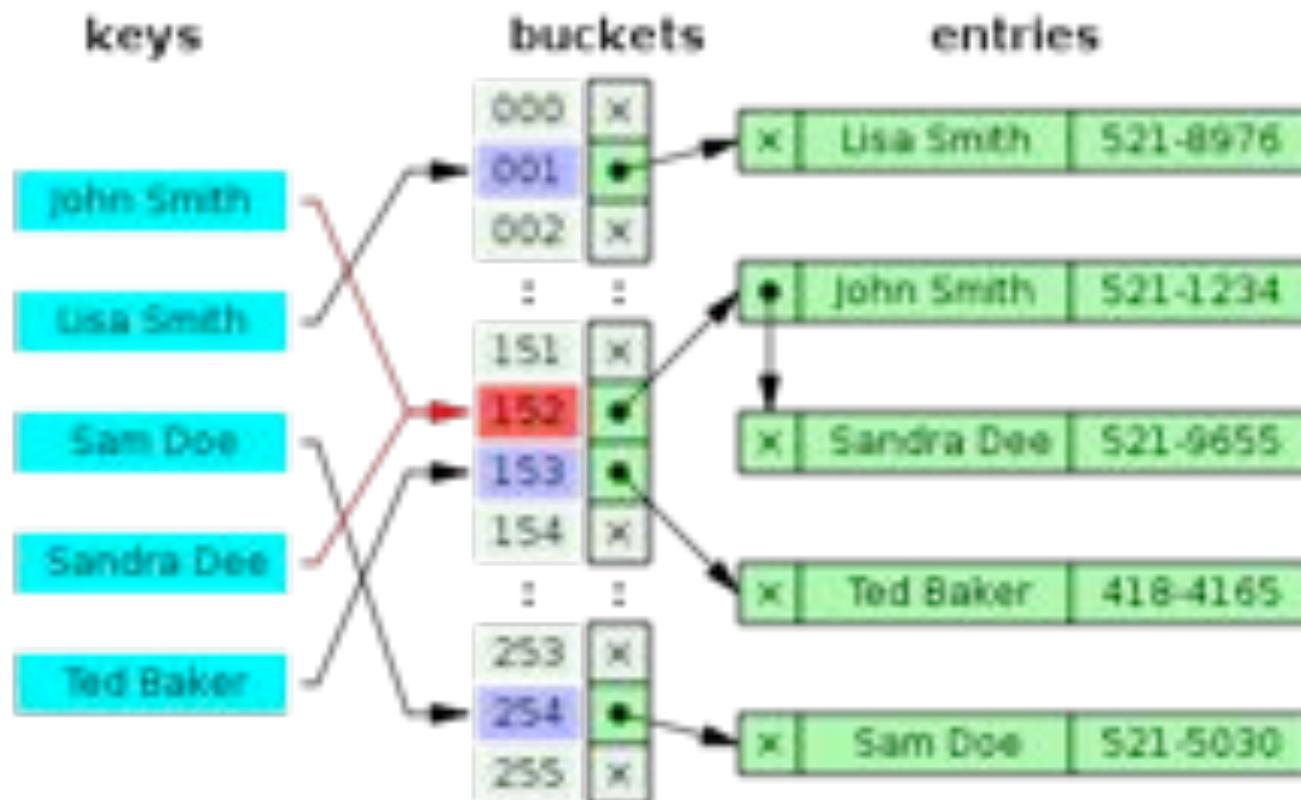


Hash Tables and Hash Functions

- Number of possible sequences of length $k = 4^k$
 - $4^7 = 16,384$ (easy to store)
 - $4^{20} = 1,099,511,627,776$ (impossible to directly store in RAM)
 - There are only 3B 20-mers in the genome
 - ⇒ Even if we could build this table, 99.7% will be empty
 - ⇒ But we don't know which cells are empty until we try
- Hash Function: $\text{hash}(n) \rightarrow h$
 - Maps a number n in $[0, R]$ to h in $[0, H]$ where $H \ll R$
 - More than one n will have the same h
 - A good hash function evenly distributes the values
 - R/H have the same hash value
 - A really good hash function also spreads out the values
 - $\Pr(\text{hash}(n) == \text{hash}(m)) = 1/H$
 - A common (decent) choice is $\text{hash}(n) = n \bmod H$

Hash Table Lookup

- By construction, multiple keys have the same hash value
 - Store elements with the same key in a bucket chained together
 - Looking up a value scans the entire bucket
 - Slows down the search as a function of the hash table load
 - Warning: This complexity is usually hidden in the hash table code



http://en.wikipedia.org/wiki/Hash_table

Variable Length Queries

- Where are GATTACA and GATTACCA in the human genome?
 - $s = \min(\text{length of all queries})$
 - Build an inverted index of all s -mers (seeds) in the genome
 - GATTACA => 2, 5000, 32000000, ...
 - GATTACC => 5500, 10101, 1000000, ...
- Seed-and-extend to find end-to-end exact matches
 - Check every occurrence of the qry seed (first s characters)
 - ~1 in 4 are GATTACCA, 1 in 4 are GATTACCC, etc
 - The specificity of the seed depends on $\text{length}(q)$ & s
 - Works best if $\max(\text{length}) = \sim \min(\text{length})$
 - Works best if $e\text{-value}(m) \ll 1$

Exact Matching Review

- E-value depends on length of genome and inversely on query length
 - $E = (n-m+1)/4^m$

Brute Force
(3 GB)

BANANA
BAN
ANA
NAN
ANA

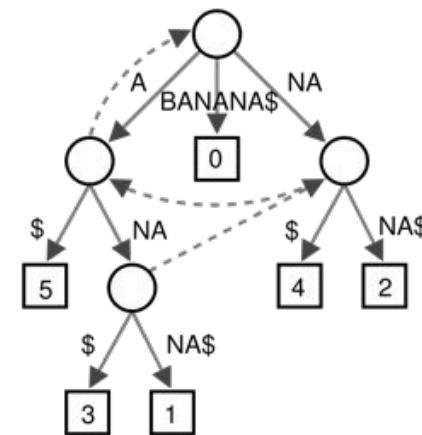
Naive
Slow & Easy

Suffix Array
(>15 GB)

6	\$
5	A\$
3	ANA\$
1	ANANA\$
0	BANANA\$
4	NA\$
2	NANA\$

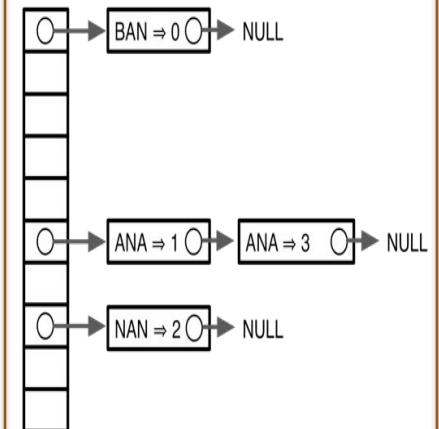
Vmatch, PacBio Aligner
Binary Search

Suffix Tree
(>51 GB)



MUMmer, MUMmerGPU
Tree Walking & DFS

Hash Table
(>15 GB)

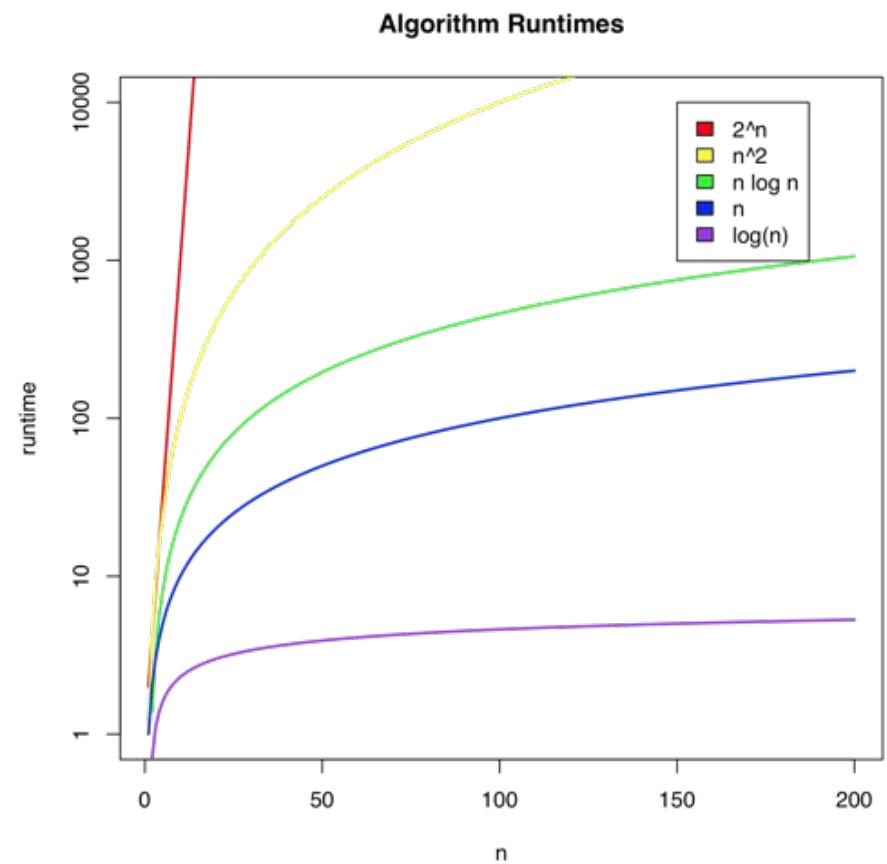
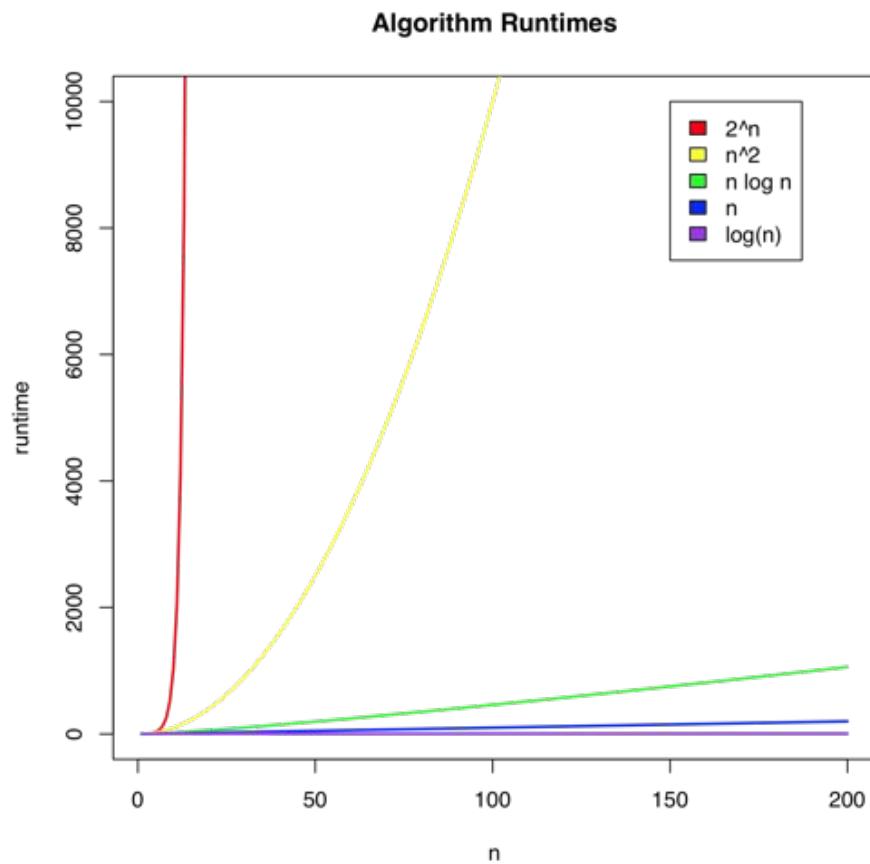


BLAST, MAQ, ZOOM,
RMAP, CloudBurst
Seed-and-extend

Algorithms Summary

- Algorithms choreograph the dance of data inside the machine
 - Algorithms add provable precision to your method
 - A smarter algorithm can solve the same problem with much less work
- Techniques
 - Binary search: Fast lookup in any sorted list
 - Divide-and-conquer: Split a hard problem into an easier problem
 - Recursion: Solve a problem using a function of itself
 - Randomization: Avoid the demon
 - Hashing: Storing sets across a huge range of values
 - Indexing: Focus on the search on the important parts
 - Different indexing schemes have different space/time features
- Data Structures
 - Primitives: Integers, Numbers, Strings
 - Lists / Arrays / Multi-dimensional arrays
 - Trees
 - Hash Table

Algorithmic Complexity



What is the runtime as a function of the input size?

Next Time

- In-exact alignment
 - Smith & Waterman (1981) *Identification of Common Molecular Subsequences*. J. of Molecular Biology. 147:195-197.
- Sequence Homology
 - Altschul SF, Gish W, Miller W, Myers EW, Lipman DJ (1990). *Basic local alignment search tool*. J of Molecular Biology. 215 (3): 403–410.
- Whole Genome Alignment
 - A.L. Delcher, S. Kasif, R.D. Fleischmann, J. Peterson, O.White, and S.L. Salzberg (1999) *Alignment of Whole Genomes*. Nucleic Acids Research (27):11 2369-2376.
- Short Read Mapping
 - Langmead B, Trapnell C, Pop M, Salzberg SL. (2009) *Ultrafast and memory-efficient alignment of short DNA sequences to the human genome*. Genome Biology. 10:R25.