

1. Exact string matching
2. Boyer Moore
3. Indexing structures

Lesson 05

Exact string matching algorithms

- Online exact matching algorithms (no preparation of the text)
 - Boyer-Moore
- Offline exact matching algorithms (prepare some kind of index of the text)
 - Multimap table
 - Hash table
 - Suffix array
 - Burrows–Wheeler transformation, FM index

String definitions

- String S is a finite sequence of characters
- Characters are drawn from alphabet Σ :
Usually, $\Sigma = \{ A, C, G, T \}$
- $| S | =$ number of characters in S
- ϵ is “empty string” $| \epsilon | = 0$

Exact matching

- At what offsets does pattern P occur within text T?
- What's a simple algorithm for exact matching?

Text: There would have been a time for such a word

Pattern: word

Answer: 40

Try all possible alignments. For each, check whether it's an occurrence. “Naïve algorithm”.

Exact matching: Naïve algorithm

- Looking for places where a pattern P occurs as a substring of a Text
- Let $n = |P|$, and let $m = |T|$, and assume $n \leq m$
- An **alignment** is a way of putting P 's characters opposite T 's characters. It may or may not correspond to an occurrence:

T: There would have been a time for such a word

P: word

Alignment 1: word

Alignment 2: word

Exact matching

```
def naive(p, t):  
    occurrences = []  
    for i in range(len(t) - len(p) + 1): # loop over alignments, L-to-R  
        match = True  
        for j in range(len(p)):          # loop over characters, L-to-R  
            if t[i+j] != p[j]:           # character compare  
                match = False            # mismatch; reject alignment  
                break  
        if match:  
            occurrences.append(i)         # all chars matched; record  
    return occurrences
```

Python demo: <http://nbviewer.ipython.org/6513059>

There would have been a time for such a word

-----word-----word-----word
----->----->----->

Exact matching: Naïve algorithm

- How many alignments are possible given n and m ($|P|$ and $|T|$)?

$$m - n + 1$$

- What is the lowest and greatest number of possible character comparisons?

$$m - n + 1, n(m - n + 1)$$

- How many character comparisons in this example?

There would have been a time for such a word

-----word-----word-----word
 -----> -----> ----->

$m - n$ mismatches, 6 matches

Exact matching: Naïve algorithm

Greatest # character
comparisons:
 $n(m - n + 1)$

Least:
 $m - n + 1$

P: aaaa

T: aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa
aaaa aaaa aaaa aaaa aaaa aaaa aaaa aaaa aaaa
aaaa aaaa aaaa aaaa aaaa aaaa aaaa aaaa aaaa
aaaa aaaa aaaa aaaa aaaa aaaa aaaa aaaa aaaa
aaaa aaaa aaaa aaaa aaaa aaaa aaaa aaaa aaaa
aaaa aaaa aaaa aaaa aaaa aaaa aaaa aaaa aaaa

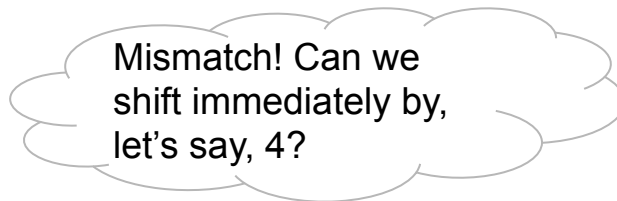
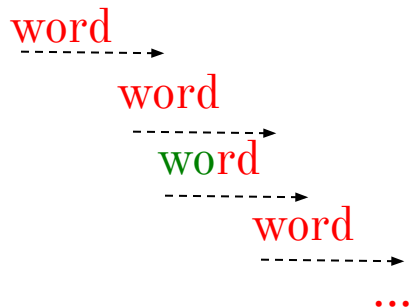
Worst-case time bound of naïve algorithm is $O(nm)$

In the best case, we do only $\sim m$ character comparisons

Exact matching: Can it be done better?

- Can we skip some alignments?
- Define some heuristic that could increase the shifts of pattern!
- Preprocess Text or Pattern and extract some information.

There would have been a time for such a word



Online exact matching: Boyer Moore algorithm

Use knowledge gained from character comparisons to skip future alignments that definitely won't match:

1. **Bad character rule:** If we mismatch, use knowledge of the mismatched text character to skip alignments
2. **Good suffix rule:** If we match some characters, use knowledge of the matched characters to skip alignments
3. **For longer skips:** If we match some characters, use knowledge of the matched characters to skip alignments

Boyer Moore: Bad character rule

- Upon mismatch, let b be the mismatched character in T .
Skip alignments until (a) b matches its opposite in P , or (b)
 P moves past b .

T: GCTT**CT**GTACCTTTTGCGCGCGCGCGGAA
P: CCTT**TT**GC

b - mismatched character

Case (a)

T: GCTTCTGCT**AC**CTTTTGCGCGCGCGCGGAA
P: CCTTTT**GC**

Case (b)

T: GCTTCTGCTAC**CCTTTT**GTGCGCGCGCGCGGAA
P: CCTTTT**GC**

Compare characters
from right to left!

We skipped 2 + 6
alignments!

Boyer Moore: Good suffix rule (weak)

Let t be the substring of T that matched a suffix of P . Skip alignments until (a) t matches opposite characters in P , or (b) a prefix of P matches a suffix of t , or (c) P moves past t , whichever happens first.

T: CGTGCCCTACTTACTTACTTACTTACGCGAA

Diagram: A dashed double-headed arrow labeled t is positioned above the text, spanning from the start of the first 'CTACT' to the end of the last 'CTACT'.

P: CTTACTTACT

Diagram: A box highlights the 'CTTACT' prefix of P . A dashed double-headed arrow labeled t is positioned below the text, spanning from the start of the first 'CTACT' to the end of the last 'CTACT'.

Case (a)

T: CGTGCCCTACTTACTTACTTACTTACGCGAA

Diagram: A box highlights the 'TACTTACT' suffix of t . A dashed double-headed arrow labeled t is positioned above the text, spanning from the start of the first 'CTACT' to the end of the last 'CTACT'.

P: CTTACTTACT

Diagram: A box highlights the 'CTTACT' prefix of P . A dashed double-headed arrow labeled t is positioned below the text, spanning from the start of the first 'CTACT' to the end of the last 'CTACT'.

Case (b)

Prefix(P) = Suffix(t) = CTTACT

T: CGTGCCCTACTTACTTACTTACTTACGCGAA

Diagram: A dashed double-headed arrow labeled t is positioned above the text, spanning from the start of the first 'CTACT' to the end of the last 'CTACT'.

P: CTTACTTACT

Boyer Moore: Good suffix rule (strong)

Let t be the substring of T that matched a suffix of P . Skip alignments until (a) t matches opposite characters in P **and character to the left of t is the same as it opposite character in P** , or (b) a prefix of P matches a suffix of t , or (c) P moves past t , whichever happens first.

T: CGTGCC**CTACT**TTACTTTACTTTACTTTACGCGAA
P: C**TTACT****TAC**

Diagram illustrating Case (a): A dashed arrow labeled t points to the suffix **CTACT** of T . A red arrow points from the **CTACT** in T to the **TTACT** in P . A dashed arrow points from the **TAC** in $P to the **TTACT** in T .$

Case (a)

T: CGTGCCCTA**CTTACTTAC**TTACTTTACTTTACGCGAA
P: **CTTACTTAC**

Boyer Moore: Good suffix rule

Like with the bad character rule, the number of skips possible using the good suffix rule can be precalculated into a few tables (Gusfield 2.2.4 and 2.2.5)

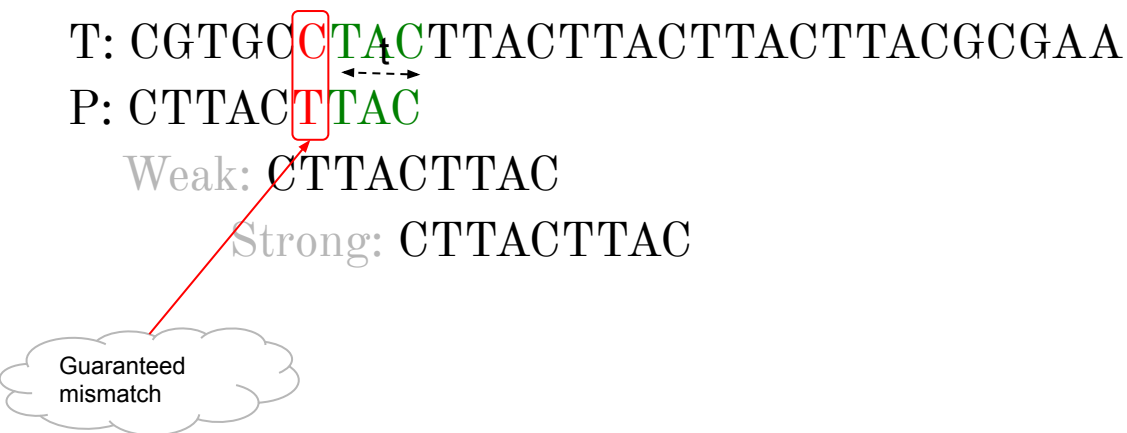
Strong good suffix rule (Gusfield 2.2.3)

T: CGTGCCCTACTTACTTACTTACGCGAA

P: CTTACTTAC

Weak: CTTACTTAC

Strong: CTTACTTAC



Guaranteed mismatch

Boyer Moore: Putting it all together

After each alignment, use bad character or good suffix rule, whichever skips more.

Bad character rule:

Upon mismatch, let b be the mismatched character in T . Skip alignments until (a) b matches its opposite in P , or (b) P moves past b .

T: GTTATAGCTGATCGCGGCGTAGCGGCGAA
P: GTAGCGGCG



bc: 6, gs: 0 (Part (a) of bad character rule)

T: GTTATAGCTGATCGCGGCGTAGCGGCGAA
P: GTAGCGGCG

bc: 0, gs: 2 (Part (b) of good suffix rule)

T: GTTATAGCTGATCGCGGCGTAGCGGCGAA
P: GTAGCGGCG

bc: 2, gs: 7 (Part (b) of good suffix rule)

T: GTTATAGCTGATCGCGGCGTAGCGGCGAA
P: GTAGCGGCG

Good suffix rule:

Let t be the substring of T that matched a suffix of P . Skip alignments until (a) t matches opposite characters in P , or (b) a prefix of P matches a suffix of t , or (c) P moves past t , whichever happens first.

*15 alignments skipped, 11 text characters never examined

Slide adapted from Ben Langmead

Boyer Moore: Preprocessing

- Pre-calculate skips. For bad character rule, $P = \text{TCGC}$:

		P			
		T	C	G	C
Σ	A	0	1	2	3
	C	0	-	0	-
	G	0	1	-	0
	T	-	0	1	2

Boyer-Moore
exercise in
Python

T : A A T C A A T A G C
 P : T C G C

Boyer Moore: Worst and best cases

Boyer-Moore (or a slight variant) is $O(m)$ worst-case time

What's the best case?

Every character comparison is a mismatch, and bad character rule always slides P fully past the mismatch

How many character comparisons?

$\text{floor}(|T| / |P|)$

Boyer Moore: Performance comparison

	Naïve matching		Boyer-Moore		
	# character comparisons	wall clock time	# character comparisons	wall clock time	
P: "tomorrow" T: Shakespeare's complete works	5,906,125	2.90 s	785,855	1.54 s	17 matches $ T = 5.59 \text{ M}$
P: 50 nt string from Alu repeat* T: Human reference (hg19) chromosome 1	307,013,905	137 s	32,495,111	55 s	336 matches $ T = 249 \text{ M}$

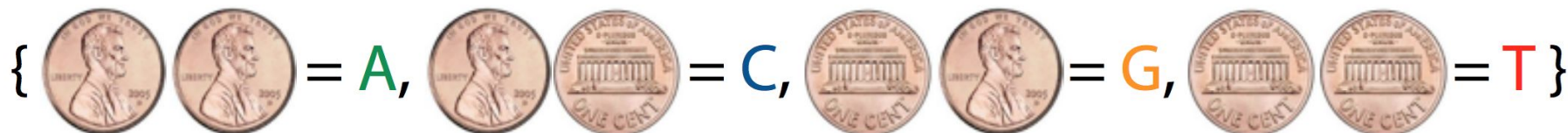
*

GCGCGGTGGCTCACGCCTGTAATCCCAGCACTTTGGGAGGCCGAGGCGGG

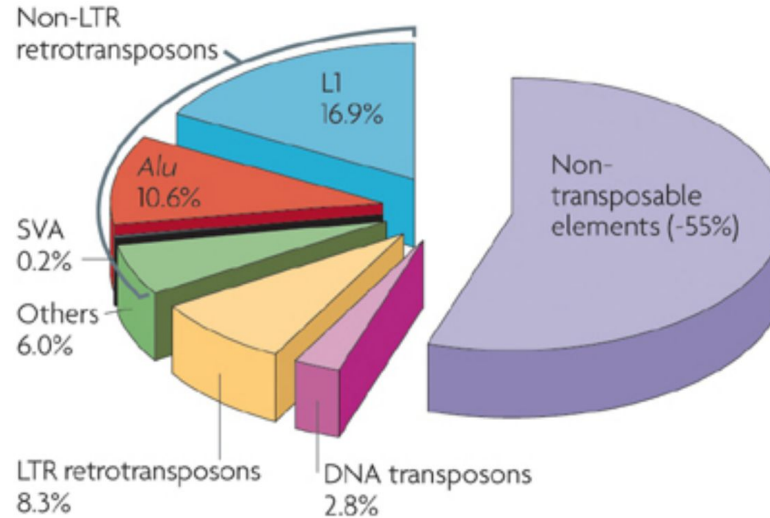
Slide adapted from Ben Langmead

Small digression

- Real genomes are not like “random” genomes



Repetitive sequences

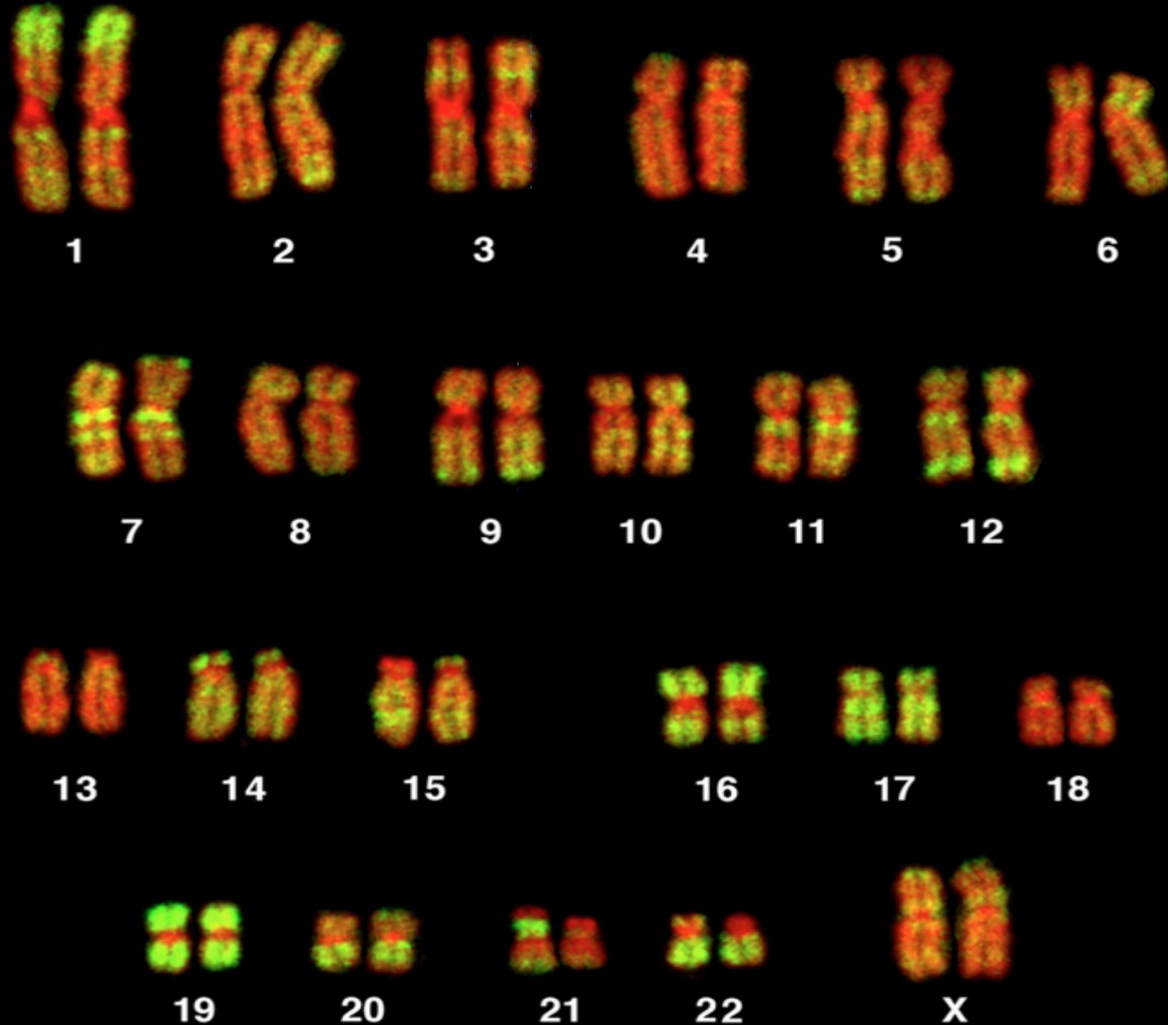


human genetic
identification based
on short tandem
repeats

Cordaux R, Batzer MA. The impact of retrotransposons on human genome evolution. Nat Rev Genet. 2009 Oct;10(10):691-703

Alu repeats cover
11% of the human
genome

Image: *Alus*
glowing green
in human
chromosomes





Offline exact matching: Create sorted index - Multimap

- T: CGTGCGTGCTT

- Index of T:

CGTGC : 0,4

GCGTG : 3

GTGCC : 1

GTGCT : 5

TGCCT : 2

TGCTT : 6

5-mer index

Preprocessing: Use index

- Index of T:

CGTGC : 0,4

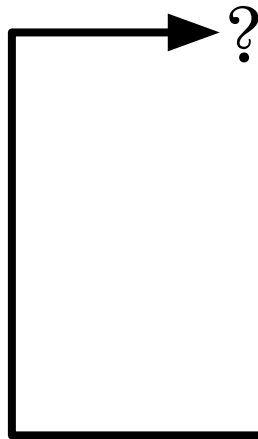
GCGTG : 3

GTGCC : 1

GTGCT : 5

TGCCT : 2

TGCTT : 6



T: CGTGCGTGCTT

P: GCGTGC

Preprocessing: Use index

- Index of T:

CGTGC : 0,4

GCGTG : 3

GTGCC : 1

GTGCT : 5

TGCCT : 2

TGCTT : 6

3

T: CGTGCGTGCTT

P: GCGTGC

Preprocessing: Use index

- Index of T:

CGTGC : 0,4

GCGTG : 3

GTGCC : 1

GTGCT : 5

TGCCT : 2

TGCTT : 6

3

T: CGTGCGTGCCTT

P: GCGTGC

What about the rest?

Preprocessing: Use index - different 5-mer

- Index of T:

CGTGC : 0,4

GCGTG : 3

GTGCC : 1

GTGCT : 5

TGCCT : 2

TGCTT : 6

0,4

T: CGTGCGTGCTT

P: GCGTGC

Preprocessing: Use index - different 5-mer

- Index of T:

CGTGC : 0,4

GCGTG : 3

GTGCC : 1

GTGCT : 5

TGCCT : 2

TGCTT : 6

0

T: CGTGCGTGCTT

P: GCGTGC

Preprocessing: Use index - different 5-mer

- Index of T:

CGTGC : 0,4

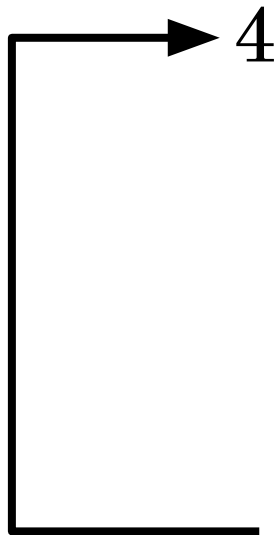
GCGTG : 3

GTGCC : 1

GTGCT : 5

TGCCT : 2

TGCTT : 6



T: CGTGCGTGCTT

P: GCGTGC

Preprocessing: Use index - different pattern

- Index of T:

CGTGC : 0,4

GCGTG : 3

GTGCC : 1

GTGCT : 5

TGCCT : 2

TGCTT : 6

3

T: CGTGCGTGCTT

P: GCGTGA

Preprocessing: Use index - different pattern

- Index of T:

CGTGC : 0,4

GCGTG : 3

GTGCC : 1

GTGCT : 5

TGCCT : 2

TGCTT : 6

3

We had index hit but
pattern mismatch!

T: CGTGCGTGCTT

P: GCGTGA

Preprocessing: Use index - different pattern

- Index of T:

CGTGC : 0,4

GCGTG : 3

GTGCC : 1

GTGCT : 5

TGCCT : 2

TGCTT : 6

?

T: CGTGCGTGCTT

P: GCGTAC



Preprocessing: Use index - different pattern

- Index of T:

CGTGC : 0,4

GCGTG : 3

GTGCC : 1

GTGCT : 5

TGCCT : 2

TGCTT : 6

We had index miss!

T: CGTGCGTGCTT

P: GCGTAC

Multimap


- T: GTGCGTGTGGGGG

GTG 0
TGC 1
GCG 2
CGT 3
GTG 4
TGT 5
GTG 6
TGG 7
GGG 8
GTG 9
GGG 10

Multimap

Alphabetical by k-mer

- T: GTGCGTGTGGGGG




CGT 3
GCG 2
GGG 8
GGG 9
GGG 10
GTG 0
GTG 4
GTG 6
TGC 1
TGG 7
TGT 5

Binary search

- T: GTGCGTGTGGGGG
- P: GCGTGG

TGG > GTG



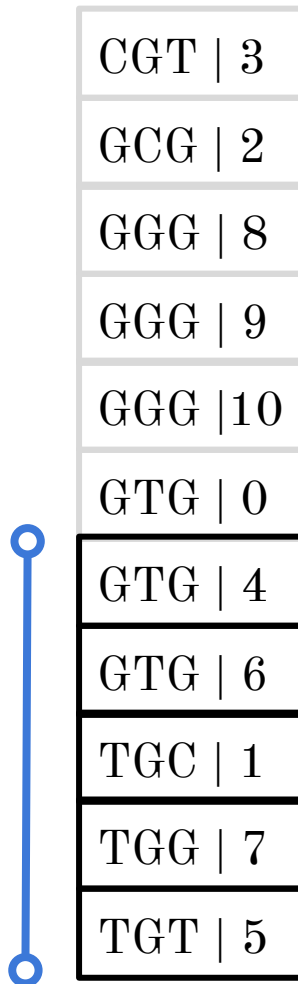
CGT 3
GCG 2
GGG 8
GGG 9
GGG 10
GTG 0
GTG 4
GTG 6
TGC 1
TGG 7
TGT 5

Binary search

After 1st bisection

TGG > TGC

- T: GTGCGTGTGGGGG
- P: GCGTGG

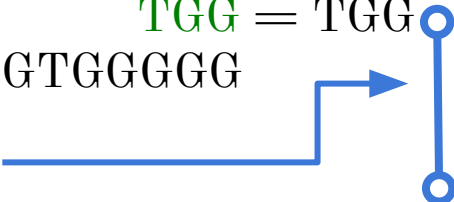


CGT 3
GCG 2
GGG 8
GGG 9
GGG 10
GTG 0
GTG 4
GTG 6
TGC 1
TGG 7
TGT 5

Binary search

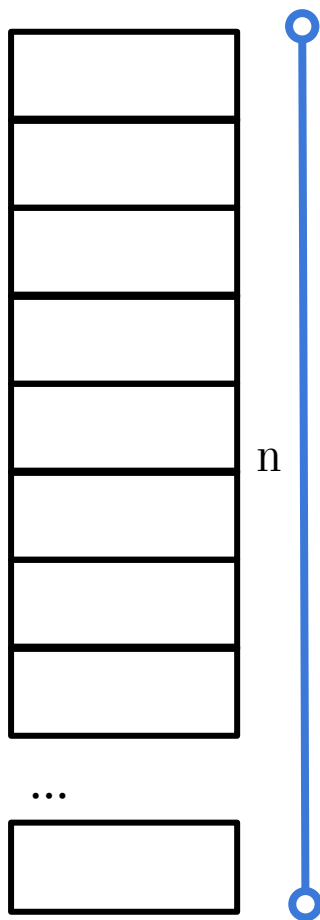
After 2nt bisection



- T: GTGCGTGTGGGGG
 - P: GCGTGG
- $\text{TGG} = \text{TGG}$
- 

CGT 3
GCG 2
GGG 8
GGG 9
GGG 10
GTG 0
GTG 4
GTG 6
TGC 1
TGG 7
TGT 5

Binary search




How many bisections per query?

$$\log_2(n)$$

Binary search - python

bisect.bisect_left(a, x): Leftmost offset where x can be inserted into a to maintain order



```
>>> a = [1, 3, 3, 6, 8, 8, 9, 10]
>>> import bisect
>>> bisect.bisect_left(a, 2)
1
>>> bisect.bisect_left(a, 4)
3
>>> bisect.bisect_left(a, 8)
4
```


Binary search - python

`bisect_left(index, 'GTG')`

- T: GTGCGTGTGGGGG
- P: GCGTGG

CGT 3
GCG 2
GGG 8
GGG 9
GGG 10
GTG 0
GTG 4
GTG 6
TGC 1
TGG 7
TGT 5

Index exercise
in Python

Indexing subsequences

- Subsequence of S: string of characters also occurring in S in the same order
- Substrings are also subsequences, subsequences are not necessarily substrings

```
>>> seq = 'AACCGTT'  
>>> seq[0] + seq[1] + seq[5] + seq[7]  
'AAGT' # subsequence  
>>> seq.find('AAGT')  
-1 #not a substring
```

Indexing subsequences

- Index of T:

CGGGT : 0

CGGTT : 4

GCTCT : 3

GTCTG : 1

TGGGC : 2

Find CGGGT



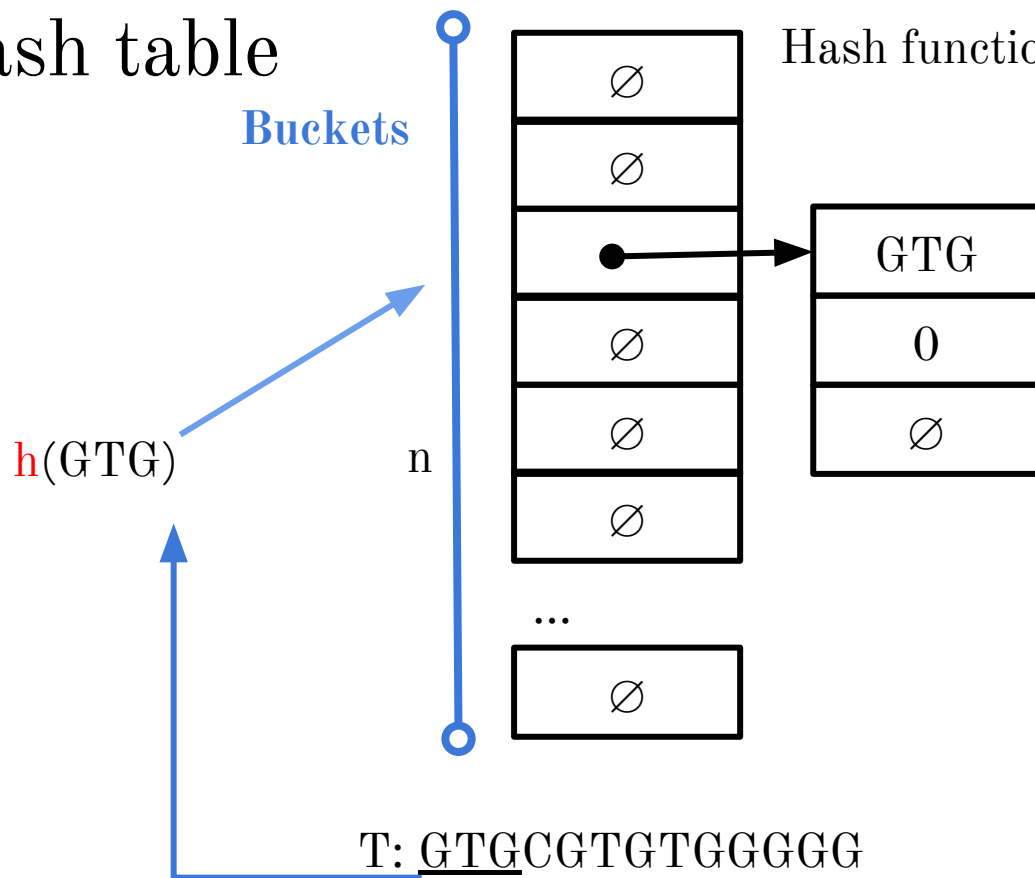
T: CGTGCGTGCTT

Using subsequences
improves specificity!
Why?

Hash table

Buckets

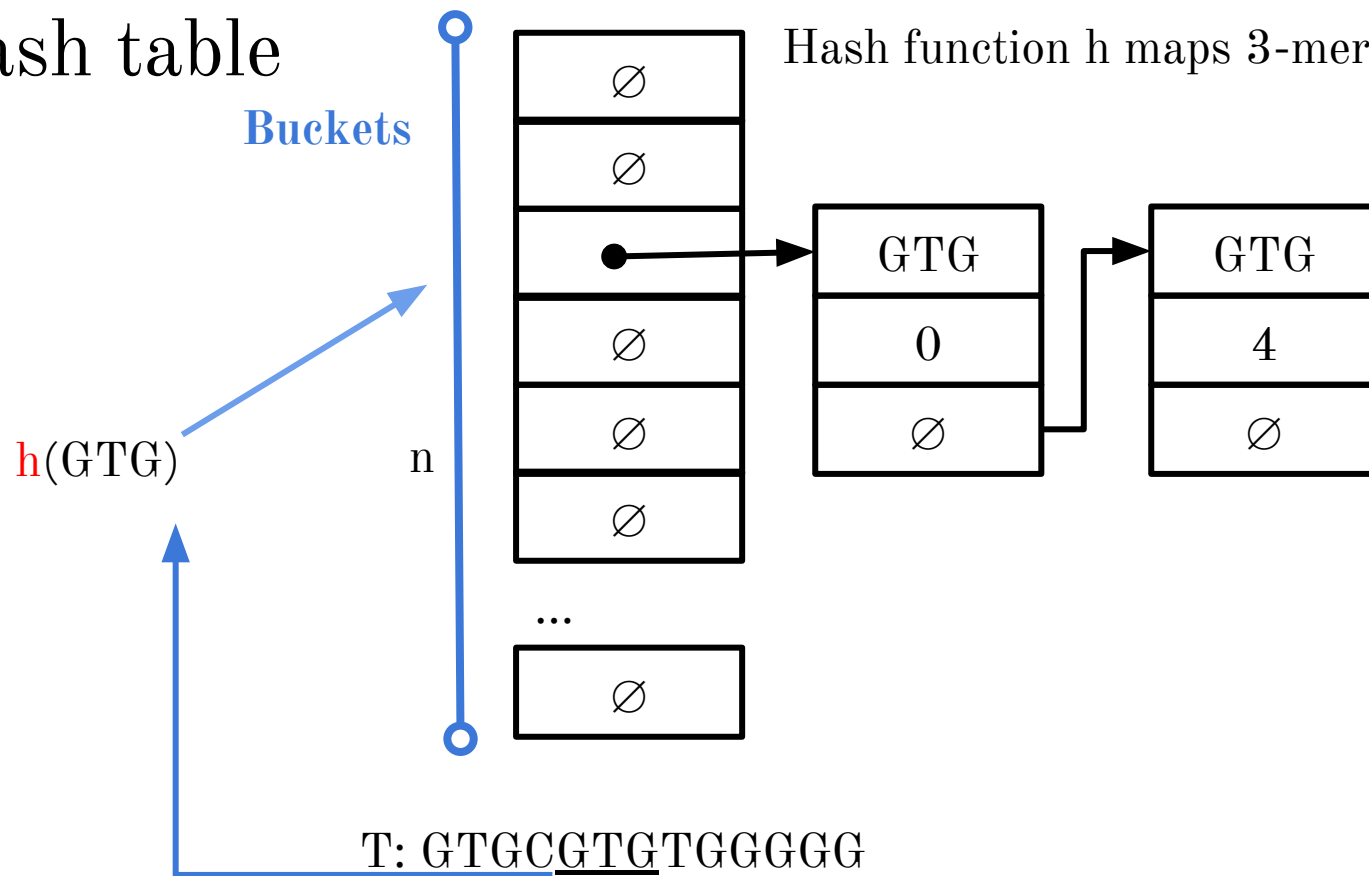
Hash function h maps 3-mers to buckets



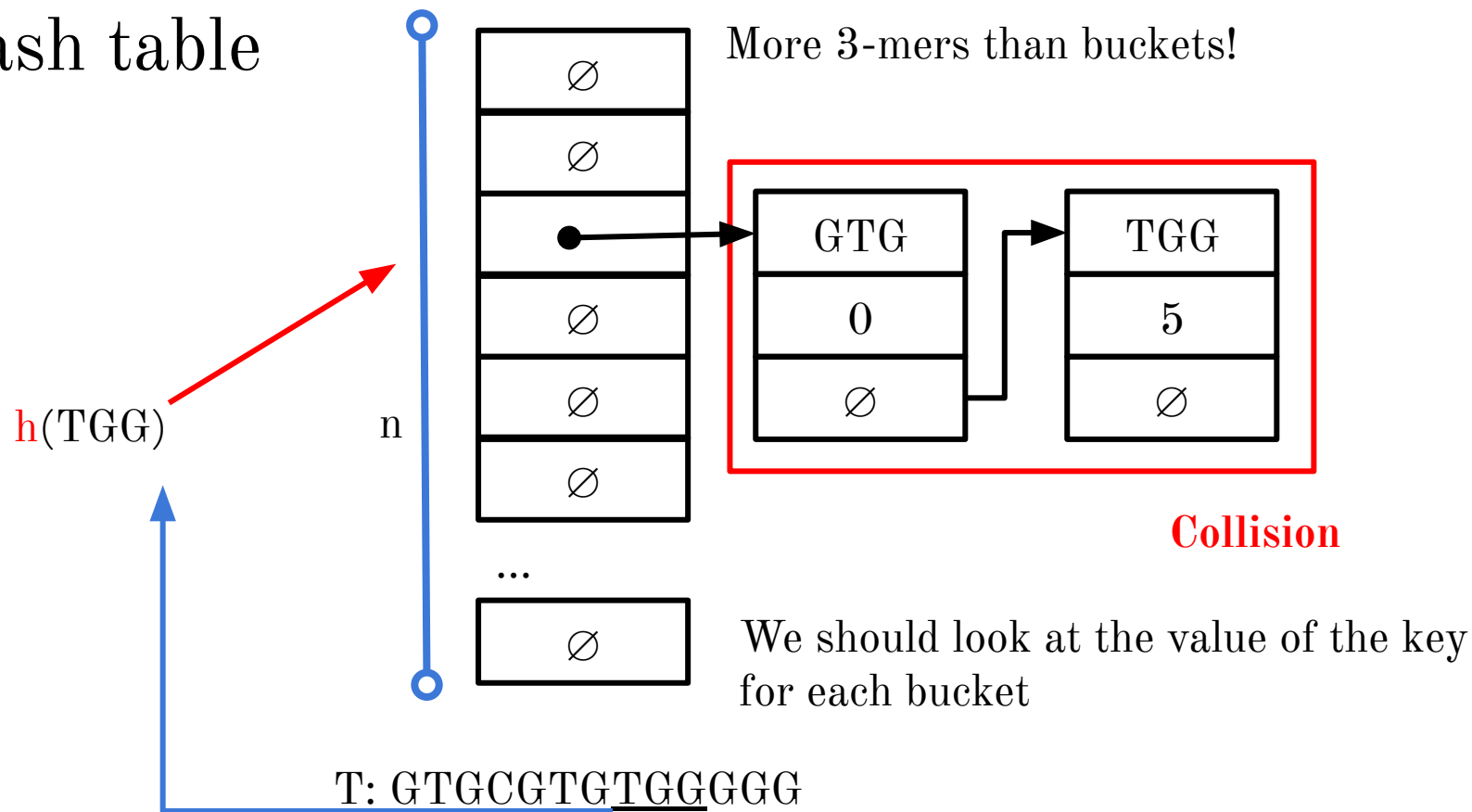
Hash table

Buckets

Hash function h maps 3-mers to buckets



Hash table



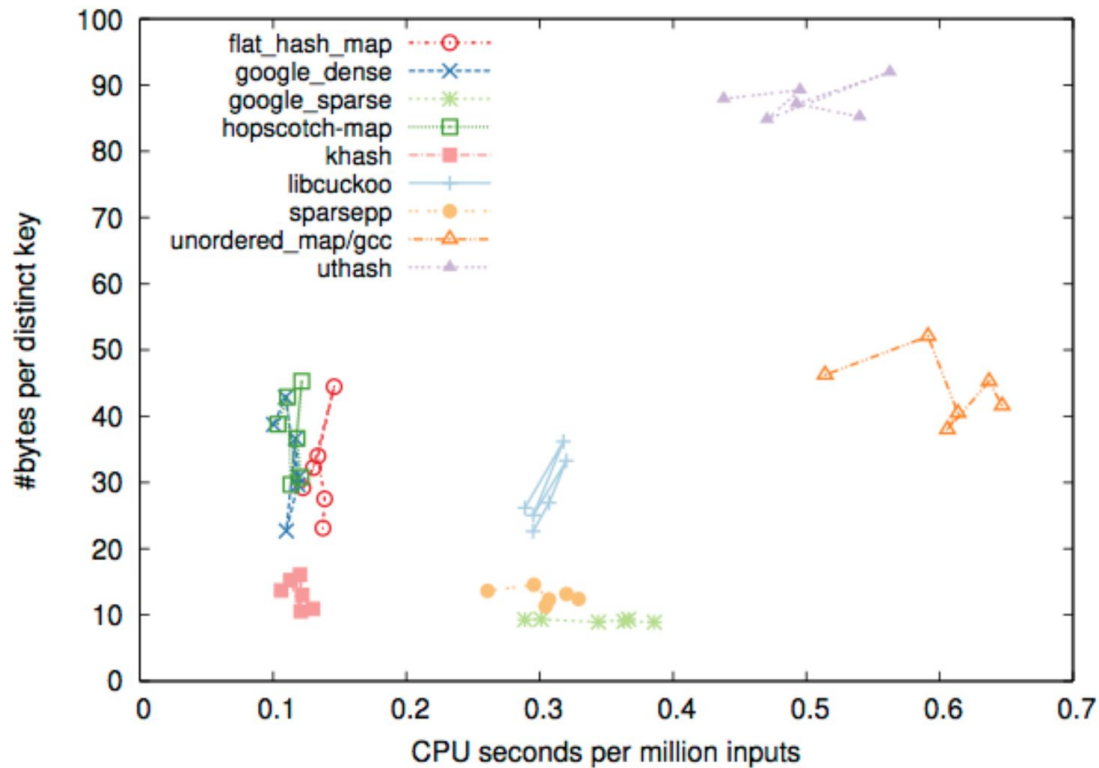
Dictionary in Python

```
>>> t = 'GTGCGTGTGGGGG'
>>> table = {'GTG':[0, 4, 6], 'TGC':[1],
             'GCG':[2], 'CGT':[3], 'TGT':[5],
             'TGG':[7], 'GGG':[8, 9, 10]}
>>> table['GGG']
[8, 9, 10]
>>> table['CGT']
[3]
```

Hash table comparison

Each line - 6 dots, corresponding to
N=10,18,26,34,42,50 million inputs

10 years ago google_danse was
fastest



Suffix index

T = GTTATAGCTGATCGCGGCGTAGCGG\$
GTTATAGCTGATCGCGGCGTAGCGG\$
TTATAGCTGATCGCGGCGTAGCGG\$
TATAGCTGATCGCGGCGTAGCGG\$
ATAGCTGATCGCGGCGTAGCGG\$
TAGCTGATCGCGGCGTAGCGG\$
AGCTGATCGCGGCGTAGCGG\$
GCTGATCGCGGCGTAGCGG\$
CTGATCGCGGCGTAGCGG\$
TGATCGCGGCGTAGCGG\$
GATCGCGGCGTAGCGG\$
ATCGCGGCGTAGCGG\$
TCGCGGCGTAGCGG\$
CGCGGCGTAGCGG\$
GCGGCGTAGCGG\$
CGGCGTAGCGG\$
GGCGTAGCGG\$
GCGTAGCGG\$
CGTAGCGG\$
GTAGCGG\$
TAGCGG\$
AGCGG\$
GCGG\$
CGG\$
GG\$
G\$
\$

Suffix Array

T = abaaba

abaaba

baaba

aaba

aba

ba

a

Alphabetical
order



a

aaba

aba

abaaba

ba

baaba



P = ab

- Querying uses binary search

Suffix index

Modern genomics
algorithms still use
Suffix index? How
come?

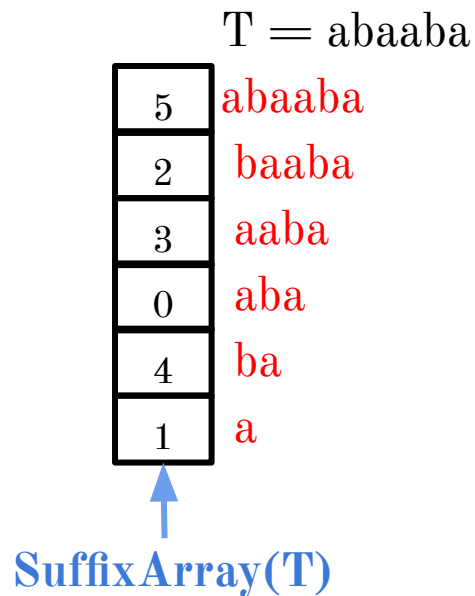
- Imagine suffix index of 3 billion nucleotides long human reference genome

T = GTTATAGCTGATCGCGGCGTAGCGG\$
GTTATAGCTGATCGCGGCGTAGCGG\$
TTATAGCTGATCGCGGCGTAGCGG\$
TATAGCTGATCGCGGCGTAGCGG\$
ATAGCTGATCGCGGCGTAGCGG\$
TAGCTGATCGCGGCGTAGCGG\$
AGCTGATCGCGGCGTAGCGG\$
GCTGATCGCGGCGTAGCGG\$
CTGATCGCGGCGTAGCGG\$
TGATCGCGGCGTAGCGG\$
GATCGCGGCGTAGCGG\$
ATCGCGGCGTAGCGG\$
TCGCGGCGTAGCGG\$
CGCGGCGTAGCGG\$
GCGGCGTAGCGG\$
CGGCGTAGCGG\$
GGCGTAGCGG\$
GCGTAGCGG\$
CGTAGCGG\$
GTAGCGG\$
TAGCGG\$
AGCGG\$
GCGG\$
CGG\$
GG\$
G\$
\$

$n(n+1)/2$ chars $\approx (n^2)/2$

Suffix array

Suffix array is $|T|$
integers long



- Save in index only positions of suffixes in T

References

- Dan Gusfield: **Algorithms on Strings, Trees, and Sequences: Computer Science and Computational Biology**, Cambridge University Press
- Pavel Pevzner, Neils Jones: **An Introduction to Bioinformatics Algorithms (Computational Molecular Biology)**, MIT Press
- R. Durbin, S. Eddy, A. Krogh, G. Mitchinson: **Biological Sequence Analysis: Probabilistic Models of Proteins and Nucleic Acids**, Cambridge University Press
- Veli Mäkinen, Djamel Belazzougui, Fabio Cunial, Alexandru I. Tomescu: **Genome-Scale Algorithm Design: Biological Sequence Analysis in the Era of High-Throughput Sequencing**, Cambridge University press