

Jumbled String Matching: Motivations, Variants, Algorithms

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Workshop

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Jumbled String Matching

Parikh vectors:

Given string t over constant-size ordered alphabet Σ , with $|\Sigma| = \sigma$.

The **Parikh vector** $p(t)$ counts the multiplicity of characters in t .

Ex.: $p(aabbcac) = (3, 1, 2)$.

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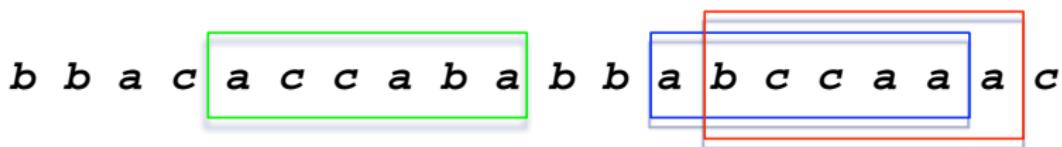
(a.k.a. jumbled string = compomer = composition = . . .)

Problem Statement

JUMBLED STRING MATCHING

Given string s of length n , and query Parikh vector $q \in \mathbb{N}^\sigma$.
Find all occurrences of substrings t of s s.t. $p(t) = q$.

Ex.: $\Sigma = \{a, b, c\}$, query $q = (3, 1, 2)$



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The diagram shows two occurrences of a jumbled string matching query. The string s is represented as a sequence of characters: $b\ b\ a\ c\ a\ c\ c\ a\ b\ a\ b\ b\ a\ b\ c\ c\ a\ a\ a\ c$. The first occurrence of the query is highlighted with a green rectangle, covering the substring $a\ c\ c\ a\ b\ a$. The second occurrence is highlighted with a blue rectangle, covering the substring $a\ b\ c\ c\ a\ a$. Both occurrences correspond to the query $(3, 1, 2)$, which represents the Parikh vector $p(a) = (3, 1, 2)$.

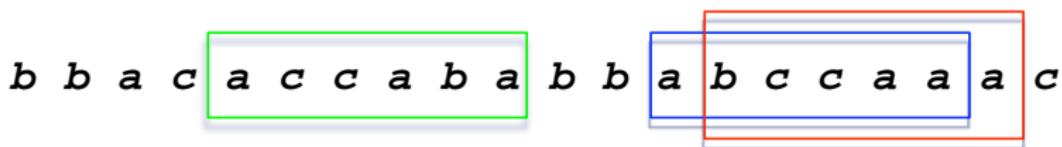
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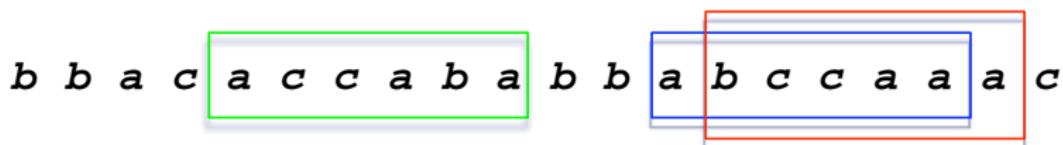
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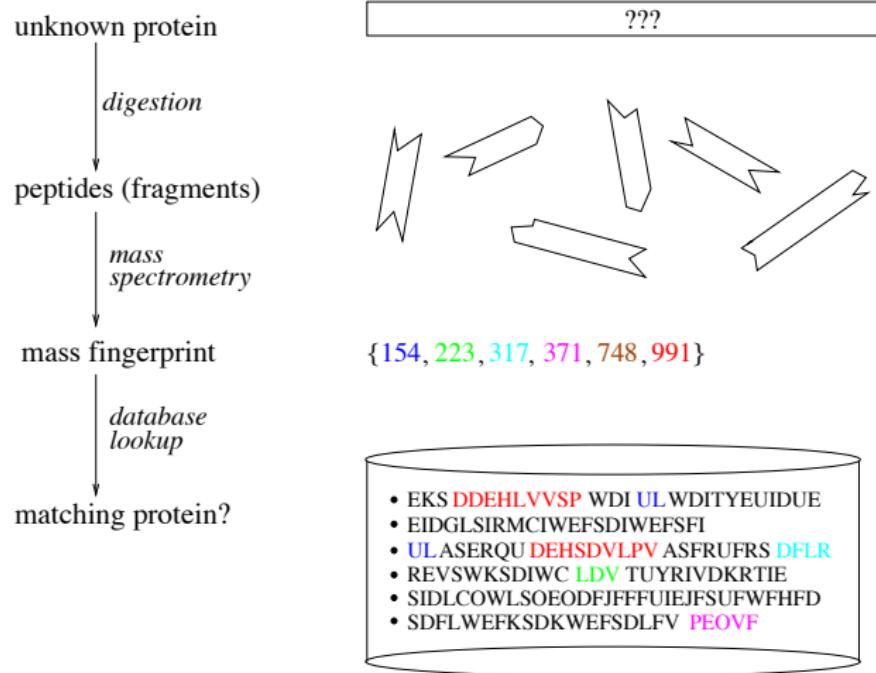
= any permutation of $aabdac$ = any jumble of $aabdac$

a.k.a. permutation matching, Parikh vector matching, abelian matching

Motivations, Applications

- Mass spectrometry
- Gene clusters
- Motif search in graphs and trees
- Filter for exact pattern matching

Protein identification with mass spectrometry (here: PMF)

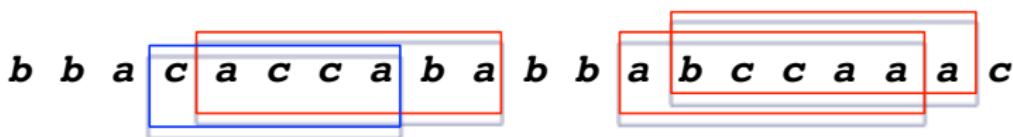


Takes advantage of different molecular masses of “characters” (AAs, nucleotides, . . .)

Modelling sample identification with MS

Every character has a mass: $\mu : \Sigma \rightarrow \mathbb{R}^+$ mass function, $\mu(t) = \sum_i \mu(t_i)$.

Ex: $\Sigma = \{a, b, c\}$ with $\mu(a) = 2, \mu(b) = 3, \mu(c) = 5$. Query $M = 19$



Actually we can also look for all Parikh vectors with query mass $M!$
⇒ Jumbled String Matching!

Application 2: Gene clusters

Given: k genomes

Find: maximal blocks consisting of same genes

1 2 **3 4 3 5 1 5 4** 7 2 5

5 3 1 4 4 7 1 7 2 2 1 3

1 2 6 7 **5 1 3 5 4** 2 2 5

gene cluster: {1, 3, 4, 5}

Application 2: Gene clusters

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1 2 **3 4 3 5 1 5 4** 7 2 5

5 3 1 4 4 7 1 7 2 2 1 3

1 2 6 7 **5 1 3 5 4** 2 2 5

gene cluster: {1, 3, 4, 5}

Caveat: Problem slightly different (so far).

1. Simple solutions

Window algorithm

Jumbled string matching query $q = (3, 1, 2)$

b b a c a c c a b a b b a b c c a a a c

- sliding window: either fixed-size ($m = |q| = \sum_i q_i$), or variable-size

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- sliding window: either fixed-size ($m = |q| = \sum_i q_i$), or variable-size
- worst-case optimal for one query: $O(n)$ time, $O(\sigma)$ additional space.

Indexed jumbled string matching

What about many queries? \rightsquigarrow indexed version of problem

simple solutions (K queries):

1. no index: $O(Kn)$ query time
2. store all: $O(n^2)$ index size, $O(K \log n)$ query time.

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simple solutions (K queries):

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For exact string matching, elaborate solutions exist:
suffix trees, suffix arrays, ...

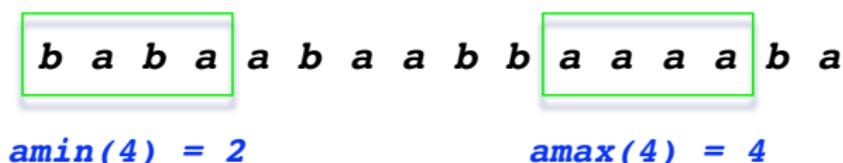
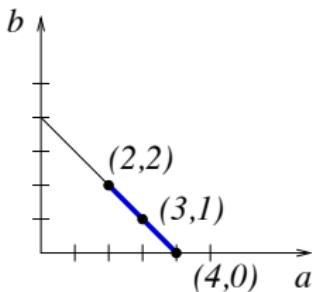
- index has $O(n)$ size (size of text)
- construction time and space $O(n)$
- query time $O(m)$ (size of query) – so $O(Km)$ for K queries

2. Binary alphabets

Binary alphabets: Interval property

Lemma

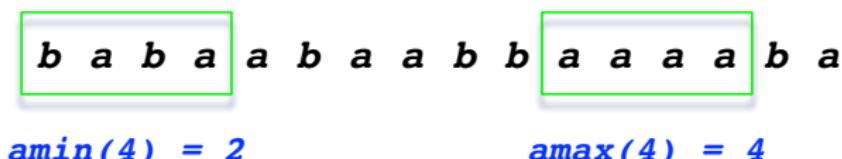
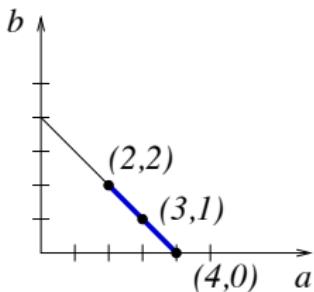
If $(x, m - x)$ and $(y, m - y)$ both occur in s , then so does $(z, m - z)$ for any $x \leq z \leq y$.



Binary alphabets: Interval property

Lemma

If $(x, m - x)$ and $(y, m - y)$ both occur in s , then so does $(z, m - z)$ for any $x \leq z \leq y$.



Corollary

All sub-Parikh vectors of s of length m build a set
 $\{(x, m - x) : \text{amin}(m) \leq x \leq \text{amax}(m)\}$.

Binary alphabets: Interval algorithm for **decision** queries

- **Index:** Table of $\text{amin}(m)$ and $\text{amax}(m)$, for $1 \leq m \leq n$ size $O(n)$
- **Query** (x, y) with occurs in s iff $\text{amin}(x + y) \leq x \leq \text{amax}(x + y)$.
- **Query time** $O(1)$.

m	amin	amax
...		
4	2	4
...		

query (3, 1) — YES
query (1, 3) — NO

Construction of index

Goal

Given a binary string of length n , find, for all $1 \leq m \leq n$, the minimum (maximum) number of a's in a window of size m .

- $O(n^2)$ time—Cicalese, Fici, L. (PSC 2009)
- $O(n^2 / \log n)$ time
 - Burcsi, Cicalese, Fici, L. (FUN 2010); Moosa, Rahman (IPL 2010)
- $O(n^2 / \log^2 n)$ time in word-RAM model
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- approximate index with one-sided error in $O(n^{1+\epsilon})$ time
 - Cicalese, Laber, Weimann, Yuster (CPM 2012)
- Corner Index: construction time and index size depend on $r =$ runlength enc. of s
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Index for binary JPM

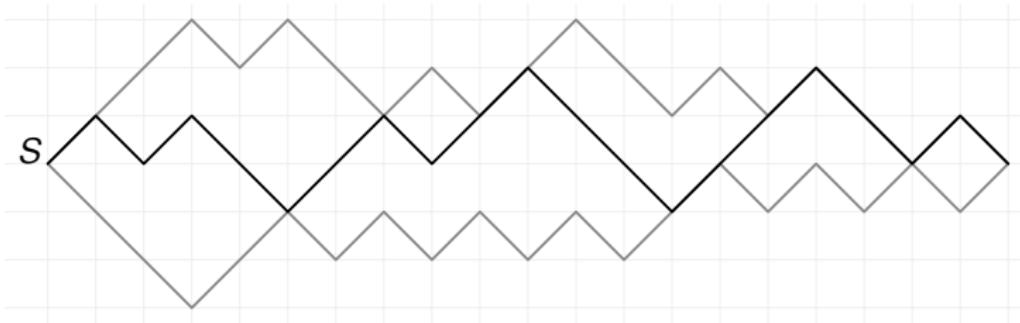


Figure : $\diagup = a$, $\diagdown = b$, $s = ababbaabaabbbaaabab$. Verticals are fixed length sub-Parikh vectors. The region is the **Parikh set** of w .

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Open problem: Faster construction of index?

3. General alphabets: Jumping Algorithm

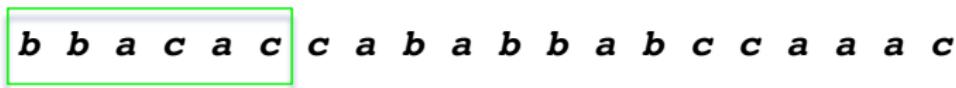
Jumping Algorithm for Jumbled String Matching

Cicalese, Fici, L. (PSC 2009, FUN 2010)

Recall the window algorithm.

fixed size window → variable size window

$$q = (312)$$



b b a c a c c a b a b b a b c c c a a a c

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The image shows a sequence of characters: **b b a c a c c** a b a b b a b c c c a a a c. The first seven characters, **b b a c a c c**, are enclosed in a green rectangular box, indicating they form a window or pattern being compared against a larger string.

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The Jumping Algorithm simulates these moves by jumps.

Jumping algorithm: update rules

$q = (312)$

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
L		b	b	a	c	a	c	c	a	b	a	b	b	a	b	c	c	a	a	a	c
a	0	0	1	1	2	2	2	3	3	4	4	4	5	5	5	5	6	7	8	8	
b	1	2	2	2	2	2	2	2	3	3	4	5	5	6	6	6	6	6	6	6	
c	0	0	0	1	1	2	3	3	3	3	3	3	3	3	4	5	5	5	5	6	

Jumping algorithm: update rules

$q = (312)$

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
L	b	b	a	c	a	c	c	a	b	a	b	b	a	b	c	c	a	a	a	c	
R									b	a	b	b	a	b	c	c	a	a	a	a	
a	0	0	1	1	2	2	2	3	3	4	4	4	5	5	5	5	6	7	8	8	
b	1	2	2	2	2	2	2	2	3	3	4	5	5	6	6	6	6	6	6	6	
c	0	0	0	1	1	2	3	3	3	3	3	3	3	3	4	5	5	5	5	6	

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L	b	b	a	c	a	c	c	a	b	a	b	b	a	b	c	c	a	a	a	c	
R									b	a	b	b	a	b	c	c	a	a	a	a	
a	0	0	1	1	2	2	2	3	3	4	4	4	5	5	5	5	6	7	8	8	
b	1	2	2	2	2	2	2	2	3	3	4	5	5	6	6	6	6	6	6	6	
c	0	0	0	1	1	2	3	3	3	3	3	3	3	3	4	5	5	5	5	6	

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	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
L	b	b	a	c	a	c	c	a													
R									b	a	b	b	a	b	c	c	a	a	a	c	
a	0	0	1	1	2	2	2	3	3	4	4	4	5	5	5	5	6	7	8	8	
b	1	2	2	2	2	2	2	2	3	3	3	4	5	5	6	6	6	6	6	6	
c	0	0	0	1	1	2	3	3	3	3	3	3	3	3	4	5	5	5	5	6	

update R : $R \leftarrow \max_{a \in \Sigma} \underbrace{\text{select}_a(\text{rank}_a(L) + q_a)}_{\text{necessary char's}}$

Jumping algorithm: update rules

$$q = (312)$$

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
	b	b	a	c	a	c	c	a		b	a	b	b	a	b	c	c	a	a	a	c
a	0	0	1	1	2	2	2	2	3	3	4	4	4	5	5	5	5	6	7	8	8
b	1	2	2	2	2	2	2	2	3	3	3	4	5	5	6	6	6	6	6	6	6
c	0	0	0	1	1	2	3	3	3	3	3	3	3	3	3	4	5	5	5	5	6

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	b	b	a	c	a	c	c	a		b	a	b	b	a	b	c	c	a	a	a	c
a	0	0	1	1	2	2	2	2	3	3	4	4	4	5	5	5	5	6	7	8	8
b	1	2	2	2	2	2	2	2	3	3	3	4	5	5	6	6	6	6	6	6	6
c	0	0	0	1	1	2	3	3	3	3	3	3	3	3	3	4	5	5	5	5	6

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update L : $L \leftarrow \max_{a \in \Sigma} \underbrace{\text{select}_a(\text{rank}_a(R) - q_a)}_{\text{unnecessary char's}}$ (no match),

Jumping algorithm: update rules

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	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
	<i>b</i>	<i>b</i>	<i>a</i>	<i>c</i>	a	c	c	a	b	a	b	b	a	b	c	c	a	a	a	c		
a	0	0	1	1	2	2	2	2	3	3	4	4	4	4	5	5	5	5	6	7	8	8
b	1	2	2	2	2	2	2	2	3	3	3	4	5	5	6	6	6	6	6	6	6	6
c	0	0	0	1	1	2	3	3	3	3	3	3	3	3	3	4	5	5	5	5	6	

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Jumping algorithm: update rules

$q = (312)$

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
	<i>b</i>	<i>b</i>	<i>a</i>	<i>c</i>	<i>a</i>	L	<i>c</i>	<i>c</i>	<i>a</i>	<i>b</i>	<i>a</i>	R	<i>b</i>	<i>b</i>	<i>a</i>	<i>b</i>	<i>c</i>	<i>c</i>	<i>a</i>	<i>a</i>	<i>a</i>
a	0	0	1	1	2	2	2	2	3	3	4	4	4	4	5	5	5	5	6	7	8
b	1	2	2	2	2	2	2	2	3	3	3	4	5	5	6	6	6	6	6	6	6
c	0	0	0	1	1	2	3	3	3	3	3	3	3	3	3	4	5	5	5	5	6

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$L \leftarrow L + 1$ (match).

Jumping algorithm: update rules

$q = (312)$

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
	b	b	a	c	a	L	c	c	a	b	a	b	b	a	R	b	c	c	a	a	a
a	0	0	1	1	2	2	2	2	3	3	4	4	4	5	5	5	5	6	7	8	8
b	1	2	2	2	2	2	2	2	3	3	4	5	5	6	6	6	6	6	6	6	6
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	b	b	a	c	a	c	c	a	b	a	b	a	b	c	c	a	a	a	c		
a	0	0	1	1	2	2	2	3	3	4	4	4	5	5	5	5	6	7	8	8	
b	1	2	2	2	2	2	2	3	3	3	4	5	5	6	6	6	6	6	6	6	
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	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
	b	b	a	c	a	c	c	a	b	a	b	a	b	c	c	a	a	a	a	c		
a	0	0	1	1	2	2	2	3	3	3	4	4	4	4	5	5	5	5	6	7	8	8
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c	0	0	0	1	1	2	3	3	3	3	3	3	3	3	3	4	5	5	5	5	5	6

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update L : $L \leftarrow \max_{a \in \Sigma} \underbrace{\text{select}_a(\text{rank}_a(R) - q_a)}_{\text{unnecessary char's}}$ (no match),

$L \leftarrow L + 1$ (match).

Jumping algorithm: update rules

$q = (312)$

	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	
	b	b	a	c	a	c	c	a	b	a	b	b	a	b	c	c	a	a	a	c		
a	0	0	1	1	2	2	2	3	3	4	4	4	4	5	5	5	5	5	6	7	8	8
b	1	2	2	2	2	2	2	2	3	3	3	4	5	5	6	6	6	6	6	6	6	6
c	0	0	0	1	1	2	3	3	3	3	3	3	3	3	3	4	5	5	5	5	6	

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	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
	b	b	a	c	a	c	c	a	b	a	b	b	a	b	c	c	a	a	a	c	
a	0	0	1	1	2	2	2	3	3	4	4	4	5	5	5	5	5	6	7	8	8
b	1	2	2	2	2	2	2	2	3	3	4	5	5	6	6	6	6	6	6	6	6
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	b	b	a	c	a	c	c	a	b	a	b	b	a	b	c	c	a	a	a	c		
a	0	0	1	1	2	2	2	3	3	4	4	4	4	5	5	5	5	5	6	7	8	8
b	1	2	2	2	2	2	2	2	3	3	3	4	5	5	6	6	6	6	6	6	6	6
c	0	0	0	1	1	2	3	3	3	3	3	3	3	3	3	4	5	5	5	5	6	

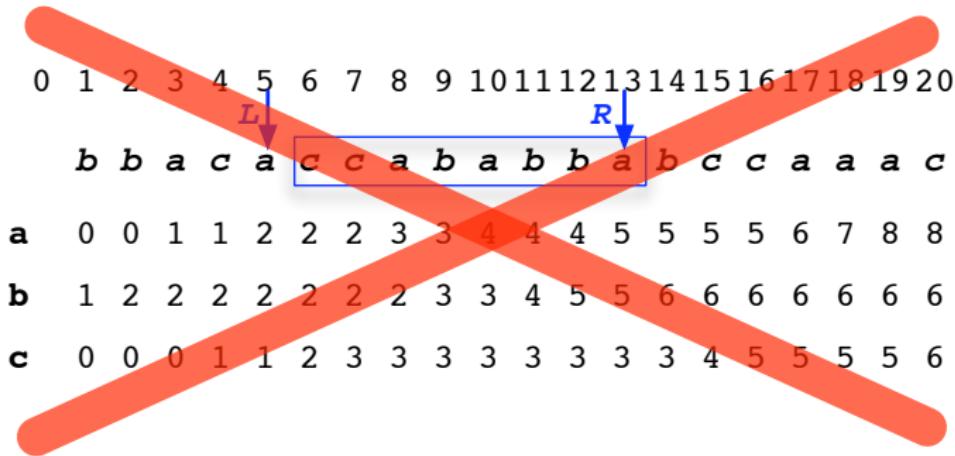
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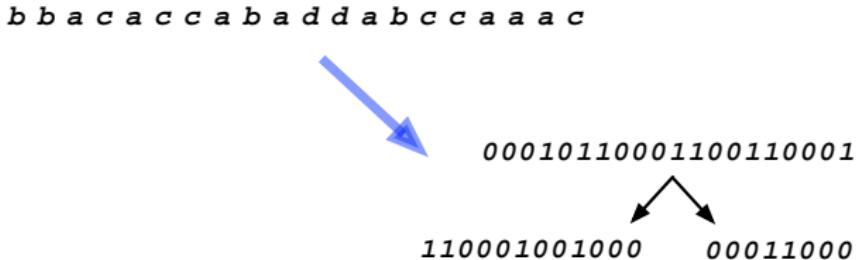
$L \leftarrow L + 1$ (match).

Jumping algorithm: Analysis

Note that we do not need to store the prefix table, nor the string s .



Jumping algorithm: Analysis



Using a wavelet tree [Grossi et al., SODA 2003] as index, we have

- space $O(n)$ (for wavelet tree)
- construction time $O(n \log \sigma)$
- every update (jump) in $O(\sigma)$ time
- query time $O(J\sigma)$, where $J = \text{number of jumps (updates)}$
- expected running time: $O(n \sqrt{\frac{\sigma}{\log \sigma}} \frac{1}{\sqrt{m}})$, where $m = \sum_i q_i$.

Jumbled string matching on general alphabets

Latest result: Kociumaka, Radoszewski, Rytter (ESA 2013)

- for arbitrary constant size alphabet
- $o(n^2)$ index size
- $o(n)$ query time (worst-case)
- $O(n^2)$ construction time

(for any $\delta \in (0, 1)$ construct index of size $O(n^{2-\delta})$ with query time $O(m^{\delta(2\sigma-1)})$)

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Compare to:

1. no index: $O(n)$ space, $O(n)$ query time
2. store all: $O(n^2)$ index size, $O(\log n)$ query time
3. Jumping algo: $O(n)$ index size, $o(n)$ query time **in expectation**

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Open problem: Find something better.

4. Prefix normal words

Prefix normal words

Fici, L. (DLT 2011)

Definition

A word $s \in \{a, b\}^*$ is a **prefix normal word** (w.r.t. a) if $\forall 0 \leq m \leq |s|$ no substring of length m has more a 's than the prefix of s of length m .

Example

$$s = ababbaabaabbbaaaabbab$$

$$s' = aaababbabaabbababbab$$

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Example

$s = ababbaabaabbbaaaabbab$ NO

$s' = aaababbabaabbabababbab$ YES

Prefix normal forms

Recall $\text{amax}_a(m) = \text{maximum number of } a\text{'s in a substring of } s \text{ of length } m$.

$$s = ababbaabaabbbaaaabbab$$

m	0	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
$\text{amax}_a(m)$	0	1	2	3	3	4	4	4	5	5	6	7	7	7	8	8	9	9	9	10	10

Theorem

Let $s \in \{a, b\}^*$. Then there exists a unique prefix normal word s' s.t. for all $0 \leq m \leq |s|$, $\text{amax}_a(s, m) = \text{amax}_a(s', m)$, called its **prefix normal form w.r.t. a**, $\text{PNF}_a(s)$.

The **Parikh set** of a word s is the set of Parikh vectors of the substrings of s .

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Theorem

Two strings $s, t \in \{a, b\}^$ have the same Parikh set if and only if $PNF_a(s) = PNF_a(t)$ and $PNF_b(s) = PNF_b(t)$.*

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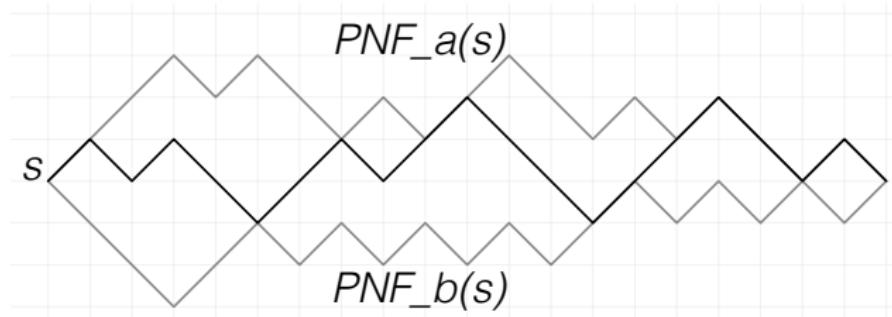


Figure : $\swarrow = a$, $\searrow = b$, $s = ababbaabaabbbaaabab$ and its prefix normal forms. The region delimited by $PNF_a(s)$ and $PNF_b(s)$ is the **Parikh set** of s .

Computation of PNFs

Open problem: Compute the PNFs in $o(n^2 / \log^2 n)$

~~ would lead to faster index construction for binary jumbled string matching.

Other variants

- approximate jumbled string matching: e.g. find all occurrences between (12, 5, 7) and (8, 2, 4): variant of jumping algorithm expected sublinear (Burcsi, Cicalese, Fici, L., FUN 2010, ToCS 2012)
- (mostly binary) on **trees** and **graphs with bounded treewidth** (Gagie, Hermelin, Landau, Weimann, ESA 2013)
- (mostly binary) locating one occurrence in **strings, trees, graphs** (Cicalese, Gagie, Giaquinta, Laber, L., Rizzi, Tomescu, SPIRE 2013)

THANK YOU!

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