Ch32 String Matching

- Introduction
- Naïve Algorithm 朴素算法
- Rabin-Karp Algorithm
- String Matching using Finite Automata 自动机方法
- Knuth-Morris-Pratt (KMP) Algorithm
- Indexing Method: BWT (Suppl.)

To various sources, including Profs. Ananth Grama, Mehmet Koyuturk, Michael Raymer, Wiki sources (pictures), and other noted attributions

Introduction

- What is *string matching*?
  - 模式串
  - Finding all occurrences of a *pattern* in a given *text* (or *body of text*).
- Many applications:
  - While using editor/word processor/browser.
  - Login name & password checking.
  - Virus detection.病毒检查
  - Header analysis in data communications.
  - DNA sequence analysis.

History of String Search

- The brute force algorithm
  - invented in the dawn of computer history.
  - re-invented many times, *still* common.
- Knuth & Pratt invented a better one in 1970
  - published 1976 as “Knuth-Morris-Pratt”.
- Boyer & Moore found a better one before 1976
  - Published 1977.
- Karp & Rabin found a “better” one in 1980
  - Published 1987.

n 文本串
m 模式串

对模式串做预处理

Algorithm	Preprocessing Time	Matching Time
Naive	0	$O((n-m+1)m)$
用指纹 Rabin-Karp	$\Theta(m)$	$O((n-m+1)m)$
Finite Automaton	$O(m\|\Sigma\|)$	$\Theta(n)$
从左到右 Knuth-Morris-Pratt	$\Theta(m)$	$\Theta(n)$
Boyer-Moore	$\Theta(m)$	$\Theta(n)$

适合模式串只出现几次
出现几次

适合流处理

String-Matching Problem

- The *text* is in an array $T[1..n]$ of length n.
- The *pattern* is in an array $P[1..m]$ of length m.
- Elements of T and P are characters from a *finite alphabet* Σ.
  - E.g., $\Sigma = \{0,1\}$ or $\Sigma = \{a, b, \ldots, z\}$. ⬅字符来自于
- Usually T and P are called *strings* of characters.

String-Matching Problem ...contd

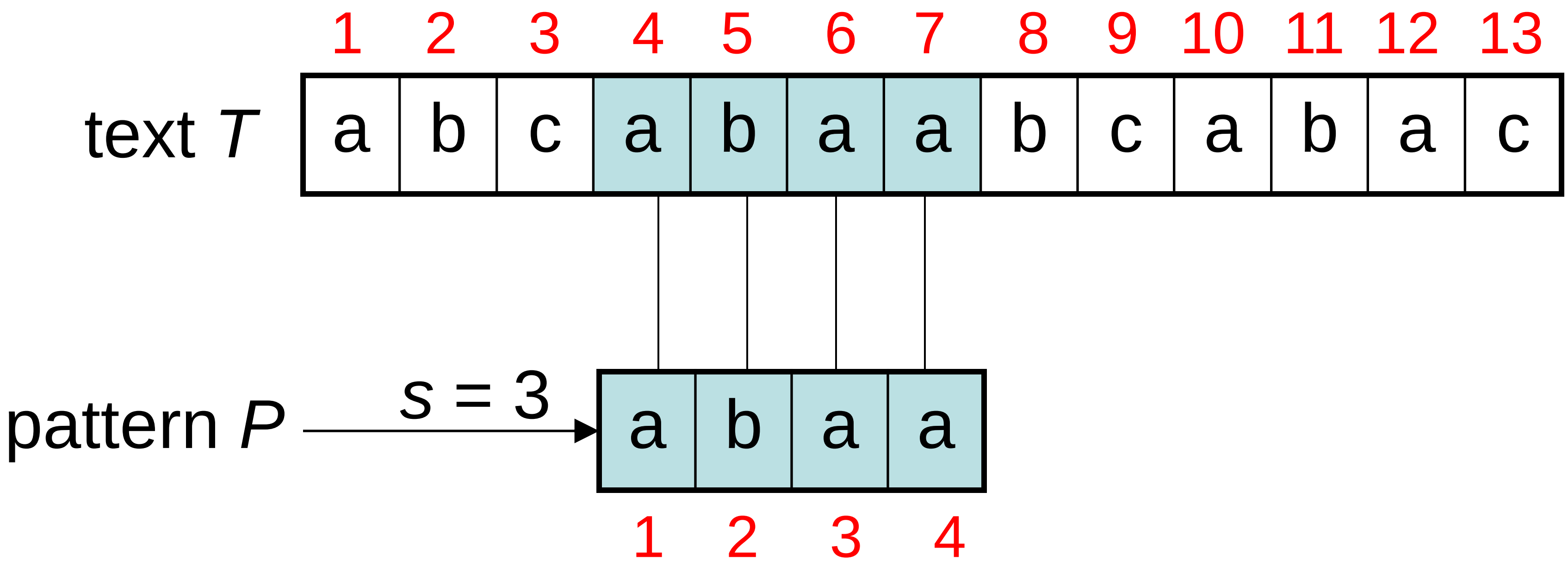
- We say that pattern P *occurs with shift s* in text T if:

a) $0 \le s \le n-m$ 可以检查的位置，哪些是合法的匹配 and

b) $T[(s+1)..(s+m)] = P[1..m]$.

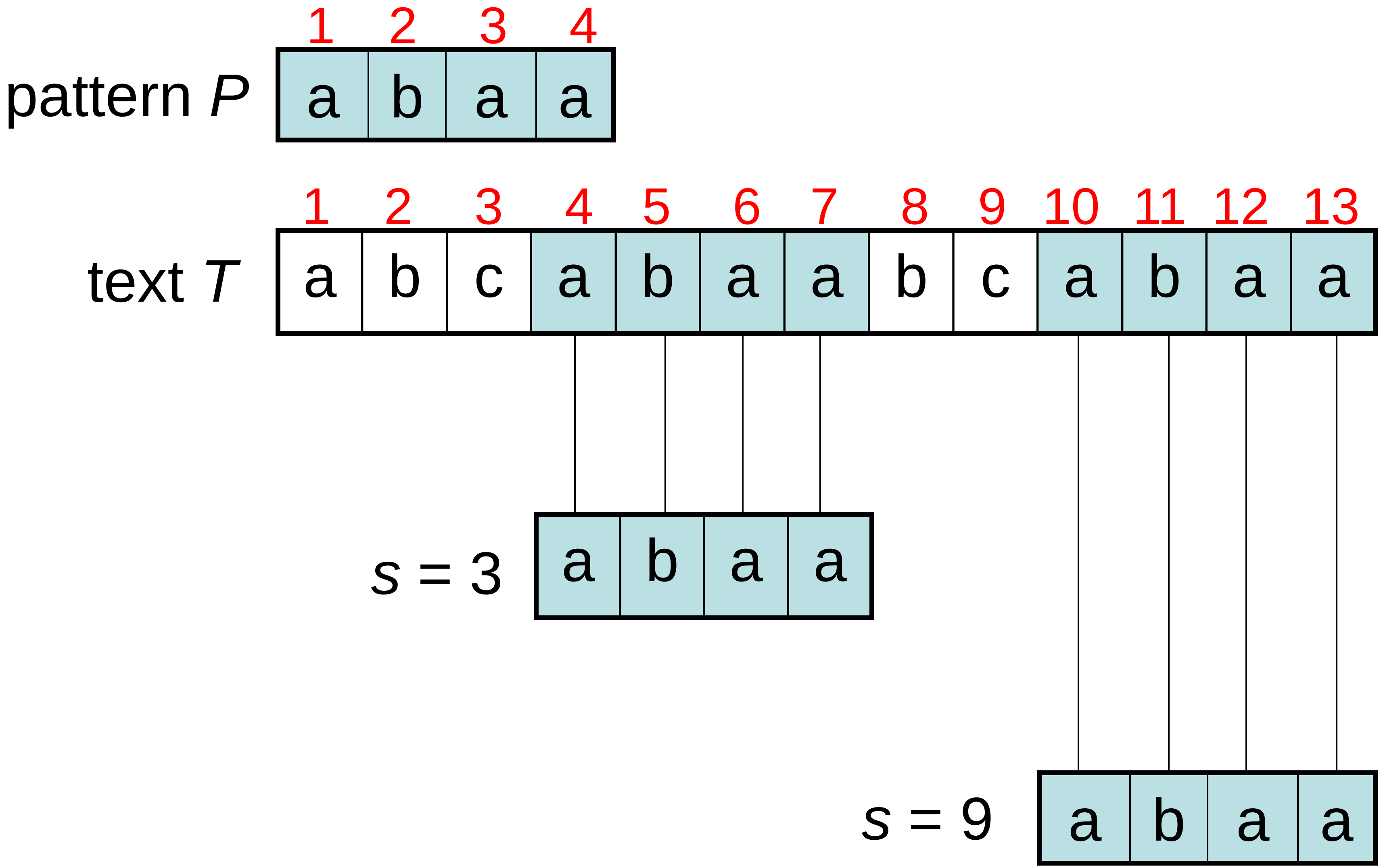
- If P occurs with shift s in T, then s is a *valid shift*, otherwise s is an *invalid shift.*
- String-matching problem: finding all valid shifts for a given T and P.

Example 1



shift s = 3 is a valid shift
(n=13, m=4 and $0 \leq s \leq n\text{-}m$ holds)

Example 2


1 2 3 4
pattern P
a b a a
1 2 3 4 5 6 7 8 9 10 11 12 13
text T
a b c a b a a b c a b a a
$s = 3$
a b a a
$s = 9$
a b a a

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Naïve String-Matching Algorithm

Input: Text strings T [1..n] and P[1..m].

Result: All valid shifts displayed.

NAÏVE-STRING-MATCHER (T, P)

$n \leftarrow length[T]$ 文本串

$m \leftarrow length[P]$ 模式串

for $s \leftarrow 0$ **to** $n\text{-}m$

窗口 起始s

if $P[1..m] = T[(s+1)..(s+m)]$

print "pattern occurs with shift" s

Example

P="abxyabxz" and T="xabxyabxyabxz"

T	x	a	b	x	y	a	b	x	y	a	b	x	z
P						a	b	x	y	a	b	x	z

Worst-case Analysis

- There are *m* comparisons for each shift in the worst case.
- There are n-m+1 shifts.
- So, the worst-case running time is $\Theta((n-m+1)m)$.

  0开始到n-m
- Naïve method is inefficient because information from a shift is not used again.

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对朴素算法的改造

Rabin-Karp Algorithm

- Has a worst-case running time of $O((n-m+1)m)$ but average-case is $O(n+m)$.
  - Also works well in practice.
- Based on number-theoretic notion of *modular equivalence.*

适合于能够配上的串不是很多
适合于数字串的处理

- We assume that $\Sigma = \{0,1, 2, \ldots, 9\}$, i.e., each character is a decimal digit.
  - In general, use radix-d where $d = |\Sigma|$.

模等价类方法

Modular Equivalence

- If $(a \bmod n) = (b \bmod n)$, then we say "*a* is equivalent to *b*, modulo *n*".
- Denoted by $a \equiv b \pmod{n}$.
- That is, $a \equiv b \pmod{n}$ if *a* and *b* have the same remainder when divided by *n*.
  - E.g., $23 \equiv 37 \equiv -19 \pmod{7}$.

模式串很长的情况下，大整数除一个素数，余数可以作为数的特征（指纹）

Rabin-Karp Approach

- We can view a string of k characters (digits) as a length-k decimal number.
  - E.g., the string "31425" corresponds to the decimal number 31,425.
    文本串
    数值
- Given a pattern P [1..m], let p denote the corresponding decimal value.
- Given a text T [1..n], let t_s denote the decimal value of the length-m substring T [(s+1)..(s+m)] for s=0,1,…,(n-m).

Rabin-Karp Approach ...contd

- $t_s = p$ iff $T\,[(s+1)..(s+m)] = P\,[1..m]$.
- s is a valid shift iff $t_s = p$.
- p can be computed in $O(m)$ time.

把字符串转为数值： 低位 个位 十位

  - $p = P[m] + 10\,(P[m\text{-}1] + 10\,(P[m\text{-}2]+\ldots))$. 霍恩算法

- t_0 can similarly be computed in $O(m)$ time.
- Other $t_1, t_2,\ldots, t_{n\text{-}m}$ can be computed in O(n-m) time since t_{s+1} can be computed from t_s in constant time.

Rabin-Karp Approach …contd

- $t_{s+1} = 10(t_s - 10^{m-1} \cdot T[s+1]) + T[s+m+1]$
  - E.g., if T={…,3,1,4,1,5,2,…}, m=5 and t_s= 31,415, then $t_{s+1} = 10(31415 - 10000 \cdot 3) + 2$
- We can compute p, t_0, $\underline{t_1, t_2, \ldots, t_{n-m}}$ in $O(n+m)$ time.

  2m+O(1) · (n-m)=)(n+m)

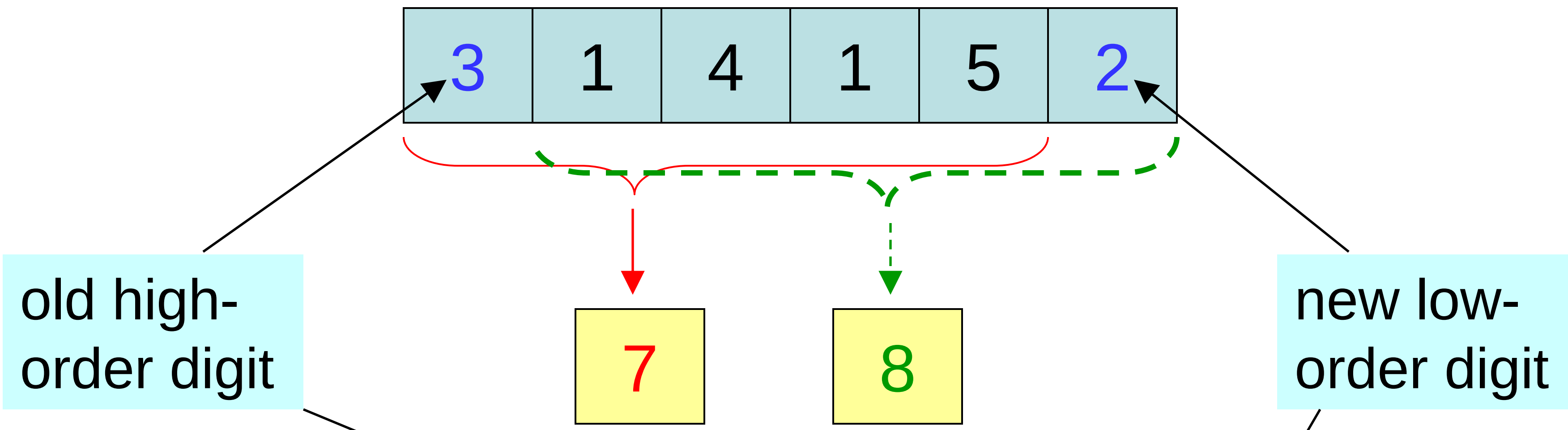
- But…a problem: this is assuming p and t_s are small numbers.
  - They may be too large to work with easily.

Rabin-Karp Approach …contd

- Solution: we can use modular arithmetic with a suitable modulus, *q.*
  - E.g., $t_{s+1} \equiv 10(t_s - \ldots) + T\,[s+m+1] \pmod{q}$.

- *q* is chosen as a small *prime number*, e.g., 13 for radix 10.
  - Generally, if the radix is *d*, then *dq* should fit within one computer word.

How values modulo 13 are computed



$$14152 \equiv (31415 - 3 \cdot 10000) \cdot 10 + 2 \pmod{13}$$

$$\equiv (7 - 3 \cdot 3) \cdot 10 + 2 \pmod{13}$$

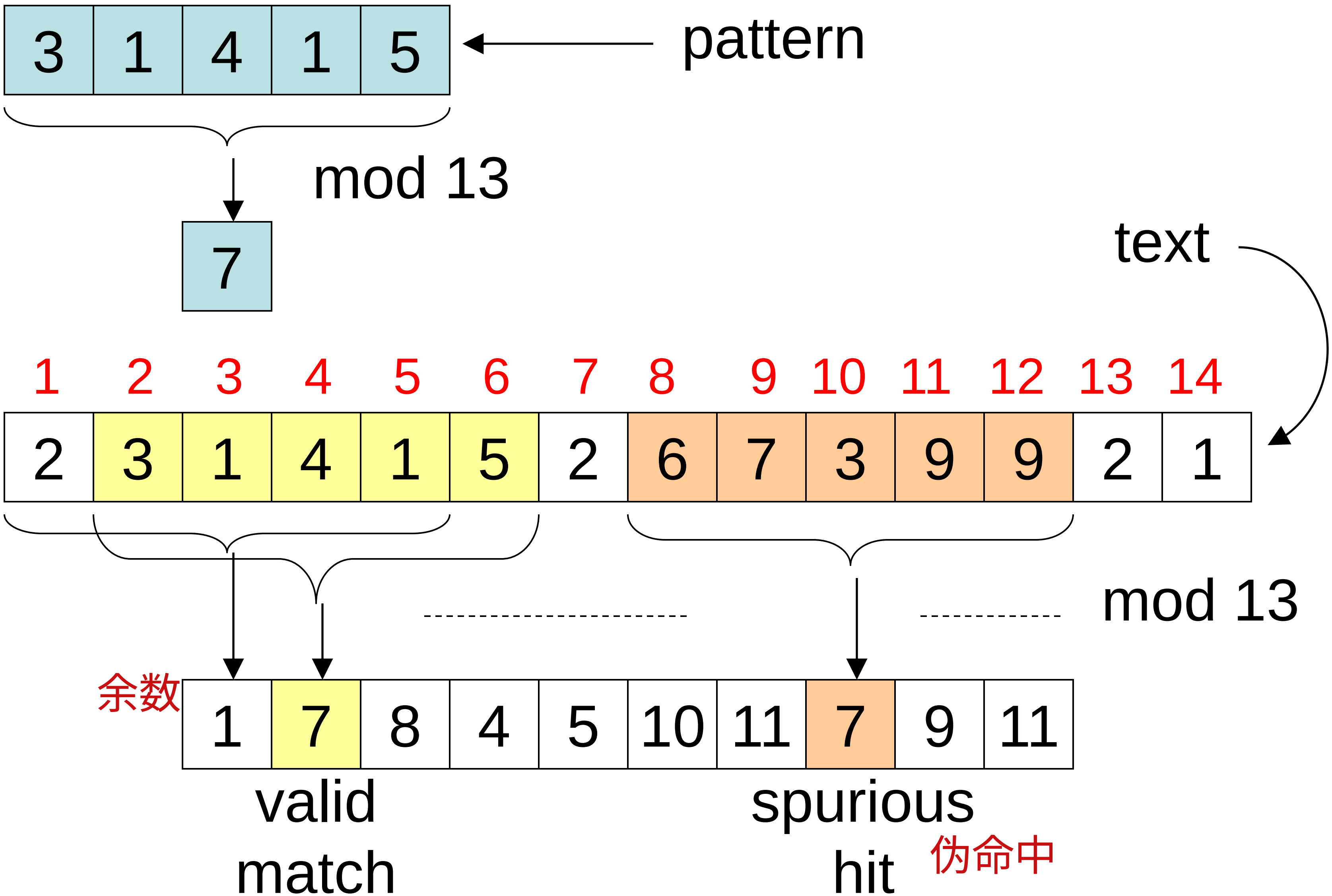
$$\equiv 8 \pmod{13}$$

伪命中问题

Problem of Spurious Hits

- $t_s \equiv p \pmod{q}$ does not imply that $t_s = p$.
  - Modular equivalence does not necessarily mean that two integers are equal.
- A case in which $t_s \equiv p \pmod{q}$ when $t_s \neq p$ is called a *spurious hit.* 余数相等但值不相等
- On the other hand, if two integers are not modular equivalent, then they cannot be equal.

Example


3 1 4 1 5
pattern
mod 13
7
text
1 2 3 4 5 6 7 8 9 10 11 12 13 14
2 3 1 4 1 5 2 6 7 3 9 9 2 1
mod 13
余数
1 7 8 4 5 10 11 7 9 11
valid match
spurious hit
伪命中

Rabin-Karp Algorithm

- Basic structure like the naïve algorithm, but uses modular arithmetic as described.
- For each *hit*, i.e., for each s where $t_s \equiv p \pmod{q}$, verify character by character. whether s is a valid shift or a spurious hit
- In the worst case, every shift is verified.
  - Running time can be shown as $O((n-m+1)m)$.
- Average-case running time is $O(n+m)$.

O(n-m+1)+O(m)

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Finite Automata 自动机方法

- A *finite automaton* M is a 五元组 5-tuple $(Q, q_0, A, \Sigma, \delta)$, where
  - Q is a finite set of *states*. 有限的状态集
  - q_0 属于 ε Q is the *start state*. 开始状态
  - A 子集 $\subseteq Q$ is a set of *accepting states*. 接收状态
  - Σ is a finite *input alphabet*. 有限字符集
  - δ is the *transition function* 状态变化函数 that gives the next state for a given current state and input.

How a Finite Automaton Works

- The finite automaton *M* begins in state q_0.
- Reads characters from $\sum$ one at a time.
- If *M* is in state *q* and reads input character *a*, *M* moves to state $\delta(q,a)$.
- If its current state *q* is in *A*, *M* is said to have *accepted* the string read so far.
- An input string that is not accepted is said to be *rejected.*

Example

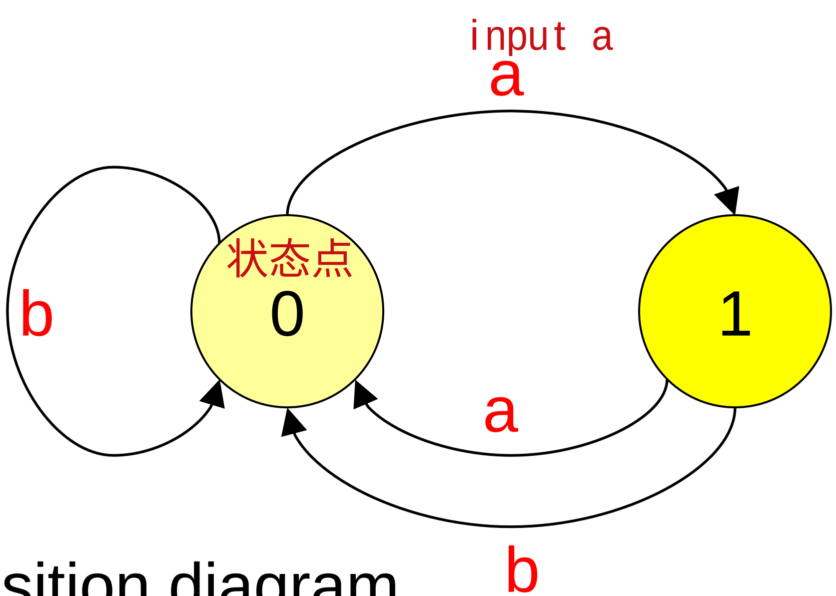
初始状态 可接受 a b两个字符

- $Q = \{0,1\}$, $q_0 = 0$, A={1}, $\Sigma = \{a, b\}$.
- $\delta(q,a)$ shown in the transition table/diagram.
- This accepts strings that end in an odd number of a's; e.g., abbaaa is accepted, aa is rejected.

可以判别出第一个a后面 a出现的个数是奇数个还是偶数个

state	input a	input b
0	1	0
1	0	0

transition table
状态转换



transition diagram

String-Matching Automata

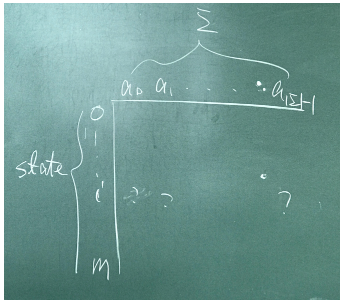
- Given the pattern P [1..m], build a finite automaton M.
  - 开始 找到m个位置和字符串匹配
  - The state set is $Q=\{0, 1, 2, \ldots, m\}$. 状态集合 状态0-m
  - The start state is 0.
  - The only accepting state is m.

- Time to build M can be large if Σ is large.
  根据模式串构造

String-Matching Automata ...contd

- Scan the text string *T* [1..*n*] to find all occurrences of the pattern *P* [1..*m*].

- String matching is efficient: Θ(*n*).
  - Each character is examined exactly once.
  - Constant time for each character.
- But …time to compute δ is $O(m\ |\Sigma|)$.
  - δ Has $O(m\ |\Sigma|\ )$ entries.



Algorithm

Input: Text string T [1..n], δ and m

Result: All valid shifts displayed

FINITE-AUTOMATON-MATCHER (T, m, δ)

$n \leftarrow length[T]$

$q \leftarrow 0$

for $i \leftarrow 1$ **to** n

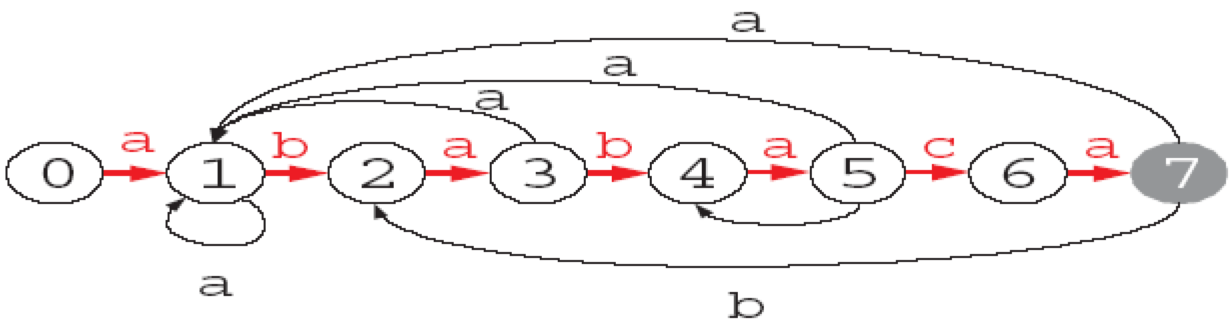
$q \leftarrow \delta\,(q, T\,[i])$

if $q = m$

print "pattern occurs with shift" i-m

比如第一个窗口匹配上就print 0

Example



状态 / 模式串

state	a	b	c	P
0	1	0	0	a
1	1	2	0	b
2	3	0	0	a
3	1	4	0	b
4	5	0	0	a
5	1	4	6	c
6	7	0	0	a
7	1	2	0	

有2个一样的

输入a
右3个
一样

看a,b,c 能对上几个

做法：找后缀与前缀一样的最大长度

i	—	1	2	3	4	5	6	7	8	9	10	11
$T[i]$	—	a	b	a	b	a	b	a	c	a	b	a
$\phi(T_i)$	0	1	2	3	4	5	4	5	6	7	2	3

i-m=9-7=2

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Knuth-Morris-Pratt (KMP) Method

- Avoids computing δ (transition function).
- Instead computes a *prefix function* π in $O(m)$ time.
  - π has only m entries.

- Prefix function stores info about how the pattern matches against shifts of itself.
  - Can avoid testing useless shifts.

Terminology/Notations

前缀

- String w is a *prefix* of string x, if x=wy for some string y (e.g., “srilan” of “srilanka”).

后缀

- String w is a *suffix* of string x, if x=yw for some string y (e.g., “anka” of “srilanka”).
- The k-character prefix of the pattern P [1..m] denoted by P_k.
  - E.g., $P_0 = \varepsilon$, $P_m = P = P$ [1..m].

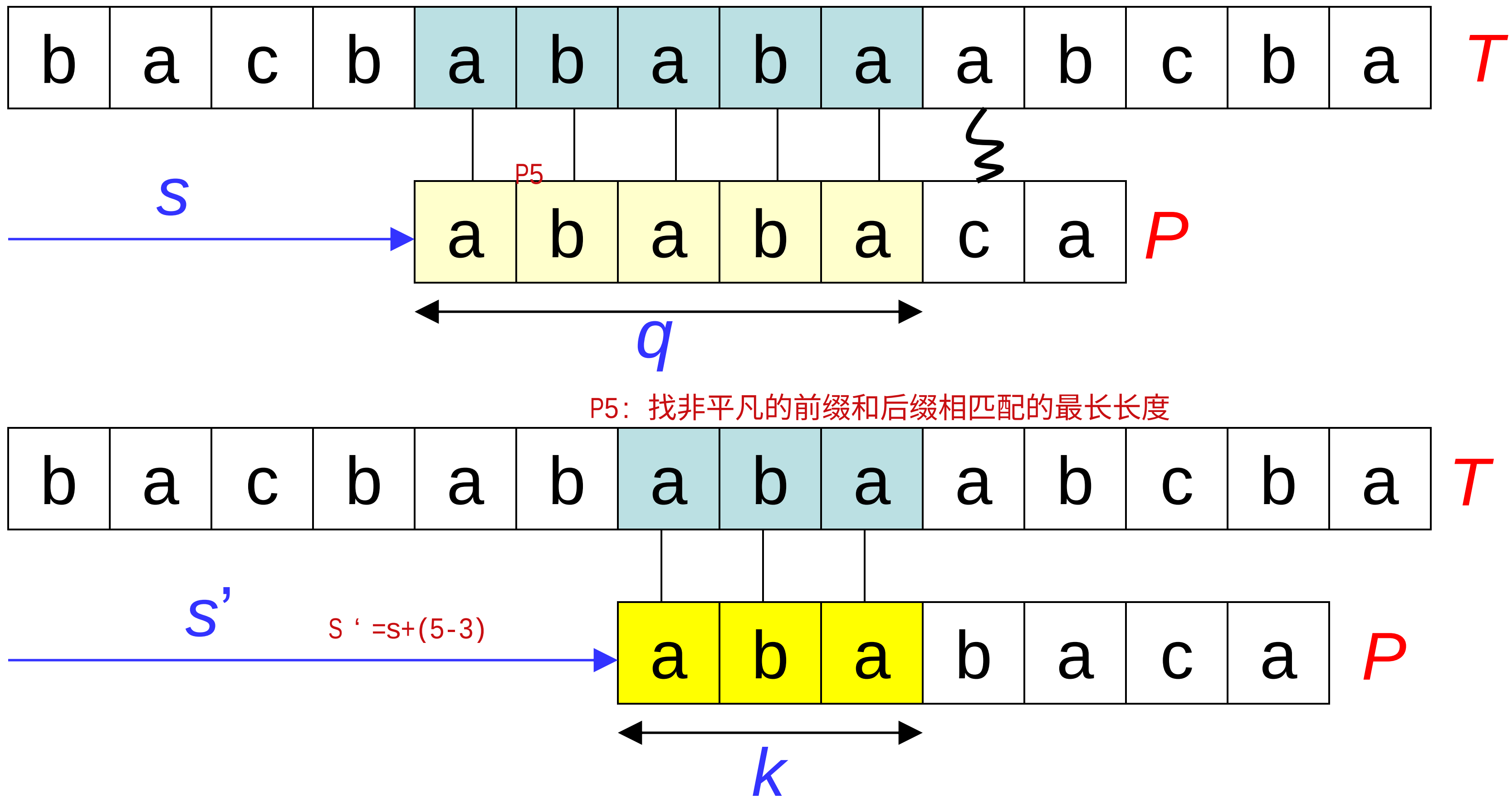
Prefix Function for a Pattern

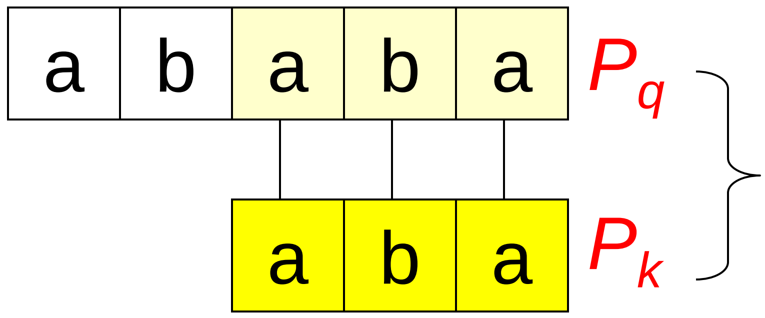
- Given that pattern prefix $P\,[1..q]$ matches text characters $T\,[(s+1)..(s+q)]$, what is the least shift $s' > s$ such that

  $P\,[1..k] = T\,[(s'+1)..(s'+k)]$ where $s'+k=s+q$?

- At the new shift s', no need to compare the first k characters of P with corresponding characters of T.
  - Since we know that they match.

Prefix Function: Example 1





Compare pattern against itself; longest prefix of P that is also a suffix of P_5 is P_3; so $\pi[5]= 3$

Prefix Function: Example 2

i	1	2	3	4	5	6	7	8	9	10
$P[i]$	**a**	**b**	**a**	**b**	**a**	**b**	**a**	**b**	**c**	**a**
$\pi[i]$ 最长前缀后缀	0	0	1	2	3	4	5	6	0	1

$\pi[q] = \max \{ k \mid k<q \text{ and } P_k \text{ is a suffix of } P_q \}$

Illustration: given a String ‘S’ and pattern ‘p’ as follows:

S	b	a	c	b	a	b	a	b	a	b	a	c	a	c	a

p	a	b	a	b	a	c	a

Let us execute the KMP algorithm to find whether ‘p’ occurs in ‘S’.

For ‘p’ the prefix function, Π was computed previously and is as follows:

q	1	2	3	4	5	6	7
p	a	b	a	b	a	c	a
Π	0	0	1	2	3	0	1

Initially: n = size of S = 15;
m = size of p = 7

Step 1: i = 1, q = 0
comparing p[1] with S[1]

S	b	a	c	b	a	b	a	b	a	b	a	c	a	a	b
p	a	b	a	b	a	c	a								

P[1] does not match with S[1]. ‘p’ will be shifted one position to the right.

Step 2: i = 2, q = 0
comparing p[1] with S[2]

S	b	a	c	b	a	b	a	b	a	b	a	c	a	a	b
p		a	b	a	b	a	c	a							

P[1] matches S[2]. Since there is a match, p is not shifted.

Step 3: i = 3, q = 1

Comparing p[2] with S[3]   p[2] does not match with S[3]

S	b	a	c	b	a	b	a	b	a	b	a	c	a	a	b

p	a	b	a	b	a	c	a

Backtracking on p, comparing p[1] and S[3]

Step 4: i = 4, q = 0

comparing p[1] with S[4]   p[1] does not match with S[4]

S	b	a	c	b	a	b	a	b	a	b	a	c	a	a	b

p	a	b	a	b	a	c	a

Step 5: i = 5, q = 0

comparing p[1] with S[5]   p[1] matches with S[5]

S	b	a	c	b	a	b	a	b	a	b	a	c	a	a	b

p	a	b	a	b	a	c	a

Step 6: i = 6, q = 1

Comparing p[2] with S[6]   p[2] matches with S[6]

S	b	a	c	b	a	b	a	b	a	b	a	c	a	a	b
p					a	b	a	b	a	c	a				

Step 7: i = 7, q = 2

Comparing p[3] with S[7]   p[3] matches with S[7]

S	b	a	c	b	a	b	a	b	a	b	a	c	a	a	b
p					a	b	a	b	a	c	a				

Step 8: i = 8, q = 3

Comparing p[4] with S[8]   p[4] matches with S[8]

S	b	a	c	b	a	b	a	b	a	b	a	c	a	a	b
p					a	b	a	b	a	c	a				

Step 9: i = 9, q = 4

Comparing p[5] with S[9] p[5] matches with S[9]

S	b	a	c	b	a	b	a	b	a	b	a	c	a	a	b
p					a	b	a	b	a	c	a				

Step 10: i = 10, q = 5

Comparing p[6] with S[10] p[6] doesn’t match with S[10]

S	b	a	c	b	a	b	a	b	a	b	a	c	a	a	b
p					a	b	a	b	a	c	a				

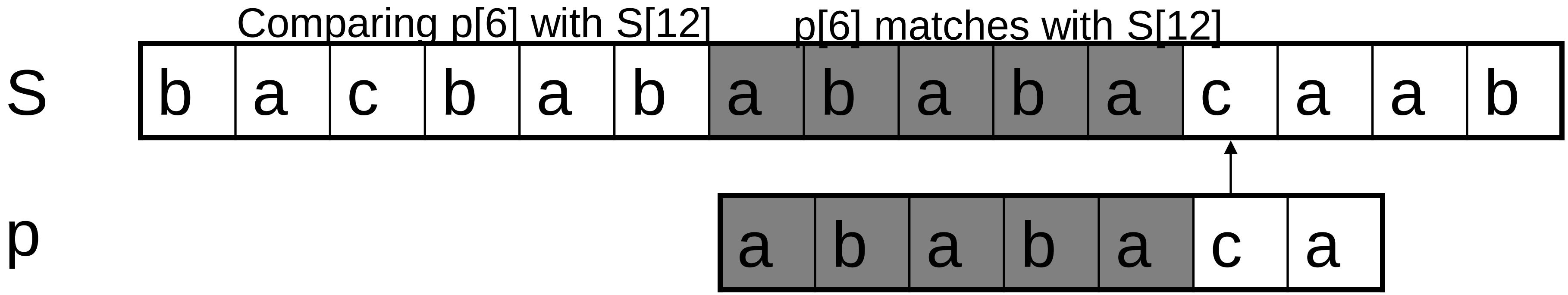
Backtracking on p, comparing p[4] with S[10] because after mismatch q = Π[5] = 3

Step 11: i = 11, q = 4

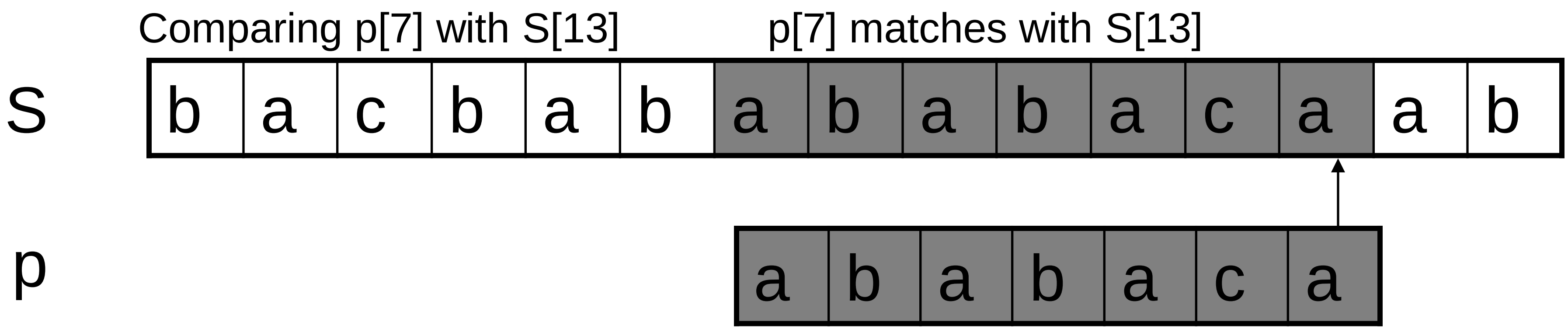
Comparing p[5] with S[11] p[5] matches with S[11]

S	b	a	c	b	a	b	a	b	a	b	a	c	a	a	b
p							a	b	a	b	a	c	a		

Step 12: i = 12, q = 5



Step 13: i = 13, q = 6



Pattern ‘p’ has been found to completely occur in string ‘S’. The total number of shifts that took place for the match to be found are: i – m = 13 – 7 = 6 shifts.

Knuth-Morris-Pratt (KMP) Algorithm

- Information stored in prefix function
  - Can speed up both the naïve algorithm and the finite-automaton matcher.
- KMP Algorithm
  - 2 parts: KMP-MATCHER, PREFIX.
    匹配 算前缀
- Running time
  - PREFIX takes $O(m)$.
  - KMP-MATCHER takes $O(m+n)$.

Boyer-Moore Algorithm

从右向左

- Published in 1977.
- The longer the pattern is, the faster it works.
- Starts from the end of pattern, while KMP starts from the beginning.
  从左向右
- Works best for character string, while KMP works best for binary string.
- KMP and Boyer-Moore
  - Preprocessing existing patterns.
  - Searching patterns in input strings.

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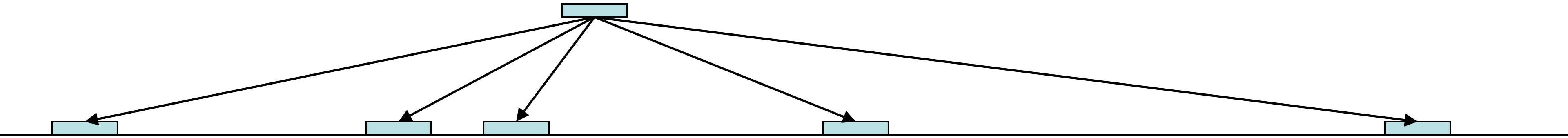
Short read mapping

- Input:
  - A reference genome.
  - A collection of many 25-100bp reads.
  - User-specified parameters (best or all mapping…).
- Output:
  - One or more genomic coordinates for each read.

Multiple mapping



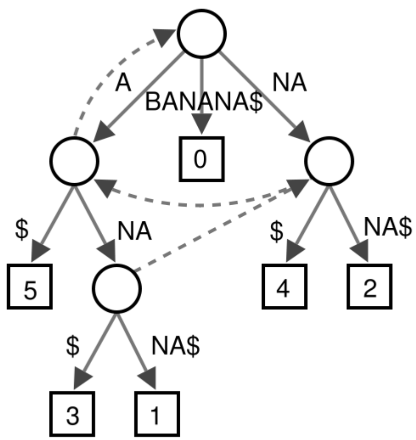
Mapping Reads Review

- Hash Table (Lookup table): exact match
  - Fast, but only for with fixed length. [O(α(n)N), lookup time α(n)]
- Suffix Trees or Suffix Array: exact match
  - Can handle patterns with variable length. [O(mN)]
  - Constructing suffix array require at least $n\lceil \log_2 n \rceil$ bits of working space.
- Dynamic Programming (Smith Waterman): approximate match
  - Mathematically optimal solution for Indels (插入/删除) .
  - Slow, needs filter out impossible positions in practice. [O(mnN)]
- FM-index with Burrows-Wheeler Transform: exact match
  - Fast for small alphabet. [O($mN\log_2\alpha$), α is the size of alphabet]
  - Memory efficient, total is less than 1.5GB for human genome.

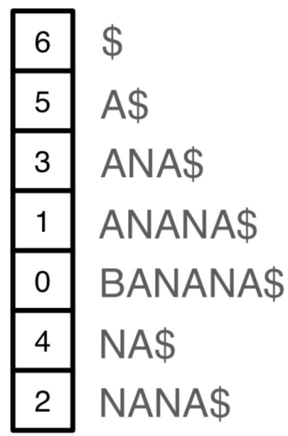
Where *m* is the length of reads, *n* is the length of genome, *N* is the number of reads.

Indexing (1)

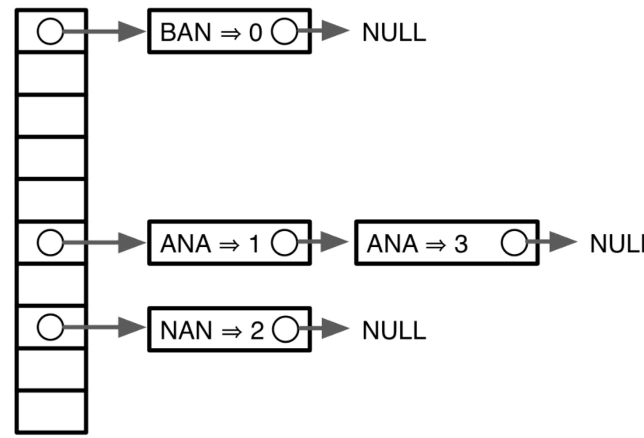
- *Indexing* is required



Suffix tree



Suffix array

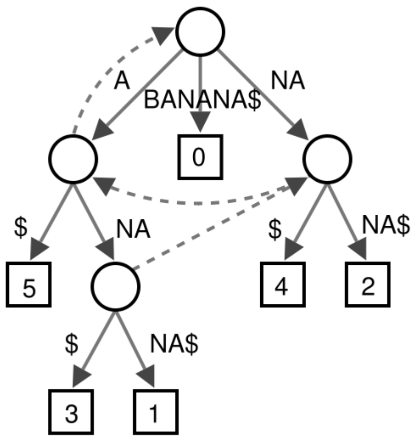


Seed hash tables
Many variants, incl. spaced seeds

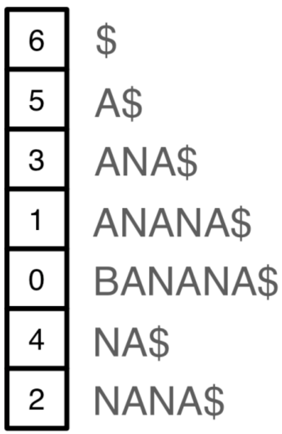
- Choice of index is key to performance.

Indexing (2)

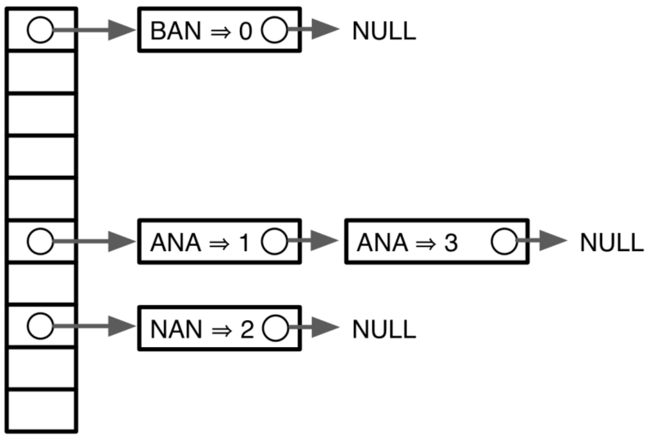
- Genome indices can be big. For human:



> 35 GBs



> 12 GBs



> 12 GBs

- Large indices necessitate painful compromises:
  1. Require big-memory machine
  2. Use secondary storage
  3. Build new index each run
  4. Subindex and do multiple passes

Building: From T to BWT(T)

- Reversible permutation used originally in compression.

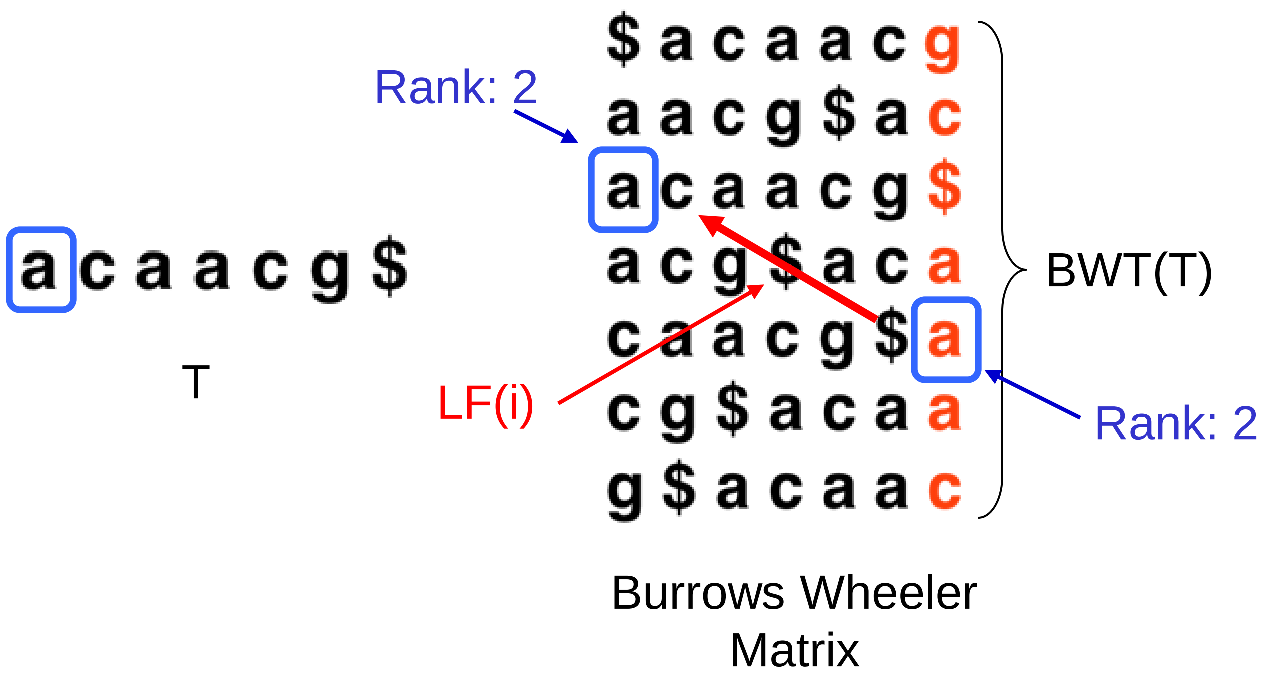
T		Burrows Wheeler Matrix		Last column		BWT(T)
		$ a c a a c g		$ a c a a c g		
		a a c g $ a c		a a c g $ a c		
		a c a a c g $		a c a a c g $		
a c a a c g $	→	a c g $ a c a	→	a c g $ a c a	→	g c $ a a a c
		c a a c g $ a		c a a c g $ a		
		c g $ a c a a		c g $ a c a a		
		g $ a c a a c		g $ a c a a c		

- Once BWT(T) is built, *all else shown here is discarded.*
  - Matrix will be shown for illustration only.

Burrows M, Wheeler DJ: A block sorting lossless data compression algorithm. *Digital Equipment Corporation, Palo Alto, CA* 1994, Technical Report 124; 1994

LF Mapping of BWT

- Property that makes BWT(T) reversible is “LF Mapping”.
  - Property: i^{th} occurrence of a character in **L**ast column is same *text* occurrence as the i^{th} occurrence in **F**irst column.
  - E.g. LF(5)=3 is the map from last row to first row, where 5 is line# of last and 3 is line# of first for the same a of rank 2.



Recover: From BWT(T) to T

- To recreate T from BWT(T), repeatedly apply rule:
  - **T** = **BWT**[**LF**(i)] + **T**; j = **LF**(i).
  - Where **LF**(i) maps row i to row j whose first column character corresponds to j's last column per LF Mapping.

- Could be called "unpermute (解置换)" or "walk-left" algorithm.

FM Index

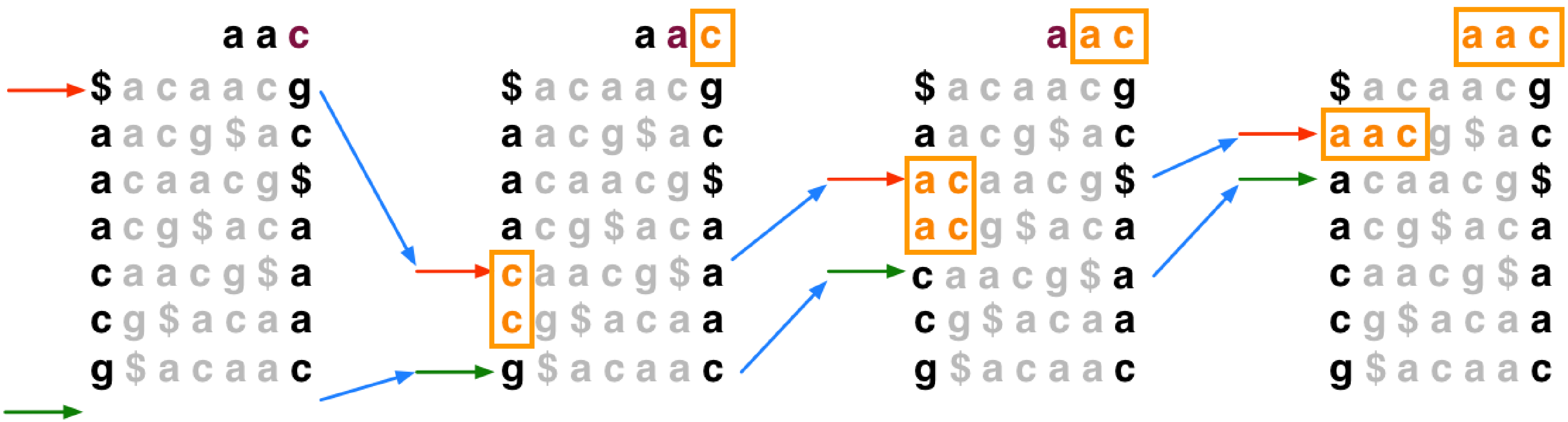
- Ferragina & Manzini propose "FM Index" based on BWT.

- Observed:
  - LF Mapping also allows *exact matching* within T.
  - **LF**(i) can be made fast with *checkpointing.*
  - …and more (see FOCS paper).

- Ferragina P, Manzini G: Opportunistic data structures with applications. *FOCS. IEEE Computer Society; 2000.*
- Ferragina P, Manzini G: An experimental study of an opportunistic index. *SIAM symposium on Discrete algorithms*. Washington, D.C.; 2001.

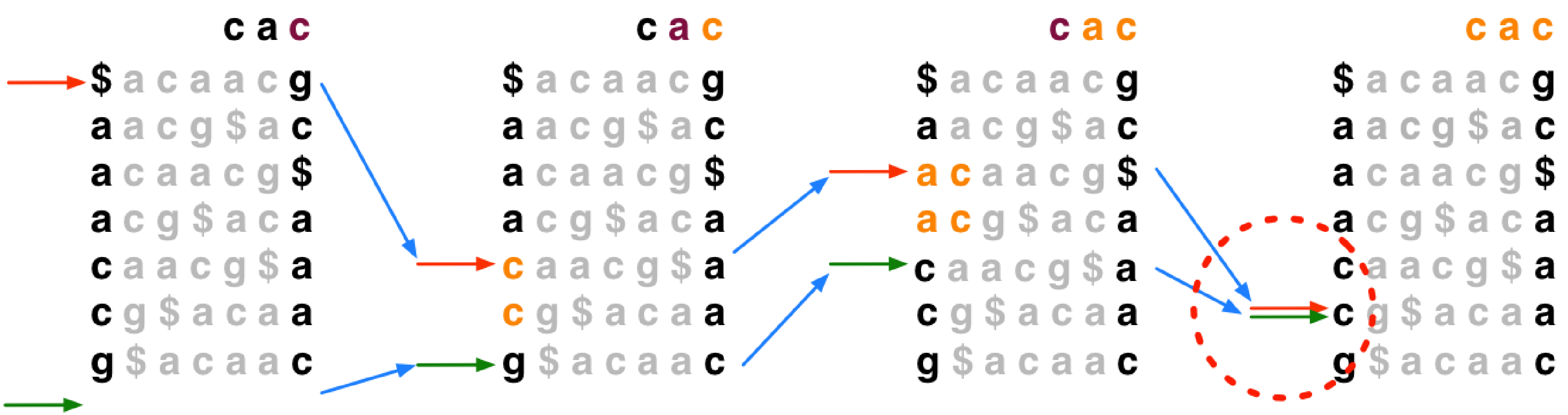
Searching with FM Index: Existed

- To match Q in T using BWT(T), repeatedly apply rule:
  - **top** = **LF**(**top**, **qc**) //also by sp; **bot** = **LF**(**bot**, **qc**) //also by ep
  - Where **qc** is the next character in Q (right-to-left) and **LF**(i, **qc**) maps row i to the row whose first column character corresponds to i's last column character *as if it were* ***qc.***



- In progressive rounds, **top** & **bot** delimit the range of rows beginning with progressively longer suffixes of Q.

Searching with FM Index: Inexisted



- If range becomes empty (**top** = **bot**) the query suffix (and therefore the query) does not occur in the text.

Auxiliary data structures

Key for efficient pattern matching: how to find the corresponding chars in the first column efficiently, in terms of both time and space.

	a	c	g	T
rank	1	5	8	11

	SA		BWT	a	c	g	t
		$agcagcagac**t**	t				
1	9	**a**ct$agcagca**g**	g	0	0	1	1
2	7	**a**gact$agcag**c**	c	0	1	1	1
3	4	**a**gcagact$ag**c**	c	0	2	1	1
4	1	**a**gcagcagact**$**	$	0	2	1	1
5	6	**c**agact$agca**g**	g	0	2	2	1
6	3	**c**agcagact$a**g**	g	0	2	3	1
7	10	**c**t$agcagcag**a**	a	1	2	3	1
8	8	**g**act$agcagc**a**	a	2	2	3	1
9	5	**g**cagact$agc**a**	a	3	2	3	1
10	2	**g**cagcagact$**a**	a	4	2	3	1
11	11	**t**$agcagcaga**c**	c	4	3	3	1

FM indices

Checkpoints

Auxiliary data structures

Key for efficient pattern matching: how to find the corresponding chars in the first column efficiently, in terms of both time and space.

TOTAL

	a	c	g	t
rank	1	5	8	11

FM indices

gca

	SA		BWT	OCC a	OCC c	OCC g	OCC t
		$agcagcagac**t**	t				
1	9	**a**ct$agcagca**g**	g	0	0	1	1
2	7	**a**gact$agcag**c**	c	0	1	1	1
3	4	**a**gcagact$ag**c**	c	0	2	1	1
4	1	**a**gcagcagact**$**	$	0	2	1	1
5	6	**c**agact$agca**g**	g	0	2	2	1
6	3	**c**agcagact$a**g**	g	0	2	3	1
7	10	**c**t$agcagcag**a**	a	1	2	3	1
8	8	**g**act$agcagc**a**	a	2	2	3	1
9	5	**g**cagact$agc**a**	a	3	2	3	1
10	2	**g**cagcagact$**a**	a	4	2	3	1
11	11	**t**$agcagcaga**c**	c	4	3	3	1

Next block:
From 1 + 0 = 1
to 1 + (4-1) = 4

Auxiliary data structures

Key for efficient pattern matching: how to find the corresponding chars in the first column efficiently, in terms of both time and space.

	a	c	g	T
rank	1	5	8	11

gca

	SA		BWT
		$agcagcagact	t
1	9	act$agcagcag	g
2	7	agact$agcagc	c
3	4	agcagact$agc	c
4	1	agcagcagact$	$
5	6	cagact$agcag	g
6	3	cagcagact$ag	g
7	10	ct$agcagcaga	a
8	8	gact$agcagca	a
9	5	gcagact$agca	a
10	2	gcagcagact$a	a
11	11	t$agcagcagac	c

FM indices

a	c	g	t
0	0	1	1
0	1	1	1
0	2	1	1
0	2	1	1
0	2	2	1
0	2	3	1
1	2	3	1
2	2	3	1
3	2	3	1
4	2	3	1
4	3	3	1

Checkpoints

Next block:
From 5 + 0 = 5
to 5 + (2-1) = 6

Auxiliary data structures

Key for efficient pattern matching: how to find the corresponding chars in the first column efficiently, in terms of both time and space.

	a	c	g	T
rank	1	5	8	11

gca

	SA		BWT
		$agcagcagac**t**	t
1	9	**a**ct$agcagca**g**	g
2	7	**a**gact$agcag**c**	c
3	4	**a**gcagact$ag**c**	c
4	1	**a**gcagcagact**$**	$
5	6	**c**agact$agca**g**	g
6	3	**c**agcagact$a**g**	g
7	10	**c**t$agcagcag**a**	a
8	8	**g**act$agcagc**a**	a
9	5	**g**cagact$agc**a**	a
10	2	**g**cagcagact$**a**	a
11	11	**t**$agcagcaga**c**	c

a	c	g	t
0	0	1	1
0	1	1	1
0	2	1	1
0	2	1	1
0	2	2	1
0	2	3	1
1	2	3	1
2	2	3	1
3	2	3	1
4	2	3	1
4	3	3	1

FM indices

Next block:
From 8 + 1 = 9
to 8 + (3-1) = 10

Checkpoints

FM Index: small memory footprint

Components of the FM Index:

First column (*F*):	~ $\vert\Sigma\vert$ integers
Last column (*L*):	*m* characters
SA sample:	$m \cdot a$ integers, where *a* is fraction of rows kept
Checkpoints:	$m \times \vert\Sigma\vert \cdot b$ integers, where *b* is fraction of rows checkpointed

Example: DNA alphabet (2 bits per nucleotide), *T* = human genome, $a = 1/32$, $b = 1/128$

First column (*F*):	16 bytes
Last column (*L*):	2 bits * 3 billion chars = 750 MB
SA sample:	3 billion chars * 4 bytes/char / 32 = ~ 400 MB
Checkpoints:	*3 billion* * 4 bytes/char / *128* = ~ 100 MB

Total < 1.5 GB

End of Ch32