String Matching Algorithms

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(with basic contributions from M. J. Dinneen, Wikipedia, and web materials by Ch. Charras and Thierry Lecroq, Russ Cox, David Eppstein, etc.)

COMPSCI 369 Computational Science

1 String matching algorithms

2 Naïve, or brute-force search

3 Automaton search

4 Rabin-Karp algorithm

5 Knuth-Morris-Pratt algorithm

6 Boyer-Moore algorithm

7 Other string matching algorithms

Learning outcomes: Be familiar with string matching algorithms

Recommended reading:
http://www-igm.univ-mlv.fr/~lecroq/string/index.html

C. Charras and T. Lecroq: Exact String Matching Algorithms. Univ. de Rouen, 1997

String Matching (Searching)

String matching or searching algorithms try to find places where one or several strings (also called **patterns**) are found within a larger string (**searched text**):

```
...␣try␣to␣find␣places␣where␣one␣or␣several␣strings␣(also...
PATTERN: ace
...␣try␣to␣find␣places␣where␣one␣or␣several␣strings␣(also...
```

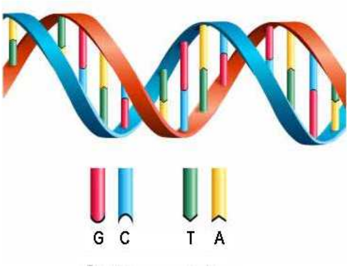
Formally, both the pattern and searched text are concatenation of elements of an **alphabet** (finite set) Σ

- Σ may be a usual human alphabet, for example, the Latin letters a through z or Greek letters α through ω
- Other applications may include binary alphabet, $\Sigma = \{0, 1\}$, or DNA alphabet, $\Sigma = \{A, C, G, T\}$, in bioinformatics

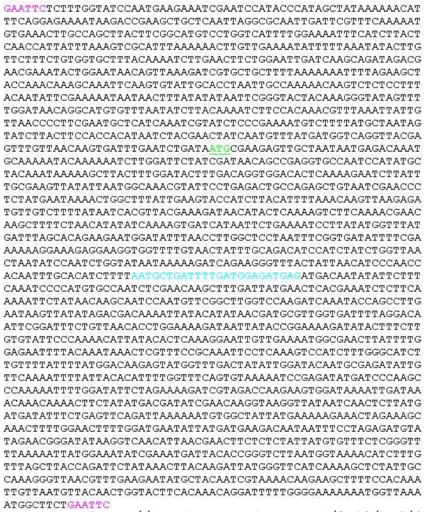
String Searching: DNA alphabet

DNA alphabet contains only four "letters", forming fixed pairs in the double-helical structure of DNA

- A – adenine: A pairs with T
- C – cytosine: C pairs with G
- G – guanine: G pairs with C
- T - thymine: T pairs with A



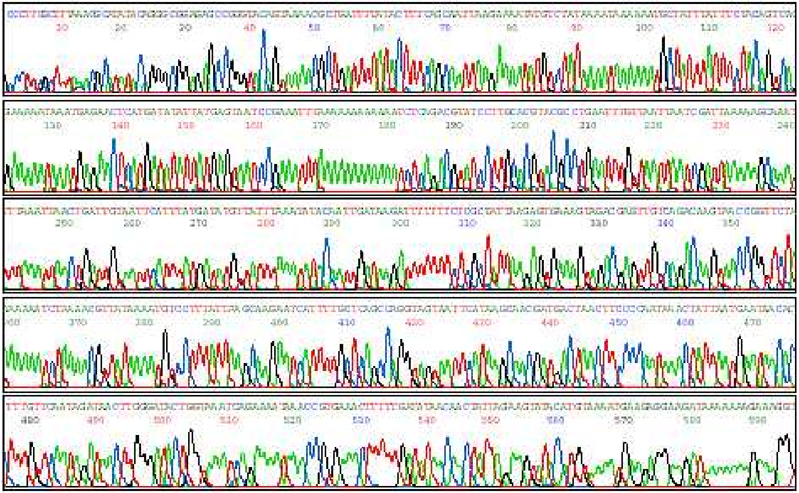
http://www.biotechnologyonline.gov.au/popups/img_helix.html



```
GAATTCTCTTTGGTATCCAATGAAGAAATCGAATCCATACCCATAGCTATAAAAAACAT
TTCAGGAGAAAATAAGACCGAAGCTGCTCAATTAGGCGCAATTGATTCGTTTCAAAAAT
GTGAAACTTGCCAGCTTACTTCGGCATGTCCTGGTCATTTTGGAAAATTTCATCTTACT
CAACCATTATTTAAAGTCGCATTTAAAAAACTTGTTGAAAATATTTTTAAATATACTTG
TTCTTTCTGTGGTGCTTTACAAAATCTTGAACTTCTGGAATTGATCAAGCAGATAGACG
AACGAAATACTGGAATAACAGTTAAAGATCGTGCTGCTTTTAAAAAAATTTTAGAAGCT
ACCAAACAAAGCAAATTCAAGTGTATTGCACCTAATTGCCAAAAACAAGTCTCTCCTTT
ACAATATTCGAAAAATAATAACTTTATATATAATTCGGGTACTACAAAGGGTATAGTTT
TGGATAACAGGCATGTGTTTAATATCTTACAAAATCTTCCACAAACGTTTAAATTATTG
TTAACCCCTTCGAATGCTCATCAAATCGTATCTCCCGAAAATGTCTTTTATGCTAATAG
TATCTTACTTCCACCACATAATCTACGAACTATCAATGTTTATGATGGTCAGGTTACGA
GTTTGTTAACAAGTGATTTGAATCTGATAATGCGAAGAGTTGCTAATAATGAGACAAAT
GCAAAAATACAAAAAATCTTGGATTCTATCGATAACAGCCGAGGTGCCAATCCATATGC
TACAAATAAAAAGCTTACTTTGGATACTTTGACAGGTGGACACTCAAAAGAATCTTATT
TGCGAAGTTATATTAATGGCAAACGTATTCCTGAGACTGCCAGAGCTGTAATCGAACCC
TCTATGAATAAAACTGGCTTTATTGAAGTACCATCTTACATTTTAAACAAGTTAAGAGA
TGTTGTCTTTTATAATCACGTTACGAAAGATAACATACTCAAAAGTCTTCAAAACGAAC
AAGCTTTTCTAACATATATCAAAAGTGATCATAATTCTGAAAATCCTTATATGGTTTAT
GATTTAGCACAGAAGAATGGATATTTAACCTTGGCTCCTAATTTCGGTGATATTTTCGA
AAAAAGGAAAGAGGAAGGTGGTTTTGTAACTATTTGCAGACATCCATCTATCTGGTTAA
CTAATATCCAATCTGGTATAATAAAAAGATCAGAAGGGTTTACTATTAACATCCCAACC
ACAATTTGCACATCTTTTAATGCTGATTTTGATGGAGATGAGATGACAATATATTCTTT
CAAATCCCCATGTGCCAATCTCGAACAAGCTTTGATTATGAACTCACGAAATCTCTTCA
AAAATTCTATAACAAGCAATCCAATGTTCGGCTTGGTCCAAGATCAAATACCAGCCTTG
AATAAGTTATATAGACGACAAAATTATACATATAACGATGCGTTGGTGATTTTAGGACA
ATTCGGATTTCTGTTAACACCTGGAAAAGATAATTATACCGGAAAAGATATACTTTCTT
GTGTATTCCCAAAACATTATACACTCAAAGGAATTGTTGAAAATGGCGAACTTATTTTG
GAGAATTTTACAAATAAACTCGTTTCCGCAAATTCCTCAAAGTCCATCTTTGGGCATCT
TGTTTTATTTTATGGACAAGAGTATGGTTTGACTATATTGGATACAATGCGAGATATTG
TTCAAAATTTTATTACACATTTTGGTTTCAGTGTAAAAATCCGAGATATGATCCCAAGC
CCAAAAATTTTGGATATTCTAGAAAAGATCGTAGACCAAGAAGTGGATAAAATTGATAA
ACAAACAAAACTTCTATATGACGATATCGAACAAGGTAAGGTTATAATCAACTCTTATG
ATGATATTTCTGAGTTCAGATTAAAAAATGTGGCTATTATGAAAAAGAAACTAGAAAGC
AAACTTTTGGAACTTTTGGATGAATATTATGATGAAGACAATAATTTCCTAGAGATGTA
TAGAACGGGATATAAGGTCAACATTAACGAACTTCTCTCTATTATGTGTTTCTCGGGTT
TTAAAAATTATGGAAATATCGAAATGATTACACCGGGTCTTAATGGTAAAACATCTTTG
TTTAGCTTACCAGATTCTATAAACTTACAAGATTATGGGTTCATCAAAAGCTCTATTGC
CAAAGGGTTAACGTTTGAAGAATATGCTACAATCGTAAAACAAGAAGCTTTTCCACAAA
TTGTTAATGTTACAACTGGTACTTCACAAACAGGATTTTTGGGGAAAAAAATGGTTAAA
ATGGCTTCTGAATTC
```

http://www.insectscience.org/2.10/ref/fig5a.gif

String Searching: DNA alphabet



http://biology.kenyon.edu/courses/biol114/Chap08/longread_sequence.gif

String Searching (Matching) Problems

http://www-igm.univ-mlv.fr/∼lecroq/string/index.html

String matching: Find one, or more generally, all the occurrences of a pattern $x = [x_0 x_1 .. x_{m-1}]$; $x_i \in \Sigma$; $i = 0, \ldots, m-1$, in a text (string) $y = [y_0 y_1 .. y_{n-1}]$; $y_j \in \Sigma$; $j = 0, \ldots, n-1$

- Two basic variants:
  1. Given a pattern, find its occurrences in any initially unknown text
     - Solutions by preprocessing the pattern using finite automata models or combinatorial properties of strings
  2. Given a text, find occurrences of any initially unknown pattern
     - Solutions by indexing the text with the help of trees or finite automata
- In COMPSCI 369: only algorithms of the first kind
- Algorithms of the second kind: look e.g. at Google…

String Matching: Sliding Window Mechanism

- Sliding window: Scan the text by a window of size, which is generally equal to m
- An attempt: Align the left end of the window with the text and compare the characters in the window with those of the pattern
    - Each attempt (step) is associated with position j in the text when the window is positioned on $y_j..y_{j+m-1}$
- Shift the window to the right after the whole match of the pattern or after a mismatch

Effectiveness of the search depends on the order of comparisons:

1. The order is not relevant (e.g. naïve, or brute-force algorithm)
2. The natural left-to-right order (the reading direction)
3. The right-to-left order (the best algorithms in practice)
4. A specific order (the best theoretical bounds)

Single Pattern Algorithms (Summary)

Notation:

m – the length (size) of the pattern; n – the length of the searched text

String search algorithm	**Time complexity for**	
	preprocessing	matching
Naïve	0 (none)	$\Theta(n \cdot m)$
Rabin-Karp	$\Theta(m)$	avg $\Theta(n+m)$ worst $\Theta(n \cdot m)$
Finite state automaton	$\Theta(m\|\Sigma\|)$	$\Theta(n)$
Knuth-Morris-Pratt	$\Theta(m)$	$\Theta(n)$
Boyer-Moore	$\Theta(m+\|\Sigma\|)$	$\Omega(n/m)$, $O(n)$
Bit based (approximate)	$\Theta(m+\|\Sigma\|)$	$\Theta(n)$

See `http://www-igm.univ-mlv.fr/∼lecroq/string` for some animations of these and many other string algorithms

Naïve (Brute-Force) Algorithm

```
for ( j = 0; j <= n - m; j++ ) {
   for ( i = 0; i < m && x[i] == y[i + j]; i++ );
   if ( i >= m ) return j;
}
```

Main features of this easy (but slow) $O(nm)$ algorithm:

- No preprocessing phase
- Only constant extra space needed
- Always shifts the window by exactly 1 position to the right
- Comparisons can be done in any order
- mn expected text characters comparisons

Naïve Algorithm: An Example

Pattern: abaa; *searched string*: ababbaabaaab

```
ababbaabaaab             ............

abaa________  step 1     ABA#        mismatch: 4th letter
_abaa_______  step 2     _#...       mismatch: 1st letter
__abaa______  step 3     __AB#.      mismatch: 3rd letter
___abaa_____  step 4     ___#...     mismatch: 1st letter
____abaa____  step 5     ____#...    mismatch: 1st letter
_____abaa___  step 6     _____A#..   mismatch: 2nd letter
______abaa__  step 7     ______ABAA  success
_______abaa_  step 8     _______#... mismatch: 1st letter
________abaa  step 9     ________.#..mismatch: 2nd letter
```

Runs with 9 window steps and 18 character comparisons

Automaton Based Search

Main features:

- Building the minimal deterministic finite automaton (DFA) accepting strings from the language $L = \Sigma^* x$
  - L is the set of all strings of characters from Σ ending with the pattern x
  - Time complexity $O(m|\Sigma|)$ of this preprocessing ($m = |x|$, i.e. the size of x)
- Time complexity $O(n)$ of the search in a string y of size n if the DFA is stored in a direct access table
- Most suitable for searching within many different strings y for same given pattern x

$$x = x_0x_1x_2x_3 \Rightarrow \left.\begin{array}{l}\epsilon\\ x_0\\ x_0x_1\\ x_0x_1x_2\\ x_0x_1x_2x_3\end{array}\right\} m+1 \text{ DFA states} \longrightarrow x = \text{abaa} \Rightarrow \left.\begin{array}{l}\epsilon \ \ \text{empty}\\ \text{a}\\ \text{ab}\\ \text{aba}\\ \text{abaa}\end{array}\right\}$$

Bulding the Minimal DFA for $L = \Sigma^* x$

- The DFA $(Q, \Sigma, \delta : Q \times \Sigma \rightarrow Q, q_0 \in Q, F \subseteq Q)$ to recognise the language $L = \Sigma^* x$:
    - Q – the set of all the prefixes of $x = x_0 \cdots x_{m-1}$:

$$Q = \{\epsilon,\ x_0,\ x_0 x_1,\ \ldots,\ x_0 \cdots x_{m-2},\ x_0 \cdots x_{m-1}\}$$

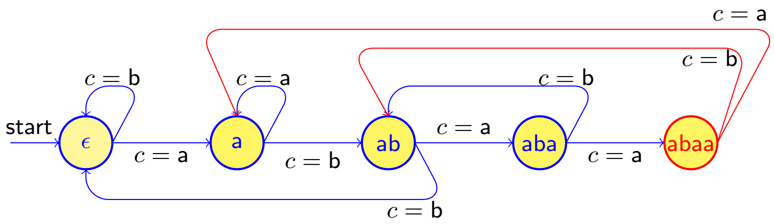
    - $q_0 = \epsilon$ – the state representing the empty prefix
    - $F = \{x\}$ – the state representing the pattern(s) x
    - δ – the state+character to state transition function
        - For $q \in Q$ and $c \in \Sigma$, $\delta(q, c) = qc$ if and only if $qc \in Q$
        - Otherwise $\delta(q, c) = p$ such that p is the longest suffix of qc, which is a prefix of x (i.e. $p \in Q$)
- Once the DFA is built, searching for the word x in a text y consists of parsing y with the DFA beginning with the initial state q_0
- Each time a unique final state F is encountered an occurrence of x is reported

Automaton Search: x = abaa and y = ababbaabaaab

$$\Sigma = \{\text{a}, \text{b}\};\ Q = \{\epsilon, \text{a}, \text{ab}, \text{aba}, \text{abaa}\};\ q_0 = \epsilon;\ F = \{x\} = \{\text{abaa}\}$$

Transitions $\delta(q, c)$:

$c \backslash q$	ϵ	a	ab	aba	abaa
a	a	a	aba	abaa	a
b	ϵ	ab	ϵ	ab	ab



See also: `http://www.ics.uci.edu/~eppstein/161/960222.html`

Automaton Search: $x =$ abaa and $y =$ ababbaabaaab

Automaton:

Initial state ϵ
Final states {abaa}
Transitions

$q_{\text{next}} = \delta(q_{\text{curr}}, c) =$

$q_{\text{curr}} \setminus c$	a	b
ϵ	a	ϵ
a	a	ab
ab	aba	ϵ
aba	abaa	ab
abaa	a	ab

Step	Text	Transition		
1	ababbaabaaab	ϵ	$\longrightarrow$	a
2	ababbaabaaab	a	$\longrightarrow$	ab
3	ababbaabaaab	ab	$\longrightarrow$	aba
4	ababbaabaaab	aba	$\longrightarrow$	ab
5	ababbaabaaab	ab	$\longrightarrow$	ϵ
6	ababbaabaaab	ϵ	$\longrightarrow$	a
7	ababbaabaaab	a	$\longrightarrow$	a
8	ababbaabaaab	a	$\longrightarrow$	ab
9	ababbaabaaab	ab	$\longrightarrow$	aba
10	ababbaabaaab	aba	$\longrightarrow$	abaa
11	ababbaabaaab	abaa	$\longrightarrow$	a
12	ababbaabaaab	a	$\longrightarrow$	ab

Runs with 12 steps and 12 character comparisons

Rabin-Karp Algorithm

Main features:

- Using hashing function
  (i.e., it is more efficient to check whether the window contents "looks like" the pattern than checking exact match)
- Preprocessing phase: time complexity $O(m)$ and constant space
- Searching phase time complexity:
  - $O(mn)$ for worst case
  - $O(n+m)$ for expected case
- Good for multiple patterns x being used

Rabin-Karp Hashing Details

Desirable hashing functions $\mathrm{hash}(\ldots)$ for string matching:

- Efficiency of computation
- High discrimination for strings
- Easy computation of $\mathrm{hash}(y_{j+1}..y_{j+m})$ from the previous window: i.e. $\mathrm{hash}(y_{j+1}..y_{j+m}) = \mathrm{rehash}\left(y_j, y_{j+m}, \mathrm{hash}(y_j..y_{j+m-1})\right)$

For a word w of length m, let $\mathrm{hash}(w)$ be defined as:

$$\mathrm{hash}(w_0..w_{m-1}) = \left(w_0 2^{m-1} + w_1 2^{m-2} + \ldots + w_{m-1} 2^0\right)_{\bmod q}$$

where q is a large number. Then $\mathrm{rehash}(a, b, h) = (2h - a2^m + b)_{\bmod q}$

- Preprocessing phase: computing $\mathrm{hash}(x)$
  - It can be done in constant space and $O(m)$ time
- Searching phase: comparing $\mathrm{hash}(x)$ with $\mathrm{hash}(y_j..y_{j+m-1})$ for $0 \leq j < n - m$
  - If an equality is found, still check the equality $x = y_j..y_{j+m-1}$ character by character

Rabin-Karp Algorithm

Using external hash and rehash functions:

```
int RabinKarp(String x, String y)
{
  m = x.length();
  n = y.length();
  hx = hash(x,0,m-1);
  hy = hash(y,0,m-1);
  for (int j = 0; j <= n - m; j++)
  {
   if (hx==hy && y.substring(j,j+m-1)==x) return j;
   hy = rehash(y[j],y[j+m],hy);
  }
  return -1; // not found
}
```

Rabin-Karp with x = abaa and y = ababbaabaaab

hash(abaa)	=	1459	$\rightarrow$	`hx` — hash value for pattern x
		`hy` $\downarrow$	$\rightarrow$	hash value for substring y
$\mathrm{hash}(y_0..y_3)$	=	1460		ababbaabaaab
$\mathrm{hash}(y_1..y_4)$	=	1466		ababbaabaaab
$\mathrm{hash}(y_2..y_5)$	=	1461		ababbaabaaab
$\mathrm{hash}(y_3..y_6)$	=	1467		ababbaabaaab
$\mathrm{hash}(y_4..y_7)$	=	1464		ababbaabaaab
$\mathrm{hash}(y_5..y_8)$	=	1457		ababbaabaaab
$\mathrm{hash}(y_6..y_9)$	=	1459		ababbaabaaab : `return 6`
$\mathrm{hash}(y_7..y_10)$	=	1463		ababbaabaaab
$\mathrm{hash}(y_8..y_11)$	=	1456		ababbaabaaab

Rabin-Karp Algorithm (searching multiple patterns)

Extending the search for multiple patterns of the *same* length:

```
void RabinKarpMult(String[] x, String y)
{
  m = x[0].length();
  n = y.length();
  for( int i = 0; i < x.length; i++ )
     hx[i] = hash( x[i], 0, m-1);
  hy = hash(y, 0, m-1);
  for( int j = 0; j <= n - m; j ++ )  {
    for( int k = 0; k < x.length; k++ )
      if ( hx[k]==hy && y.substring(j,j+m-1) == x[k] )
                                           matchProcess( k, j );
        hy = rehash( y[j], y[j+m], hy );
    }
}
```

Knuth-Morris-Pratt Algorithm

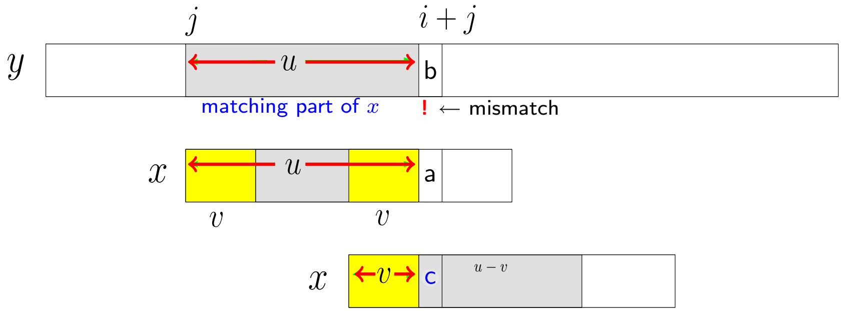
Searches for occurrences of a pattern x within a main text string y by employing the simple observation: *after a mismatch, the word itself allows us to determine where to begin the* ***next match*** *to bypass re-examination of previously matched characters*

- Preprocessing phase: $O(m)$ space and time complexity
- Searching phase: $O(n+m)$ time complexity (independent from the alphabet size)
- At most $2n-1$ character comparisons during the text scan
- The maximum number of comparisons for a single text character: $\leq \log_\eta m$ where $\eta = \frac{1+\sqrt{5}}{2}$ is the golden ratio

The algorithm was invented in 1977 by Knuth and Pratt and independently by Morris, but the three published it jointly

Knuth-Morris-Pratt Window Shift Idea

Let offset i; $0 < i < m$, be the first mismatched position for a pattern x matched to the text string y starting at index position j (i.e. $x_0..x_{i-1} = y_j..y_{j+i-1} = u$, but $x_i =$ a $\neq y_{j+i} =$ b):



The length of the largest substring v being a prefix and suffix of u, which are followed by different characters (like va and vc above), gives the next search index `next[i]`

Knuth-Morris-Pratt Preprocessing

All the shift distances `next[i]` can be actually computed for $0 \leq i \leq m$ in total time $O(m)$ where $m = |x|$

```
void computeNext( String x, int[] next ) {
 int i = 0;
 int j = next[0] = -1;  // end of window marker
 while ( i < x.length() ) {
    while ( j > -1 && x[i] != x[j] ) j = next[ j ];
    i++;
    j++;
    if ( x[ i ] == x[ j ] )
              next[ i ]= next[ j ];
    else next[ i ]= j;
  }
}
```

Knuth-Morris-Pratt Main Algorithm

The main search runs in time $O(n)$ where $n = |y|$.

```
int KMP(String x, String y) {
 int m = x.length(); int n = y.length();
 int[ m+1 ] next;
 computeNext( x, next );
 int i = 0; int j = 0;   // indices in x and y
 while ( j < n ) {
   while ( i > -1 && x[i] != y[j] ) i = next[ i ];
   i++;
   j++;
   if ( i >= m ) return j - i; // Match
 }
 return -1; // Mismatch
}
```

So the total time of the KMP algorithm is $O(m + n)$

KMP with $x =$ abaa and $y =$ ababbaabaaab

Preprocessing phase:

x	a	b	a	a	-
i	0	1	2	3	4
next$[i]$	-1	0	-1	1	1

Searching phase:

```
ababbaabaaab
ABAa           Shift by 2 (next[3]=1)

  .Ba.         Shift by 3 (next[2]=-1)

     Ab..      Shift by 1 (next[1]=0)

      ABAA     Shift by 3 (match found)
```

Boyer-Moore Algorithm

Main features of this “best practical choice” algorithm:

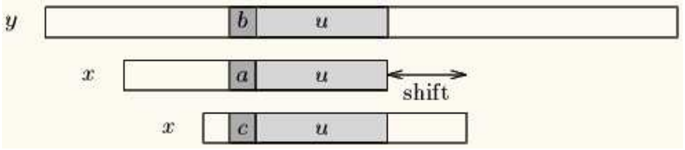
- Performing the comparisons from right to left
- Preprocessing phase: $O(m + |\Sigma|)$ time and space complexity
- Searching phase: $O(m + n)$ time complexity;
- $3n$ text character comparisons in the worst case when searching for a non periodic pattern
- $O(n/m)$ best performance

Two precomputed functions to shift the window to the right:

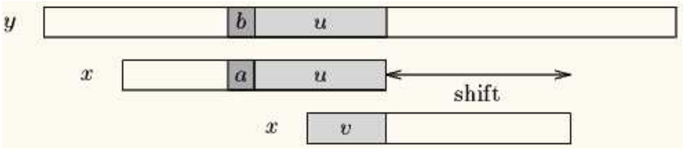
- The good-suffix shift (also called *matching shift*)
- The bad-character shift (also called *occurrence shift*)

Good-Suffix (Matching) Shifts

A mismatch $x_i \neq y_{j+i}$ for a matching attempt at position j, so that $x_{i+1}..x_{m-1} = y_{j+i+1}..y_{j+m-1} = u$
The shift: by aligning the segment u in y with its rightmost occurrence in x that is preceded by a character different from x_i:



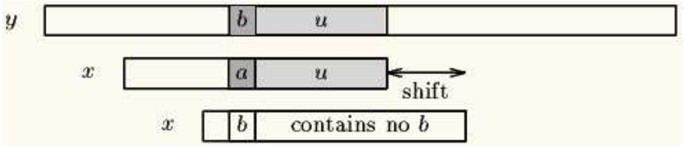
or if no such segment in x exists, by aligning the longest suffix of u in y with a matching prefix v of x:



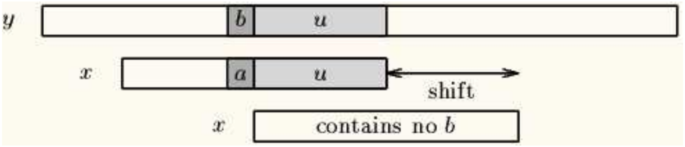
See details in http://www-igm.univ-mlv.fr/~lecroq/string/index.html

Bad-Character (Occurrence) Shifts

A mismatch $x_i \neq y_{j+i}$ for a matching attempt at position j, so that $x_{i+1}..x_{m-1} = y_{j+i+1}..y_{j+m-1} = u$
The shift: by aligning the text character y_{i+j} with its rightmost occurrence in $x_0..x_{m-2}$:



or if y_{j+i} does not occur in x, the left end of the window is aligned with the character y_{j+i+1} immediately after y_{j+i}:



See details in http://www-igm.univ-mlv.fr/~lecroq/string/index.html

Boyer-Moore with $x =$ abaa and $y =$ ababbaabaaab

Bad-character shifts `Bc[a]=1` and `Bc[b]=2`.
Good-suffix shifts `Gs` are 3, 3, 1, and 2, respectively.

```
ababbaabaaab

...a        Shift by 2

  ..aA      Shift by 1

   aBAA     Shift by 3

      ABAA  Shift by 3
```

Shift-AND Matching Algorithm

Also known as the **Baeza-Yates–Gonnet** algorithm and is related to the **Wu-Manber** k-differences algorithm.

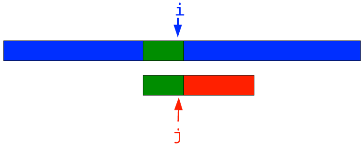
The main features of this bit based algorithm are:

- efficient if the pattern length is no longer than the memory-word size of the machine;
- preprocessing phase in $O(m + |\Sigma|)$ time and space complexity;
- searching phase in $O(n)$ time complexity;
- adapts easily to approximate string matching.

Shift-AND Matching Algorithm (continued)

Algorithm uses (for fixed i) a state vector $\hat{s}$, where

$$s[j] = 1 \text{ iff } y[i-j,\ldots,i] = x[0,\ldots,j]$$



For $c \in \Sigma$ let $T[c]$ be a (Boolean) bit vector of length $m = |x|$ that indicates where c occurs in x.
The next state vector at postions $i+1$ is computed very fast:

$$\hat{s} = ((\hat{s} << 1) + 1)\ \&\ T[y[i+1]]$$

A match is found whenever $s[m-1] = 1$.

Shift-AND with X=abaa and Y=ababbaabaaab

The character vectors for the pattern x are:

x \ $T[]$	a	b
a	1	0
b	0	1
a	1	0
a	1	0

The main search progresses as follows:

x \ $s[]$	a	b	a	b	b	a	a	b	a	a	a	b
a	1	0	1	0	0	1	1	0	1	1	1	0
b	0	1	0	1	0	0	0	1	0	0	0	1
a	0	0	1	0	0	0	0	0	1	0	0	0
a	0	0	0	0	0	0	0	0	0	$\boxed{1}$	0	0

Wu-Manber Approximation Matching Algorithm

The **Shift-AND** algorithm can be modified to detect string matching with at most k errors (or k differences).

The possibilities for matching $x[0,\ldots,j]$ with a substring of y that ends at position i with e errors:

1. *Match:* $x[j] = y[i]$ and a match with e errors between $x[0,\ldots,j-1]$ and a substring of y ending at $i-1$.
2. *Substitution:* a match with $e-1$ errors between $x[0,\ldots,j-1]$ and a substring of y ending at $i-1$.
3. *Insertion:* a match with $e-1$ errors between $x[0,\ldots,j]$ and a substring of y ending at $i-1$.
4. *Deletion:* a match with $e-1$ errors between $x[0,\ldots,j-1]$ and a substring of y ending at i.

Wu-Manber State Update Procedure

We introduce new state vectors $\hat{s_e}$ that represent the matches where $0 \leq e \leq k$ errors have occurred. [Note: $\hat{s} = \hat{s_0}$.]

The state updating is a generalization of the **Shift-AND** rule:

$$\begin{aligned} s'_e \quad = \quad & (((s_e << 1) + 1) \textbf{ AND } T[y[i+1]]) \textbf{ OR} \\ & ((s_{e-1} << 1) + 1) \textbf{ OR} \\ & ((s'_{e-1} << 1) + 1) \textbf{ OR} \\ & s_{e-1} \end{aligned}$$

Here, the s_* and s'_* denote the state at character position i and $i+1$, respectively, of the text string y

The **OR**'s in the above rule account for the 4 possible ways to approximate the pattern with errors