Computing Patterns in Strings I: Specific, Generic, Intrinsic

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Outline

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Computing patterns in strings constitutes the combinatorial nuts and bolts of many more general technologies: pattern “recognition”, data mining, data compression, bioinformatics, cryptography, information retrieval, security systems.

In this series of three lectures, I give a nontechnical overview, guaranteed intelligible to the non-mathematician, of these methods, organized into three categories:

* specific patterns (pattern-matching);
* generic patterns (“regularities” in strings);
* intrinsic patterns (always there, they make things happen!).

Outline

What is a string?

A string is just a sequence of "letters" (symbols) drawn from some (finite or infinite) "alphabet" (set):

- a word in the English language, whose letters are the upper and lower case English letters;
- a text file, whose letters are the ASCII characters;
- a book written in Chinese, whose letters are Chinese ideograms;
- a computer program, whose elements are certain "separators" (space, semicolon, colon, and so on) together with the "words" between separators; also a compiled .exe program;
- a DNA sequence, perhaps three *billion* letters long, containing only the letters C, G, A and T, standing for the nucleotides cytosine, guanine, adenine and thymine, respectively;
- a stream of *trillions* of bits beamed from a space vehicle;
- a list of the lengths of the sides of a convex polygon, whose values are drawn from the real numbers.

Why are strings important?

Because everything is a string!

Examples

* Fibonacci

$$
\begin{array}{cccccccccccccc}
 & 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 & 11 & 12 & 13 \\
\boldsymbol{f} = & a & b & a & a & b & a & b & a & a & b & a & a & b & \cdots
\end{array}
$$

* WWW (courtesy Lewis Carroll)

1	2	3	4	5	6	7	8	9	10	
'Twas	*brillig*	*and*	*the*	*slithy*	*toves*	*did*	*gyre*	*and*	*gimble*	···

* highly periodic

$$001010010110100101001011010010100 \cdots$$

Conferences on String Processing

* AFL: International Conference on Automata & Formal Languages
* CIAA: International Conference on Implementation & Application of Automata;
* CPM: Symposium on Combinatorial Pattern Matching;
* DLT: Developments in Language Theory;
* ECCB: European Conference on Computational Biology;
* FSMNLP: Finite-State Methods & Natural Language Processing;
* LATA: International Conference on Language & Automata Theory & Applications;
* LSD: London Stringology Days;
* PSC: Prague Stringology Conference;
* SPIRE: Symposium on String Processing and Information Retrieval;
* StringMasters (@ McMaster): “How long is a piece of string?”
* WABI: Workshop on Algorithms in Bioinformatics;
* WORDS: International Conference on Words.

In 1980 AFL started, the next one was CPM in 1990 — all the others have started since then.

Important Ideas

* combinatorial
* specific
* generic
* intrinsic

Outline

The Pattern-Matching Task

The problem: to find all occurrences of a given pattern $\boldsymbol{p} = \boldsymbol{p}[1..m]$ in a given text $\boldsymbol{x} = \boldsymbol{x}[1..n]$ – hundreds, if not thousands, of algorithms have been proposed. More than 30 are given, with descriptions and C code, at

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

Two approaches:

(1) skip sections of $\boldsymbol{x}$ where $\boldsymbol{p}$ cannot occur;
(2) use the bit-parallel property of computer words to go through $\boldsymbol{x}$ fast!
(3) hybrid – do first one, then the other.

Two modes:

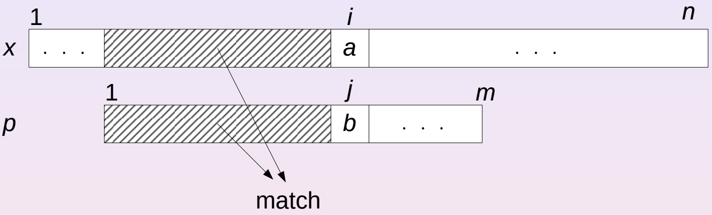
(1) exact – *issi* occurs twice in *Mississippi*;
(2) approximate – *ipsi* occurs three times with one error in *Mississippi*!

Outline

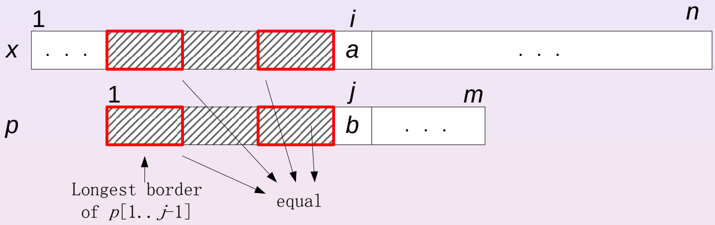
The Knuth-Morris-Pratt Algorithm

- The most famous pattern-matching algorithm.
- Preprocessing: compute the border of every prefix of $\boldsymbol{p}$.
- Requires at most $2n$ letter comparisons (linear!).
- However, not very fast in practice.

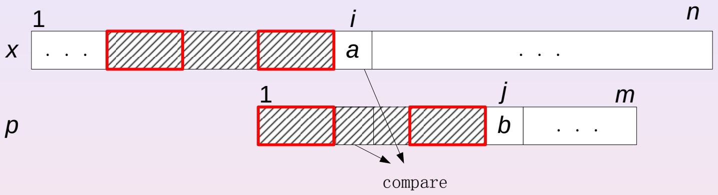
The KMP Algorithm - 1



The KMP Algorithm - 2



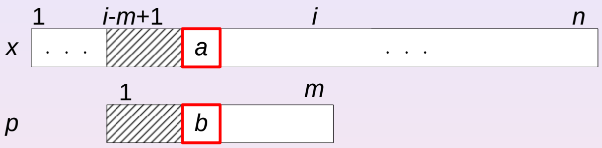
The KMP Algorithm - 3



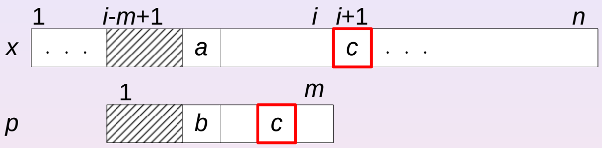
Sunday Variant of Boyer-Moore

- A simplified version of the Boyer-Moore algorithm.
- Preprocessing: find the rightmost occurrence of each letter in $\boldsymbol{p}$.
- Time complexity $O(mn)$.
- However, very fast in practice.

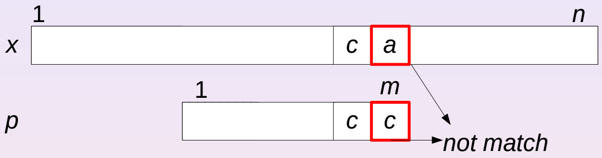
The BMS Algorithm - 1



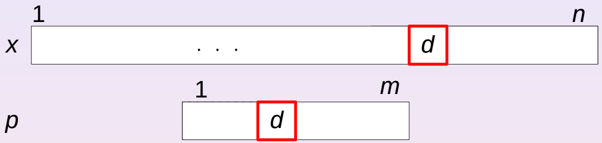
The BMS Algorithm - 2



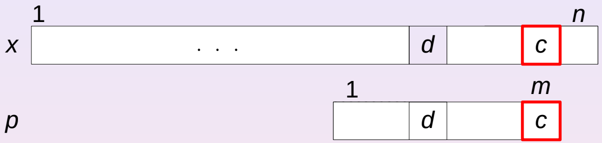
The BMS Algorithm - 3



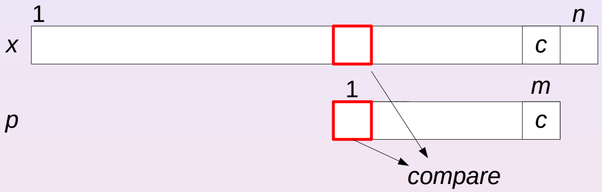
The BMS Algorithm - 4



The BMS Algorithm - 5



The BMS Algorithm - 6



The DBG Shift-Or Algorithm

- Makes use of the bit-parallel nature of computer words.
- Preprocessing: computes a bit array $\boldsymbol{B}$ identifying each letter in $\boldsymbol{p}$.
- Time complexity $O(mn/w)$, where w is the computer word length.
- Fast for shorter patterns.
- Very flexible – easily modified for approximate matching.

DBG Shift-Or

		$\boldsymbol{B}$		
$\boldsymbol{p} \backslash \Sigma$	A	C	G	T
A	0	1	1	1
A	0	1	1	1
T	1	1	1	0
C	1	0	1	1
G	1	1	0	1

Preprocess($\boldsymbol{B}$)
$\boldsymbol{s}[0..m] \leftarrow 0(1^m)$ — *initialize state vector*
for $i \leftarrow 1$ **to** n **do**
    $\boldsymbol{s} \leftarrow rightshift(\boldsymbol{s}, 1) \lor \boldsymbol{B}\big[1..m, \boldsymbol{x}[i]\big]$
    if $\boldsymbol{s}[m] = 0$ **then output** $i - m + 1$

At each step the state vector $\boldsymbol{s}$ is shifted right one bit (0 enters from the left) and a logical OR is done with the column of $\boldsymbol{B}$ corresponding to the current position i in $\boldsymbol{x}$.

Franek-Jennings-Smyth

- Combines KMP & BMS.
- So inherits the merits of both algorithms: very fast both asymptotically ($O(n)$) and in practice.

Here it is:

1. Perform **Sunday** shift along text.
2. When a match of letters is found at the end of the pattern, switch to **KMP** matching.
3. Continue **KMP** matching until no border can be used, then switch back to **Sunday** shift.

Smyth-Wang-Yu

- Combines BMS & Shift-Or.
- Adapts to the nature of the text, thus on average faster than either component.

Here it is:

1. Perform **Sunday shift** along text.
2. When a match of letters is found at the end of the pattern, switch to **Shift-Or matching**.
3. Continue **Shift-Or** until no match can be found at the current position (the state vector $\boldsymbol{s}$ is all ones), then skip to next possible position and switch back to **Sunday** shift.

Outline

Overview

There are four main paradigms of approximate pattern-matching:

- pattern $\boldsymbol{p}$ and text $\boldsymbol{x}$ are well-defined; handled by dynamic programming in $O(mn)$, maybe $O(n \log m)$, time;
- letters in either $\boldsymbol{p}$ or $\boldsymbol{x}$ may be indeterminate; handled by modifications to exact pattern-matching algorithms (especially DBG & Sunday);
- letters are exact or indeterminate, with bounds given on both maximum and total distance (for example, (δ, γ)-matching of musical texts in musical databases);
- match is exact but positions may be scrambled (Abelian matching); handled by convolutions.

Applications of Approximate Matching

- Recognition/correction of misspellings or word inversion in database/internet search.
- Tolerance of transcription errors in DNA sequences copied elsewhere in the genome.
- Appropriate handling of legitimate ambiguity, such as in protein/DNA entries, or in spelling variants (among dialects, or between past and present — for example, "itemise" and "itemize", or Smyth and Smith).
- Matching of inherently approximate texts, such as musical passages or rhythms (to detect plagiarism, for example).

$\boldsymbol{p}$ & $\boldsymbol{x}$ Well-Defined

- Hamming distance (substitution only)
- Edit distance (plus insertion & deletion)
- Scoring distance (distinct scores for each pair of letters)

Usually a threshhold k is given; if the pattern $\boldsymbol{p}$ is no more than distance k from a substring $\boldsymbol{u} = \boldsymbol{x}[i..i+m-1]$, then $\boldsymbol{u}$ is a k-match for $\boldsymbol{p}$.

Hamming distance

$$
\begin{array}{lccccccccccc}
 & 1 & 2 & 3 & 4 & 5 & 6 & 7 & 8 & 9 & 10 & 11 \\
\boldsymbol{x} = & m & i & \underline{s} & s & i & \underline{s} & s & i & p & \underline{p} & i \\
\boldsymbol{p} = & & i & \underline{p} & s & i & & & & & & \\
 & & & & & i & \underline{p} & s & i & & & \\
 & & & & & & & & i & p & \underline{s} & i
\end{array}
$$

Hamming distance $d(\boldsymbol{p}, \boldsymbol{x}[2..5]) = 1$ implies that one substitution yields a match.

Edit/Scoring distance I

Using deletions and insertions can sometimes reduce the distance:

$$\boldsymbol{x} = abcd; \quad \boldsymbol{p} = adbc.$$

Here the Hamming distance $d(\boldsymbol{p}, \boldsymbol{x}) = 3$, but deleting d from $\boldsymbol{x}$, then reinserting it after position 1 (two operations), yields edit distance $d'(\boldsymbol{p}, \boldsymbol{x}) = 2$.

More generally, scoring distance (often used in DNA analysis) gives different weights (or scores) to each operation — for exxample, reflecting the probability that letter A is deleted, or that $C \rightarrow G$.

Pattern-matching using all of these forms of distance is implemented using dynamic programming.

Edit/Scoring distance II

	1	2	3	4	5	6	7	8	9	10	11
$\boldsymbol{x} =$	m	i	$\underline{s}$	s	i	$\underline{s}$	s	i	p	$\underline{p}$	i
$\boldsymbol{p} =$		i		s	i						
					i		s	i			

Edit distance $d(\boldsymbol{p}, \boldsymbol{x}[2..5]) = 1$ since deleting $\boldsymbol{x}[3]$ yields a match. (Also $d(\boldsymbol{p}, \boldsymbol{x}[2..4] = 1$ by substituting $\boldsymbol{x}[4] \leftarrow i$, $d(\boldsymbol{p}, \boldsymbol{x}[3..5]) = 1$ by substituting $\boldsymbol{x}[3] \leftarrow i$.)

Indeterminate Pattern-Matching

This is common in applications to DNA/protein sequences, where a letter may legitimately take one of several values, and so match with each of them. For example, the string

$$h\{a, i, o, u\}t$$

matches

$$hat,\ hit, h\{o, u\}t.$$

A new area of research since 2003; the subject of Shu Wang's Ph.D. dissertation. Bit-parallel and hybrid approaches are effective.

(δ, γ)-Matching

In musical texts, the notes can be represented by integers. A match occurs if

$$\begin{aligned} \max_{j=1}^{m} |\boldsymbol{p}[j] - \boldsymbol{x}[i+j-1]| &\leq \delta, \\ \Sigma_{j=1}^{m} |\boldsymbol{p}[j] - \boldsymbol{x}[i+j-1]| &\leq \gamma. \end{aligned}$$

Shift-Or is used, and modifications of other exact methods.

Abelian Pattern-Matching

This is an even newer area of research, again motivated by applications in bioinformatics. In

$$\boldsymbol{x} = mississippi,$$

under Abelian matching, we find five matches with $\boldsymbol{p} = sis$!