Fast nGram-Based String Search Over Data Encoded Using Algebraic Signatures

W. Litwin (Dauphine),R. Mokadem (Dauphine),Ph. Rigaux (Dauphine)T. Schwarz (U. Santa Clara)

Plan

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- Our Proposal
- Key Idea
 - □ Algebraic Signatures
 - Record Encoding
 - □ Pattern Preprocessing
- Search Example
- Performance Study
- Conclusion

Problem

String Search (Pattern Matching) in A Database or File

□ Find every record matching pattern = "Dauphine"

- What about record "Universite de Technologie Paris Dauphine" ?
- Records are searched often, and updated rarely
 - We especially target large Scalable and Distributed DBs and Files
 - on Grids and P2P networks



Our Proposal

Fast String Search Method
Several Times Faster than Boyer-Moore
In our experiments:
Up to eleven times for ASCII
Up to six times for XML
Up to seventy times for DNA

Key Idea : Pre-processing

- We aggregate (encode) all *n*-symbol long substrings (*ngrams*) in visited strings (*records*) and in the searched pattern into single-symbol *algebraic signatures*
 - Records are encoded while coming for storage
 - Pattern is encoded during search preprocessing



Key Idea : Search

- We compare signatures for attempted matches and shifts like Boyer-Moore (BM) does
 - "Bad character" shift
- However, matching ngram signatures matching n symbols at the time

Key Benefit

- Matching attempts usually more discriminative than matching a single (original) symbol at the time.
 - The latter is the current approach
 - BM and all other major pattern matching algorithms we are aware of
 - □ KMP, Quick Search, KR...

Key Benefit

- Longer shifts
- Fewer comparisons
- Faster search
- Local search over encoded data only
- No local user can claim unintentional disclosure of stored data
 - Important for P2P
 - Thought determined fraud is not that difficult
- Idem for the data transfer to the client

Algebraic Signature

- Condenses information in a string into a single character
- Defined over Galois Fields (GF) of size 2^f
 - \Box Elements are bit strings of length *f*
 - \Box In our case, typically f = 8
 - □ Hence our symbols are bytes
 - \Box We realize GF addition \oplus as XOR
 - We realize GF multiplication through log/antilog tables

Algebraic Signature

$$AS(r_1 \dots r_k) = r_1 \alpha \oplus r_2 \alpha^2 \oplus \cdots \oplus r_k \alpha^k$$

- $\Rightarrow \alpha$ is a primitive element, e.g., $\alpha = 2$
- ⇒ if $AS(R_1) \neq AS(R_2)$ then $R_1 \neq R_2$ for sure ⇒ if $AS(R_1) = AS(R_2)$ then for sure or very likely $R_1 = R_2$

□ The latter case is a *collision*

Record Encoding

■ We encode every stored record : $r_1...r_k$ □ Either into full *Cumulative Algebraic Signature* $r'_k = r_1 \alpha \oplus r_2 \alpha^2 \oplus \cdots \oplus r_k \alpha^k$ □ Or into partial (moving) CAS of ngrams $r'_k = r_{k-n+1} \alpha \oplus \cdots \oplus r_k \alpha^n$

Full CAS







- Partial CAS can be stored or dynamically calculated from full CAS
 - See the paper

Pattern Preprocessing

- We aggregate ngram signatures in the pattern in a BM-like shift table T
- Conceptual result for "Dauphine"
- Actually:
 - shift table size is f and entry is by AS value
 - Rightmost ngram value is in variable V

2-gram	Shift
33 = AS(d	a) 6
23 = AS(a	u) 5
133 = AS(u	p) 4
24 = AS(p)	h) 3
07 = AS(h)	i) 2
62 = AS(i	n) <u>1</u>
67 = AS(n	e) 0
Any other digram 7	

- Pattern = "Dauphine" of length / = 8
- Record = "Universite de Technologie Paris Dauphine"





- Attempt to match the rightmost 2-gram of pattern against the visited 2-gram in the record
 - AS(ne) =? AS(si) at offset of "i"

- Pattern = "Dauphine" of length / = 8
- Record = "Universite de Technologie Paris Dauphine"
- - 67 =? 11
 - No
 - Lookup shift table T at offset 11 = (AS(si))
 - T shows shift of 7 symbols since AS(si) is not in "Dauphine"
 - Maximal shift here
 - Equal in general to l n + 1

S



- AS(ne) =? AS(T)
- Mismatch
- What in element AS(T) in table T?
- Maximal shift by 7
 - Since "T" is nowhere in "Dauphine"

- Idem
- Mismatch
- Shift by 7
 - Again maximal shift since 'lo' not in "Dauphine"

- Idem
- Mismatch
- Shift by 7
 - Maximal shift since 'ar' not in "Dauphine"



- Compare by signature digrams "ne" and "up"
- Mismatch
- shift by 4 according to T
 - To align on 'up' in "Dauphine"



- Match 'ne' and 'ne', 'hi' and 'hi', 'up' against 'up', 'Da' and 'Da'
- Full match



- Test for false positive : full CAS
 - Compare all the matching symbols at the server
- No test if ngram signatures never collide
 - e.g., through the method proposed for DNA in the paper



- Test for false positive : partial CAS
 - Compare matching symbols at the server except for AS(D) in the record
 - Match D after decoding at the client
 - Remaining n 1 leftmost symbols in general
- No test if ngram signatures never collide
 - e.g., through the method proposed for DNA in the paper

Match attempts and shifts compare single symbol at the time

- Compare right-most character
- Mismatch, hence move Dauphine 2 slots to the right where 'i' appears in Dauphine

- Compare right-most character
- Match, hence compare next character
- Mismatch, hence move Dauphine 7 slots to the right since 'e' appears only once in Dauphine

- Compare 'h' against 'e'
- Mismatch, move pattern three to the right

- Compare 'l' against 'e'
- No 'l' in Dauphine, move by 8

BM: Looking for "Dauphine" in "Universite de Technologie Paris Dauphine:

No 'r' in Dauphine, move by 8

BM: Looking for "Dauphine" in "Universite de Technologie Paris Dauphine:



There is a 'p' in Dauphine, move by 5



- Compare 'e' against 'e', then 'n' against 'n', ...
- A match

Comparison

- 2-gram search has fewer shifts (6 vs 8)
- The shifts are on average longer
- Even though maximum shift size for 2gram is here only 7 vs. 8 for BM
- Much larger gain to expect for larger patterns

N-gram Search in Nutshell



Performance

Zero Storage Overhead

□ No indexing

□ Like BM, KMP…

□ Unlike suffix trees and arrays or ngram indexes...

• Search cost is O(s), *s* the number of shifts

 \Box Maximal shift size is *I* - *n* + 1

 \Box Expected shift size converges towards *f*

Galois Field size used for CAS calculus

Performance

Depends on tuning of n

- □ Larger *n* decreases the maximum shift
- But makes ngrams more discriminative
- □ Up to some value of *n*
 - depending on the alphabet size, symbol value distribution...
- Our experiments show:
 - □ N=4 for DNA records
 - □ N=2 for ASCII & XML in natural language text

Analytical Calculus



Expected Shift Size for 4-gram search on DNA

• Random distribution of symbol values

Experiments

- We compare experimentally performance of N-gram search with BM
- We use mostly partial CAS encoding for: DNA
 - ASCII natural language text
 - □ XML code

Experiments: DNA (homo sap.)



Search Times

Experiments: DNA (homo sap.)



Shifts

Experiments (ASCII nat. lang.)



Experiments (ASCII nat. lang.)



Conclusion

- A new algorithm suitable for data stored once and read many times
 - At least as fast as the most used pattern-matching technique (Boyer-Moore);
 - □ Much faster for small alphabets and/or large patterns;
 - Search without decoding is valuable for P2Pn and Grid environment.
- Current work on:
 - □ Approximate string matching
 - Multiple pattern matching
 - Stronger privacy preservation

Thank You

for

Your Attention