Extended XML Tree Pattern Matching Using TREEMATCH Algorithm

Dr D.Suresh Babu, B.Shiva kiran

Department of Computer Science,
KITS Warangal, AP, India

Abstract: In most of the pattern matching algorithms finding all the distinct matching's of the query tree pattern is the core operation of xml query evaluation. The existing algorithms for tree pattern matching may produce large useless intermediate results using some different notations such as wild cards, negation function, and/or order restrictions for which query processing gets bit complicated.
We propose a TREEMATCH algorithm to achieve a large optimal query class using which leads to the reduction of useless intermediate results

Index Terms—Query processing, XML/XSL/RDF, algorithms

INTRODUCTION

As business and enterprisers generate and exchange XML data more often, there is an increasing need for efficient processing of queries on XML data. An XML query pattern commonly can be represented as a rooted, labeled tree (or called twig). For example, Figure 1(a) shows an example XPath query: *A*[*B*]=*C* and the corresponding XML tree pattern. This query finds all node *C* that has the parent *A* which has another child *B*. In Figure 1(b), the query answers are nodes "*C*1" and "*C*2".
Considered as a core operation in XML query processing. In recent years, many methods ([9], [13], [3], [11], [4], [25]) have been proposed to match XML tree queries efficiently particular, Khalifa et al. [1] proposed a stack-based algorithm to match binary structural relationship including parent-child (P-C) and ancestor-descendant (A-D) relationships. The limitation of their method is that the size of useless intermediate results may become very large, even if the final results are small. Bruno et al. [3] proposed a novel holistic twig join algorithm named TwigStack, which processes the tree pattern *holistically* without decomposing it into several small binary relationships.

EXISTING SYSTEM:-

ALL the Previous algorithms focus on XML tree pattern queries with XML tree queries which may contain wildcards, negation function and order restriction, all of which are frequently used in XML query languages such as XPath and XQuery, for which the query processing gets bit complicated.

PROPOSED SYSTEM:-

We develop theoretical framework on optimal processing of XML tree pattern queries using TREEMATCH ALGORITHM for notations such as Negation functions, ordered restrictions and wild cards of three types of patterns , Query processing gets bit complicated using XPATH,XQUERY languages .we develop
A little work on TREEMATCH algorithm by which we can reduce the useless intermediate results by using different traversal techniques and increase "optimality of algorithm "for large optimal query class to address the problem of sub optimality of different holistic algorithms.

MODULES

1. Matching Cross:

"Matching cross" demonstrates the intrinsic reason for the sub-optimality of existing holistic algorithms. The purpose of our study are (i) to provide insight into the characteristics of the holistic algorithms, and thus promotes our understanding about their behaviors; and (ii) to lead to novel algorithms that can guarantee a larger optimal query class and realize better query performance. The existing holistic algorithms consist of two phases: (i) in the first phase, a list of path solutions is output as intermediate path solutions and each solution matches the individual root-to-leaf path expression; and (ii) in the second phase, the path solutions are merged to produce the final answers for the whole twig query. However, for queries with parent-child (P-C) relationships, the state-of-the-art algorithms cannot guarantee that each intermediate solution output in the first phase is useful to merge in the second phase. In other words, many useless intermediate results (i.e. path solutions) may be produced in the first phase, which is called the sub optimality of algorithms.

2. Return nodes in twig pattern queries:

In a practical application, only parts of query nodes belong to return nodes (or called output nodes interchangeably). Take the Path "//A[B]//C" as an example, only C element and its sub tree are answers. The current "modus operandi" is that they first find the query answer with the combinations of all query nodes, and then do an appropriate projection on those return nodes. Such a post-processing approach has an obvious disadvantage: it outputs many matching elements of non-return nodes that are unnecessary for the final results. Here, we develop a new encoding method to record the mapping relationships and avoid outputting non-return nodes.

3. Modeling of XML data and extended tree pattern query:

An XML database D is usually modeled as a rooted, node labeled tree, element tags and attributes are mapped to nodes in the trees and the edges are used to represent the direct nesting relationships. Our primary focus is on element nodes; and it is not difficult to extend our methods to process the

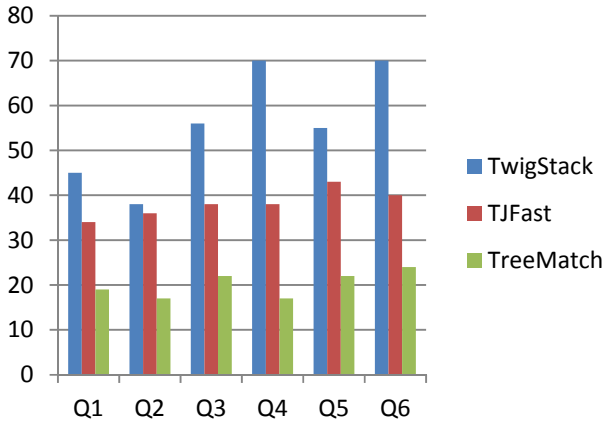
other types of nodes, including attribute and character data. For convenience, we distinguish between query nodes and database nodes by using the term "node" to refer to a query node and the term "element" to refer to a data element in D. An extended tree query Q describes a complex traversal of the XML document and retrieves relevant tree-structured portions of it. The nodes in Q include element tags, attributes and character data. We use "*" to denote the wildcard, which can match any single tree element. There are four kinds of query edges, which are the four combinations between (positive, negative) and (parent-child, ancestor-descendant).

Query	D1		D2		D3	
	O	P	O	P	O	P
Q1	1321	100%	6576	100%	13290	100%
Q2	3558	100%	17757	100%	35649	100%
Q3	9575	98.8%	95291	99.9%	156954	94.5%
Q4	6635	100%	33055	100%	65691	100%
Q5	296	100%	1313	100%	2782	100%
Q6	7506	100%	94132	100%	127478	99.9%

Table for Number of output elements (O) andthe percentage (P)of useful elements for TreeMatch on random data

	D_1	D_2	D_3
Q1	5	6	6
Q2	9	10	11
Q3	528	27067	89779
Q4	6	7	8
Q5	7	8	10
Q6	520	26808	89627

Table of required buffered elements (Randomdata)



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