IMPROVING REAL WORLD SCHEMA MATCHING WITH DECOMPOSITION PROCESS

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Abstract: This paper tends to provide an answer to a difficult problem: Matching large XML schemas. Scalable Matching acquires a long execution time other than decreasing the quality of matches. In this paper, we propose an XML schema decomposition approach as a solution for large schema matching problem. The presented approach identifies the common structures between and within XML schemas, and decomposes these input schemas. Our method uses tree mining techniques to identify these common structures and to select the most relevant sub-parts of large schemas for matching. As proved by our experiments in e-business domain, the proposed approach improves the performance of schema matching and offers a better quality of matches in comparison to other existing matching tools.

1 INTRODUCTION

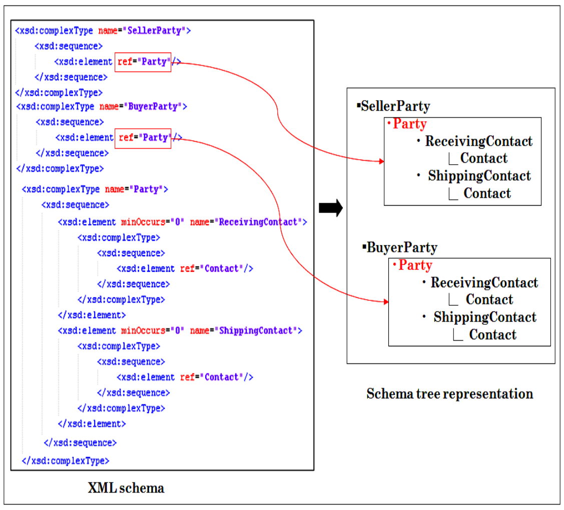
Nowadays, within the business area, the industry builds large scale distributed systems and middlewares that are more and more based on XML technology. In fact, there are many databases and information sources available through the web covering different domains: semantic Web, deep Web, E-business, digital libraries, etc. In such domains, the generated data (XML schemas, ontologies, etc) are heterogeneous and voluminous. The presence of vast heterogeneous collections of data arises one of the greatest challenges in data integration field. For example, real-life E-business schemas of catalogs and messages such as BMEcat, OAGIS[1] or XCBL[2] present an "amazing scale" of elements ($20 \approx 10000$ elements). One of the most critical steps to integrate heterogeneous e-Business applications that contain different XML schemas is to use large schema matching.

Matching techniques are solutions to automatically search correspondences between these data in order to obtain useful information. In fact, matching is an operation that takes data as input (e.g XML schemas, ontologies, relational database schemas) and returns the semantic similarity values of their elements. Schema matching has attracted the attention of research community (Do et al., 2002) (Rahm et al., 2001). However, most matching tools are applied on two schemas with human intervention, whereas in practice, real world schemas are voluminous. Matching these schemas at large scale represents a laborious process. Moreover, matching the whole input schemas will take long execution time. Then, one of the challenges of the matching community is to efficiently search for correspondences between large schemas and to compute reasonable results in a reasonable time.

Our main motivation is to decrease scalable match overload. E-business domain has to deal with large schemas. Matching XML business schemas have two main characteristics. First, an XML business schema may include identical redundant structures called intra-schemas structures or shared sub-structures. Intra-schemas structures are frequent within large XML schemas. In fact, there are many shared XML schema components (elements, attributes, and types) that are referenced in several places (figure 1) in a schema.

Second, schemas from the same domains may share common structures called inter-schemas structures (i.e. similar structures in different schemas). These structures represent an important source of structural and semantic information.

Figure 2 shows an example of the inter-schemas structures. Both schemas share {Invoice To, Contact, Tel, Name, E-mail} and {Deliver To, Contact, Tel, Name, E-mail} sub-schemas.



```
<xsd:complexType name="SellerParty">
    <xsd:sequence>
        <xsd:element ref="Party"/>
    </xsd:sequence>
</xsd:complexType>
<xsd:complexType name="BuyerParty">
    <xsd:sequence>
        <xsd:element ref="Party"/>
    </xsd:sequence>
</xsd:complexType>
<xsd:complexType name="Party">
    <xsd:sequence>
        <xsd:element minOccurs="0" name="ReceivingContact">
            <xsd:complexType>
                <xsd:sequence>
                    <xsd:element ref="Contact"/>
                </xsd:sequence>
            </xsd:complexType>
        </xsd:element>
        <xsd:element minOccurs="0" name="ShippingContact">
            <xsd:complexType>
                <xsd:sequence>
                    <xsd:element ref="Contact"/>
                </xsd:sequence>
            </xsd:complexType>
        </xsd:element>
    </xsd:sequence>
</xsd:complexType>
```

Figure 1: Schema tree representation.

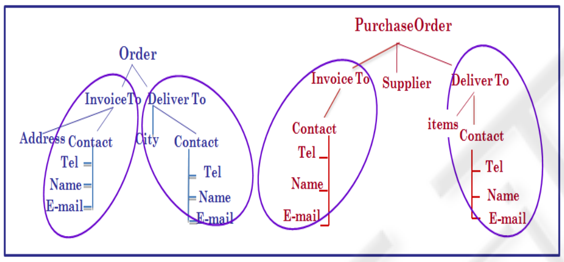


Figure 2: Example of inter-schemas structures.

Motivated by these observations, we propose an XML schema decomposition approach based on inter-schemas and intra-schemas identification. Our approach attempts to find the most similar parts between all the schemas, at once. To this end, we use tree mining techniques to identify these common structures between and within XML schemas. Tree mining is a classical data mining problem which has received lots of efforts in this last years.

Our approach is composed of three steps: transforming XML schemas into trees, extracting frequent trees from these transformed schemas and processing these sub-trees to find the more relevant candidates for matching.

The goal of our paper is then to provide a pre matching approach based on decomposing large schemas into smaller ones to improve the quality and performance of large schema matching. Then matching will be performed between small schemas.

The remainder of this paper is organized as follows. Section 2 reviews the research works related to the different matching strategies. The aim of this study is to show how existing works deal with scalability problem. In section 3, we present our decomposition approach. Section 4 presents experimental evaluation results. Finally, we conclude and discuss future works.

2 RELATED WORK: MATCHING STRATEGIES

Being a central process for several research topics like data integration, data transformation, schema evolution, etc, matching has attracted much attention by research community. Several matching tools have been proposed in the literature including different strategies to deal with scalability problem. These approaches represent an effective attempt to resolve large scale matching problem. We distinguish three different strategies: fragmentation, clustering and statistical approaches.

- *Fragmentation Strategy:* This is a divide and conquers strategy which decomposes a large matching problem into smaller sub-problems by matching at the level of fragments. The issue of fragmentation large-scale schemas and ontologies has been recently addressed by (Hu et al., 2008), (Rahm et al., 2004) and (Wang et al., 2006). The authors (Rahm et al., 2004) presented the fragment-based approach as an effective solution to decompose two large schemas into small fragments. The fragment can be a schema, or sub-schema that represents parts of a schema which can be separately instantiated, or shared that is identified by a node with multiple parents. The proposed strategy is composed of two matching steps: The first step is the fragments identification of two schemas and the second step is to match fragments. This approach has been implemented in COMA++ tool (Do and Rahm, 2007). The authors (Hu et al., 2008) propose a method for partition-based block matching that considers both linguistic and structural characteristics of domain entities based on virtual documents for the relatedness measure. Partitioning ontologies is achieved by a hierarchical bisection algorithm to provide block mappings. Like partitioning approach, Modularization-based Ontology Matching approach (MOM) (Wang et al., 2006) decomposes a large matching problem into smaller sub-problems by matching at the level of ontology modules. This approach includes sub-steps for large ontology partitioning, finding similar modules, module matching and result combination. This method uses the ε-connection to transform the input ontology into an ε-connection with the largest possible number of connected knowledge bases.

• *Clustering Strategy:* This approach has been proposed by (Pei et al., 2006). First, schemas are clustered based on their contextual similarity. Second, attributes of the schemas that are in the same schema cluster are clustered to find attribute correspondences between these schemas. Third, attributes are clustered across different schema clusters using statistical information gleaned from the existing attribute clusters to find attribute correspondences between more schemas.

• *Statistical Strategy:* This approach has been introduced by (He et al., 2003) and (He et al., 2004) with MGS (for hypothesis modeling, generation, and selection) and a DCM (Dual Correlation Mining) framework. The MGS framework is an approach for global evaluation, building upon the hypothesis of the existence of a hidden schema model that probabilistically generates the schemas we observed. This evaluation estimates all possible "models," where a model expresses all attributes matchings. Nevertheless, this approach does not take into consideration complex mappings. DCM framework has been proposed for local evaluation, based on the observation that co-occurrence patterns across schemas often reveal the complex relationships of attributes. However, these approaches suffer from noisy data. HSM (Holistic Schema Matching) and PSM (Parallel Schema Matching) have been proposed by (Su et al., 2006) to find matching attributes across a set of Web database schemas of the same domain. HSM integrates several steps: matching score calculation that measures the probability of two attributes being synonymous, grouping score calculation that estimates whether two attributes are grouping attributes. PSM forms parallel schemas by comparing two schemas and deleting their common attributes. HSM and PSM are purely based on the occurrence patterns of attributes and require neither domain-knowledge, nor user interaction.

In our work, we propose a decomposition approach which divides XML schemas into small sub-schemas with the use of linguistic and tree mining techniques. Our approach is similar to the fragmentation strategy. The main difference lies in the way to find intra-schemas structures called shared sub-structures in COMA++ (Do and Rahm, 2007). More precisely, our approach extends fragmentation method to find inter-schemas structures in automatic manner and is applied on several schemas at once.

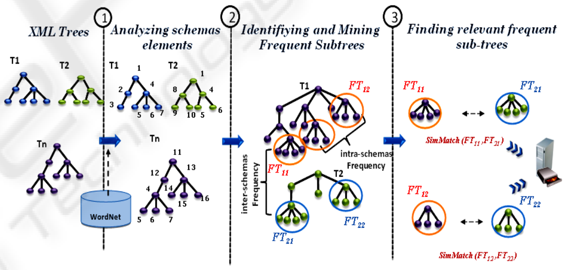
3 XML SCHEMAS DECOMPOSITION APPROACH

We propose a decomposition approach, as a pre-matching phase, which break down large XML schemas into smaller sub-schemas to improve the performance of large schema matching. Our approach identifies and extracts common structures between and within XML schemas (inter and intra-schemas) and finds the sub-schemas candidates for matching.

As illustrated in figure 3, our proposed approach is composed of three phases: (1) converting XML schemas in trees, (2) identifying and mining frequent sub-trees, (3) finding relevant frequent sub-trees.

Our approach is based on the following observations and assumptions: a) Schemas at large scale are various and voluminous, b) Schemas in the same domain contain the same domain concepts, and c) In one schema, several sub-schemas are redundant.

We discuss in this section the different phases of decomposition approach.



1
2
3
XML Trees
Analyzing schemas elements
Identifiying and Mining Frequent Subtrees
Finding relevant frequent sub-trees
T1
T2
Tn
WordNet
intra-schemas Frequency
inter-schemas Frequency
FT_{11}
FT_{12}
FT_{21}
FT_{22}
SimMatch (FT_{11},FT_{21})
SimMatch (FT_{12},FT_{22})

Figure 3: Decomposition approach.

3.1 XML Trees: From Schemas to Trees

The goal of this initial phase is to transform XML schemas into trees and to find linguistic relations between elements. This aims at improving decomposition with considering not only exactly the same labels of elements but also the linguistic similar elements.

We firstly need to parse the XML schemas and transforming them into trees. The main feature of these large schemas is that they contain referential constraints. Then parsing these schemas becomes a difficult exercise. To cope with these constraints, we duplicate the segment which they refer to resolve their multiple contexts. We notice that most previous match systems focused on simple schemas without referential elements.

An XML schema is then modeled as a labeled unordered rooted tree. Each element or attribute of the schema is translated into a node. The child elements and attributes are translated into children of the element node. The names, types and constraints of elements and attributes represent the labels of the nodes.

We present the formal definition of basic XML tree concept.

Definition 1 (XML Tree). T= (r, N, E, φ) is a labeled unordered rooted tree, where r is the root, N is a set of nodes (elements or attributes), E is the set of edges, and φ is a labeling application $\varphi : N \rightarrow L$ assigning a label (element name, type or constraint) to each node of the tree, where L is the set of labels of nodes.

Definition 2 (Tree Size and Depth). T= (r, N, E, φ) is a labeled unordered rooted tree. The size of T, denoted |T| is the number of nodes in T. The depth of a node N is the number of ancestors of N. The root node is at depth zero.

Moreover, we parse the element names and gather them into sequences of tokens. A tokenizer identifies punctuation (e.g PARTY_ID→ <Party, ID>), special symbols, etc. We use WorldNet thesaurus to find synonym elements. This analysis allows the identification of the most relevant elements in the next step. These elements are then mapped into integer representation to make faster the mining process.

3.2 Identifying and Mining Frequent Sub-trees

The main goal of this phase is to decompose the input schemas into smaller ones. To this end, we identify and extract the common sub-structures from XML schemas describing the same domains. Then we distinguish between two sub-structures: inter and intra schemas structures.

- Inter-schemas: They are the common structures between different XML schemas. They represent an important source of structural and semantic information
- Intra-schemas: They are the frequent structures within an XML schema. Identifying such structures plays a key role for decomposition.

The problem of discovering these structures can be defined as follows:

Frequent Tree Mining. Given a set of trees F (also called the forest) and a user defined threshold σ, the problem is to find all the sub-trees *included* at least σ times in F. The solutions are called the frequent trees of F w.r.t. σ.

Definition 3 (Tree Inclusion). Let $T_1 = (r_1, N_1, E_1, \varphi_1)$ be a labeled unordered sub-tree and $T_2 = (r_2, N_2, E_2, \varphi_2)$ be a labeled unordered tree. T_1 is included into T_2 (noted $T_1 \subseteq T_2$) if there exists an injective mapping $\mathscr{M}: N_1 \rightarrow N_2$ that satisfies the following rules:

***R*₁** : $\mathscr{M}$ preserves the labels : $\forall u \in N_1$, $\varphi_1(u) = \varphi_2(\mathscr{M}(u))$ ($\varphi : N \rightarrow L$ is an application that assigns a label to each node).

***R*₂** : $\mathscr{M}$ preserves the parent (a) and ancestor relationship (b) :

(a) $\forall u, v \in N_1$, $(u, v) \in E_1 \Leftrightarrow (\mathscr{M}(u), \mathscr{M}(v)) \in E_2$

(b) $\forall u, v \in N_1$ si $(u, v) \in E_1 \Leftrightarrow (\mathscr{M}(u), \mathscr{M}(v)) \in E_2^{+}$

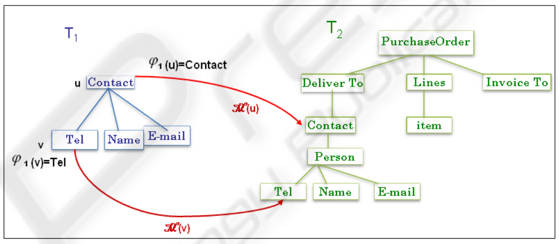


Figure 4: Example of tree inclusion.

We consider the tree inclusion as shown in Figure 4 $T_1 = (r_1, N_1, E_1, \varphi_1)$ and $T_2 = (r_2, N_2, E_2, \varphi_2)$ are two trees.

$T_1 \subseteq T_2$ means That:

*R*₁: $\exists u \in N_1 \mid \varphi_1(u) = \text{Contact} \Rightarrow \varphi_1(u) = \varphi_2(\mathscr{M}(u)) = \text{Contact}$

*R*₂: $\exists u, v \in N_1 \mid (u, v) \in E_1 \Leftrightarrow (\mathscr{M}(u), \mathscr{M}(v)) \in E_2^{+}$

The frequency is computed using the notion of *frequency support*. The support of a tree X is noted *Support(*X,F). The basic definitions of these concepts are listed as follows:

Definition 4 (Frequency Support). Let F = {T_1, T_2,… T_n} be a set of trees (or forest).

The *frequency Support* of a tree X noted *Support*(X,F) is defined as:

$$Support(X,F) = \sum_{i=1}^{n} intra\text{-}support(X,T_i)$$

Where *intra-support*(X, T_i) is the number of occurrence of X in T_i Note that this support definition considers both intra and inter-schemas.

Definition 5 (Frequent Tree). A tree X is said to be frequent in a forest F w.r.t. a minimum support threshold σ iff *Support*(X,F) $\geq \sigma$.

The set of all frequent trees of a forest is noted FT = $\{FT_1, FT_2, \ldots, FT_i\}$ and $FT_i = \{FT_{i1}, FT_{i2}, \ldots, FT_{in}\}$ represents the set of elements in the frequent tree FT_i

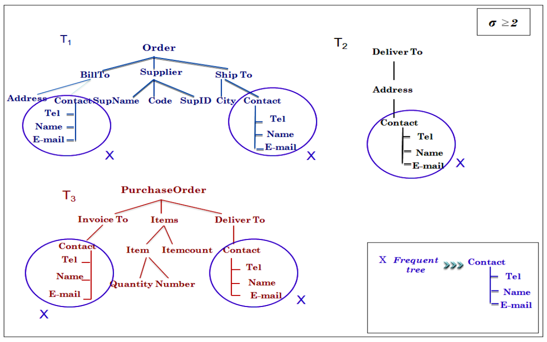


Figure 5: Example of frequent tree mining.

Figure 5 illustrates an example of frequent tree mining. For a threshold σ=2, the sub-tree X containing the nodes {Contact, Tel, Name and E-mail} appears in T_1, T_2 and T_3. The intra-support of X in T_1, T_2 and T_3 is respectively 2, 1 and 2. Consequently, *Support* (X, F) = 5 ◘ σ and X is a frequent tree FT.

We propose to use tree mining techniques to identify these common structures. More precisely, we use the algorithm proposed by (Termier et al., 2004). Tree mining is a classical pattern mining problem (an important class of data mining problem) which aims at discovering automatically sub-trees that appear frequently in a set of trees.

3.3 Relevant Frequent Sub-trees Calculus

The focus of this phase is to identify the sub-trees candidates for matching. This aims at reducing match effort by only matching relevant parts from the other schemas. These sub-schemas are then selected for matching.

This pre-matching phase includes two main steps:

3.3.1 Selection of Maximal Sub-trees

The goal of this operation is to find the maximal frequent trees to avoid redundant calculation between the same nodes. Our approach pruned out all the minimal ones (FT_{min}) (see Def. 6).

Definition 6 (Minimal Frequent Sub-tree). A frequent sub-tree is said to be minimal (FT_{min}) $\Leftrightarrow \neg\exists$ **FT** $\subseteq FT_{min}$ / **FT** is a frequent sub-tree

3.3.2 Finding Similar Sub-trees

The goal of this step is to identify the most similar sub-trees (FT_{Sim}) for matching. This is done in two phases:

a) Testing the Linguistic Similarity between Element Sub-trees to Find the Most Related Nodes

The objective is to find similar nodes between the frequent sub-trees. This similarity (Sim_{edit}) is done with the use of edit distance function (Cohen et al., 2003).

$Sim_{edit}\ (FT_{si},\ FT_{Tj}) = 1-\ (edit\_distance\ (FT_{si},\ FT_{Tj})\ /\ max\ (length\ (FT_{si}),\ length\ (FT_{Tj})))$

b) Computing the Similarity Measure between Frequent Trees:

Definition 7 (Frequent Tree Similarity). Let FT_S and FT_T two frequent trees source and target

N_c represents the set of all the common and similar element pairs between FT_S and FT_T : $N_c = \{(FT_{si}, FT_{Tj}) \mid Sim_{edit}\ (FT_{si}, FT_{Tj}) \geq 0.4\}$

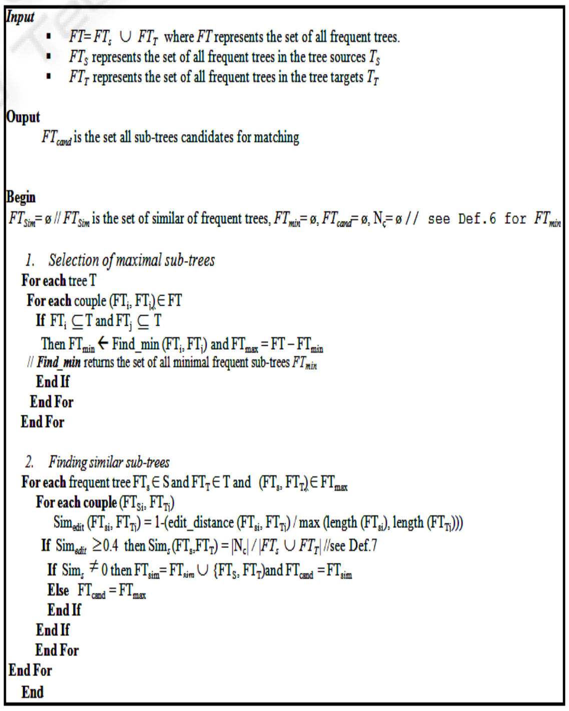
The similarity (Sim_s) between FT_s and FT_T is:

$$Sim_s\ (FT_S\ , FT_T\ )= \mid N_c\mid / \mid FT_s \cup FT_T \mid$$

where $Sim_s\ (FT_S\ , FT_T\ )$ value is included in [0,1].

$\mid N_c \mid$: represents the cardinality of N_c

3.3.3 Pre-matching Algorithm



```
Input
  ▪ $FT= FT_s \cup FT_T$ where FT represents the set of all frequent trees.
  ▪ $FT_S$ represents the set of all frequent trees in the tree sources $T_S$
  ▪ $FT_T$ represents the set of all frequent trees in the tree targets $T_T$

Ouput
    $FT_{cand}$ is the set all sub-trees candidates for matching

Begin
$FT_{Sim}$= ø // $FT_{Sim}$ is the set of similar of frequent trees, $FT_{min}$= ø, $FT_{cand}$= ø, $N_c$= ø // see Def.6 for $FT_{min}$

  1. Selection of maximal sub-trees
  For each tree T
   For each couple $(FT_i, FT_j) \in FT$
     If $FT_i \subseteq T$ and $FT_j \subseteq T$
      Then $FT_{min} \leftarrow$ Find_min $(FT_i, FT_j)$ and $FT_{max} = FT - FT_{min}$
   // Find_min returns the set of all minimal frequent sub-trees $FT_{min}$
     End If
    End For
  End For

  2. Finding similar sub-trees
  For each frequent tree $FT_s \in S$ and $FT_T \in T$ and $(FT_s, FT_T) \in FT_{max}$
     For each couple $(FT_{Si}, FT_{Tj})$
        $Sim_{edit} (FT_{si}, FT_{Tj}) = 1-(edit\_distance (FT_{si}, FT_{Tj}) / max (length (FT_{si}), length (FT_{Tj})))$
      If $Sim_{edit} \geq 0.4$ then $Sim_s(FT_s,FT_T) = |N_c| / |FT_s \cup FT_T|$ //see Def.7
       If $Sim_s \neq 0$ then $FT_{sim} = FT_{sim} \cup \{FT_S, FT_T)$ and $FT_{cand} = FT_{sim}$
       Else  $FT_{cand} = FT_{max}$
       End If
     End If
     End For
End For
  End
```

Figure 6: Pseudo-code of pre-matching phase.

3.4 Matching Sub-schemas

In this phase, the resulted sub-schemas of decomposition approach are selected for matching. Then matching large schemas is reduced to the matching of much smaller ones. For every pair of schemas of FT_{cand} set, we apply our matching algorithm called EXSMAL (Chukmol et al., 2005) to discover semantic and structural correspondences between pair of schema elements (figure 7). Our algorithm considers the element types, descriptions (basic similarity) and structural similarities. Structural similarity is very important because, the same element may appear in many different contexts, for example, DeliverTo.Address and BillTo.Address which should be differentiated for a correct matching.

Algorithm EXSMAL
Input: FT_S, FT_T : two XML sub-schemas source and target
Ouput: set of triplets < FT_{si} , FT_{Tj} , V_{sim}>
With FT_{si} , an element of FT_s,
FT_{Tj} , an element of FT_{Tj}
V_{sim} the similarity value between FT_{si} *and* FT_{Tj}

```
Begin
  Matching (FT_s, FT_T)
   {
  For each pair of elements < FT_si,FT_Tj >
      Compute {
                  Basic similarity value
                  Structural similarity value
                  Pair-wise element similarity value
              }
  Filter: eliminate the element pairs having their V_sim below
  an acceptation threshold value
  }
End
```

Figure 7: Short description of EXSMAL algorithm.

4 EVALUATION

We conducted our experiments on real XML schemas (XCBL[1] and OAGIS[2]). XCBL (XML Common Business Library) is a set of XML schemas for business-to-business e-commerce. The standard OAGIS (Open Application Group Inc.) represents a set of business process schemas. The main goal of our experiments is to show that our approach deals with both *quality* and *performance* of large schema matching. We have implemented the XML schema parser, the decomposition approach in our PLASMA (Platform for LArge Schema MAtching) prototype. Firstly, we evaluate the performance of schema parsing comparing to COMA++ tool and schema matching execution. Secondly, we determine the quality of matching that we use to compare with fragmentation results of COMA++ tool.

Experimental Environment. Our experiments were conducted on a Windows machine with a 2.80GHz Intel Pentium and 2Go RAM.
Table 1 summarizes the major characteristics E-business schemas

Table 1: Characteristics of E-business schemas.

XCBL and OAGIS schemas	Smallest/ Largest schema size (number of elements)	Min/Max depth	Average schema size	Number of schemas
Medium	116-143	10-11	130	5
Large	554-708	12-14	631	10
Very Large	1339-3796	16-19	2568	25

[1] www.xcbl.org, [2]www.oagi.org

4.1 Parsing XML Schemas Evaluation

We have evaluated the time elapsed in loading and parsing XML schemas by our parser implemented within PLASMA and compared in the same conditions with the time elapsed by COMA++. This experience was done on medium schemas with 245 elements (154ko), large schemas with 630 elements (330ko) and very large with 3796 elements (950ko). Parsing schemas depends on elements number and on files size. Figure 8 illustrates these results showing clearly a better performance of the PLASMA parser. In fact, COMA++ loads schemas in a repository before parsing. This step is very low and can spent several minutes for very large schemas.

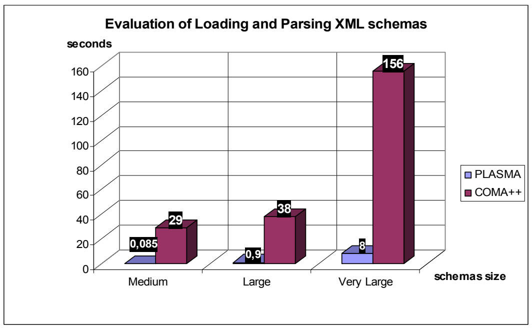


Figure 8: Parsing XML schemas by PLASMA and COMA++.

4.2 Performance of Decomposition Approach

We have evaluated the performance of the decomposition approach applied on different size of schemas (medium, large and very large) and compare it with the approach without decomposition (direct matching with EXSMAL). The performance is described in terms of the *execution time gain* (figure 9) defined as follows:

$$Execution\_time\_gain = \frac{time\_execution\_without\_decomposition - time\_execution\_decomposition}{time\_execution\_without\_decomposition}$$

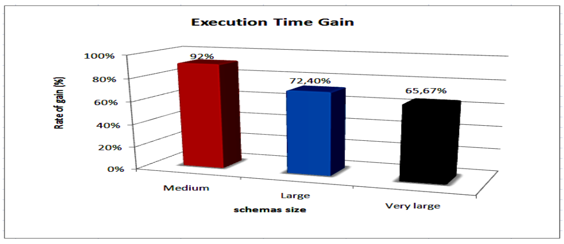


Figure 9: Execution time gain with decomposition approach.

We have observed that using our decomposition approach, we optimize the EXSMAL matcher's execution (e.g 65.67% for the very large schemas). Note that, in our experimentations, the execution time of the tree mining algorithm is only few seconds.

4.3 Quality of Matching

To determine the quality of a decomposition approach, we use the three metrics namely precision, recall and f-measure (Do et al., 2002). We compared our decomposition results with those of fragmentation COMA++ approach. PLASMA and COMA ++ have been tested within the same experimental conditions. Furthermore, COMA ++ is configured to be as close as possible to PLASMA.

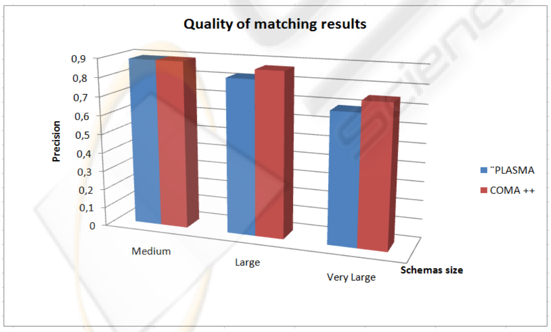


Figure 10: Precision obtained by decomposition approach in PLASMA and fragmentation approach in COMA++.

Figure 10 shows the precision for the PLASMA decomposition and COMA++ fragmentation approaches. In the medium schemas, PLASMA and COMA++ achieve a higher precision value. However, precision decreases with growing schema size.

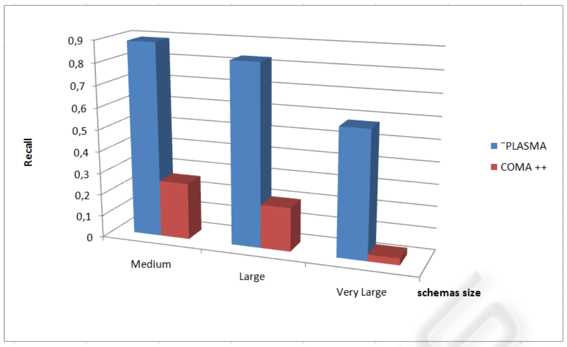


Figure 11: Recall obtained by decomposition approach in PLASMA and fragmentation approach in COMA++.

Figure 11 depicts the recall of the both matching strategies in PLASMA and COMA++. The results proved that our decomposition approach outperforms the fragmentation approach. This is due to limitation of the fragmentation approach to find only the shared fragments (or intra-schemas). Unlike our approach, fragmentation does not cover all the possible matches. F-measure is given in figure 12. Due to its previous recall results, COMA++ obtains a lowest f-measure than PLASMA.

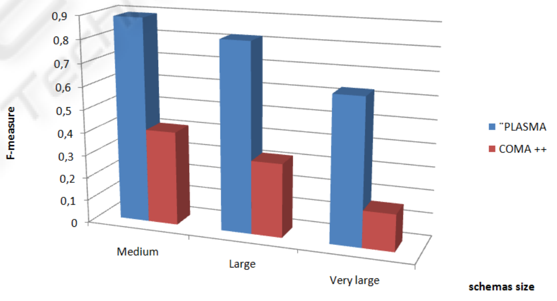


Figure 12: F-measure obtained by decomposition approach in PLASMA and fragmentation approach in COMA++.

5 CONCLUSIONS

In this paper we have proposed a decomposition approach as a first attempt to reduce large scale matching problem. Our approach identifies common structures between and within XML schemas and tries to break down these input schemas. Our aim is to find the most similar sub-schemas between large input schemas using scalable and efficient techniques. Then we have described the way to effectively decompose large XML schemas using tree mining and our proposed pre-matching algorithms. The originality of our work w.r.t.

existing approaches is the techniques used to decompose several schemas at once in a scalable and automatic manner. Our experiments confirm that the most of schemas from the same sub-domains share an important rate of common structures and matching is more efficient. Moreover, experiments show that decomposition approach provides a better quality of matching in comparison to the fragmentation approach in COMA++.

In the future, we plan to do further experiments with more XML schemas and complete our PLASMA system implementation with Wordnet and edit distance function.

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