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<tr>
<th>Title(English)</th>
<th>SLAX: An Improved Leaf-Clustering Based Approximate XML Join Algorithm for Integrating XML Data at Subtree Classes</th>
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XML is widely applied to represent and exchange data on the Internet. However, XML documents from different sources may convey nearly or exactly the same information but may be different on structures. In previous work, we have proposed LAX (Leaf-clustering based Approximate XML join algorithm), in which the two XML document trees are divided into independent subtrees and the approximate similarity between them are determined by the tree similarity degree based on the mean value of the similarity degrees of matched subtrees. Our previous experimental results show that LAX, comparing with the tree edit distance, is more efficient in performance and more effective for measuring the approximate similarity between XML documents. However, because the tree edit distance is extremely time-consuming, we only used bibliography data of very small sizes to compare the performance of LAX with that of the tree edit distance in our previous experiments. Besides, in LAX, the output is oriented to the pair of documents that have larger tree similarity degree than the threshold. Therefore, when LAX is applied to the fragments divided from large XML documents, the hit subtree selected from the output pair of fragment documents that has large tree similarity degree might not be the proper one that should be integrated. In this paper, we propose SLAX (Subtree-class Leaf-clustering based Approximate XML join algorithm) for integrating the fragments divided from large XML documents by using the maximum match value at subtree classes. And we conduct further experiments to evaluate SLAX, comparing with LAX, by using both real large bibliography and bioinformatics data. The experimental results show that SLAX is more effective than LAX for integrating both large bibliography and bioinformatics data at subtree classes.

1. Introduction

The Extensible Markup Language (XML) is widely applied to represent and exchange data on the Internet, because it can represent different kinds of data from multiple sources. Nowadays more and more data, especially bioinformatics such as Swiss-Prot, TrEMBL and bibliography data such as DBLP and ACM SIGMOD Record, are published and exchanged by XML on the Internet. However, XML documents from different data sources might contain nearly or exactly the same information but might be constructed by different structures. Besides, even the two XML documents convey the same contents, both of them may have some extra information what the other does not do. Therefore, it becomes important that an algorithm can efficiently measure the similarity between XML documents for integrating such data sources so that the users can conveniently access and acquire more complete information.

The Document Type Descriptor (DTD) is recognized as a helpful tool to detect the structural information from XML documents. However, even if XML documents have the same DTDs, they may not have identical tree structures because of the repeating and optional elements and attributes. Figure 1 shows an example of two XML documents (sample fragments from the XML files of Swiss-Prot and TrEMBL, respectively) with very similar DTDs. Although these two documents are structurally different due to the repeating and optional elements, they express very similar information. Besides, each of the document has some information what the other does not do. For instance, comment in Fig. 1(a); and evidence in Fig. 1(b).

The tree edit distance is widely used as an effective metric for measuring the structural similarity between XML documents. However, it is a very expensive operation; in the worst case, the time complexity is $O(n^4)$ for the document of size $n$, where $n$ is the number of the nodes of the document.

In previous work, we have proposed LAX...
Fig. 1 Example XML documents.

(Leaf-clustering based Approximate XML join algorithm), in which the two XML document trees are divided into subtrees representing independent information units, and the output is oriented to the pair of documents that has larger tree similarity degree than the user-defined threshold. We have also proposed an effective algorithm for segmenting XML documents into independent subtrees for LAX. We have shown that LAX is more efficient in performance comparing to the tree edit distance, because it is an \( O(n^2) \) operation for the document of size \( n \) in the worst case. Because the tree edit distance is extremely time-consuming, we only used bibliography data of very small sizes to compare the performance of LAX with that of the tree edit distance in our previous experiments. In addition, in order to compare with the work based on the tree edit distance \(^9,10\), the output of LAX is oriented to the pair of documents that have larger tree similarity degree (mean value of the similarity degrees of matched subtrees) than the threshold. The large XML documents sometimes can not be loaded into the main memory, they must be divided into small fragments. In this case, the target subtrees are distributed in each fragment document. Therefore, when LAX is applied to such fragment documents, the hit subtrees selected from the output pair of fragment documents that has large tree similarity degree might not be the proper one that should be integrated.

In this paper, we propose SLAX (Subtree-class Leaf-clustering based Approximate XML join algorithm) to integrate fragments divided from large XML documents by using the maximum match value at subtree classes. We conduct further experiments to compare SLAX with LAX on the performance and effectiveness by using both large real bibliography and bioinformatics data. The experimental results indicate that the precision of subtree matching using SLAX is twice larger than that using LAX for bibliography data. And SLAX is useful and valuable for people to acquire similar proteins belonging to the same species, organisms, and so on, even if the two XML documents do not contain exactly the same proteins.

The rest of this paper is organized as follows. Section 2 briefly introduces the work related to the paper and the requirements for the issues of measuring approximate similarity between XML documents. In Section 3, we introduce the basic knowledge of LAX. Section 4 describes the problem of LAX when it handles fragments divided from large XML documents and proposes SLAX for solving this problem. In Section 5, we conduct experiments to compare SLAX with LAX by using both large real bioinformatics and bibliography data. In the end, Section 6 concludes the paper and outlines the future work.

2. Related Work and Requirements

A well formed XML document can be parsed into an ordered labeled tree \(^{19}\). The tree structure represents the nesting of its elements, and node labels record the contents of the elements by element tags, attribute names, attribute values and PCDATA values.

Many researches have been done to solve the problem of measuring the edit distance between ordered labeled trees \(^{3,5,8,12,14,16,18,23,25}\). The edit distance between two ordered labeled trees is defined as the minimum cost edit operations (insertions, deletions and substitutions) required to transform one tree to another. It can be figured out by a mapping between the nodes of the two trees \(^{25}\). The tree edit distance is regarded as an effective metric for measuring the structural similarity in XML documents \(^{8,9,13}\). However, its computational cost is extremely expensive; in the worst case, it is an \( O(n^4) \) operation for the document of size \( n \). Thus, it is of difficulty for the tree edit distance to handle the XML documents of large sizes.

In order to avoid the expensive tree edit
distance operation as much as possible, S. Guha, et al. proposed the lower and upper bound as inexpensive substitutions for the tree edit distance operation. However, when the upper bound is greater than the threshold distance \( \tau \) and meanwhile the lower bound is less than \( \tau \), the tree edit distance will still must be calculated. Therefore, we need a more efficient metric for measuring the approximate similarity between XML documents. As the matter of fact, many real XML documents are constructed by repeating elements, entry in the uniprot_sprot.xml and uniprot_tremb.xml for example. Such kind of XML documents can be segmented into subtrees representing independent units by rooting the subtrees at the repeating elements. The approximate similarity between the well-segmented documents can be effectively determined by computing the similarity degree based on the clustered leaf nodes of each pair of subtrees even without considering the structural and semantic heterogeneity.

3. Introduction of LAX

3.1 Overview

In previous work, we have proposed LAX for evaluating the approximate similarity between XML documents. In LAX, the two XML documents to be joined are segmented into subtrees representing independent information units. And the approximate similarity between them are determined by the tree similarity degree that is the mean value of the similarity degrees of the matched subtrees.

Notation. Let \( T_1 \) and \( T_2 \) be two XML document trees. Let \( T_1 \) be the base tree, and \( T_2 \) be the target one. Assume \( T_1 \) and \( T_2 \) are segmented into \( k_1 \) and \( k_2 \) sub-trees \( t_{1i} \) (\( 1 \leq i \leq k_1 \)) and \( t_{2j} \) (\( 1 \leq j \leq k_2 \)), respectively.

The subtree similarity degree between \( t_{1i} \) and \( t_{2j} \), \( S_S(t_{1i}, t_{2j}) \), is defined by Equation (1) as the percentage of the number of matched leaf nodes (the pair of leaf nodes that has the same PCDATA value) out of the number of leaf nodes in the base subtree \( t_{1i} \), where \( n \) and \( n_{1i} \) denote the number of matched leaf nodes and the number of leaf nodes in the base subtree \( t_{1i} \).

\[
S_S(t_{1i}, t_{2j}) = \frac{n}{n_{1i}} \times 100 \, \% \tag{1}
\]

The matched subtree, \( T_M[i] \), is defined as the pair of subtrees that has the maximum subtree similarity degree in one join loop; that is, the similarity degree of \( T_M[i] \), \( S_M[i] \), can be calculated as follows.

\[
S_M[i] = \max_{j=1}^{k_2}(S_S(t_{1i}, t_{2j})) \tag{2}
\]

In the \( i \)th join loop, the matched subtree \( T_M[i] \) is a hit subtree, iff \( S_M[i] \geq \tau \) (\( 0 < \tau \leq 1 \)), where \( \tau \) is the user defined threshold for the output subtrees.

The tree similarity degree between \( T_1 \) and \( T_2 \), \( S_T(T_1, T_2) \), is determined by Equation (3) based on the mean value of the similarity degrees of matched subtrees.

\[
S_T(T_1, T_2) = \frac{\sum_{i=1}^{k_1} S_M[i]}{k_1} \times 100 \, \% \tag{3}
\]

3.2 Segmentation Algorithm

Many real XML documents are constructed by repeating elements, and they can be divided into independent subtrees at the repeating elements. However, there might be many different repeating elements with the same tag names in different levels. For instance, entry and name in Fig.1(a). Therefore, it is not an easy task to segment the XML document tree into subtrees at the proper positions. In previous work, we have proposed an effective algorithm for segmenting XML document trees, in which the spot for segmentation is determined by the weighting factor \( w \). For a candidate element \( E(n, d) \), where \( n \) denotes the number of candidate elements among its children, and \( d \) represents the the distance to its furthest descendant. The weighting factor \( w \) can be calculated by the following equation,

\[
w = n \times d^\theta \quad (0 < \theta \leq 1) \tag{4}
\]

where, \( \theta \) is an adjustable constant.

3.3 Join Process

Let \( S_1 \) and \( S_2 \) be two XML data sources. Assume each document \( d_1 \in S_1 \) and \( d_2 \in S_2 \) are parsed into XML document trees \( T_1 \) and \( T_2 \). Let \( T_1 \) and \( T_2 \) be segmented into \( k_1 \) and \( k_2 \) subtrees \( t_{1i} \) and \( t_{2j} \). Given a user-defined threshold \( \tau \), the join process of LAX is illustrated by Algorithm LAX shown in Fig.2.

3.4 Comparison with Tree Edit Distance

For the document of size \( n \), in the worst case, LAX is an \( O(n^2) \) operation while the tree edit distance is an \( O(n^4) \) one. Our previous experimental results indicate that as the size of document increases, LAX becomes overwhelmingly faster relative to the tree edit distance. As for two XML documents with different DTDs that have the same number of nodes, the tree
edit distance of them will not increase much when the PCDATA values of the leaf nodes change. While in LAX, the tree similarity degree will change in a large scale as the values of the leaf nodes change. Our previous experimental results show that LAX can effectively distinguish the similarity differences between XML documents even the tree edit distances of them are almost the same.

4. SLAX

4.1 Problem of LAX

In this paper, we just use the original real large XML documents without storing them into RDBs. When the XML documents are too large to be loaded into the main memory, they must be divided into small fragments. In this case, the target subtrees are distributed in each fragment document. Besides, in LAX, the output is oriented to the pair of documents that have larger tree similarity degree (mean value of the similarity degrees of matched subtrees) than the threshold. Therefore, when LAX is applied to such fragment documents, the hit subtrees selected from the output pair of fragment documents that has large tree similarity degree might not be the proper one that should be integrated.

Example 1. For the base document tree $T_{B1}$, and the target ones $T_{T1}$ and $T_{T2}$ divided from a large XML document tree $T_T$ in Fig. 3, the tree similarity degrees $S_T(T_{B1}, T_{T1}) = 66.7\%$ and $S_T(T_{B1}, T_{T2}) = 50\%$. Assume the threshold for the output $0.5 < \tau \leq 0.667$, and the threshold for the hit subtree $T \leq 0.667$. Because $S_T(T_{B1}, T_{T1}) = 66.7\% > \tau > S_T(T_{B1}, T_{T2}) = 0.5$, the document tree pair $(T_{B1}, T_{T1})$ will be output. Therefore, the subtree pair $(t_{B12}, t_{T12})$ $(S_S(t_{B12}, t_{T12}) = 66.7\% > T)$ will be selected as the hit subtree by LAX. However, the most proper subtree pair is actually the $(t_{B12}, t_{T21})$, because $S_S(t_{B12}, t_{T21}) = 100\% > S_S(t_{B12}, t_{T12}) = 66.7\%$.

4.2 Key Definitions for SLAX

Before we propose the improved algorithm SLAX to solve the problem mentioned in Section 4.1, we present the following notations and definitions.

Definition 1 (Match Value). The match value $M[n]$ for the subtree $t_{Bmi}$ and each target tree $T_{Tn}$ $(1 \leq n \leq L)$ is defined as the following equation.

$$M[n] = \max_{j=1}^{k_T} (S_S(t_{Bmi}, t_{Tnj})) \quad (5)$$

Definition 2 (Maximum Match Value). The maximum match value $M_M[i]$ for the sub-
Definition 4 (Matched Pair). Let $t_B$ and $t_T$ be two XML data sources, and each $d_B[i] \in S_B$ and $d_T[i] \in S_T$ be parsed into XML document trees $T_B[i]$ and $T_T[i]$. Assume $T_B[i]$ and $T_T[i]$ are segmented into $k_B[i]$ and $k_T[i]$ subtrees $t_{B[i]}$ and $t_{T[i]}$, respectively. The matched pairs $P_i$ and $P_j$ of the subtree $T_B[i]$ and $T_T[j]$ are the hit pairs and should be output as the final results.

4.3 Algorithm SLAX

Let $S_B$ and $S_T$ be two XML data sources, and each $d_B[i] \in S_B$ and $d_T[i] \in S_T$ be parsed into XML document trees $T_B[i]$ and $T_T[i]$. Assume $T_B[i]$ and $T_T[i]$ are segmented into $k_B[i]$ and $k_T[i]$ subtrees $t_{B[i]}$ and $t_{T[i]}$. Given a user-defined threshold $T$, the algorithm SLAX is illustrated by Fig. 4.

![Algorithm SLAX](image)

Example 2. For the base tree $T_{B1}$ and the target ones $T_{T1}$ and $T_{T2}$ in Fig. 3, The matched trees $T_{M1}$ and $T_{M2}$ for the subtree $T_{B1}$ and $T_{B12}$ are $T_{T1}$ and $T_{T2}$, respectively. And the matched pairs $P_1$ and $P_2$ of the subtree $T_{B11}$ and $T_{B12}$ are $(t_{B11}, t_{T11})$ and $(t_{B12}, t_{T21})$, respectively. Assume $T < 0.667$, both of the matched $P_1$ and $P_2$ are the hit pairs and should be output as the final results.

4.4 Comparison with LAX

The main differences between the improved algorithm SLAX and the original one LAX are summarized as follows:

- **Application Object** The application object for LAX is to measure the approximate similarity between XML documents, while that for SLAX is to detect the subtrees that represent the same or similar information in XML documents from different sources, so that the XML documents can be integrated at subtree classes.

- **Join Base and Target** The join base and target for LAX are oriented to XML documents, while those for SLAX are subtree-oriented.

- **Basis for Subtree Matching** In LAX, the subtree matching must be selected from the pair of XML documents that has larger tree similarity degree than the threshold. While in SLAX, the subtree matching is directly based on the maximum match value for the base subtree and the target one.

5. Experimental Evaluation

In our previous experiments\(^{11}\), we have compared the performance of LAX with the tree edit distance for measuring the approximate similarity between XML documents. Because the tree edit distance is extremely time-consuming, we only used very small bibliography XML documents; the mean size of the fragment files of SIGMOD Record\(^1\) and DBLP\(^2\) we used was 4.32 KB (about 200 nodes). In this paper, we conduct experiments to compare SLAX with LAX by using different types of large XML data. We should have compared SLAX and LAX with the tree edit distance. However, the tree edit distance is too time-consuming to be applied to the large data. But anyway, our previous experimental results have shown that LAX is more efficient and effective for measuring the approximate similarity between XML documents than the tree edit distance even for small data\(^{11}\).
In order to observe and compare how effectively SLAX and LAX determine the matched subtree by using the maximum match value and the tree similarity degree, respectively, we define the precision of subtree matching, $P$ as follows.

**Definition 6 (Precision of Subtree Matching).** The precision of subtree matching ($P$) is the percentage of the number of correctly matched subtree ($N_c$) out of the total number of subtrees ($N$) in the base document as the following equation.

$$P = \frac{N_c}{N} \times 100(\%) \quad (7)$$

We use both real bibliography and bioinformatics data that are more than 100 times larger of sizes to evaluate SLAX and LAX in the following aspects.

- How do the document size and the number of the segmented subtrees impact the execution time of SLAX and LAX for different types of large XML data?
- What is the difference in the characteristic and performance for SLAX and LAX to integrate different types of large XML data?
- What is the difference in the precision of subtree matching for bibliography documents using the maximum match value and the tree similarity degree, respectively?

### 5.1 Data Used

#### 5.1.1 Bibliography Data

The main characteristic of the bibliography document is that the number of leaf nodes of each segmented subtree is small. A bibliography XML document can be generally divided into a large number of subtrees representing a literature item such as an article and a book. The size of each subtree in the bibliography document is quite small. For example, the mean number of leaf nodes of an segmented subtree in SigmodRecord.xml is only 5.8. In our experiments, we use SigmodRecord.xml (482 KB, about 20,000 nodes) and 955 fragments divided from DBLP.xml into fragment files. The size of each fragment of SigmodRecord.xml is 3 MB (about 80,000 nodes). We randomly sample 100 base subtrees from SigmodRecord.xml to compose a document, named sigmod.xml, using the same DTD as SigmodRecord.xml. Then, we join the sigmod.xml with the 955 fragments of DBLP.xml by using the tree similarity degree and maximum match value, respectively. The number of correctly matched subtrees ($N_c$), the number of incorrectly matched subtrees ($N_i$) and the precision of subtree matching ($P$) using LAX and SLAX are shown in Table 2.

#### 5.1.2 Bioinformatics Data

Comparing with the bibliography data, bioinformatics data, such as protein data, contains a lot of information in each entry. Therefore, the size of each segmented subtree becomes much larger in the bioinformatics data. For instance, the mean number of leaf nodes of a 3 MB fragment of uniprot_sprot.xml$^{20}$ is 42.4.

Because the original protein XML documents are too big to be loaded into the main memory, we divide the uniprot_sprot.xml$^{20}$ and uniprot_trembl.xml$^{21}$ into fragment files. The size of each fragment of uniprot_sprot.xml$^{20}$ is 3 MB (about 80,000 nodes), and that of uniprot_trembl.xml$^{21}$ is 1 MB (about 25,000 nodes).

### 5.2 Experimental Environment

The experiments have been done under the environment shown in Table 1.

### 5.3 Experimental Results

#### 5.3.1 Bibliography Data

For the bibliography data, we take the SigmodRecord.xml as the base document, and all the 955 fragments of DBLP.xml, named DBLP1.xml-DBLP955.xml as the target ones. The number of segmented subtrees of the SigmodRecord.xml is 1504, and the mean number of those of the DBLP fragment files is 640. The mean execution time for handling each pair of documents by SLAX is 3.77 seconds.

We randomly sample 100 base subtrees from SigmodRecord.xml to compose a document, named sigmod.xml, using the same DTD as SigmodRecord.xml. Then, we join the sigmod.xml with the 955 fragments of DBLP.xml by using the tree similarity degree and maximum match value, respectively. The number of correctly matched subtrees ($N_c$), the number of incorrectly matched subtrees ($N_i$) and the precision of subtree matching ($P$) using LAX and SLAX are shown in Table 2.

Here we show a real example of mismatching using LAX. We use SigmodRecord.xml as the base document, and randomly choose 40 fragments of DBLP.xml as the target ones. Figure 5 shows the match values for the sample subtree and each fragment of DBLP.xml, and Figure 6 shows the source code of a sub-

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1) SigmodRecord.xml
20) uniprot_sprot.xml
21) uniprot_trembl.xml
Fig. 5 Match values for the sample subtree and dblp1.xml-dblp40.xml.

Fig. 6 Sample subtree from sigmod.xml.

Fig. 7 The matched subtree selected by SLAX from dblp24.xml.

tree sampled from SigmodRecord.xml. The matched subtree for the sample subtree is selected by SLAX from dblp24.xml because of the maximum match value, and its source code is shown in Fig. 7. It is evident that the matched subtree determined by SLAX represents exactly the same article as the sample subtree. Figure 8 shows the tree similarity degrees for SigmodRecord.xml and each fragment of DBLP.xml. Because the tree similarity degree between dblp14.xml and SigmodRecord is the largest among the 40 fragments, the number of hit pairs in dblp14.xml is larger than those in dblp24.xml; that is the number of similar subtrees in dblp14.xml is larger than that in dblp24.xml. However, the source code in Fig. 9 shows that the matched subtree determined by LAX from dblp14.xml is not exactly the same article as the sample one but written by the same authors.

5.3.2 Bioinformatics Data
In order to learn how the document size and the number of segmented subtrees impact the execution time for SLAX and LAX, we randomly choose 5 fragments of uniprot_treml.xml, named trembl1.xml-trembl5.xml, and join them with 40 fragments of uniprot_sprot.xml, named sprot1.xml-sprot40.xml. N, T_S and T_L in Table 3 indicate the number of subtrees in trembl1-5.xml and the mean execution time to join a pair of fragment files by SLAX and LAX, respectively.

Because the documents from TrEMBL and Swiss-Prot do not contain exactly the same protein information, it is difficult to quantitatively define the precision of subtree matching for the protein data without expert knowledge. Therefore, in this paper we only conduct experiments to verify if our algorithm can find the similar protein from the target fragments for a
sample protein in the base fragment.

We choose trembl4.xml as the base document and sprot1.xml-sprot40.xml as the target ones. The number of segmented subtrees of trembl4.xml is 414 and the mean number of those of sprot1-40.xml is 387. Figure 10 shows the source code of the base subtree sampled from trembl4.xml, and Fig. 11 indicates the match values for the sample subtree and sprot1-40.xml. The matched subtree for the sample one will be selected from sprot31.xml by SLAX. Figure 12 shows the source code of the matched subtree determined by SLAX.

Figure 10 and Fig. 12, we can observe that the matched subtree pair determined by SLAX represents very similar proteins belonging to the same organism. In respect of LAX, the tree similarity degrees for trembl4.xml and sprot1-40.xml are shown in Fig. 13. Figure 14 shows the source code of the matched subtree for the sample one selected by LAX from sprot22.xml.

It is apparent that the matched subtree determined by LAX is totally a different protein corresponding to the base one. Although the matched pairs for protein data selected by SLAX sometimes may not denote exactly the same proteins, it is still helpful and valuable for people to obtain the group of proteins belonging to the same species, organisms, and so on.

5.4 Discussion and Comparison

According to the results of the experiments, we outline the following discussions and comparisons to summarize the characteristics and the differences of SLAX and LAX when they handle different types of large XML documents.

- From Table 3 and Fig. 15, we can observe that SLAX is slightly faster than LAX. Besides, the execution time for joining a pair of documents for both SLAX and LAX increases tardily as the number of segmented subtrees increases. With regard to the impact of document sizes, the integration of large documents might be faster than
Fig. 14 The Matched subtree selected by LAX from sprot22.xml.

Fig. 15 Execution time for joining a pair of bioinformatics fragments.

that of small ones. For example, the total mean size of SigmodRecord.xml and DBLP fragment files is about 0.8 MB and that of the protein fragment files is about 4.0 MB. However, the mean time for handling the protein data by SLAX is 3.63 seconds while that for processing the bibliography data is 3.77 seconds. It takes less time for SLAX to handle the protein data, because the number of segmented subtrees of bibliography data is much larger than that of the protein data.

- We can easily find the maximum peak (maximum match value) from Fig. 5 and Fig. 11 for both bibliography and bioinformatics data. While it is of difficulty to discriminate the max peak from Fig. 8 and Fig. 13, because there are many peaks that have very close tree similarity degrees with the maximum one. Therefore, the most proper matched subtree sometimes does not exist in the maximum peak but other peaks having the close value to the maximum one.

- For the bibliography data, the similarity degree of subtrees with smaller number of leaf nodes are easier to be the same because of the smaller $n_{11}$ in Eq. (1). Therefore, it may happen to get multiple subtrees that have the same similarity degree. On the other hand, the maximum match value for the hit subtrees for bioinformatics data might be small because of the large number of leaf nodes in each subtree.

- SLAX can more precisely detect the proper matched subtree for integrating the fragments divided from large XML documents than LAX. For the bibliography data, SLAX can effectively detect the matched subtree that contains exactly the same information as the base one. The precision of subtree matching using SLAX is twice larger than that using LAX. For the protein data, SLAX is useful and valuable for people to acquire similar proteins belonging to the same species, organisms, and so on, even the two XML documents do not contain exactly the same proteins. Therefore, we consider that SLAX is applicable and effective for integrating both large bibliography and bioinformatics data at subtree classes.

6. Conclusions and Future Work

As more and more data are increasingly represented and exchanged by XML on the Internet, a method that can efficiently measure the approximate similarity between XML documents for integrating multiple XML data sources becomes more important. We have proposed LAX (Leaf-clustering based Approximate XML join algorithm) in previous work, in which the two XML document trees are segmented into subtrees representing independent units, and the output is oriented to the pair of documents that has larger tree similarity degree than the user-defined threshold.

In this paper, we have proposed SLAX by using the maximum match value for integrating the fragments divided from large XML documents at subtree classes. We have done experiments to evaluate SLAX, comparing with LAX, by using both real large bibliography and bioinformatics data. Our experimental results indicate that the precision of subtree matching us-
ing SLAX is twice larger than that using LAX for bibliography data. And SLAX is useful and valuable for people to acquire similar proteins belonging to the same species, organisms, and so on, even if the two XML documents do not contain exactly the same proteins. Therefore, We consider that SLAX performs more effectively than LAX for integrating both large bibliography and bioinformatics data at subtree classes.

Due to the limitation of the main memory, we plan to do further experiments for evaluating LAX and SLAX by using different types of large XML data stored RDBs. We are also going to improve the segmentation algorithm for handling more complex XML data. Besides, the semantic heterogeneity is to be taken into account to improve the precision of our algorithms.

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