Exploring Lattice Structures in Mining Multi-Domain Sequential Patterns

Zhung-Xun Liao and Wen-Chih Peng
Department of Computer Science
National Chiao Tung University
Hsinchu, Taiwan, ROC
E-mail:{wcpeng, g9113}@cs.nctu.edu.tw

ABSTRACT

Since sequential patterns may exist in multiple sequence databases, we propose algorithm PropagatedMine+ to efficiently discover multi-domain sequential patterns. Prior works have shown that algorithm PropagatedMine outperforms other methods. In this paper, by exploring lattice structures, we develop algorithm PropagatedMine+ for propagating. Note that the lattice structure provides some guidelines when mining sequential patterns in other domain databases. Thus, exploiting the lattice structure devised could further reduce the number of candidate patterns, thereby improving the performance of mining sequential patterns across multiple domain sequence databases. A comprehensive performance study is conducted and experimental results show the scalability and the efficiency of algorithm PropagatedMine+.

1. INTRODUCTION

Existing sequential pattern mining algorithms [1][2][3] only discover the sequential behavior (e.g., buying behavior) in one domain, which are not sufficient. One would like to discover sequential patterns across multiple domains. Such a sequential pattern across multiple domains is referred to as a multi-domain sequential pattern [4]. Consider a mobile computing environment, where mobile users can access three services (i.e., location tracking service, data searching service, and credit payment service) via mobile devices and each service is referred to one domain. Thus, exploiting the lattice structure devised could further reduce the number of candidate patterns, thereby improving the performance of mining sequential patterns across multiple domain sequence databases. A comprehensive performance study is conducted and experimental results show the scalability and the efficiency of algorithm PropagatedMine+.

Table 1: An example of a multi-domain sequential pattern.

<table>
<thead>
<tr>
<th></th>
<th>(A)</th>
<th>(B, C)</th>
<th>(D)</th>
</tr>
</thead>
<tbody>
<tr>
<td>Location tracking</td>
<td>(1, 2)</td>
<td>(3, 4, 5)</td>
<td>(6, 7)</td>
</tr>
<tr>
<td>Search</td>
<td>(1, 2)</td>
<td>(3, 4, 5)</td>
<td>(6, 7)</td>
</tr>
<tr>
<td>Payment</td>
<td>(α, β)</td>
<td>(γ)</td>
<td>(θ, δ)</td>
</tr>
</tbody>
</table>

Table 1: An example of a multi-domain sequential pattern.

then moves to area \(B, C\), searches data \(3, 4, 5\), and buys goods \(γ\); and finally moves to area \(D\), searches data \(6, 7\), and buys goods \(θ, δ\). Such a sequential pattern consists of sequences across multiple domains and provides more information to analyze user behaviors.

2. CHALLENGES

Table 2 depicts multiple domain sequence databases and each domain sequence database is stored individually. Notice that time instance sequences represent the occurred time slots for the corresponding sequences in each domain sequence database. The prior work [4] has formulated the problem of mining sequential patterns across multiple domain sequence databases. Therefore, the main challenge is to discover sequential patterns across multiple sequence databases without joining every domain sequence database via time instance sequences.

3. ALGORITHM PROPAGATEDMINE+

The prior work in [4] developed algorithm PropagatedMine to propagate sequential patterns mined to other domain sequence databases. Though algorithm PropagatedMine is able to outperform other methods, the cost of propagating sequential patterns could be further reduced. Thus, in this paper, we propose algorithm PropagatedMine+. The same to the work in [4], algorithm PropagatedMine+ consists of two phases: the mining phase and the deriving phase. In the mining phase, algorithm PropagatedMine+ utilizes existing sequential pattern mining algorithms to discover sequential patterns in a starting domain and then propagates time instance sets of only 1-sequences (referred to as atomic patterns) to next domains. However, the sequential patterns in the starting domain are represented as the lattice graph structure to facilitate the generation of candidates and provide guidelines for mining multi-domain sequential patterns. For example, assume that the starting domain is set to \(D_1\) in Table 2. Those sequential patterns mined are represented as a lattice structure shown in Figure 1, where each node...
represents a sequential pattern and the linkages of nodes (standing for intra-domain links) represent itemset relationships. Furthermore, those nodes having the same number of elements are further arranged level-by-level. Explicitly, it can be seen in Figure 1 for the nodes with their number of elements is 1; these nodes are put level-by-level in increasing order of length of sequences.

**Definition 1 (Propagated table):** Let $M$ be a multi-domain sequential pattern across $k$ domain sequence databases with $TIS(M) = \{<T_{S_1}: t_1>,<T_{S_2}: t_2>,...,<T_{S_k}: t_k>\}$, where $T_{S_i}$ is a time instance sequence and $t_i$ is the corresponding integer list. Assume that domain $D_i = \{s_1,s_2,...,s_{n_i}\}$, where $s_i = <X_{s_1},X_{s_2},...,X_{s_{n_i}}>$ and each sequence $s_i$ has the corresponding time instance sequence, denoted as $T_{S_{s_i}}$. When propagating time instance sets of $M$ to domain $D_1$, we could have a propagated table defined as $D_1||M = \{X_{s}\mid T_{S_{s}}\text{ and } T_{S_{s}} \supseteq \{T_{S_a} = T_{S_b}\}\}$.

For example, in Table 2, by propagating $TIS(<b>)$ to sequence database $D_2$, we could have the propagated table $D_2||<b>$ shown in Table 3. After obtaining propagated tables, we could mine frequent itemsets by association rule mining algorithms. Then, those frequent itemsets could be combined by the corresponding patterns propagated to generate multi-domain sequential patterns. From the above example, given a minimum support 3, we can easily obtain $\{b\}$ and $\{b, c\}$ as multi-domain sequential patterns across 2 domain sequence databases, where $\{2\}$ and $\{3\}$ are the frequent items of $D_2||<b>$. The detailed steps for deriving phase are described as follows:

**Step 1: Derive through propagated table:**

In Table 2, we first derive atomic patterns in sequence database $D_2$. Specifically, in Figure 2, time instance sets of atomic patterns in sequence database $D_1$ (i.e., the top-level nodes) are propagated to sequence database $D_2$. From the propagated table of each atomic pattern, atomic patterns are easily obtained. For each atomic pattern in $D_1$, there is a inter-domain link representing that these two patterns are able to form multi-domain sequential patterns. Consequently, we have the lattice structure in domain $D_2$.

**Step 2: Derive through union operation:**

In this step, we will derive multi-domain sequential patterns with their number of elements to be one. For example, let $Q = <b, c>$, a sequential pattern with $e(Q) = 1$ in domain $D_1$ of Table 2. Through the intra-domain links, we can find atomic patterns that are components of $Q$ (i.e., $<b>$ and $<c>$). In Figure 3 following inter-domain links of $<b>$ and $<c>$, we could obtain the atomic patterns in domain $D_2$ (i.e., $<2>$ and $<3>$). Consequently, two possible unions of $P$ are generated (i.e., $\{b\}$ and $\{c\}$).

Once we have the possible candidate multi-domain sequential patterns, support values of these patterns are examined by checking their time instance sets. Given a minimum support 3, since the support values of $\{b, c\}$ and $\{b, c\}$ are 3 and 2, respectively, $\{b, c\}$ is a frequent multi-domain sequence. Thus, the lattice structure in domain $D_2$ contains
Figure 3: An example of generating sequential patterns whose number of elements is 1 in domain D2.

Figure 4: An example of generating sequential patterns with their number of elements larger than 1 in domain D2.

< (2) > and inter-domain links are built between lattice structures in domain D1 and that in domain D2.

Step 3: Derive through concatenate operation:

Before describing this step, we first define the concatenate operation.

Definition 2 (concatenate operation of TIS): Let M and N be two multi-domain sequences. TIS(M) = {< S1 : l_{i1}, l_{i2}, ..., l_{i_{|M|}}>}, < S2 : l_{j1}, l_{j2}, ..., l_{j_{|M|}}>, ..., < Sn : l_{m1}, l_{m2}, ..., l_{m_{|M|}}>} and TIS(N) = {< T1 : k_{i1}, k_{i2}, ..., k_{i_{|M|}}>}, < T2 : k_{j1}, k_{j2}, ..., k_{j_{|M|}}>, ..., < Tk : k_{m1}, k_{m2}, ..., k_{m_{|M|}}>}. The concatenation of TIS(M) and TIS(N) is denoted as TIS(M) \cap_c TIS(N) = {< S1 : l_{i1}, l_{i2}, ..., l_{i_{|M|}}, k_{j1}, k_{j2}, ..., k_{j_{|M|}}>, < S2 : l_{j1}, l_{j2}, ..., l_{j_{|M|}}, k_{j1}, k_{j2}, ..., k_{j_{|M|}}>, ..., < Sn : l_{m1}, l_{m2}, ..., l_{m_{|M|}}, k_{j1}, k_{j2}, ..., k_{j_{|M|}}>} such that S_i = T_j and l_{i_{|M|}} < k_{j_{|M|}}. In other words, TIS(M) \cap_c TIS(N) is the time instance set of the multi-domain sequence < M, N >.

For example, given M = [(a) (1) ] and the multi-domain sequence database in Table 2 with a minimum support as 3, it can be verified that TIS(M) = {< T1(T2(T3))T4(T5) : 1 >, < T2(T3)(T4)T5 : 1 >, < T1(T2(T3))T4(T5) : 1 >}, TIS(N) = {< T2(T3)(T4)T5 : 2 >, < T2(T3)(T4)T5 : 2 >, < T1(T2(T3))T4(T5) : 3 >}, and TIS(M) \cap_c TIS(N) = {< T2(T3) T4 : 1.2 >, < T2(T3)T4 : 1.2 >, < T1(T2(T3))T4(T5) : 1.3 >}. If T(M) \cap_c T(N), we further merge these sequential patterns into [(b,c) (2)]. Therefore, P = [(a)(b,c) (1)(2)] is generated.

Algorithm PropagatedMine:

Input: Multi-domain sequence database with n domains, D1, D2, ..., Dn, and the minimum support \( \delta \).

Output: Multi-domain sequential patterns with n domains.

Begin
Apply sequential pattern mining on D1.
Let \( SP_1 \) be the set of sequential patterns mined in D1.
For each domain \( D_i \), \( i = 2, 3, ..., n \)
For each \( P \in SP_{i-1} \)
If \( |P| = 1 \) Then
Construct Propagation Table \( D_i||P \).
Find frequent items in \( D_i||P \) with min_sup \( \delta \).
Let \( FI \) be the set of frequent items in \( D_i||P \).
For each \( q \in FI \)
Append \( [P \ q] \) to \( SP_i \).
Let \( TIS(\ [P \ q] \ ) = TIS(P) \cap TIS(q) \).
If \( e(P) = 1 \) Then
Compose \( [P \ q] \) with \( e(\ [P \ q] \ ) = 1 \).
If Support(\ [P \ q] \ ) \geq \delta \) Then
append \( P \ q \) to \( SP_i \).
If \( e(P) > 1 \) Then
Compose \( [P \ q] \) with \( e(\ [P \ q] \ ) > 1 \).
If Support(\ [P \ q] \ ) \geq \delta \) Then
append \( P \ q \) to \( SP_i \).
Output = \( SP_n \).
End

Correctness of PropagatedMine: The correctness of step 1 is omitted. Interested readers could refer to the prior work in [4]. In this paper, we only prove the correctness of step 2 and step 3. Let \( P \) be a k-domain sequential pattern and \( P' \) be a \((k+1)\)-domain sequential pattern derived from \( P \), where \( e(P') = e(P) = 1 \), \( |P'| \geq |P| > 1 \), and the corresponding frequent itemset of \( P \) and \( P' \) is Z. In other words, \( P' = [PZ] \). Given an arbitrary division \( X \) and \( Y \) of \( P \), such that \( X \cup Y = P \). Clearly, there are intra-domain links from \( X \) to \( Y \) and \( X \). In addition, there are inter-domain \( Z \) \( (P(Z) \) P \) the power set of \( Z \) and \( Z' \neq \emptyset \), due to the anti-monotone property (i.e., if \( P' \) is frequent, all multi-domain sequences contained by \( P' \) must be frequent, too). Hence, both \([X \ Z']\) and \([Y \ Z']\) are frequent. Therefore, the lattice structures could derive every pairs of \( P \) and \( P' \). Following the above operations, the correctness of step 3 is also applied.
Figure 5: The execution time of algorithms with various minimum support values.

Figure 6: The performance of algorithms with the number of domain varied.

4. EXPERIMENTAL RESULTS

We first investigate the performance of algorithms PropagatedMine and PropagatedMine+ with the value of minimum support varied from 0.5% to 5%. The execution time of these two algorithms is shown in Figure 5. With the smaller minimum support, the number of sequential patterns will be larger, thereby increasing the execution time of both algorithms. Since algorithm PropagatedMine needs to propagate more multi-domain sequential patterns, the execution time of algorithm PropagatedMine is larger than that of algorithm PropagatedMine+.

Next, we conduct experiments with the number of domains varied from 2 to 5 and the minimum support is set to 0.3%. The performance is shown in Figure 6. Clearly, when the number of domains increases, the execution time of both algorithms PropagatedMine and PropagatedMine+ increases. It is expected that with a larger number of domains, algorithm PropagatedMine performs worse than algorithm PropagatedMine+ since more propagated tables are generated.

The experiments of varying the number of sequences is now evaluated. The numbers of sequences are set to 1000, 2000, 3000, 4000, 5000 and 6000, respectively. The setting of the minimum support is 1%. As can be seen in Figure 7, the execution time of both algorithms increases with the number of sequences. Furthermore, algorithm PropagatedMine+ outperforms algorithm PropagatedMine due to the same reason that algorithm PropagatedMine needs to process every multi-domain sequential patterns. As the number of sequences increases, the total number of multi-domain sequential patterns becomes larger.

5. CONCLUSIONS

In this paper, we proposed algorithm PropagatedMine+ for mining sequential patterns across multiple domain sequence databases. Algorithm PropagatedMine+ first mines sequential patterns in a starting domain sequence database, and then uses a lattice structure to store these sequential patterns. In light of the lattice structure, algorithm PropagatedMine+ is able to propagate time instance sets of only atomic patterns to next domains for mining sequential patterns in a level-by-level manner. A comprehensive performance study was conducted. Experimental results show that by only propagating time instance sets of atomic patterns to other domains, algorithm PropagatedMine+ outperforms algorithm PropagatedMine.

6. REFERENCES


