SLPMiner: An Algorithm for Finding Frequent Sequential Patterns Using Length-Decreasing Support Constraint*

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Abstract

Over the years, a variety of algorithms for finding frequent sequential patterns in very large sequential databases have been developed. The key feature in most of these algorithms is that they use a constant support constraint to control the inherently exponential complexity of the problem. In general, patterns that contain only a few items will tend to be interesting if they have a high support, whereas long patterns can still be interesting even if their support is relatively small. Ideally, we desire to have an algorithm that finds all the frequent patterns whose support decreases as a function of their length. In this paper we present an algorithm called SLPMiner, that finds all sequential patterns that satisfy a length-decreasing support constraint. Our experimental evaluation shows that SLPMiner achieves up to two orders of magnitude of speedup by effectively exploiting the length-decreasing support constraint, and that its runtime increases gradually as the average length of the sequences (and the discovered frequent patterns) increases.

1 Introduction

Data mining research during the last years has led to the development of a variety of algorithms for finding frequent sequential patterns in very large sequential databases [7, 9, 5]. These patterns can be used to find sequential association rules or extract prevalent patterns that exist in the sequences, and have been effectively used in many different domains and applications.

The key feature in most of these algorithms is that they control the inherently exponential complexity of the problem by finding only the patterns that occur in a sufficiently large fraction of the sequences, called the *support*. A limitation of this paradigm for generating frequent patterns is that it uses a constant support value, irrespective of the length of the discovered patterns. In general, patterns that contain only a few items will tend to be interesting if they have a high support, whereas long patterns can still be interesting even if their support is relatively small. Unfortunately, if constant-support-based frequent pattern discovery algorithms are used to find some of the longer but infrequent patterns, they will end up generating an exponentially large number of short patterns. Ideally, we desire to have an algorithm that finds all the frequent patterns whose support decreases as a function of their length. Developing such an algorithm is particularly challenging because the downward closure property of the constant support constraint cannot be used to prune short infrequent patterns.

Recently [6], we introduced the problem of finding frequent itemsets whose support satisfies a non-increasing function of their length. An itemset is frequent only if its support is greater than or equal to the minimum support value determined by the length of the itemset. We found a property that an itemset must have in order to support longer itemsets given a length-decreasing support constraint. This property, that we call the *smallest valid extension* or *SVE* for short, enabled us to prune many short itemsets that are irrelevant to finding longer itemsets. We developed an algorithm called LPMiner that efficiently finds frequent itemsets given a length-decreasing support constraint by pruning large portion of search space.

In this paper, we extend the problem of finding patterns that satisfy a length-decreasing support constraint to the much more challenging problem of finding sequential patterns. We developed an algorithm called SLPMiner that finds all frequent sequential patterns that satisfy a length-decreasing support constraint. SLPMiner follows the database-projection-based approach for frequent pattern generation, that was shown to lead to efficient algorithms, and serves as a platform to evaluate our new three pruning methods based on the SVE property. These pruning methods exploit different aspects of the sequential pattern discovery process and prune either entire sequences, items

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within certain sequences, or entire projected databases. Our experimental evaluation shows that SLPMiner achieves up to two orders of magnitude of speedup by effectively exploiting the SVE property, and that its runtime increases gradually as the average length of the sequences (and the discovered patterns) increases.

The rest of this paper is organized as follows. Section 2 provides some background information. Section 3 describes the basic pattern discovery algorithm of SLPMiner and how the length-decreasing support constraint can be exploited to prune the search space of frequent patterns. The experimental results of our algorithm are shown in Section 4, followed by a conclusion in Section 5.

2 Background

2.1 Sequence Model and Notation

The basic sequence model that we will use was introduced by Srikant et al [7] and is defined as follows. Let $I = \{i_1, i_2, \ldots, i_n\}$ be the set of all items. An *itemset* is a subset of items. A *sequence* $s = \langle t_1, t_2, \ldots, t_l \rangle$ is an ordered list of itemsets, where $t_j \subseteq I$ for $1 \leq j \leq l$. A sequential database D is a set of sequences. The length of a sequence s is defined to be the number of items in s and denoted as $|s|$. Similarly, given an itemset t, let $|t|$ denote the number of items in t. Given a sequential database D, $|D|$ denotes the number of sequences in D. This model can describe a wide range of real data. For example, at a retail shop, customer transactions can be modeled by this sequence model such that an itemset represents a set of goods (or items) purchased by a customer at a visit and a sequence represents an ordered purchased itemsets history of a customer.

Sequence $s = \langle t_1, t_2, \ldots, t_l \rangle$ is called a *sub-sequence* of sequence $s' = \langle t'_1, t'_2, \ldots, t'_m \rangle$ $(l \leq m)$ if there exist l integers $i_1, i_2, \ldots i_l$ such that $1 \leq i_1 < i_2 < \ldots < i_l \leq m$ and $t_j \subseteq t'_{i_j}$ $(j = 1, 2, \ldots, l)$. If s is a sub-sequence of s', then we write $s \subseteq s'$ and say sequence s' *supports* s. The *support* of a sequence s in a sequential database D, denoted as $\sigma_D(s)$, is defined to be $|D_s|/|D|$, where $D_s = \{s_i | s \subseteq s_i \wedge s_i \in D\}$. From the definition, it always holds that $0 \leq \sigma_D(s) \leq 1$. We use the term *sequential pattern* to refer to a sequence when we want to emphasize that the sequence is supported by many sequences in a sequential database.

We assume that we can give a lexicographic ordering on the items in I. Although an itemset is just a set of items without the notion of ordering, it is essential to be able to define an ordering among the items for our algorithm. When we represent the items in an itemset, we order the items according to the lexicographic ordering and put those ordered items within matched parentheses (). When we represent the items in a sequence, we represent each itemset in this way and arrange these itemsets according to the ordering in the sequence within matched angled parentheses $\langle\rangle$.

2.2 Sequential Pattern Mining with Constant Support

The problem of finding frequent sequential patterns given a constant minimum support constraint [7] is formally defined as follows:

Definition 1 (Sequential Pattern Mining with Constant Support) *Given a sequential database D and a minimum support σ $(0 \leq \sigma \leq 1)$, find all sequences each of which is supported by at least $\lceil \sigma|D| \rceil$ sequences in D.*

Efficient algorithms for finding frequent itemsets or sequences [2, 8, 1, 4, 3, 5, 10] in very large itemset or sequence databases have been one of the key success stories of data mining research. The key feature in these algorithms is that they control the inherently exponential complexity of the problem by using the downward closure property [7]. This property states that in order for a pattern of length l to be frequent, all of its sub-sequences must be frequent as well. As a result, once we find that a sequence of length l is infrequent, we know that any longer sequences that include this particular sequence cannot be frequent, and thus eliminate such sequences from further consideration.

2.3 Finding Patterns with Length-Decreasing Support

Recently, we introduced the idea of length-decreasing support constraint [6] that helps us to find long itemsets with low support as well as short itemsets with high support. A length-decreasing support constraint is given as a function of the itemset length $f(l)$ such that $f(l_a) \geq f(l_b)$ for any l_a, l_b satisfying $l_a < l_b$. The idea of introducing this kind of support constraint is that by using a support function that decreases as the length of the itemset increases, we may be able to find long itemsets that may be of interest without generating an exponentially large number of shorter itemsets. We can naturally extend this idea to the sequence model by using the length of the sequence instead of the length of the itemset. Figure 1 shows a typical length-decreasing support constraint. In this example, the support constraint decreases linearly to the minimum value and then stays the same for sequential patterns of longer length. Formally, the problem of finding this type of patterns is stated as follows:

Definition 2 (Sequential Pattern Mining with Length-Decreasing Support) *Given a sequential database D and a length-decreasing support constraint $f(l)$, where $f(l)$ is a non-increasing function defined over all the positive integers and always $0 \leq f(l) \leq 1$, find all the sequential patterns each s of which satisfies $\sigma_D(s) \geq f(|s|)$.*

Finding the complete set of frequent sequential patterns that satisfy a length-decreasing support constraint is particularly challenging since we cannot rely solely on the

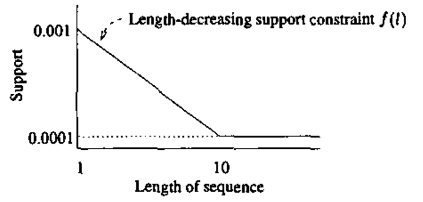


Figure 1. An example of typical length-decreasing support constraint

downward closure property of the constant support pattern mining. Notice that, under a length-decreasing support constraint, a sequence can be frequent even if its subsequences are infrequent since the minimum support value decreases as the length of a sequence increases. We must use $\min_{l \geq 1} f(l)$ as the minimum support value to apply the downward closure property, which will result in finding an exponentially large number of uninteresting infrequent short patterns.

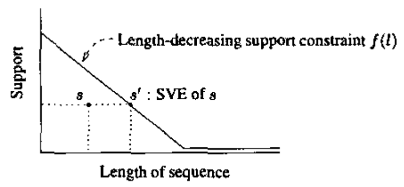


Figure 2. Smallest valid extension (SVE)

A key property regarding sequences whose support decreases as a function of their length is the following. Given a sequential database D and a particular sequence $s \in D$, if the sequence s is currently infrequent ($\sigma_D(s) < f(|s|)$), then $f^{-1}(\sigma_D(s)) = \min(\{l | f(l) \leq \sigma_D(s)\})$ is the minimum length that a sequence s' such that $s' \supset s$ must have before it can potentially become frequent. Figure 2 illustrates this relation graphically. The length of s' is nothing more than the point at which a line parallel to the x-axis at $y = \sigma_D(s)$ intersects the support curve; here, we essentially assume that the best case in which s' exists and it is supported by the same set of sequences as its sub-sequence s. This property is called the *smallest valid extension* property or *SVE* property for short and was initially introduced for the problem of finding itemsets that satisfy a length-decreasing support constraint [6].

3 SLPMiner Algorithm

We developed an algorithm called SLPMiner that finds all the frequent sequential patterns that satisfy a given length-decreasing support constraint. SLPMiner serves as a platform to develop and evaluate pruning methods for reducing the complexity of finding this type of patterns. Our design goals for SLPMiner was to make it generic enough so that any conclusions drawn from our experiments can carry through other database-projection-based sequential pattern mining algorithms [3, 5].

This section consists of two main parts. First, we will explain how SLPMiner finds frequent sequential patterns. Second, we will explain how SLPMiner prunes unnecessary data by using three different pruning methods that exploit the SVE property.

3.1 Sequential Database-Projection-based Algorithm

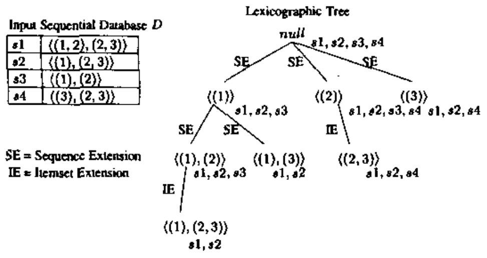
SLPMiner finds frequent sequential patterns using the database-projection-based approach. First, we describe the general idea of the the database-projection-based approach and then discuss about details specific to SLPMiner. The description of the database-projection-based approach is based on [3].

SLPMiner grows sequential patterns by adding an item at a time. It uses a prefix tree that determines which items are to be added to grow each pattern. Each node in the tree represents a frequent sequential pattern with one item added to the end of the sequential pattern that its parent node represents. As a result, if a node represents a sequential pattern p, its parent node represents the length-($|p| - 1$) prefix of p. For example, if a node represents a pattern $\langle(1), (2, 3)\rangle$, its parent node represents $\langle(1), (2)\rangle$.

SLPMiner starts from the root node that represents the null sequence to find all the frequent items in the input database and expands the root node into the child nodes corresponding to the frequent items. Then it recursively moves to each child node and expands it into child nodes that represent frequent sequential patterns.

SLPMiner grows each pattern in two different ways, namely, *itemset extension* and *sequence extension*. Itemset extension grows a pattern by adding an item to the last itemset of the pattern, where the added item must be larger than any item in the last itemset of the original pattern. For example, $\langle(1), (2)\rangle$ is extended to $\langle(1), (2, 3)\rangle$ by itemset extension, but cannot be extended to $\langle(1), (2, 1)\rangle$ or $\langle(1), (2, 2)\rangle$. Sequence extension grows a pattern by adding an item as a new itemset next to the last itemset of the pattern. For example, $\langle(1), (2)\rangle$ is extended to $\langle(1), (2), (2)\rangle$ by sequence extension.

Figure 3 shows a sequential database D and its prefix tree that contains all the frequent sequential patterns given minimum support 0.5. Since D contains a total of four sequences, a pattern is frequent if and only if at least two sequences in D support the pattern. The root of the tree represents the null sequence. At each node of the tree in the figure, its pattern and its supporting sequences in D are depicted together with symbol SE or IE on each edge representing itemset extension or sequence extension respectively.


Input Sequential Database D

$s1$	$\langle(1,2),(2,3)\rangle$
$s2$	$\langle(1),(2,3)\rangle$
$s3$	$\langle(1),(2)\rangle$
$s4$	$\langle(3),(2,3)\rangle$

Figure 3. The prefix tree of a sequential database

At each node we need to know the support of each possible extension to see whether it is frequent or not. In principle, we can count the number of supporting sequences at each node by scanning the input sequential database D. However, if only a small number of sequences in D support the pattern, scanning the whole database costs too much for a pattern. We can avoid this overhead by scanning a database called *projected database*, which is generally much smaller than the original sequential database D. The projected database of a sequential pattern p has only those sequences in D that support p. For example, at the node $\langle(2,3)\rangle$ in Figure 3, its projected database needs to contain only $s1, s2, s4$ since $s3$ does not support this pattern. Furthermore, we can eliminate preceding items in each sequence that will never be used to extend the current pattern. For example, at the node $\langle(2)\rangle$ in Figure 3, we can store sequence $s1' = \langle(2,3)\rangle$ instead of $s1$ itself in its projected database. Overall, database projection reduces the amount of sequences that need to be processed at each node and enhances efficient pattern discovery.

There are various database-projection-based algorithms for both finding frequent itemsets and finding frequent sequential patterns [1, 3, 4, 5]. SLPMiner builds the tree in depth first order and generates a projected database at every node explicitly to maximize opportunities for applying the various pruning methods. As a result, its overall approach is similar to that used by PrefixSpan [5]. However, the main difference between them is that SLPMiner generates several projected databases at a time before exploring those generated child nodes, whereas PrefixSpan generates and explores one projected database at a time.

3.2 Performance Optimizations

Expanding each node of the tree, SLPMiner performs the following two steps. First, it calculates the support of each item that can be used for itemset extension and each item that can be used for sequence extension by scanning the projected database D' once. Second, SLPMiner projects D' into a projected database for each frequent extension found in the previous step.

Since we want SLPMiner to be able to run against large input sequential databases, the access to the input database and all projected databases is disk-based. To facilitate this, SLPMiner uses two kinds of buffers: a read-buffer and a write-buffer. The read-buffer is used to load a projected database from disk. If the size of a projected database does not fit in the read-buffer, SLPMiner reads part of the database from disk several times. The write-buffer is used to temporally store several projected databases that are generated at a node by scanning the current projected database once using the read-buffer. There are two conflicting requirements concerning how many projected databases we should generate at a time. In order to reduce the number of database scans, we want to generate as many projected databases as possible in one scan. On the other hand, if we keep small buffers for many projected databases simultaneously within the write-buffer, it will reduce the size of the buffer assigned to each projected database, leading to expensive frequent I/O between the write-buffer and disk. In order to balance these two conflicting requirements, SLPMiner calculates the size of each projected database when calculating the support of every item in the current projected database before it actually generates new projected databases. Then SLPMiner generates projected databases as many as they fit in the write-buffer by one database scan, writes those projected databases on the write-buffer to the disk, and traverses only those generated child nodes in depth first order. This method also facilitates storing each projected database in a chunk rather than fragmented small pieces, which improves and stabilizes disk I/O efficiency dramatically.

Even though the disk I/O of SLPMiner is quite efficient, it is still a bottle-neck of the total performance. In order to reduce the size of projected database, SLPMiner prunes all items from a projected database if the support is less than $\min_{l \geq 1} f(l)$ since such items will never contribute to any frequent sequential patterns.

3.3 Pruning Methods

Given a length-decreasing support constraint, SLPMiner follows the sequential database-projection-based approach explained so far using $\min_{l \geq 1} f(l)$ as the constant minimum support constraint. Then SLPMiner outputs sequential patterns if their support satisfies the given length-decreasing support constraint. But this algorithm itself does not reduce the number of discovered patterns and will be very inefficient as our experimental results will show. In this subsection, we introduce three pruning methods that exploit the length-decreasing support constraint using the SVE property.

3.3.1 Sequence Pruning, SP

The first pruning method is used to eliminate certain sequences from the projected databases. Recall from Section 3 that SLPMiner generates a projected database at every node. Let us assume that we have a projected database D' at a node N that represents a sequential pattern p. Each sequence in D' has p as its prefix. If p is infrequent, we know from the SVE property that in order for this pattern to grow to something indeed frequent, it must have a length of at least $f^{-1}(\sigma_D(p))$. Now consider a sequence s that is in the projected database at node N, i.e., $s \in D'$. The largest sequential pattern that s can support is of length $|s|+|p|$. Now if $|s|+|p| \leq f^{-1}(\sigma_D(p))$, then s is too short to support any frequent patterns that have p as prefix. Consequently, s does not need to be considered any further and can be pruned. We will refer to this pruning method as the *sequence pruning* method or *SP* for short, which is formally defined as follows:

Definition 3 (Sequence Pruning) *Given a length-decreasing support constraint $f(l)$ and a projected database D' at a node representing a sequential pattern p, a sequence $s \in D'$ can be pruned from D' if $f(|s|+|p|) > \sigma_D(p)$.*

SLPMiner checks if a sequence can be pruned before inserting it onto the write-buffer. We evaluated the complexity of this method in comparison with the complexity of inserting a sequence to a projected database. There are three parameters required to prune a sequence: $|s|$, $|p|$, and $\sigma_D(p)$. As the length of each sequence is part of sequence data structure in SLPMiner, it takes a constant time to calculate $|s|$ and $|p|$. As for $\sigma_D(p)$, we know this value when we generated the projected database for the pattern p. Evaluating function f takes a constant time because SLPMiner has a lookup table that contains all possible $(l, f(l))$ pairs. Thus, the complexity of this method is just a constant time per inserting a sequence.

3.3.2 Item Pruning, IP

The second pruning method eliminates some items of each sequence in projected databases. Let us assume that we have a projected database D' at a node N that represents sequential pattern p and consider an item i in a sequence $s \in D'$. From the SVE property we know that the item i will contribute to a valid frequent sequential pattern only if

$$|s|+|p| \geq f^{-1}(\sigma_{D'}(i)) \qquad (1)$$

where $\sigma_{D'}(i)$ is the support of item i in D'. This is because of the following. The longest sequential pattern that s can participate in is $|s|+|p|$, and we know that, in the subtree rooted at N, sequential patterns that extend p with item i have support at most $\sigma_{D'}(i)$. Now, from the SVE property, such sequential patterns must have length at least $f^{-1}(\sigma_{D'}(i))$ in order to be frequent. As a result, if equation (1) does not hold, item i can be pruned from the sequence s. Once item i is pruned, then $\sigma_{D'}(i)$ and $|s|$ decrease, possibly allowing further pruning. Essentially, this pruning method eliminates some of the infrequent items from the short sequences. We will refer to this method as the *item pruning* method, or *IP* for short, which is formally defined as follows:

Definition 4 (Item Pruning) *Given a length-decreasing support constraint $f(l)$ and a projected database D' at a node representing a sequential pattern p, an item i in a sequence $s \in D'$ can be pruned from s if $|s|+|p| < f^{-1}(\sigma_{D'}(i))$.*

We can implement this pruning method simply as follows: for each projected database D', repeat scanning D' to collect support values of items and scanning D' again to prune items from each sequence until no more items can be pruned. Then, we can project the database into a projected database for each frequent item in the pruned projected database. This algorithm, however, requires multiple scans of the projected database and hence will be too costly.

Instead, we can scan a projected database once to collect support values and use those support values for pruning items as well as for projecting each sequence. Notice that we are using approximate support values that might be higher than the real values since the support values of some items might decrease during the pruning process. SLPMiner applies IP before generating a projected sequence s' of s as well as after generating s' just before inserting s' onto the write-buffer. By applying IP before projecting sequences, we can reduce the computation of projecting sequences. By applying IP once again for projected sequence s', we can exploit the reduction of length $|s|-|s'|$ to prune items in s' furthermore. Pruning items from each sequence is repeated until no more item can be pruned or the sequence becomes short enough to be pruned by SP.

IP can potentially prune larger portion of projected database than SP since it always holds that $\sigma_D(p) \geq \sigma_{D'}(i)$ and hence $f^{-1}(\sigma_D(p)) \leq f^{-1}(\sigma_{D'}(i))$. However, the pruning overhead of IP is much larger than that of SP. Let us consider the complexity of pruning items from a sequence s. The worst case is that only one item is pruned in every iteration over the items in s. Since this can be repeated as many as the number of items in the sequence, the worst case complexity for one sequence is $O(n^2)$ where n is the number of items in the sequence.

3.3.3 Structure-based Pruning

Given two sequences s_1, s_2 of the same length k, these two sequences are treated equally under SP and IP. In fact, the two sequences can be quite different from each other. For example, $\langle(1,2,3,4)\rangle$ and $\langle(1),(2),(3),(4)\rangle$ support the same 1-sequence $\langle(1)\rangle$, $\langle(2)\rangle$, $\langle(3)\rangle$, and $\langle(4)\rangle$ but never support the same k-sequences for $k \geq 2$. From this observation, we considered ways to split a projected database into smaller equivalent classes. By having smaller databases instead of one large database, we may be able to reduce the depth of a certain path from the root to a leaf node of the tree.

As a structure-based pruning, we developed the min-max pruning method. The basic idea of the min-max pruning is to split a projected database D' into two D'_1, D'_2 such that D'_1 and D'_2 contribute to two disjoint sets of frequent sequential patterns. In order to separate D' into such D'_1 and D'_2, we consider the following two values for each sequence $s \in D'$:

1. $a(s)$ = the minimum number of itemsets in frequent sequential patterns that s supports
2. $b(s)$ = the maximum number of itemsets in frequent sequential patterns that s supports

These two values define an interval $[a(s), b(s)]$, that we call the min-max interval of sequence s. If two sequences $s, s' \in D'$ satisfy $[a(s), b(s)] \cap [a(s'), b(s')] = \emptyset$, then s and s' cannot support any common sequential pattern since their min-max intervals are disjoint.

If we have D'_1 and D'_2 satisfy $\cup_{s \in D'_1}[a(s), b(s)] \cap \cup_{s \in D'_2}[a(s), b(s)] = \emptyset$, then D'_1 and D'_2 support distinct sets of frequent sequential patterns. However, this is not possible in general. Instead, D' will be split into three sets A, B, C of sequences as shown in Figure 4. More precisely, these three sets are defined for some positive integer k as follows.

$$\begin{aligned} A(k) &= \{s | s \in D' \wedge b(s) < k\} \\ B(k) &= \{s | s \in D' \wedge a(s) \geq k\} \\ C(k) &= D' - (A \cup B) \end{aligned}$$

$A(k)$ and $B(k)$ support distinct sets of frequent sequential patterns, whereas $A(k)$ and $C(k)$ as well as $B(k)$ and $C(k)$ support overlapping sets of frequent sequential patterns. From these three sets, we form $D'_1 = A(k) \cup C(k)$ and $D'_2 = B(k) \cup C(k)$. If we mine frequent sequential patterns of length up to $k-1$ from D'_1 and patterns of length no less than k from D'_2, we can gain the same patterns as we would from original D'.

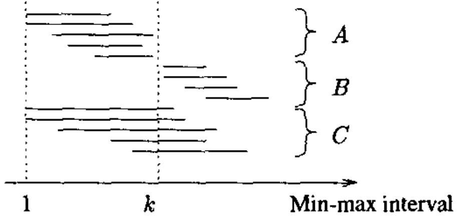


Figure 4. Min-max intervals of a set of sequences

Through our experiments, we observed $|C|$ is so close to $|D'|$ that mining D'_1 and D'_2 defined above will cost more than mining the original database D'. However, we can prune entire D' if both $|D'_1|$ and $|D'_2|$ are smaller than the $\min_{l \geq 1} f(l)$. Furthermore, we can increase this minimum support by the fact that any sequential patterns that the current pattern p can extend to is of length at most $\max_{s \in D'}(|s|) + |p|$. Now, from the SVE property, we know that if both $|D'_1|$ and $|D'_2|$ are smaller than $f^{-1}(\max_{s \in D'}(|s|) + |p|)$, then we can eliminate entire D'. Essentially, this means that if we can split a projected database into two subsets each of which is too small to be able to support any frequent sequential pattern, then we can eliminate the entire original projected database. We call this pruning method the *min-max pruning* or *MP* for short, which is formally defined as follows:

Definition 5 (Min-Max Pruning) *Given a length-decreasing support constraint $f(l)$ and a projected database D' at a node representing a sequential pattern p, entire D' can be pruned if there exists a positive integer k such that*

$$\begin{aligned} |D'_1| &= |A(k)| + |C(k)| < f(\max_{s \in D'}(|s|) + |p|)|D|, \textit{ and} \\ |D'_2| &= |B(k)| + |C(k)| < f(\max_{s \in D'}(|s|) + |p|)|D|. \quad (2) \end{aligned}$$

We apply MP just after a new projected database D' is generated if the entire sequences in D' is still kept on the write-buffer and if $|D'| \leq 1.2 f(\max_{s \in D'}(|s|))|D|$. The first condition is necessary to avoid costly disk I/O and the second condition is necessary to increase the probability of successfully eliminating the projected database. The algorithm of MP consists of two parts: the first part to calculate the distribution of the number of sequences over possible min-max intervals and the second part to find k that satisfies condition (2). The first part requires scanning D' on memory once and finding the min-max interval for each sequence. For each sequence s, SLPMiner generates a histogram of itemset size and calculates $a(s)$ by summing up itemset sizes from the largest one. The other value $b(s)$ is simply the number of itemsets in s. This part requires $O(m)$ where m is the total number of itemsets in D'. The second part uses an $n \times n$ upper triangular matrix $Q = (q_{ij})$ where $q_{ij} = |\{s | a(s) = i \wedge b(s) = j \wedge s \in D'\}|$ and n is the maximum number of itemsets in a sequence in D'. Matrix Q is generated during the database scan of the first part. Given matrix Q, we have

$$\begin{aligned} |A(k)| + |C(k)| &= \sum_{i=1}^{k-1} \sum_{j=i}^{n} q_{ij} \\ |B(k)| + |C(k)| &= \sum_{j=k}^{n} \sum_{i=1}^{j} q_{ij} \end{aligned}$$

parameter	DS1	DS2
$\lvert D\rvert$	25000	25000
$\lvert C\rvert$	$x = 10, 12, \cdots, 30$	3 to 10
$\lvert T\rvert$	2.5	$x = 2.5, 3.0, \cdots, 7.0$
N	10000	10000
$\lvert S\rvert$	$x/2$	5
$\lvert I\rvert$	1.25	$x/2$

Table 1. Parameters for datasets used in our tests

Using relations

$$(|A(k+1)| + |C(k+1)|) - (|A(k)| + |C(k)|) = \sum_{j=k}^{n} q_{kj}$$

$$(|B(k+1)| + |C(k+1)|) - (|B(k)| + |C(k)|) = -\sum_{i=1}^{k} q_{ik}$$

we can calculate $|A(k)|+|C(k)|$ and $|B(k)|+|C(k)|$ incrementally for all k in $O(n^2)$. So the total complexity of the min-max pruning for one projected database is $O(m+n^2)$. This complexity may be much larger than the runtime reduction by eliminating projected databases. However, our experimental results show that the min-max pruning method generally reduces the total runtime substantially when other pruning methods are not used together.

4 Experimental Results

We experimentally evaluated the performance of SLPMiner using a variety of datasets generated by the synthetic sequence generator that is provided by the IBM Quest group and was used in evaluating the AprioriAll algorithm [7]. All of our experiments were performed on Linux workstations with AMD Athlon at 1.5GHz and 2GB of main memory. All the reported runtime values are in seconds.

We used two classes of datasets DS1 and DS2, each of which contained 25K sequences. For each class we generated different problem instances as follows. For DS1, we varied the average number of itemsets in a sequence from 10 to 30 by interval 2, obtaining a total of 11 datasets, DS1-10, DS1-12, $\cdots$, DS1-30. For DS2, we varied the average number of items in an itemset from 2.5 to 7.0 by interval 0.5, obtaining a total of 10 datasets, DS2-2.5, DS2-3.0, $\cdots$, DS2-7.0. For DS1-x, we set the average size of maximal potentially frequent sequences to be $x/2$. For DS2-x, we set the average size of maximal potentially frequent itemsets to be $x/2$. Thus, the dataset contains longer frequent patterns as x increases. The characteristics of these datasets are summarized in Table 1, where $|D|$ is the number of sequences, $|C|$ is the average number of itemsets per sequence, $|T|$ is the average number of items per itemset, N is the number of items, $|S|$ is the average size of maximal potentially frequent sequences, and $|T|$ is the average size of maximal potentially frequent itemsets.

In all of our experiments, we used a minimum support constraint that decreases linearly with the length of the frequent sequential pattern. In particular, the initial value of support was set to 0.001 and it was decreased linearly down to 0.0001 for sequences of up to length $\lfloor |C||T|/2 \rfloor$.

We ran SPADE [9] to compare runtime values with SLPMiner. When running SPADE, we used the depth first search option, which leads to better performance than the breadth first search option on our datasets. We set the minimum support value to be $\min_{l \geq 1} f(l)$.

4.1 Results

Tables 2 and 3 show the experimental results that we obtained for the DS1 and DS2 datasets respectively. Each row of the tables shows the results obtained for a different DS1-x or DS2-x dataset, specified on the first column. The column labeled "SPADE" shows the amount of time taken by SPADE, which includes the runtime of preprocessing to transform the input sequential database into the vertical format [9]. The column labeled "None" shows the amount of time taken by SLPMiner using a constant support constraint that corresponds to the smallest support of the support curve, that is 0.0001 for all datasets. The other columns show the amount of time required by SLPMiner that uses the length-decreasing support constraint and a total of five different varieties of pruning methods and their combinations. For example, the column label "SP" corresponds to the pruning scheme that uses only sequence pruning, whereas the column labeled "SP+IP+MP" corresponds to the scheme that uses all the three pruning methods. Note that values with a "–" correspond to experiments that were aborted because they were taking too long time.

A number of interesting observations can be made from the results in these tables. First, even though SLPMiner without any pruning method is slower than SPADE, the ratio of runtime values is stable ranging from 1.9 to 2.7 with average 2.3. This shows that the performance of SLPMiner is comparable to SPADE and good enough as a platform to evaluate our pruning methods.

Second, either one of pruning methods performs better than SLPMiner without any pruning method. In particular, SP, IP, SP+IP, and SP+IP+MP have almost the same speedup. For DS1, the speedup by SP is about 1.76 times faster for DS1-10, 7.61 times faster for DS1-16, and 141.16 times faster for DS1-22. Similar trends can be observed for DS2, in which the performance of SLPMiner with SP is 1.76 times faster for DS2-2.5, 8.78 times faster for DS2-3.5, and 296.59 times faster for DS2-5.0.

Third, SP pruning alone can achieve almost the best performance among all the other tested combinations. This was counter-intuitive for us since we expected SP+IP would be much better than SP or IP alone. On the other hand, this result shows that many other sequential pattern mining algorithms can exploit the SVE property by using SP since it

		SLPMiner					
Dataset	SPADE	None	SP	IP	MP	SP+IP	SP+IP+MP
DS1-10	10.562	20.219	11.514	11.570	12.641	12.006	11.839
DS1-12	18.245	41.420	15.316	15.430	17.804	15.358	15.935
DS1-14	46.216	98.359	21.290	21.583	24.453	21.429	21.297
DS1-16	87.289	208.187	27.342	26.635	31.230	26.186	27.383
DS1-18	273.325	592.886	39.228	39.030	43.490	38.790	40.172
DS1-20	594.777	1438.932	46.147	48.440	54.727	47.864	47.723
DS1-22	4702.697	8942.943	63.351	65.123	74.905	65.232	65.907
DS1-24	–	–	82.756	85.622	94.640	82.377	83.148
DS1-26	–	–	106.986	112.180	126.647	111.699	106.567
DS1-28	–	–	139.369	142.760	162.062	137.955	138.411
DS1-30	–	–	180.715	189.029	212.848	185.601	184.105

Table 2. Comparison of pruning methods using DS1

		SLPMiner					
Dataset	SPADE	None	SP	IP	MP	SP+IP	SP+IP+MP
DS2-2.5	10.562	20.219	11.514	11.570	12.641	12.006	11.839
DS2-3.0	21.159	45.887	16.627	16.940	18.719	15.871	15.902
DS2-3.5	117.486	279.617	31.851	35.319	43.267	31.445	31.696
DS2-4.0	333.786	899.025	32.783	32.488	39.805	31.940	32.107
DS2-4.5	731.402	1784.572	35.871	37.955	43.138	38.030	36.539
DS2-5.0	6460.641	17106.370	57.677	61.654	77.835	59.115	59.096
DS2-5.5	–	–	59.500	62.617	73.759	61.187	61.798
DS2-6.0	–	–	77.752	78.684	96.951	77.925	75.186
DS2-6.5	–	–	98.061	105.475	144.387	101.213	102.184
DS2-7.0	–	–	116.986	119.907	136.513	113.443	117.602

Table 3. Comparison of pruning methods using DS2

is easy to implement. For example, it is straight-forward to implement SP in PrefixSpan [5], for both its disk-based projection and pseudo-projection. Even SPADE [9], which has no explicit sequence representation during pattern mining, can use SP by adding the length of sequence to each record in the vertical database representation.

Fourth, among the three pruning methods, SP leads to the largest runtime reduction, IP leads to the second largest runtime reduction, and MP achieves the smallest reduction. The problem with MP is the overhead of splitting a database into two subsets. Even so, it seems surprising to gain such a great speedup by MP alone. This shows a large part of the runtime of SLPMiner with no pruning method is accounted for by many small projected databases that never contribute to any frequent patterns. As for SP and IP, SP is slightly better than IP because IP and SP prune almost the same amount of projected databases for those datasets but IP has much larger overhead than SP.

Fifth, the runtime with three pruning methods increases gradually as the average length of the sequences (and the discovered patterns) increases, whereas the runtime of SLP-Miner without any pruning increases exponentially.

5 Conclusion

In this paper we presented an efficient algorithm for finding all frequent sequential patterns that satisfy a length-decreasing support constraint. The key insight that enabled us to achieve high performance was the smallest valid extension property of the length-decreasing support constraint.

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