An Efficient and Incremental System to Mine Contiguous Frequent Sequences

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Abstract

Mining frequent patterns is an important component of many prediction systems. One common usage in web applications is the mining of users' access behavior for the purpose of predicting and hence pre-fetching the web pages that the user is likely to visit.

Frequent sequence mining approaches in the literature are often based on the use of an Apriori-like candidate generation strategy, which typically requires numerous scans of a potentially huge sequence database. In this paper we instead introduce a more efficient strategy for discovering frequent patterns in sequence databases that requires only two scans of the database. The first scan obtains support counts for subsequences of length two. The second scan extracts potentially frequent sequences of any length and represents them as a compressed frequent sequences tree structure (FS-tree). Frequent sequence patterns are then mined from the FS-tree. Incremental and interactive mining functionalities are also facilitated by the FS-tree. As part of this work, we developed the FS-Miner, an system that discovers frequent sequences from web log files. The FS-Miner has the ability to adapt to changes in users' behavior over time, in the form of new input sequences, and to respond incrementally without the need to perform full re-computation. Our system also allows the user to change the input parameters (e.g., minimum support and desired pattern size) interactively without requiring full re-computation in most cases.

We have tested our system using two different data sets, comparing it against two other algorithms from the literature. Our experimental results show that our system scales up linearly with the size of the input database. Furthermore, it exhibits excellent adaptability to support threshold decreases. We also show that the incremental update capability of the system provides significant performance advantages over full re-computation even for relatively large update sizes.

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Chapter 1

Introduction

1.1 Web Usage Mining

A sequence database stores a collection of sequences, where each sequence is a collection of ordered data items or events. Examples of sequences are DNA sequences, web usage data files or customers' transactions logs. For web applications, where users' requests are satisfied by downloading pages to their local machines, the use of mining techniques to predict access behaviors and hence help with prefetching of the most appropriate pages to the local machine cache can dramatically increase the runtime performance of those applications. These mining techniques analyze web log files composed of listings of page accesses (references) organized typically into sessions. These techniques are part of what is called **Web Usage Mining**, a term first introduced by Cooley et al. [CSM97].

Typically web usage mining techniques rely on a Markov assumption with depth n. This means that it is assumed that the next request page depends only on the last n pages visited. A study conducted in [JPT03] showed that Markov based structures for web usage mining is best suited for prefetching, targeted ads, and personalization.

Web usage mining approaches can be classified based on the type of patterns they produce into three categories [GH03]: association rules, frequent sequences, and frequent generalized sequence. With association rules, the problem of finding web pages visited together is similar to finding association among item sets in transaction databases. Frequent sequences can be thought of as an ordered (by time) list of non-empty item sets, and hence frequent sequence mining can be thought of as association rule mining over temporal data sets. A frequent generalized sequence is a frequent sequence that allows wildcards in order to reflect the user's navigation in a flexible way [GST00]. [GH03] evaluated the three approaches and found that the frequent sequence approach gives better results than the association rules and the frequent generalized sequence approaches when we need to find the correct predictions within the fist predictions.

Frequent sequences are also known as **Traversal Patterns**. According to [Dun03], traversal patterns can be classified based on four main features:

- Whether or not the order of page references in a pattern matters.

- Whether or not duplicate page references are allowed. A duplicate page occurrence in a sequence can be either backward traversal (the same page reference can appear more than one time in the sequence in a non-contiguous manner), or page refresh/reload (the same page reference can appear more than one time in the sequence in a contiguous manner). For example, in the sequence $<abcafr>$ page a has a backward traversal pattern, and in the sequence $<abcccafr>$ page c has a page refresh/reload pattern.

- Whether patterns must consist of contiguous page references or they can have gaps. In other words, whether wildcards are allowed or not.

- Whether or not only maximal patterns are considered. A pattern is maximal when it is not part of another pattern. For example, if a mining algorithm outputs as a frequent sequence the pattern $<abcd>$ this implies that all subsequences of that frequent pattern: $<ab>$, $<abc>$, $<abcd>$, $<bc>$, $<bcd>$, and $<cd>$ are indeed frequent. And since the algorithm output only the maximal pattern of these smaller patterns we classify this algorithm a maximal pattern algorithm. Note that although it is visible to extract all those subsequences from the discovered maximal pattern, this is not exactly equivalent to discovering the same frequent subsequences as frequent patterns by another mining algorithm that generates them as well their maximal pattern. The reason is that, besides generating the patterns themselves, the second approach can also give their frequency, while the first approach will give the frequency of the maximal pattern and can not give the frequencies of its subsequences.

1.2 Problem Description

In this work we are particularly interested in web usage mining for the purpose of extracting frequent sequence patterns that can be used for pre-fetching and caching. For pre-fetching and caching, knowledge of such ordered contiguous page references is useful for predicting future references [Dun03]. Furthermore, knowledge of frequent backward traversal is useful for improving the design of web pages [Dun03]. In other words we are interested in mining for *traversal patterns*, where *traversal patterns* are defined to be sequences with duplicates as well as consecutive ordering between page references [XD01]. Our goal is to introduce a technique for discovering such sequence patterns, that is efficient, yet incremental and can adapt to user parameter changes. The patterns extracted by our system follow the Markov assumption discussed above and have four properties: (1) the order of page references in patterns is important; (2) duplicate page references are allowed (backward traversals and page refreshes); (3) patterns consist of contiguous page references; and (4) maximal and non-maximal patterns are allowed.

1.3 Mining Cost

In general, discovering frequent patterns in large databases is a costly process in terms of I/O and CPU costs. One major cost associated with the mining process is the generation of potentially frequent items (or sequences), called candidate item sets. Many mining techniques use an Apriori style level-wise candidate generation approach [AS94, NLHP98, STA98] that requires multiple expensive scans of the database, one for each level, to determine which of the candidates are in fact frequent. To address this issue, Han et al. [HPY00] proposed a frequent pattern growth (FP-growth) based mining method that avoids costly repeated database scans and candidate generation. Their work focuses on the discovery of frequent item sets in transactional databases. In that work the order of the items in each record (i.e. in each transaction) is not of consideration. Hence it does not support mining for sequences where order among items is important. We now propose an extension of their technique to tackle the sequence mining case.

The mining cost is even more prohibitive for dynamic databases which are subject to updates such as the continuous insertion of new sessions to the web log. In this case the reconstruction of frequent sequences may require re-executing the mining process from the beginning. The problem of incrementally mining for association rules has been studied widely [FAAM97, TBAR97]. Parthasarathy et al. [PZOD99] introduced an interactive and incremental sequence mining approach using a lattice structure. In their approach, the discovery of frequent sequences is done by traversing the lattice and intersecting subsequences of common suffixes to obtain their support. Their performance study has shown that the incremental capability of their system is more efficient than re-computing frequent sequence mining process from scratch. However, the limitation of their approach, as they point out, is the resulting high memory utilization as well as the need to keep an intermediate vertical database layout which has the same size as the original database [PZOD99].

1.4 Contributions of this Thesis

Our work is similar to [HPY00] in that we also aim to avoid the expensive candidate generation process, particularly in the presence of large number of items (page references). We propose a frequent sequence tree structure (FS-tree) for storing compressed essential information about frequent sequences. Unlike [HPY00], which aims to discover frequent item sets in which order is not important, our work takes order among page references into consideration. We introduce an algorithm which we call Frequent Sequence mining (**FS-mine**) that analyzes the FS-tree to discover frequent sequences. Our approach is incremental in that it allows updates to the database to be incrementally reflected in the FS-tree and in the discovered frequent sequences, without the need to reload the whole database or to re-execute the whole mining process from scratch. Finally the user can interactively change key system parameters (in particular the minimum support threshold and the maximum pattern size) and the system will remove the patterns that are no longer frequent and will introduce the patterns that are now frequent according to the new parameter values, without the need for scanning and loading the entire database.

The results of the experiments that we have conducted using our approach, and compared against two other approach from the literature, show that our system, as well as the other two systems, scales up linearly with the size of the input database. Furthermore, our system shows a much better response time to the decrease in the support level than the other two systems that experience a dramatic increase in cost when they hit lower support values. The incremental update capability of the our approach provides significant performance advantages over full re-computation even for relatively large update sizes.

1.5 Outline of this Document

The rest of this document is organized as follows. Chapter 2 discusses related work. Chapter 3 introduces the FS-tree data structure design and the FS-tree construction algorithm. Chapter 4 describes the FS-mine algorithm for discovering frequent sequences from the FS-tree structure. Chapter 5 describes the incremental and interactive mining algorithms. Chapter 7 discusses our experiment results. Lastly, Chapter 8 provides some conclusions and future work ideas.

Chapter 2

Related Work

Nanpoulos et al. [NKM01] proposed a method for discovering access patterns from web logs based on a new type of association patterns. They handle the order between page accesses, and allow gaps in sequences. They use a candidate generation algorithm that requires multiple scans of the database. Their pruning strategy assumes that the site structure is known.

Srikant and Agrawal [SA96] presented an algorithm for finding generalized sequential patterns that allows user-specified window-size and user-defined taxonomy over items in the database. This algorithm required multiple scans of the database to generate candidates.

Yang et al. [YZL01] presented an application of web log mining that combines caching and prefetching to improve the performance of internet systems. In this work, association rules are mined from web logs using an algorithm called *Path Model Construction* [SYLZ00] and then used to improve the GDSF caching replacement algorithm. These association rules assumes order and adjacency information among page references. The left hand side of the association rule is a substring of length n (called n-gram substring), and is obtained by scanning through all substrings ranging between 1 and n in each user session and pruning substrings that do not satisfy a pre-defined minimum support. Like us, they assume contiguous page references in sequence patterns.

Han et al. [HPY00] proposed a technique that avoids the costly process of candidate generation by adapting a pattern growth method that uses a highly condensed data structure to compress the database. This work also used a divide-and-conquer method to decompose the mining task into a set of smaller tasks that reduce the search space. The proposed technique discovers un-ordered frequent item sets. However, is does not support the type of sequences we are interested in.

Parthasarathy et al. [PZOD99] introduced a mining technique given incremental updates and user interaction. This technique avoids re-executing the whole mining algorithm on the entire data set. A special data structure called incremental sequence lattice and a vertical layout format for the database are used to store items in the database associated with customer transaction identifiers. Sequence supports are obtained by performing intersection between different nodes in the lattice and obtaining count supports from the intermediate vertical database. Due to the size of the intermediate vertical database and lattice that together typically exceeds memory limits, this process is broken into smaller processes by forming suffix-based equivalence classes. Each class is brought to the memory and processed independently. Similar in spirit to [PZOD99], we store in the FS-Tree additional data as that reduces the work required at later stages although we use very different data structures and algorithms to achieve that.

Xiao and Dunham [XD01] proposed an incremental and adaptive algorithm for mining for traversal patterns. This work relies on a generalized suffix tree structure where all sequences in the database and their suffixes are inserted into it. This tree grows quickly in size, since inserting a sequence into the suffer tree involves inserting all its suffer into the tree. Whenever the size of the tree reaches the size of the available memory during tree construction, pruning and compression techniques are applied to reduce its size in order to be able to continue the insertion process of the remaining sequences from the database. This process of reducing the size of the tree to fit into the available memory is referenced to as adaptive property. Conversely, we do not need to interrupt the FS-Tree construction process to prune or compress the tree as we prune the input sequences before inserting them into the tree and we insert only potentially frequent subsequences. Unlike [XD01], the adaptive mining here means that the system adapts to changes in user-specific parameters.

Chapter 3

FS-tree Construction

3.1 Frequent Sequences

Let $I = \{i_1, i_2, ..., i_m\}$ be a set of unique items, such as page references. A sequence **Seq** = $<p_1p_2...p_n>$ is an ordered collection of items with $p_i \in I$ for 1 $\leq$ i $\leq$ n. A database **DB** (for web usage mining typically a web log file) stores a set of records (sessions). Each record has two fields: the record ID field, **SID**, and the input sequence field, **InSeq**. The order of the items does matter within such an input sequence. When an item p_{i+1} comes immediately after another item p_i we say that there is a link l_i from p_i to p_{i+1}. We denote that as l_i = $p_i - p_{i+1}$. We may also represent a sequence as **Seq** = $p - P$, where p is the first element in the sequence and P is the remaining subsequence.

For a link h, the *support count*, $Supp^{link}(h)$, is the number of times this link appears in the database. For example if the link $a - b$ appears in the database five times we say that $Supp^{link}(a - b)$ = 5. For a sequence Seq = $<p_1p_2...p_n>$ we define its size as n which is the number of items in that sequence. Given two sequence S = $<p_1p_2...p_n>$ and R = $<q_1q_2...q_m>$ we say that S is a subsequence of R if there is some i, 1 $\leq$ i $\leq$ $m - n + 1$, such that $p_1 = q_i$, $p_2 = q_{i+1}$, ..., $p_n = q_{i+(n-1)}$. For a given input sequence Seq = $<p_1p_2...p_n>$ we consider only subsequences of size ≥ 2. For example, if a record in the database has an input sequence $<abcd>$ we extract subsequences $<abcd>$, $<abc>$, $<bcd>$, $<ab>$, $<bc>$, and $<cd>$ from that input sequence. The support count $Supp^{seq}(Seq)$ for a sequence Seq is the number of times the sequence appears in the database either as a the full sequence or as a subsequence of sessions. We allow item duplicates in frequent sequences, which means that the same item can appear more than once in the same sequence. Duplicates can be either backward traversal, e.g. the page b in $<abcb>$, or refresh/reload of the same page, e.g. the page a in $<aabc>$.

3.2 Sequence Support

The behavior of our system is governed by two main parameters. The first parameter is ***minimum* link *support count***, $MSuppC^{link}$, which is the minimum count that a link should satisfy to be considered potentially frequent. $MSuppC^{link}$ is obtained by multiplying the total number of links in the database by a desired minimum link support threshold ratio $MSuppR^{link}$. $MSuppR^{link}$ is the frequency of the link in the database to the total number of links in the database ($Supp^{link}$/total # of links in the database) which a link has to satisfy in order to be considered potentially frequent. $MSuppR^{link}$ is a system parameter (not set by the user) and is used by the FS-tree construction algorithm to decide what links to include in the FS-tree as will be discussed later. The second parameter $MSuppC^{seq}$, is the ***minimum* sequence *support count***, that denotes the minimum number of times that a sequence needs to occur in the database to be considered frequent. $MSuppC^{seq}$ is obtained by multiplying the total number of links in the database by a desired minimum sequence support threshold ratio $MSuppR^{seq}$. This desired ratio is the frequency of the sequence in the database to the total number of links in the database

($Supp^{seq}$/total # of links in the database[1]) which a sequence has to satisfy in order to be considered frequent. $MSuppR^{seq}$ is set by the user and is used by the FS-Mining algorithm during the mining process.

$MSuppC^{seq}$ is the main parameter needed for sequence mining in our system. At all times, we assume that $MSuppC^{link} \leq MSuppC^{seq}$. The reason for having $MSuppC^{link}$ is to allow the system to maintain more data about the input database than required for the mining task at hand. This will help in minimizing the amount of processing needed when handling incremental updates to the database, or when the user changes system parameters. This issues will be discussed in more detail in the incremental and interactive mining sections. In short, we consider any sequence Seq that has $Supp^{seq}(Seq) \geq MSuppC^{seq}$ a **frequent sequence** or a **pattern**. We consider any link h that has $Supp^{link}(h) \geq MSuppC^{seq}$ a **frequent link** (also considered a frequent sequence of size 2) . And if $Supp^{link}(h) \geq MSuppC^{link}$ and $Supp^{link}(h) < MSuppC^{seq}$ we call h a **potentially frequent** link. And if $Supp^{link}(h)$ does not satisfy $MSuppC^{link}$ and $MSuppC^{seq}$ we call h a **non-frequent link**.

3.3 Frequent Sequence Tree

We now describe our proposed data structure that we use to store potentially frequent sequences to facilitate the mining process.

Definition 1 *A frequent sequence tree is a structure that consists of the following three components:*

[1] Note that this is slightly different from the definition of support ratio in other work [XD01], which has the same patterns assumptions. [XD01] defines this ratio to be the frequency of the sequence to the total number of pages in the database. We think that our ratio is more appropriate since it eliminates the effect of sessions with single page reference in the input web log on the desired ratio (given that we are interested in patterns of size $\geq$ 2).

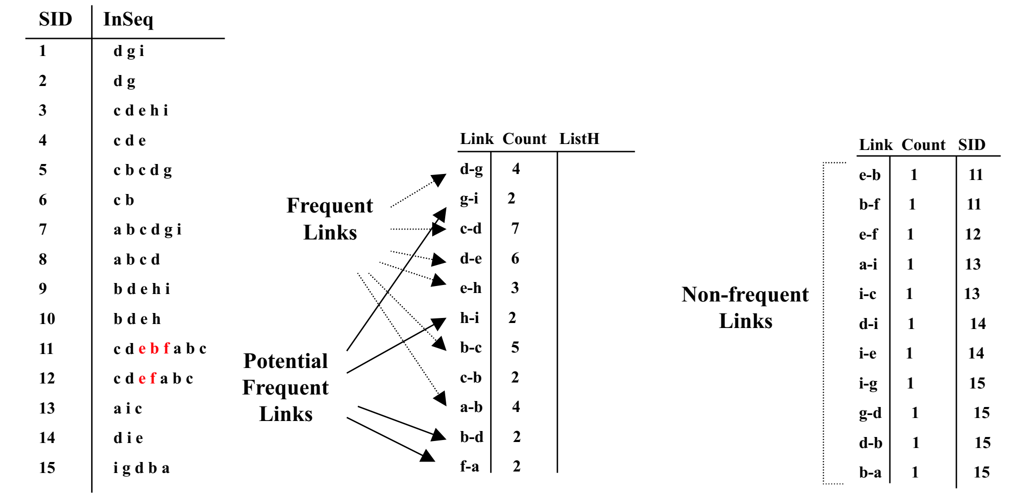
- *A tree structure with a special root node R and a set of sequence prefix subtrees as children of the root. Each node n in the FS-tree has a* ***node-name*** *field that represents an item from the input database*[2]*. Each edge in the tree represents a $link$ relationship between two nodes. Each edge has three fields:* ***edge-name****,* ***edge-count****, and* ***edge-link****.* ***Edge-name*** *represents the* ***from*** *and* ***to*** *nodes that are linked using this edge,* ***edge-count*** *represents the number of sequences that share this edge in the particular tree path, where a tree path is the prefix path that starts from the tree root to the current node.*

- *A header table HT that stores information about frequent and potentially frequent links in the database. Each entry in the header table HT has three fields:* ***Link*** *which stores the name of the link,* ***count*** *stores the count of that link in the database, and* ***listH*** *pointer, which is a linked list head pointer that points to the first edge in the tree that has the same* ***edge-name*** *as the link name. Note that the* ***edge-link*** *field in each edge in the tree is pointing to the next edge in the FS-tree with the same edge-name (or null if there is none).*

- *A non-frequent links table $NFLT$, that stores information about non-frequent links. This table is only required for supporting the incremental feature of the system. The $NFLT$ has three fields:* ***Link*** *which stores the name of the link,* ***count*** *which stores the count of that link in the database, and* ***SIDs*** *which stores the IDs of records in the database that have sequences that include that link*[3]*.*

[2] For supporting the incremental property of the system, we extent the node by adding a structure that stores a single session ID that ends at this node for certain sequences. We will introduce this structure in more details in the incremental mining chapter.

[3] For optimization, if more than one of these sessions have exactly the same sequence we might store only the ID of one of them along side with their count. For example if the link a-b was non-frequent and



SID	InSeq
1	d g i
2	d g
3	c d e h i
4	c d e
5	c b c d g
6	c b
7	a b c d g i
8	a b c d
9	b d e h i
10	b d e h
11	c d e b f a b c
12	c d e f a b c
13	a i c
14	d i e
15	i g d b a

Link	Count	ListH
d-g	4	
g-i	2	
c-d	7	
d-e	6	
e-h	3	
h-i	2	
b-c	5	
c-b	2	
a-b	4	
b-d	2	
f-a	2	

Link	Count	SID
e-b	1	11
b-f	1	11
e-f	1	12
a-i	1	13
i-c	1	13
d-i	1	14
i-e	1	14
i-g	1	15
g-d	1	15
d-b	1	15
b-a	1	15

(a) Web Log File (b) Header Table (HT) (c) Non-Frequent Links Table (NFLT)

Figure 3.1: (a) Web log file example, (b) Header table HT and (c) Non-frequent links table $NFLT$.

3.4 Frequent Sequence Tree Construction

Consider the web log file in Figure 3.1(a). It stores a set of users' sessions where each session has two fields: SID filed that stores the session id and $InSeq$ filed that stores sequence of page references accessed by the user in a certain order. Given such input web log file, and assuming $MSuppC^{link}$ = 2 and $MSuppC^{seq}$ = 3, [4] we construct the FS-tree as follows:

1) We first perform one scan of the input database (log file) to obtain counts for links in the database.

2) We identify those links that have $Supp^{link} \geq MSuppC^{link}$, and we insert them in the header table (HT), along side with their counts, as shown in Figure 3.1(b). For links that do not satisfy the predefined $MSuppC^{link}$ we insert them in the non-frequent links

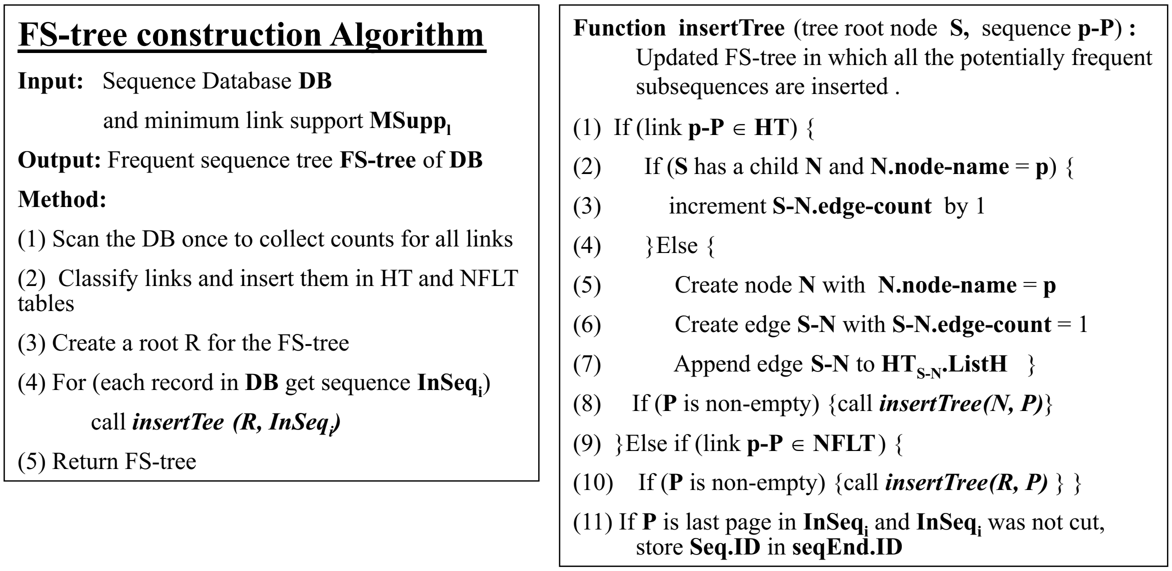
if it appeared in three sessions in the database: {5, <abc>} {9, <$eabd$>} and {15, <abc>} we may store this information in the $NFLT$ as {a-b, 3, {(5:2), (9:1)} } where a-b is the link name, 3 the link count and $\{(5:2), (9:1)\}$ means that a-b appears in a session with SID=5 and in another session that has exactly the same sequence as the one in session 5, and also appeared in a session with ID=9 that had different sequence.

[4] Frequent links are those satisfying both support thresholds, Potentially Frequent links are those satisfying only $MSuppC^{link}$ and Non-frequent links are those not satisfying any of the two support thresholds.

table ($NFLT$), along side with their counts and the SID of sessions they are obtained from[5], this is shown in Figure 3.1(c).

3) We create the root of the FS-tree.

4) We then perform a second scan of the database calling the $insertTree$ function (shown in Figure 3.2) for each input sequence. The $insertTree$ function inserts the input sequences in the FS-tree starting by the first link in the sequence, frequent links (and potentially frequent links) are stored as edges in tree branches (sharing nodes and edges when possible), until some non-frequent link is encountered, or the input sequence is exhausted. If a non-frequent link is encountered in the inserted sequence we do not insert it, rather, the insertion process is started over again from the root of the tree, with the remaining input subsequence, in a recursive manner. Besides inserting sequences into the **FS-tree** we also maintain the **ListH** linked lists that link different edges in the tree to the header table (HT).



```
FS-tree construction Algorithm
Input:   Sequence Database DB
         and minimum link support $MSupp_l$
Output: Frequent sequence tree FS-tree of DB
Method:
(1) Scan the DB once to collect counts for all links
(2) Classify links and insert them in HT and NFLT tables
(3) Create a root R for the FS-tree
(4) For (each record in DB get sequence $InSeq_i$)
        call insertTee (R, $InSeq_i$)
(5) Return FS-tree
```

```
Function insertTree (tree root node S, sequence p-P) :
    Updated FS-tree in which all the potentially frequent
    subsequences are inserted .
If (link p-P $\in$ HT) {
    If (S has a child N and N.node-name = p) {
        increment S-N.edge-count by 1
    }Else {
        Create node N with N.node-name = p
        Create edge S-N with S-N.edge-count = 1
        Append edge S-N to $HT_{S-N}$.ListH }
    If (P is non-empty) {call insertTree(N, P)}
}Else if (link p-P $\in$ NFLT) {
    If (P is non-empty) {call insertTree(R, P) } }
If P is last page in $InSeq_i$ and $InSeq_i$ was not cut,
    store Seq.ID in seqEnd.ID
```

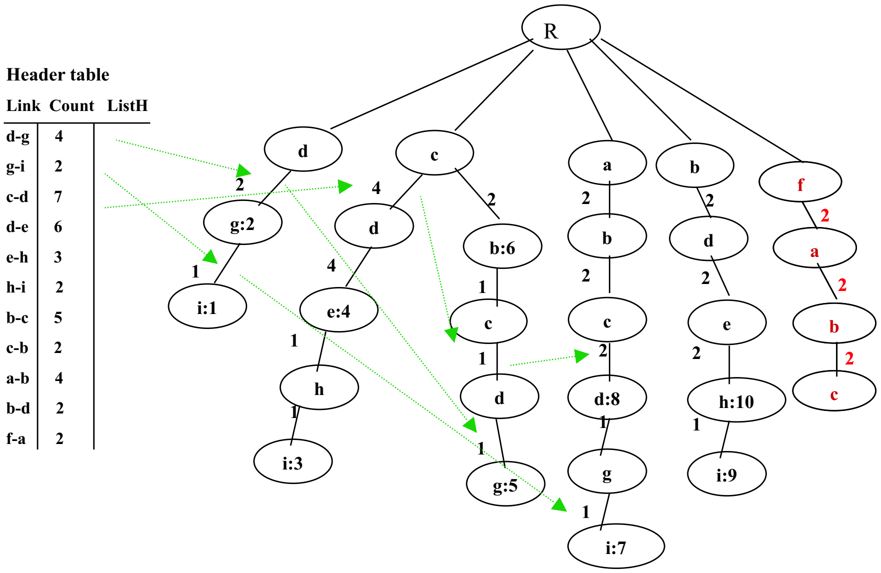
Figure 3.2: FS-tree construction.

Figure 3.3 shows the FS-tree constructed for the example in Figure 3.1[6]. The total

[5] only required for supporting incremental mining

[6] Note that we only show some of the lines that link the header table to edges in the FS-tree for simplicity

number of links in the database is 52, based on first database scan. And assuming that the system defines $MSuppR^{link}$ to be 4% and the user defines $MSuppR^{seq}$ to be 6%, we obtain $MSuppC^{link}$ = 2 and $MSuppC^{seq}$ = 3 accordingly (note that $MSuppC^{link}$ is used in FS-tree construction, while $MSuppC^{seq}$ is used later in FS-tree mining). We create the FS-tree root node R. We then insert sequences into the tree starting from the tree root using the procedure described above. For the sequence $<dgi>$ we start from the root and since the tree is empty so far, we create two new nodes with names d and g. We also create an edge $d - g$ that is assigned **edge-count** = 1. In addition, we link the **ListH** pointer for link $d - g$ in **HT** to the new edge. Lastly, we insert the node i into the **FS-tree** creating a new node and the edge $g - i$ with **edge-count** =1, and link **ListH** pointer for link $g - i$ in **HT** to that edge. When inserting the second input sequence $<dg>$, we share the nodes d and g and the edge $d - g$ and increment the count of that edge to 2.



Header table

Link	Count	ListH
d-g	4	
g-i	2	
c-d	7	
d-e	6	
e-h	3	
h-i	2	
b-c	5	
c-b	2	
a-b	4	
b-d	2	
f-a	2	

Figure 3.3: The FS-tree constructed for the example in Figure 3.1

Next we insert the sequence $<cdehi>$ by creating new nodes and edges (with counts = 1) for all the items and links in the sequence since there was no possible path sharing. Sequences in sessions with ids 3 to 10 are inserted following the same logic described above. Session 11 ($<cdebfabc>$) is a different from prior sessions, since the sequence in this session has non-frequent links, namely $e - b$ and $b - f$. First, the sub-sequence $<cde>$ is inserted in the tree. Insertion here involves sharing existing nodes and edge and incrementing edges counts. Then we ignore the two non-frequent links $e - b$ and $b - f$. The sub-sequence $<fabc>$ is inserted from the tree root by creating new nodes and edges as described above. For session 12 we insert the sub-sequence $<cde>$ into the tree, then we encounter the non-frequent link e-f, so we skip it and insert the remaining sub-sequence $<fabc>$ starting from the root node of the tree. Sessions 13, 14 and 15 are not inserted, totally or partially, into the FS-tree since all their links are non-frequent. See Figure 3.3 for the fully constructed FS-tree.

3.5 FS-Tree Size

The FS-tree is a compressed form for representing sequences scanned from the input web log file. It is compressed in two manners, first, not all sequences are stored in the tree, only those sequences/subsequence that are potentially frequent are inserted and stored in the FS-Tee. This insures that any non-potential sequence/subsequence are pruned from the beginning and are not inserted in the tree. Second, insertion into the tree involves sharing of all possible existing nodes and edges, this is even more powerful with the existence of the inial pruning step discussed earlier. So if a sequence is pruned (cut into smaller subsequence as a result of having non-frequent links in it), each of these subsequences has the chance of sharing nodes and edges when they are inserted from the top of the FS-tree. Due to these properties of the FS-tree, the size of the tree is typically much smaller than the original web log file.

To give an idea about how small our proposed FS-Tree is we examine another web usage mining work that used a tree to store and mine frequent sequences. The work presented in [XD01], that we discussed in the Background Chapter, constructs a suffix tree and mine it for frequent sequences. Insertion in the suffix tree is done as follow: for each sequence in the input log file each suffix of the sequence is inserted from the root of the tree, sharing nodes and edges if possible. For example, if we insert the sequence $<dgi>$ from session 1 in the input log file shown in Figure 3.1(a) we insert the suffix sequences: $<dgi>$, $<gi>$, and $<i>$. The same thing happens for each sequence in the input log file. This makes the suffix tree grows very quickly especially with the exitances of long sequences. For example the sequence $<cdebfabc>$ in session 11 will cause the insertion of the following suffix sequences: $<cdebfabc>$, $<debfabc>$, $<ebfabc>$, $<bfabc>$, $<fabc>$, $<abc>$, $<bc>$, $<c>$. To give an idea of how big is the initial suffix tree needed to represent the sequences in the web log file in Figure 3.1(a), we constructed this tree and are showing it in Figure 3.4. Note that for the clarity of presentation, the suffix tree in Figure 3.4 shows the accessed pages on the nodes themselves, while typically they are shown on the edges. Note that the symbol $\$$ is used to represent a terminating simple and is considered as leaf node that indicates the ending of a suffix sequence. For more details on suffix trees in general refer to [Gus97].

To overcome the problem of the suffix tree size, one can collapse nodes on tree that have single child to reduce the number of nodes and edges. Figure 3.5 shows a collapsed version of the suffix tree shown in Figure 3.4. Note that nodes with more than one child in the original tree can not be collapsed (terminating nodes $\$$ are considered as a child). Only consecutive nodes with one child are collapsed into one node. The same technique is applicable to our FS-tree. Figure 3.6 shows how the FS-tree in Figure 3.3 looks like after collapsing (note that we still maintain counts but are not shown in the figure). By comparing the collapsed FS-tree and the collapsed suffix tree we see clearly that, even after collapsing, out FS-tree continues to be much smaller in size than the suffix trees. Please refer to the Related Work Chapter for more detailed comparison between our work

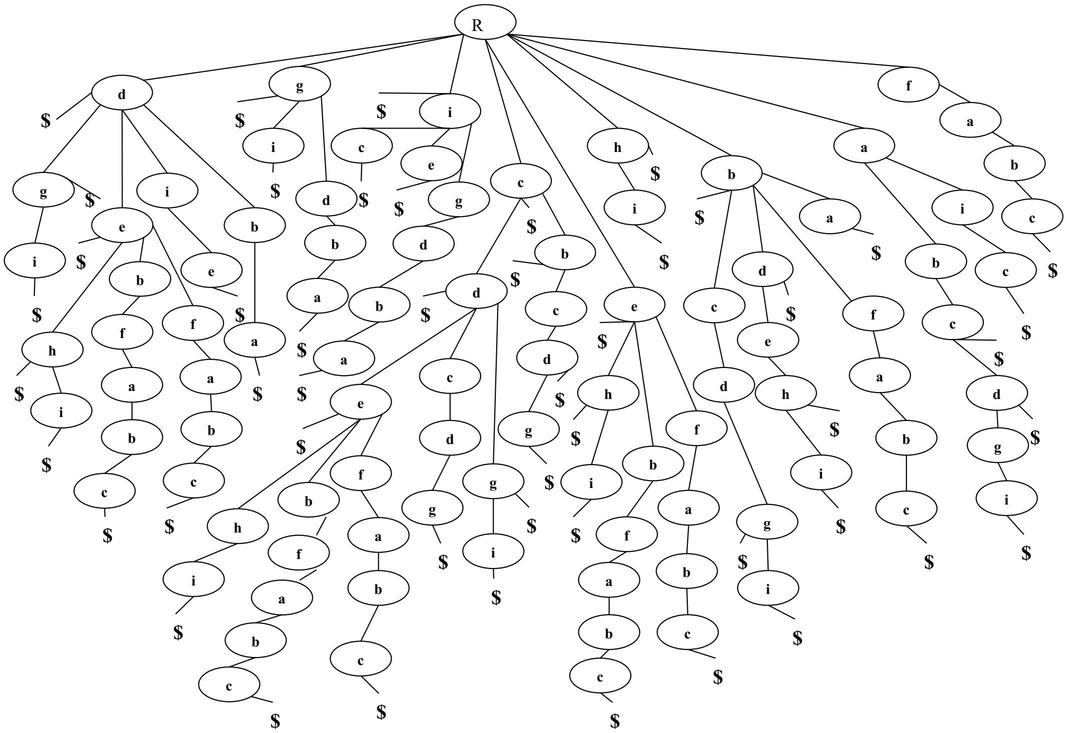

R
d g f
$ $ $ i a
i c e h a b
g $ i $ d $ $ g c $ b $ a i c
e b d $ i $ $
i $ b e $ b $ $ d $ b c $
$ f a b d $ $ c e c $ f c
h f $ a $ a d e $ $
$ a a $ $ c e $ h d h a d
i b b $ d g $ f $ $ b g $
$ c c f g $ i b i
$ $ h b g a $ $ $ a g $ c i
f i a b i f $ $ b i
$ a b $ b c $
c c c $ $ $ $

Figure 3.4: The very large suffix tree that would be needed to store the sequences in the input log file shown in Figure 3.1(a). Contrast this to the much smaller FS-tree that we propose as shown in Figure 3.3

and the work in [XD01].

Through out the reaming of this document we will be showing the non-collapsed version of the FS-tree for simplicity of illustration.

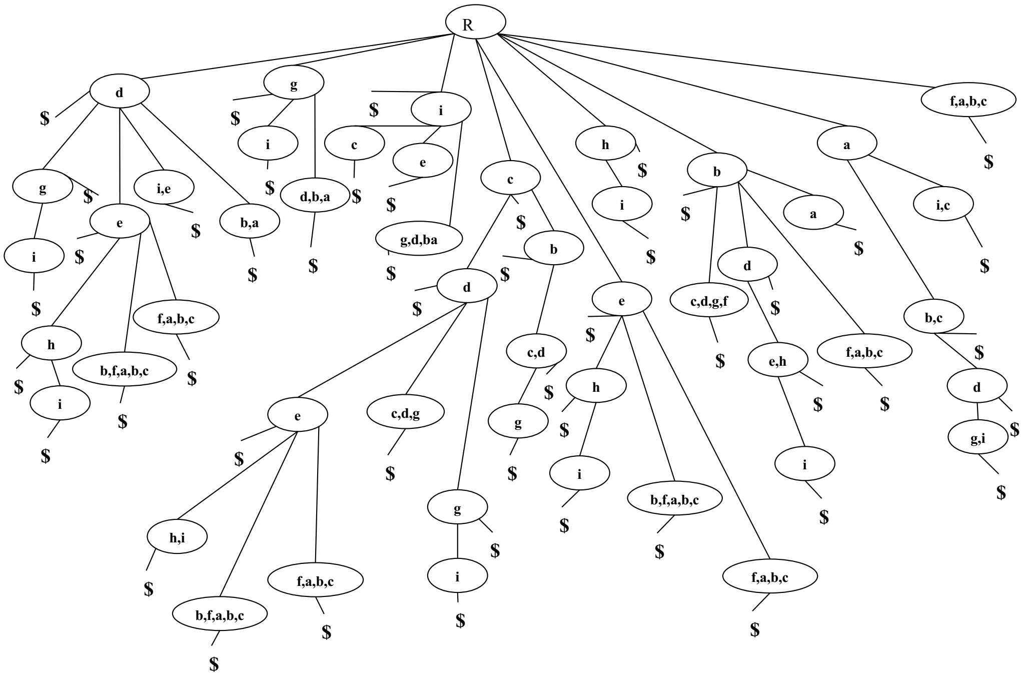
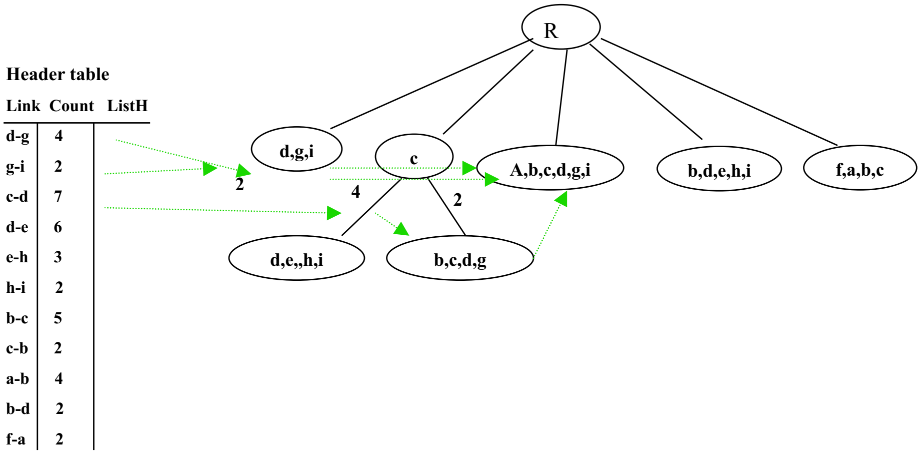


Figure 3.5: A collapsed version of the suffix tree in Figure 3.4.



Header table

Link	Count	ListH
d-g	4	
g-i	2	
c-d	7	
d-e	6	
e-h	3	
h-i	2	
b-c	5	
c-b	2	
a-b	4	
b-d	2	
f-a	2	

Figure 3.6: A collapsed version of the FS-tree in Figure 3.3.

Chapter 4

Frequent Sequences Mining from the FS-tree

Based on $MSuppC^{link}$ and $MSuppC^{seq}$ we classify the links in the database into three types (See Figure 3.1):

- *Frequent links*: links with support count $Supp^{link} \geq MSuppC^{seq} \geq MSuppC^{link}$. These links are stored in HT and are represented in the FS-tree and can be part of frequent sequences.

- *Potentially Frequent links*: links with support count $Supp^{link} \geq MSuppC^{link}$ and $Supp^{link} < MSuppC^{seq}$. These links are stored in the HT and are represented in the FS-tree but they can't be part of frequent sequences (needed for efficient incremental and interactive performance).

- *Non-frequent links*: links with support count $Supp^{link} < MSuppC^{link}$. These links are stored in $NFLT$ and are not represented in the FS-tree (needed for efficient incremental and interactive performance).

Only frequent links may appear in frequent sequences, hence, when mining the FS-tree we consider only links of this type. Before we introduce the FS-mine algorithm, we highlight the properties of the FS-tree.

4.1 Properties of the FS-trees

The FS-tree has the following properties that are important to the FS-mine algorithm:

- Any input sequence that has non-frequent link(s) is pruned before being inserted into the FS-tree. only potentially frequent subsequences of it are to be inserted in the FS-tree.

- If $MSuppC^{link} < MSuppC^{seq}$, the FS-tree is storing more information than required for the current mining task. Hence, the mining algorithm would not care about all sequences encoded in the FS-tree.

- We can obtain all possible subsequences that end with a given frequent link h by following the *ListH* pointer of h from the header table to correct FS-tree branches.

- In order to extract a sequence that ends with a certain link h from an FS-tree branch, we only need to examine the branch prefix path that ends with that link (h) backward up to the tree root. The frequency count of that sequence is equal to the count associated with the edge that ends this prefix path. We also can extract certain length of the prefix path based on user maximum pattern size preference. This feature is important for optimizing the mining phase[1].

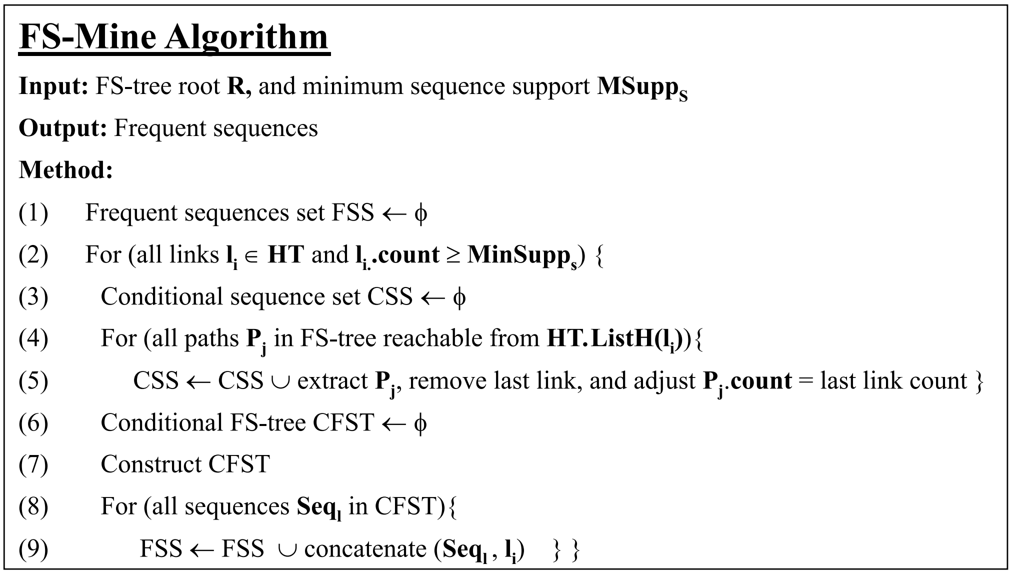
Now we describe in detail the mining steps that we use to extract frequent sequences from the FS-tree. We assume the FS-tree shown in Figure 3.3, and $MSuppC^{link}$ = 2 and

[1] For example if we follow the $ListH$ pointer for link $g - i$ from header table in Figure 3.3 to the second edge and assuming that, at the mining stage, the user is interested in patterns of maximum size of 4, we need to extract only the path prefix (c-d:2, d-g:1, g-i:1) instead of the full path starting from the tree root.

$MSuppC^{seq}$ = 3 as our running example.

4.2 FS-tree Mining Steps

Figure 4.1 lists the FS-Mine Algorithm. The algorithm has four main steps that are performed for only frequent links (potentially frequent links are excluded) in the header table (HT):



FS-Mine Algorithm

Input: FS-tree root **R,** and minimum sequence support $\mathbf{MSupp_S}$

Output: Frequent sequences

Method:

```
Frequent sequences set FSS $\leftarrow \phi$
For (all links $\mathbf{l_i} \in$ HT and $\mathbf{l_i}$.count $\geq$ $\mathbf{MinSupp_s}$) {
  Conditional sequence set CSS $\leftarrow \phi$
  For (all paths $\mathbf{P_j}$ in FS-tree reachable from HT.ListH($\mathbf{l_i}$)){
      CSS $\leftarrow$ CSS $\cup$ extract $\mathbf{P_j}$, remove last link, and adjust $\mathbf{P_j}$.count = last link count }
  Conditional FS-tree CFST $\leftarrow \phi$
  Construct CFST
  For (all sequences $\mathbf{Seq_l}$ in CFST){
      FSS $\leftarrow$ FSS $\cup$ concatenate ($\mathbf{Seq_l}$, $\mathbf{l_i}$)   } }
```

Figure 4.1: FS-Mine Algorithm.

Extracting derived paths. For link h in HT with $Supp^{link}(h) \geq MSuppC^{seq}$ we extract its derived paths by following the *ListH* pointer of h from HT to edges in the FS-tree. For each path in the FS-tree that contains h we extract its path prefix that ends at this edge and go maximum up to the tree root[2]. We call these paths *derived paths* of link h. For example, from Figure 3.3, if we follow the $ListH$ pointer for the link $e-h$ from the header table we can extract two derived paths: $(c-d:4, d-e:4, e-h:1)$ and

[2] Note the backward prefix extraction might terminate before the tree root and return a smaller prefix path in two cases: (1) reaching the limit determined by the user as the maximum pattern length he is interested in discovering or (2) encountering a potentially frequent link (since we do not mine for them).

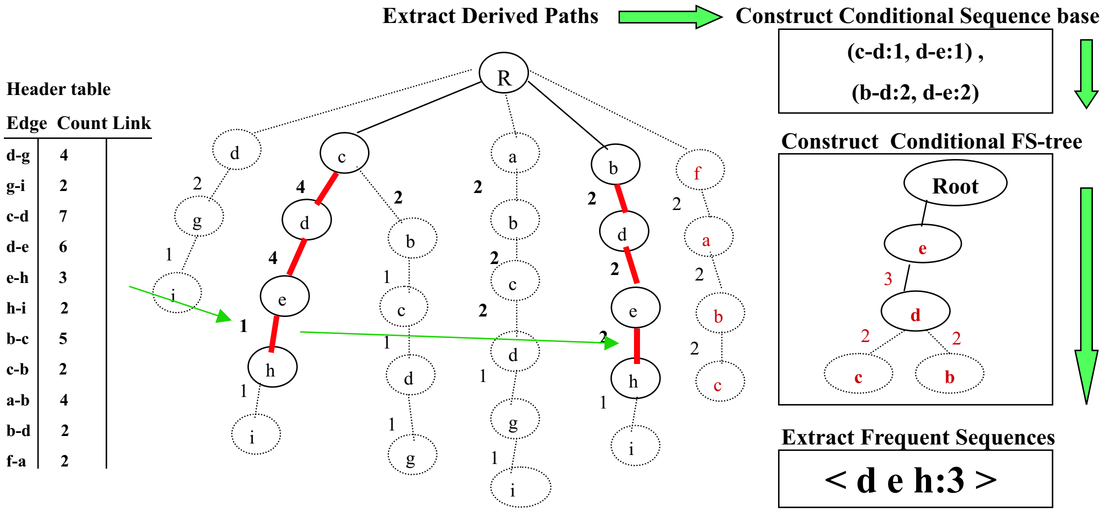
$(b - d : 3, d - e : 2, e - h : 2)$.

Constructing conditional sequence base. Given the set of derived paths of link h extracted in previous step we construct the *conditional sequence base* for h by setting the frequency count of each link in the path to the count of the h link (this gives the frequency of the full derived path). We also remove h from the end of each of the derived paths, since it is a common ending for all of them. For example, given the two derived paths extracted above for link $e - h$, the conditional base for that link consists of: $(c - d : 1, d - e : 1)$ and $(b - d : 2, d - e : 2)$ since $e - h$ frequency was 1 for the first one and 2 for the second one.

Constructing conditional FS-tree. Given the conditional base for h, we create a tree and insert each of the paths from the conditional base of h into it in a backward manner. We create necessary nodes and edges or share them when possible (incrementing edges counts). We call this tree the *conditional FS-tree* for link h. For example, given the conditional base for link $e - h$ the constructed conditional FS-tree is shown in Figure 4.2.

Extracting frequent sequences. Given a *conditional FS-tree* of a link h, we perform a depth first traversal for that tree and return only sequences satisfying $MSuppC^{seq}$. We append h to the end of each of the sequences extracted from the tree to obtain the full length frequent sequences for link h. By traversing the conditional FS-tree of link $e - h$ only the sequence $<de>$ satisfies the $MSuppC^{seq}$, so we extract it. We then append the link $e - h$ to the end of it to get the full size frequent sequence: $<deh : 3>$ where 3 represents the support (count) of that sequence.

We perform the same steps for the other frequent links in HT, namely $d - g$ $a - b$, $b - c$, $d - e$, and $c - d$. The detailed mining steps for these links are shown in Table 4.1. The last column in that table gives the final result for the mining process. The generated frequent sequences are: $<deh : 3>$, $<abc : 4>$, $<cde : 4>$, and $<bcd : 3>$ in addition to the frequent links themselves: ($<eh : 3>$, $<dg : 4>$, $<ab : 4>$, $<bc : 5>$, $<de : 6>$, and


Extract Derived Paths
Construct Conditional Sequence base
(c-d:1, d-e:1) ,
(b-d:2, d-e:2)
Construct Conditional FS-tree
Root
e
3
d
2
2
c
b
Extract Frequent Sequences
< d e h:3 >
R

Header table

Edge	Count	Link
d-g	4	
g-i	2	
c-d	7	
d-e	6	
e-h	3	
h-i	2	
b-c	5	
c-b	2	
a-b	4	
b-d	2	
f-a	2	

Figure 4.2: Mining steps for link $e - h$ from the example in Figure 3.1.

$<cd : 7>$) as they are considered frequent sequences of size 2.

Link	*Derived Paths*	*Conditional Sequence base*	*Conditional FS tree*	*Frequent Sequences generated*
e-h	(c-d:4, d-e:4, e-h:1) , (b-d:3, d-e:2, e-h:2)	(c-d:1, d-e:1) , (b-d:2, d-e:2)	(d-e:3)	$<deh : 3>$
d-g	(d-g:2), (c-b:2, b-3:1,c-d:1,d-g:1), (a-b:2,b-c:2 ,c-d:2,d-g:1)	(c-b:1, b-c:1,c-d:1), (a-b:1, b-c:1 ,c-d:1)	ϕ	ϕ
a-b	(a-b:2), (f-a:2, a-b:2)	(f-a:2)	ϕ	ϕ
b-c	(c-2:2, b-c:1), (a-b:2,b-c:2), (f-a:2, a-b:2,b-c:2)	(c-b:1), (a-b:2), (f-a:2, a-b:2)	(a-b:4)	$<abc : 4>$
d-e	(c-d:4, d-e:4), (b-d:3, d-e:2)	(c-d:4),(b-d:2)	(c-d:4)	$<cde : 4>$
c-d	(c-d:4), (c-b:2, b-c:1,c-d:1), (a-b:2,b-c:2 ,c-d:2)	(c-b:1, b-c:1), (a-b:2,b-c:2)	(b-c :3)	$<bcd : 3>$

Table 4.1: Mining for all sequences that satisfy $MSuppC^{seq}$=3.

Chapter 5

Incremental and Interactive Mining

5.1 Incremental Mining

In the presence of incremental updates $\triangle$**DB** to the sequence database, our goal is to propagate these updates into the generated frequent sequences with minimum cost. In particular, we aim to develop an incremental maintenance strategy that avoids the need for expensive scans of the complete sequence database and the complete recomputation of frequent sequences. In this section, we discuss requirements for supporting Incremental feature of the FS-miner. We then address how to maintain the FS-tree incrementally without reconstructing it from scratch and how to mine incrementally for frequent sequences.

5.1.1 Requirements for Supporting Incremental Mining in the FS-miner

We first highlight the additional information we need to maintain to support incremental mining:

1) The Non-Frequent Links Table **NFLT**, described earlier in Definition 1.

2) We extend the FS-tree node by adding to it a new structure called **seqEnd**. This

structure has two fields: **sid** and **count**. **sid** stores a record id of a sequence (from the database), or null. The value of **sid** of **seqEnd** is assigned at tree construction time. At the end of input sequence insertion into the tree, we might set **sid** of the node corresponding to the last item in the input sequence to be equivalent to the input sequence id. To assign a new value for **sid** two conditions must be satisfied: if the input sequence is inserted as one piece into the tree without being pruned[1] and if the **sid** does not contain another sequence id already (since we store only one id in this field). For each node with **sid** not equivalent to null we know that the tree branch that starts from the tree root and ends at that node is representing a complete input sequence(s) from the database. The second field, **count**, stores a count that indicates how many complete (unpruned) input sequences share the same tree branch that ends at this node. Figure 3.3 shows nodes in the tree with **sid** set to session IDs from the database [2].

5.1.2 Maintaining the FS-tree Incrementally

The FS-miner supports both database inserts and deletes. Our incremental FS-tree construction algorithm takes as input the FS-tree representing the database state before the update and $\triangle$**DB**. Then it inserts (or deletes) sequences from the tree. In some cases, the FS-tree construction algorithm performs partial restructuring of the tree, that is, some branches might be pruned or moved from one place to another in the FS-tree. Figure 5.1 shows the incremental FS-tree construction algorithm.

The algorithm first obtains the count of links in $\triangle$**DB** by performing one scan of $\triangle$**DB** (step 1 in the algorithm in Figure 5.1). In step 2, link counts in HT and $NFLT$ are incremented or decremented. $MSuppC^{seq}$ and $MSuppC^{link}$ values are updated if applicable. Link entries in $NFLT$ that now become frequent (or potentially frequent)

[1] All links in the sequence are frequent.

[2] Counts are not shown there for simplicity since they are all equal to 1 for current example.

are moved to HT. Links that were originally in HT and moved to $NFLT$, because they are no longer satisfying $MSuppC^{seq}$ and $MSuppC^{link}$ should no longer be presented in the FS-tree, so we prune edges that represent them from the FS-tree. This can be done by following their **ListH** pointer to their edge occurrences in the FS-tree. We remove each edge, then insert the subsequent tree whose root was attached to the removed edge, from the top of the FS-tree, sharing nodes and edges when possible (steps 4 through 8). For links that were originally in $NFLT$ and moved to HT, we obtain input sequences in the order which they appear from the original database[3]. We insert them into the FS-tree using the function $insertTreeInc$ (steps 9 through 12). The main difference between this function and the normal $insertTree$ function described earlier is that $insertTreeInc$ aims to compose sequences that were previously decomposed by the $insertTree$ at the initial tree construction phase[4]. For each of the obtained sequences, the $insertTreeInc$ function traverses the sub-path of it already represented in the FS-tree (staring for the root). When we encounter a link in the inserted sequence that was not frequent before the update and now is frequent (or potentially frequent), we create a new edge and node for it (or share an edge and a node and increment edge's count). After this point, we insert the remaining subsequence starting from the current node. At the same time we call the $deleteTree$ function that deletes the same remaining subsequence from the top of the FS-tree (as it had previously been inserted there). This is done by traversing the tree from the top for that subsequence and decrementing the count of any traversed edge. If the count of decremented edge becomes 0, the edge and its subsequent subtree are deleted from the FS-tree. The last phase (steps 14 through 17) inserts (or deletes) input sequences from $\triangle$**DB** into the tree using the $insertTree$ (or the $deleteTree$) function.

[3] Recall that for each we maintained a list of sequence IDs in which the link appeared in the database.

[4] This is needed because if a certain link was non-frequent before the update and became frequent later, during initial tree construction time, the $insertTree$ function has previously broken any input sequence that contained that link at this place and inserted it as subsequences in the FS-tree. But now as that link becomes frequent due to the update, the $insertTreeInc$ will bridge that gap again and put those subsequences together.

Example 1: As an example for incremental inserts, assume that the following tuples where inserted into the log file in our running example in Figure 3.1: $\{16, < efa >\}$, $\{17, < ef >\}$, $\{18, < efab >\}$. Figure 5.2 shows the effect of inserting the new input sequences. First, we scan the new records to obtain counts of links in the inserted session and we update counts of links $a - b$ and $f - a$ in HT and link $e - f$ in $NFLT$. Assuming the $MSuppC^{link}$ and $MSuppC^{seq}$ maintain the same values (2 and 3 respectively), link $a - b$ maintains the same status (frequent), links $f - a$ and $e - f$ becomes frequent thus are moved to table HT. The next step is to prune the tree by removing edges for any link transitioned from frequent to non-frequent. In this example we do not have any. Next we restructure the tree for links that were not frequent and became frequent (link $e - f$ in our example). We obtain from the **SIDs** field of link $e - f$ entry in $NFLT$ sequence id = 12 as the only sequence where the link appears in original database. We retrieve this sequence ($<cdefabc>$)from the original database and insert it into the FS-tree using the $insertTreeInc$ function. This function will first traverse the tree branch that corresponds to the subsequence represented in the tree from before ($<cde>$) and create a new edge for it when it encounters the link $e - f$. Insertion will then continue for the remaining subsequence ($<fabc>$) following this point. At the same time it calls the $deleteTree$ function for the subsequence $<fabc>$ to delete it from the root of the FS-tree. The last step in the incremental FS-tree constructions is to insert all the input sequences from $\triangle$**DB** in the FS-tree using the $insertTree$ function, resulting in the tree shown in Figure 5.1.

Example 2: As an example for incremental deletes, assume that we delete the tuple $\{$8, $<bdehi>\}$ from the **DB**. In Figure 5.3 we note that as a result of deleting that tuple the links $b - d$ and $h - i$ become non-frequent and should not be represented in the FS-tree anymore. The tree pruning step will cause the tree branch ($b - d - e - h - i$) to be cut at $b - d$ and $h - i$ edges, and the part ($b - d - e$) to be inserted at the root of the tree sharing the existing node d and creating nodes e and h. also the edge $h - i$ in the tree branch ($c - d - e - h - i$) is pruned. Now the last step is to call the function $deleteTree$ to delete the sequence $<bdehi>$. This will cause the tree branch ($b - d - e$) edges counts to decrement to 1.

Note that the incremental FS-tree construction algorithm shown in 5.1 can accept both types of updates, insertion of new sessions and deletions of existing sessions, in a batched mode, and process them together.

5.1.3 Mining the FS-tree Incrementally

After refreshing the FS-tree, the incremental mining is invoked for certain links in HT, namely those affected by the update. We first need to understand the effect of database updates on different types of links[5]. We can classify the possible change in the type of a link due to database updates into 9 different transaction types as shown in Figure 5.4[6]. We categorize how the incremental mining algorithm deals with these different transaction cases into four categories:

(1) For transaction of type 1: we mine for those links if they are affected [7].

(2) For transactions of type 2 and 4: we mine for these links.

(3) For transactions of type 3 and 5: we delete previously discovered patterns that include these links.

(4) For transactions of type 6, 7, 8 and 9: we do nothing. The incremental FS-mine algorithm is shown in Figure 5.5. The mining algorithm starts by dropping any sequence in the previously discovered frequent sequences that is either of transaction type 3 or 5 (no longer satisfying the new $MSuppC^{seq}$, if changed due to the update). Then for all links in the **HT** if the link satisfies the new $MSuppC^{seq}$ and if it is of transaction type 2,

[5] The three different types of links we discussed earlier (frequent, potentially frequent and non-frequent).

[6] The starting point of the arrow refers to where the link used to be before the database updates and the ending point of the arrow refers to where the link ends up as a result of the database update.

[7] By affected we mean if the link was in $\triangle$DB, or if the link was in one of the subsequences that were deleted from the FS-tree in the tree restructuring process described earlier.

4 or of type 1 and affected by the update, the algorithm applies the $FS - mine$ algorithm for these links.

Example 3: Consider that $\triangle$**DB** denotes an insertion of $\{16, < efa >\}$, $\{17, < ef >\}$, $\{18, < efab >\}$ described in example 3. link $a - b$ is affected by the update and maintained the same frequent status after the update. Link $f - a$ status is changed from potentially frequent to frequent due to the update. Link $e - f$ status is changed from non-frequent to frequent due to the update. These three links are the only ones affected by the update, hence we need to mine for these three links. Table 5.1 shows the steps in mining for these links and the resulting generated frequent sequences.

Link	*Derived Paths*	*Conditional Sequence base*	*Conditional FS tree*	*Frequent Sequence generated*
a-b	(c-d:4, d-e:4, e-f:1, f-a:1, a-b:1), (a-b:2), (f-a:1, a-b:1), (e-f:3, f-a:2, a-b:1)	(c-d:1, d-e:1, e-f:1, f-a:1) (f-a:1) (e-f:1, f-a:1)	(f-a:3)	$<fab : 3>$
f-a	(c-d:4, d-e:4, e-f:1, f-a:1), (f-a:1), (e-f:3, f-a :2)	(c-d:1, d-e:1, e-f:1), (e-f:2)	(e-f:3)	$<efa : 3>$
e-f	(c-d:4, d-e:4, e-f:1), (e-f:3)	(c-d:1, d-e:1)	ϕ	ϕ

Table 5.1: Incrementally Mining for link e-h where $MSuppC^{seq}$=3.

Example 4: Consider that $\triangle$**DB** denotes a deletion of the record with ID = 8 from the web file in Figure 3.1. In this case the affected links are: $b - d$, $d - e$, $e - h$, and $h - i$. And since $b - d$, $e - h$ and $h - i$ are no longer supporting the $MSuppC^{seq}$ (assuming 3) we delete any frequent sequences previously discovered that contain any of those links. Namely from the frequent sequences previously generated (and shown in Table 4.1) we delete the sequence $<deh : 3>$. Now we look in the **HT** for those link that satisfy the $MSuppC^{seq}$ and of type 2, 4, or 1 (and affected by the update). Only links $d - e$ and $e - h$ are satisfying this criteria so we apply the mining steps for each of them.

5.2 Interactive Mining

We want to allow the user to make changes to the minimum support value and get a response in a small amount of time. To achieve this goal we need to minimize the need to access the database and to re-execute the mining algorithm. We can support this goal in our system by setting the $MSuppC^{link}$ to a small enough value that is less than any value of $MSuppC^{seq}$ that the user is likely to use. The rational here is that since $MSuppC^{link}$ is responsible for determining the potentially frequent links and hence allow them to be represented in the FS-tree. This ensures that if the user lowered the $MSuppC^{seq}$ to a value that is $\geq MSuppC^{link}$ we will have enough information in the FS-tree to calculate the new frequent sequences without the need to reference the original database. This is done by applying the FS-mine algorithm for the subset of links in **HT** that is satisfying the new $MSuppC^{seq}$. On the other hand, if the user increased the $MSuppC^{seq}$, we directly provide him/her with the subset of frequent sequences previously discovered that satisfies the new $MSuppC^{seq}$ without the need for any further computation. Our system also allows the user to vary the size of the frequent patters he is interested in discovering. In this case the system does not use the input database, it only uses the FS-tree to extract the frequent sequences for the required size.

Now we give an example for lowering the $MSuppC^{seq}$. The frequent sequences shown in Table 4.1 were generated based on $MSuppC^{seq}$ = 3. Assume that $MSuppC^{link}$ = 2 was small enough to satisfy most of the expected changes to the system $MSuppC^{seq}$ and that the user later on sets $MSuppC^{seq}$ to 2, we can directly apply the FS-mine since our FS-tree already has all the information about links and sequences with minimum frequency of 2. For this we can obtain the result shown in Table 5.2 without the need for re-scanning any part of the input database.

Link	*Derived Paths*	*Conditional Sequence base*	*Conditional FS-tree*	*Frequent Sequence generated*
f-a	(f-a:2)	ϕ	ϕ	ϕ
h-i	(c-d:d,d-e:4 ,e-h:1,h-i:1), (b-d:3,d-e:3 ,e-h:2,h-i:1)	(c-d:1,d-e:1 ,e-h:1) (b-d:1,d-e:1 ,e-h:1)	(d-e:2,e-h:2)	$<dehi : 2>$
g-i	(d-g:2,g-i:1) (a-b:2,b-c:2 ,c-d:2,d-g:1,g-i:1)	(d-g:1), (a-b:1,b-3:1 ,c-d:1,d-g:1)	(d-g:2)	$<d - g - i : 2>$
c-b	(c-b:2)	ϕ	ϕ	ϕ
b-d	(b-d:2)	ϕ	ϕ	ϕ
e-h	(c-d:4, d-e:4, e-h:1) , (b-d:3, d-e:2, e-h:2)	(c-d:1, d-e:1) , (b-d:2, d-e:2)	(d-e:3), (b-d:2, d-e:2)	$<deh : 3>$ $<bdeh : 2>$
d-g	(d-g:2), (c-b:2, b-c:1,c-d:1,d-g:1), (a-b:2,b-c:2 ,c-d:2,d-g:1)	(c-b:1, b-c:1,c-d:1), (a-b:1,b-c:1 ,c-d:1)	(b-c:2 ,c-d:2)	$<bcdg : 2>$
a-b	(a-b:2), (f-a:2, a-b:2)	(f-a:2)	(f-a:2)	f-a-b :2
b-c	(c-b:2, b-c:1), (a-b:2,b-c:2), (f-a:2, a-b:2,b-c:2)	(c-b:1), (a-b:2), (f-a:2, a-b:2)	(a-b:4) (f-a:2, a-b:2)	$<abc : 4>$ $<fabc : 2>$
d-e	(c-d:4, d-e:4), (b-d:3, d-e:2)	(c-d:4), (b-d:2)	(c-d:4) (b-d:2)	$<cde : 4>$ $<bde : 2>$
c-d	(c-d:4), (c-b:2, b-c:1,c-d:1), (a-b:2,b-c:2 ,c-d:2)	(c-b:1, b-c:1), (a-b:2,b-c:2)	(b-c :3) (a-b:2, b-c:2)	$<bcd : 3>$, $<abcd : 2>$

Table 5.2: Mining for $MSuppC^{seq}$=2.

Incremental FS-tree construction Algorithm

Input: FS-tree root **R** and Δ**DB,** and new minimum link support **MSupp**$_l$

Output: updated FS-tree

Method:

```
Scan ΔDB, and collect counts (+ and -) for links
Update counts of links in HT and NFLT
Move links,between HT and NFLT, based on MinSupp$_l$
For (all links $l_l$ moved from HT to NFLT) {
    Start from $l_l$.ListH pointer
    For (every edge p-P in the FS-tree reachable from $l_l$.ListH)
        Cut the edge p-P
    Call insertTree (R, P) }
For (all links $l_l$ moved from NFLT  to HT) {
    For (every sequence ID in $l_l$.SIDs) {
        Obtain input sequence inpSeq with ID from DB
        Call insertTreeInc (R, inpSeq) } }
For (each record $Rec_i$ in ΔDB get $Rec_i$.inpSeq) {
    If ($Rec_i$ is an insert)
        Call insertTree($Rec_i$.InSeq, R)
    Else if ($Rec_i$ is a delete)
        Call deleteTree ($Rec_i$.InpSeq, R)}
```

Function insertTreeInc (tree root node **S,** sequence **p-P**) **:** Updated FS-tree.

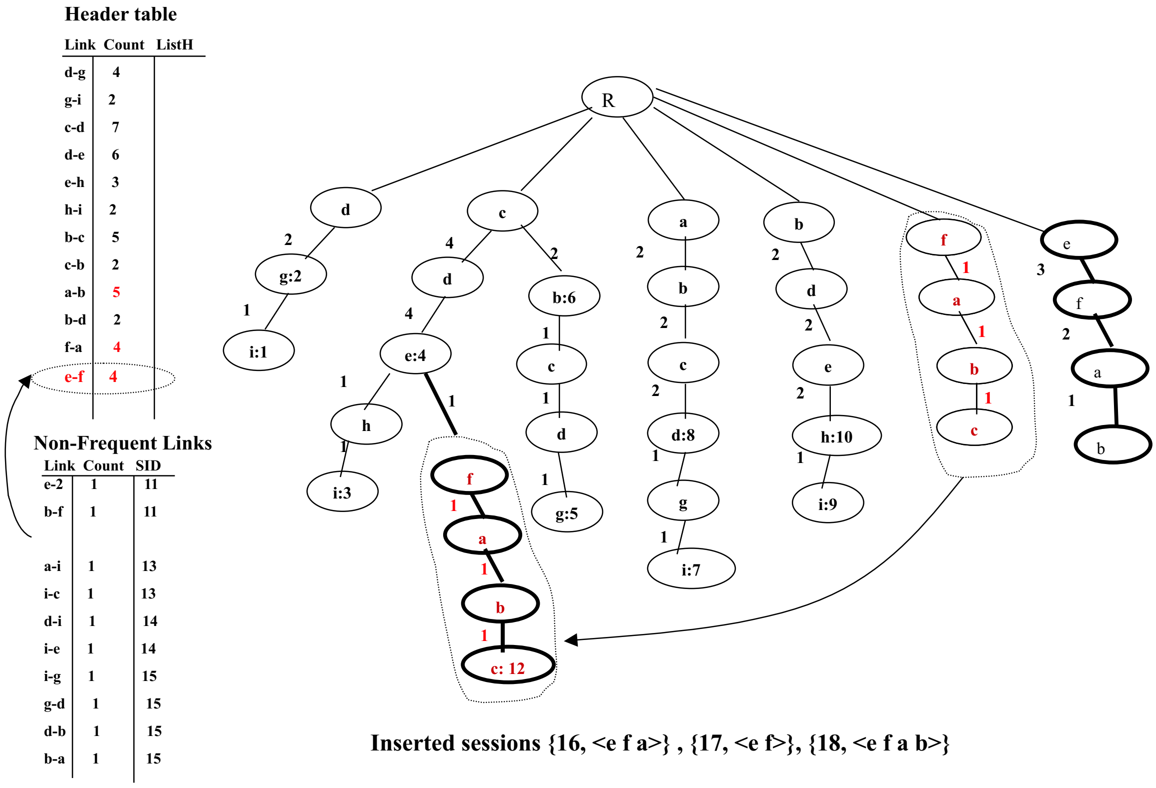
```
If (link p-P ∈ HT) {
    If (p-P was originally in HT){
        If (S has no child with name = p) {
            Create node N with  N.node-name = p
            Create edge S-N with S-N.edge-count = 1}
    }Else if (p-P was originally in NFLT){
            Node ptr = call deleteTree (R, P)
            add ptr as a child to p }
        If (P is non-empty) {call insertTreeInc(N, P)}
}Else if (link p-P ∈ NFLT) {
        If (P is non-empty) {call insertTreeInc(R, P) } }
```

Function deleteTree (tree root node **S,** sequence **p-P**) **:** Updated FS-tree.

Precondition: counts of links in **HT** and **NFLT** are already updated

```
If  (S has child N and S-N = p-P) {
        Decrement S-N.count, and deleted it if count became 0.
        If (P is non-empty){call deleteTree (N, P) }
}Else{
    If (P is non-empty) call deleteTree (R, P)}
```

Figure 5.1: Incremental FS-tree construction.



Header table

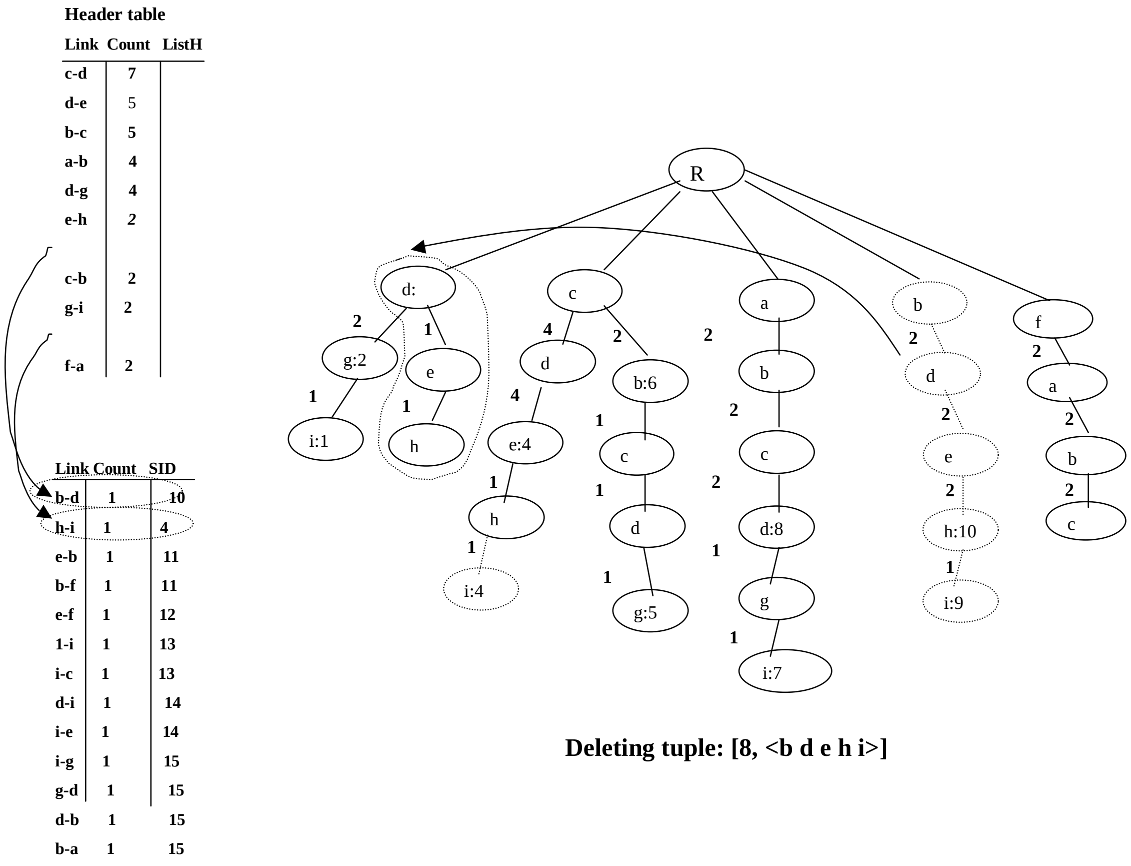
Link	Count	ListH
d-g	4	
g-i	2	
c-d	7	
d-e	6	
e-h	3	
h-i	2	
b-c	5	
c-b	2	
a-b	5	
b-d	2	
f-a	4	
e-f	4	

Non-Frequent Links

Link	Count	SID
e-2	1	11
b-f	1	11
a-i	1	13
i-c	1	13
d-i	1	14
i-e	1	14
i-g	1	15
g-d	1	15
d-b	1	15
b-a	1	15

Inserted sessions {16, <e f a>} , {17, <e f>}, {18, <e f a b>}

Figure 5.2: The effect of inserting records to the database in Figure 3.1.



Header table

Link	Count	ListH
c-d	7	
d-e	5	
b-c	5	
a-b	4	
d-g	4	
e-h	*2*	
c-b	2	
g-i	2	
f-a	2	

Link	Count	SID
b-d	1	10
h-i	1	4
e-b	1	11
b-f	1	11
e-f	1	12
1-i	1	13
i-c	1	13
d-i	1	14
i-e	1	14
i-g	1	15
g-d	1	15
d-b	1	15
b-a	1	15

Figure 5.3: The effect of deleting records from the database in Figure 3.1

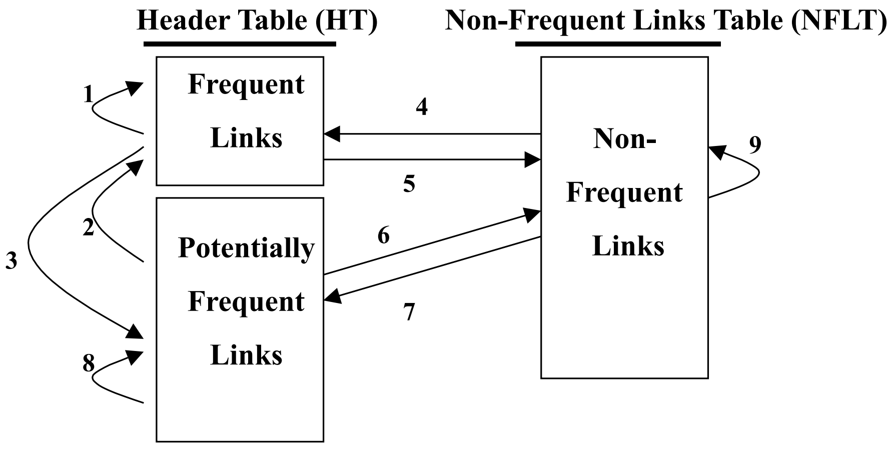


Figure 5.4: The effect of incremental updates on links in the database

Incremental FS-Mine Algorithm

Input: FS-tree root **R,** set of frequent sequences **fSeq** and **set of** affected links **affLinks**

Output: new frequent sequences based on **affLinks**

Precondition: all counts for links are updated in HT and NFLT

Method:

```
For (all frequent sequences $\mathbf{fSeq_i}$ )
    If ($\mathbf{fSeq_i}$ count < $\mathbf{Min\text{-}Supp_s}$ or $\mathbf{fSeq_i}$ has link with count < $\mathbf{Min\text{-}Supp_s}$){
        delete $\mathbf{fSeq_i}$}
For (all links $\mathbf{l_i} \in \mathbf{HT}$ where $\mathbf{l_i}$.count >= $\mathbf{Min\text{-}Supp_s}$)
        if ($\mathbf{l_i}$ moved from NFLT or $\mathbf{l_i}$ count was < $\mathbf{Min\text{-}Supp_s}$ or $\mathbf{l_i} \in$ affLinks ) {
            call FS-Mine (R) for $\mathbf{l_i}$}
```

Figure 5.5: Incremental FS-Mine Algorithm.

Chapter 6

Implementation

Figure 6.1 shows The FS-Miner system. The system has been implemented in Java on a Windows machine. It has four main parts: FS-Tree Constructor, FS-Miner, Incremental/Interactive FS-Tree Maintainer, and Incremental/Interactive FS-Miner.

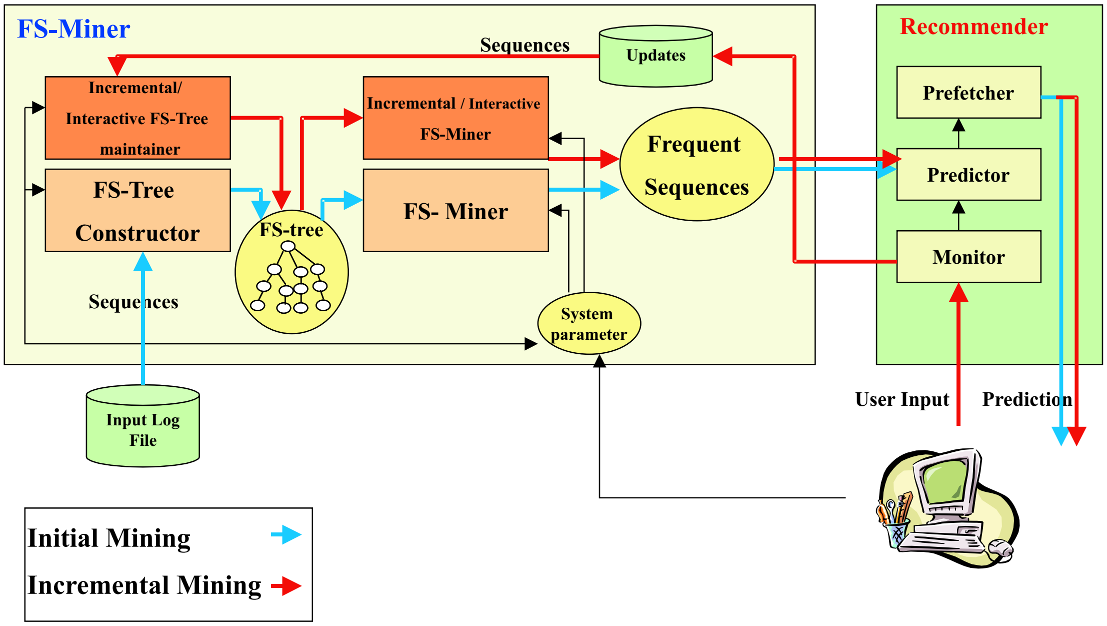


Figure 6.1: FS-Miner architecture

The **FS-tree Constructor** takes as input a web log file and two system parameters:

Minimum Link Support Ratio $MSuppR^{link}$ and a Minimum Sequence Support Ratio $MSuppR^{seq}$. It first performs one scan for the input log file and finds the count of each distinct link in the input file and the total count for all links in the input log file and depending on the last count and the $MSuppR^{link}$ it finds the $MSuppC^{link}$ that is used to decide which links are to be represented in the FS-Tree and which ones are not. Also using the count of total links in the input file and the $MSuppR^{seq}$ it calculates the $MSuppC^{seq}$ that is used later in the mining steps. The FS-tree Constructor module next constructs the FS-Tree and the HT and the $NFLT$ tables as described in section 3.4.

The **FS-Miner** uses the FS-Tree previously constructed to mine for frequent sequences given the Minimum Sequence Support $MSuppC^{seq}$ parameter. The mining process is done in four main steps as discussed in section 4.2 and will result in all frequent sequences that satisfy the predefined $MSuppC^{seq}$. The discovered frequent sequences can be used as an input for a recommender system for the purpose of predicting users' access behavior and hence prefetching pages to their machine. This can be done interactively during a user session by tracing the user current page access pattern and matching that to frequent sequences pattern previously discovered, and from this point we can predict the user next page request(s). Besides using the new page access sequences of users for predicting their access behavior, these new sequences themselves are considered as an incremental input to the input log file we started with, and hence, they might change the result (the set of frequent sequences previously discovered). This we might invalidate some previously discovered frequent sequences, introduce new frequent sequences, and/or change the frequency of perviously discovered frequent sequences. For that we collect all new users' input sessions, that were encountered after the last FS-Tree construction, and store them as an update to the web log file. This incremental input is to be used later for incremental mining as we will describe next.

The **Incremental/Interactive FS-tree Maintainer** takes as input the update web log file and performs a scan over the file to obtain link counts. Using these link counts the module updates both $MSuppC^{link}$ and $MSuppC^{seq}$. And after that it restructure the FS-Tree if needed with any added or deleted sequences and then insert the new sequences into the FS-Tree as described in section 5.1.2. This module is also responsible for maintaining the FS-Tree in case of changing $MSuppR^{link}$ and hence $MSuppC^{link}$.

The **Incremental/Interactive FS-Miner** works on the FS-Tree that was maintained by the Incremental/Interactive FS-tree Maintainer. It incrementally invalidate previously discovered frequent sequences, discover new ones, and/or modify frequencies of previously discovered ones as a result of the incremental web log file. This process is described in details in 5.1.3. This module is also responsible for maintaining discovered frequent sequences in case of change to the $MSuppC^{seq}$ by the user, as was discussed in 5.2.

Chapter 7

Experimental Evaluation

7.1 Data Sets and Experimental Setup

We use two data sets to test our system, the Microsoft Anonymous Web Data Set and the MSNBC Anonymous Web Data Set, both obtained from [Het99]. Each data set consists of a collection of sessions where each session has a sequence of page references. The Microsoft anonymous data set has 32711 sessions, each session contains from 1 up to 35 page references. The MSNBC data set has 989818 sessions. A session contains from 1 up to up to several thousands of page references [1]. The main difference between the two data sets of interest to us is the number of distinct pages. The Microsoft data set has 294 distinct pages, while the MSNBC data set has only 17 distinct pages (as each one of these pages is in fact encodes a category of pages).

We compare the performance of our algorithm against two other algorithms from the literature: the $PathModelConstruction$ algorithm [SYLZ00], and a variation of Apriori algorithm [AS94] for sequence data [2]. We have implemented the three systems in Java

[1] We preprocessed the MSNBC data sets to keep a maximum of 500 page references for each session to smooth the effect of very large sessions on experimental time.

[2] Optimized using hashing techniques and modified to provide the same sequential patterns we use.

in a Windows environment. We ran the experiments on a PC with a 733 MHz Pentium processor and 512 MB of RAM.

7.2 Experimental Results

We have conducted three different experiments using both data sets. We first tested the scalability of our approach with respect to changes in input database size.

7.2.1 Varying data set size

Figure 7.1 shows that our system, and the other two systems, scale linearly in the database size. Our system tends to outperform the other two systems with data sets that have a large number of distinct items (such as the MS data set) while Apriori tends to perform slightly better in the case of data sets with a very small distinct items (such as the MSNBC set). This is because the candidate generation cost in this case is small. Note that part of the cost of our system is due to maintaining the extra data needed for incremental and interactive tasks. So while the other two systems are only performing the mining task at hand, our system is also maintaining as a byproduct the FS-tree that can later be used for incremental and interactive operations.

7.2.2 Varying support threshold level

We also tested the scalability of the system with respect to a decrease of the support threshold level. Figure 7.2 shows that our system scales better with a decrease of support level. In fact our system shows a very smooth response time to the decrease in the support level unlike the other two systems that experience a dramatic increase in cost when they hit lower support values. This implies that even if we choose to utilize a low $MSuppC^{link}$,

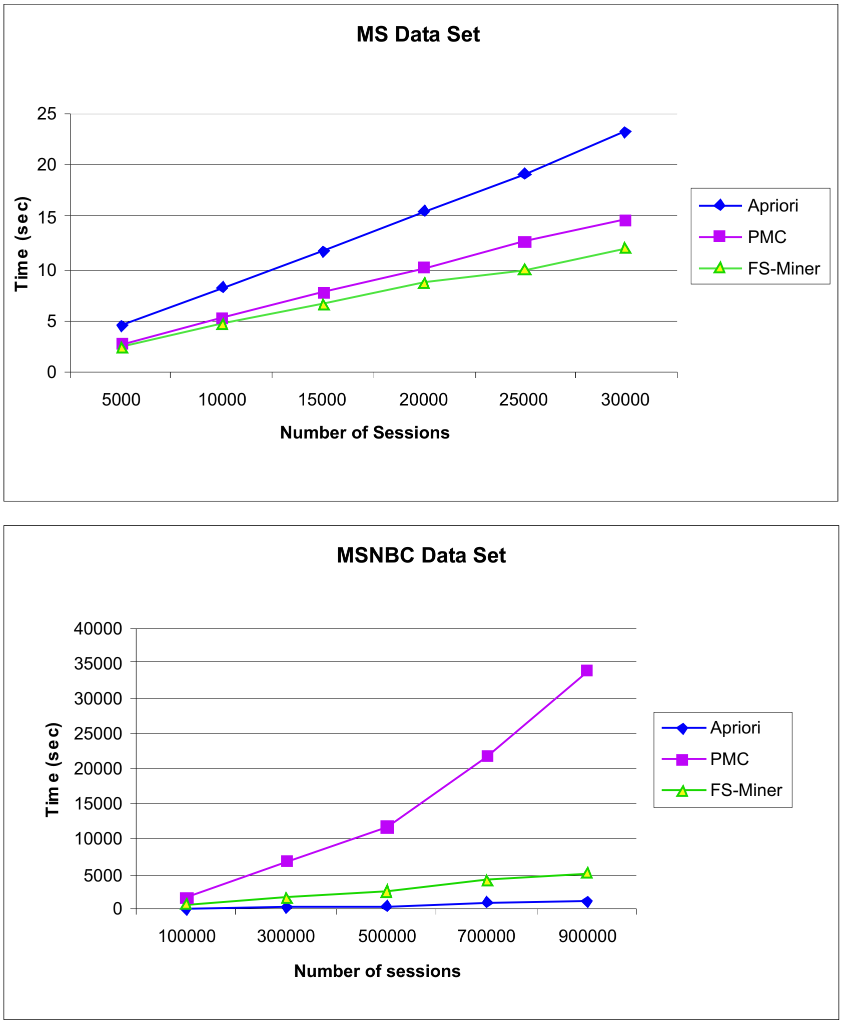


Figure 7.1: Scalability with number of input sessions

to better support the incremental and interactive tasks of the system at later stages, our system does not experience a significant overhead.

7.2.3 Incremental mining

The third experiment compares the performance of the incremental mining versus recomputation. Figure 7.3 shows that even with an incremental update size of up to one quarter of the size of the original database size, the FS-Miner's incremental feature provides significant time savings over full recomputation.

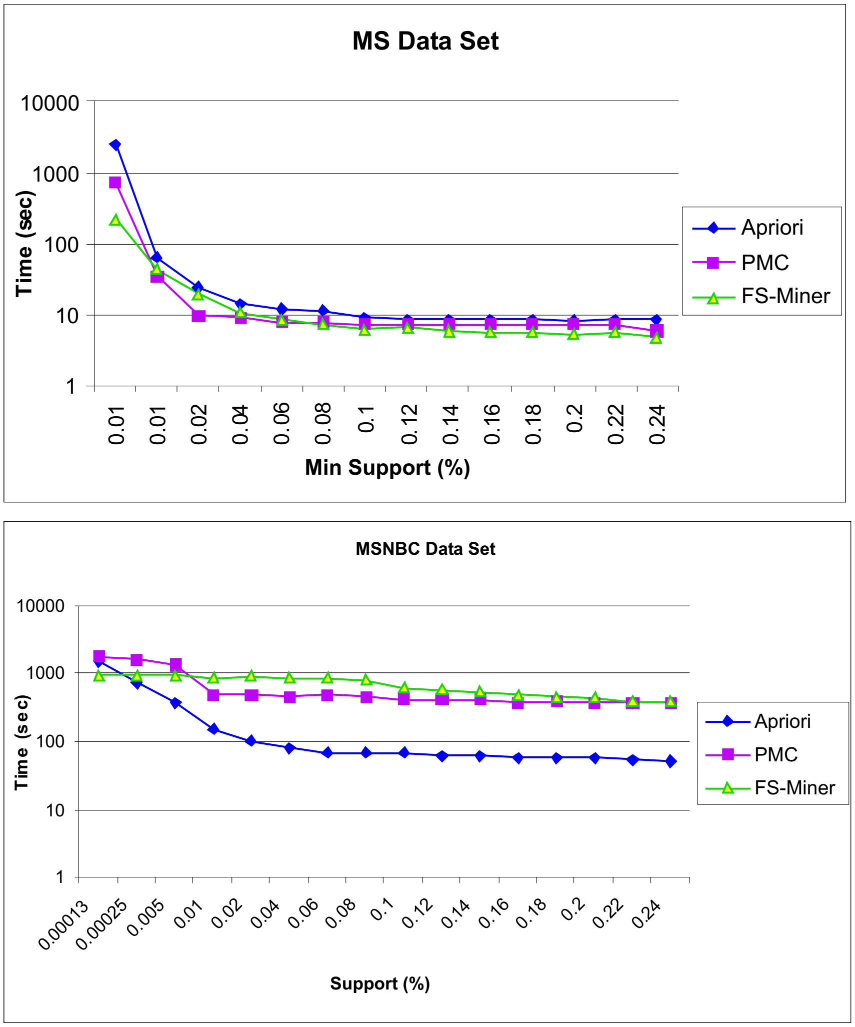


Figure 7.2: Scalability with support threshold

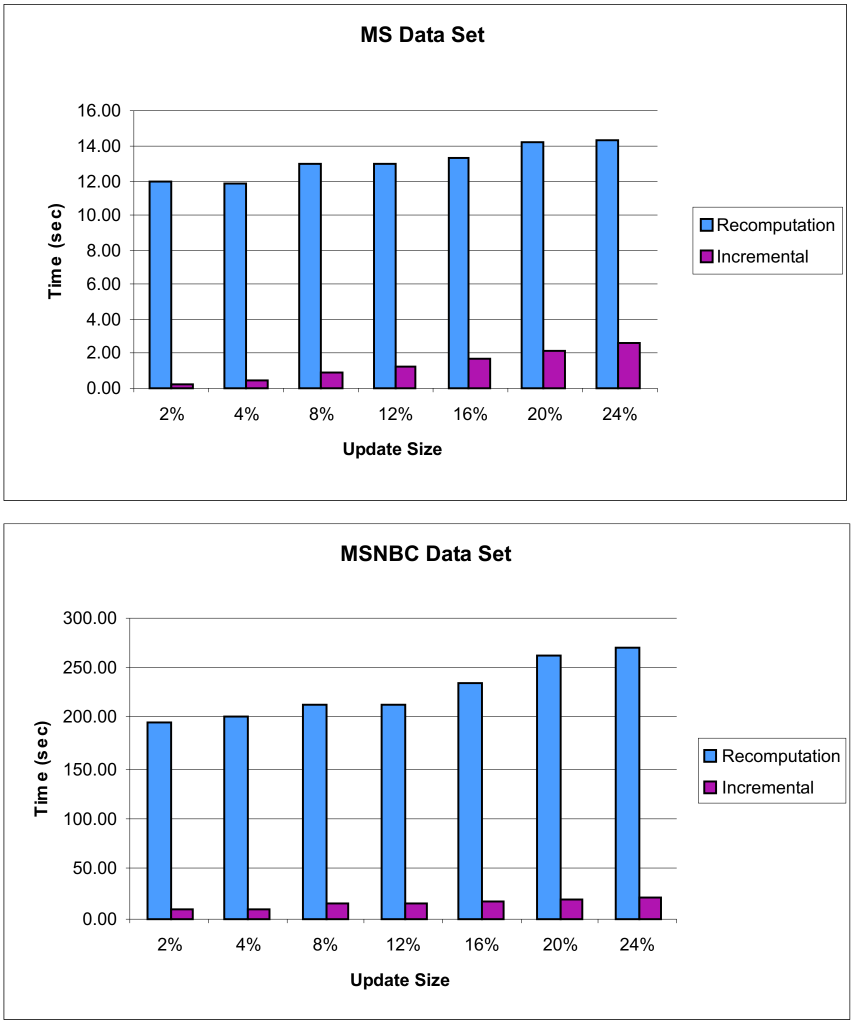


Figure 7.3: Incremental mining

Chapter 8

Conclusions and Future Work

8.1 Conclusions

In this thesis we have proposed the FS-Miner, an incremental sequence mining system. The FS-Miner constructs a compressed data structure (FS-tree) that stores potentially frequent sequences and uses that structure to discover frequent sequences. This technique requires only two scans for the input database. Our approach allows for incremental discovery of frequent sequences when the input database is updated eliminating the need for full recomputation. The FS-miner calculates the incremental effect of these updates directly from the updated FS-tree. Our approach also allows interaction with the user in the form of changes to the system minimum support, and in most cases we can satisfy these requests without having to use the original database. Our experiments show that the performance of our system scales linearly to increases in the input database size. It shows an excellent time performance when handling data sets with large number of distinct items. The FS-miner also shows great scalability with the decrease of the minimum support threshold when typically other mining algorithms tend to exhibit dramatic increases in response time. Finally the incremental functionality of our system shows a significant performance gain over recomputation even with large update sizes relative to the size of the original database.

8.2 Future Work

The mining system we have developed is basically targeted towards discovering frequent sequences for the purpose of prediction. The way we calculate the minimum sequence support threshold (by dividing the frequency of the sequence on the total number of links in the input web log file) takes into account the need to consider duplicates in sequence patterns, which is an important requirement in the context of web usage mining.

For other mining applications it might be needed that we calculate the minimum support of sequences (or item sets) as the frequency of sequences related to the total number of sessions (transactions) with no consideration to duplicates. In this case the support will be similar to the one calculated in association rule mining. It is easy to adapt our proposed system to work with this other notion of support. The main adaptation needed is to count the occurrence of each link (item) in each input session (transactions) one time regardless of how many times it appears. This involves a minor change in the tree construction subsystem only and will not affect the mining subsystem. If we run the system using this modified notion of support on a web log file we will get as output new frequent sequences, in which duplicates are not considered and the frequency is based on the total number of sessions in the input web log file.

A more interesting scenario is to extend the system to incorporate both the current support threshold (based on total number of link) and the support calculated as the frequency of sequences to the total number of sessions. This will require adding some new parameter to the system:

- *Link support (session support)*$Supp_s^{link}$

- *Sequence support (session support)* ${Supp_s}^{seq}$

- *Minimum Link support ratio (session support)* ${MSuppR_s}^{link}$

- *Minimum Sequence Support Ratio (session support)*${MSuppR_s}^{seq}$

- *Minimum Link support count (session support)*${MSuppC_S}^{link}$

- *Minimum Sequence support count (session support)*${MSuppC_s}^{seq}$

These new parameters are similar in meaning to their counterparts previously used in this document (discussed in Section 3.2). The main difference is that they do not consider duplicates and the support threshold calculation is based on the total number of sessions and not the total number of links as a cetraria for determining the frequent sequences.

We need also to extend the data structures we currently have as follows:

- Edges on the FS-tree need to have one more count field to store the count when not considering duplicates.

- Both the HT and $NFLT$ need to have one more column for storing the count of link when not considering duplicates.

With these extensions, the system can run in three modes:

- *Link support criteria*: this is the standard case that we have so far. In this mode the $FS-Tree$ the HT and $NFLT$ tables are built based on $MSuppR^{link}$, and the mining is done based on $MSuppR^{seq}$. We output patterns that are frequent based only on the total number of links.

- *Session support criteria*: in this mode the $FS{-}Tree$ and the HT and $NFLT$ tables are built based on ${MSuppR_s}^{link}$, and the mining is done based on ${MSuppR_s}^{seq}$. We output patterns that are frequent based only on the total number of sessions.

- *Both support criteria*: in this mode the $FS - Tree$ and the HT and $NFLT$ tables are built based on $MSuppR^{link}$ and ${MSuppR_s}^{link}$. This means that the HT will include links that are frequent based on $MSuppR^{link}$ or ${MSuppR_s}^{link}$, the $FS - Tree$ will include potentially frequent sequences based the same two paraments. The $NFLT$ will include links that are not frequent based on either the two paraments. These settings will allow perform three different mining tasks:

  - Mining for frequent sequences based on $MSuppR^{seq}$. We output patterns that are frequent based on total number of links.

  - Mining for frequent sequences based on ${MSuppR_s}^{seq}$. We output patterns that are frequent based on total number sessions.

  - Mining for frequent sequences based on both $MSuppR^{seq}$ and ${MSuppR_s}^{seq}$. In this mining scenario, the mining will involve less links from the HT since we have to satisfy both $MSuppR^{seq}$ and ${MSuppR_s}^{seq}$, and hence will also involve less cost on the mining phase since we will be extracting less conditional paths from the $FS - Tree$. We output patterns that are frequent based on both total number of links and total number of sessions.

Other future work might involve designing an efficient persistent storage mechanism for storing the FS-Tree, better design for the $NFLT$ to eliminate or minimize the need to access original input file in case of huge update. Also it might be interesting to study possible extension to this approach to support generalized frequent sequences that allow wildcards.

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