Mining Sequential Patterns from Temporal Streaming Data

A. Marascu and F. Masseglia

INRIA Sophia Antipolis
2004 route des Lucioles - BP 93
06902 Sophia Antipolis, France

E-mail: {Alice.Marascu,Florent.Masseglia}@sophia.inria.fr

Abstract. In recent years, emerging applications introduced new constraints for data mining methods. These constraints are typical of a new kind of data: the *data streams*. In a data stream processing, memory usage is restricted, new elements are generated continuously and have to be considered as fast as possible, no blocking operator can be performed and the data can be examined only once. At this time and to the best of our knowledge, no method has been proposed for mining sequential patterns in data streams. We argue that the main reason is the combinatory phenomenon related to sequential pattern mining. In this paper, we propose an algorithm based on sequences alignment for mining approximate sequential patterns in Web usage data streams. To meet the constraint of one scan, a greedy clustering algorithm associated to an alignment method are proposed. We will show that our proposal is able to extract relevant sequences with very low thresholds.
Keywords: data streams, sequential patterns, web usage mining, clustering, sequences alignment.

1 Introduction

The problem of mining sequential patterns from a large static database has been widely adressed [2, 11, 14, 17, 10]. The extracted relationship is known to be useful for various applications such as decision analysis, marketing, usage analysis, etc. In recent years, emerging applications such as network traffic analysis, intrusion and fraud detection, web clickstream mining or analysis of sensor data (to name a few), introduced new constraints for data mining methods. These constraints are typical of a new kind of data: the *data streams*. A data stream processing has to satisfy the following constraints: memory usage is restricted, new elements are generated continuously and have to be considered as fast as possible, no blocking operator can be performed and the data can be examined only once. Hence, many methods have been proposed for mining items or patterns from data streams [6, 3, 5]. At first, the main problem was to satisfy the constraints of the data stream environment and provide efficient methods for extracting patterns as fast as possible. For this purpose, approximation has been

recognized as a key feature for mining data streams [7]. Then, recent methods [4, 8, 16] introduced different principles for managing the history of frequencies for the extracted patterns. The main idea is that people are often more interested in recent changes. [8] introduced the *logarithmic tilted time window* for storing patterns frequencies with a fine granularity for recent changes and a coarse granularity for long term changes. In [16] the frequencies are represented by a regression-based scheme and a particular technique is proposed for segment tuning and relaxation (merging old segments for saving main memory).
However, at this time and to the best of our knowledge, no method has been proposed for mining sequential patterns in data streams. We argue that the main reason is the combinatory phenomenon related to sequential pattern mining. Actually, if itemset mining relies on a finite set of possible results (the set of combinations between items recorded in the data) this is not the case for sequential patterns where the set of results is infinite. In fact, due to the temporal aspect of sequential patterns, an item can be repeated without limitation leading to an infinite number of potential frequent sequences.
In this paper, we propose the SMDS (Sequence Mining in Data Streams) algorithm which is based on sequences alignment (such as [10, 9] as already proposed for static databases) for mining approximate sequential patterns in data streams. The goal of this paper is first to show that classic sequential pattern mining methods cannot be included in a data stream environment because of their complexity and then to propose a solution. The proposed algorithm is implemented and tested over a real dataset. Our data comes from the access log files of Inria Sophia-Antipolis. We will thus show the efficiency of our mining scheme for Web usage data streams, though our method might be applied to any kind of sequential data. Analyzing the behavior of a Web site's users, also known as Web Usage Mining, is a research field which consists in adapting the data mining methods to the records of access log files. These files collect data such as the IP address of the connected host, the requested URL, the date and other information regarding the navigation of the user. Web Usage Mining techniques provide knowledge about the behavior of the users in order to extract relationships in the recorded data. Among available techniques, the sequential patterns are particularly well adapted to the log study. Extracting sequential patterns on a log file, is supposed to provide this kind of relationship:"*On the Inria's Web Site, 10% of users visited consecutively the homepage, the available positions page, the ET*[1] *offers, the ET missions and finally the past ET competitive selection*". We want to extract typical behaviours from clickstream data and show that our algorithm meets the time constraints in a data stream environment and can be included in a data stream process at a negligible cost. The rest of this paper is organized as follows. The definitions of Sequential Pattern Mining and Web Usage Mining are given in Section 2. Section 3 gives an overview of two recent methods for extracting frequent patterns in data streams. The framework proposed in this paper is presented in Section 4 and empirical studies are conducted in Section 5.

[1] ET: Engineers, Technicians

2 Definitions

In this section we define the sequential pattern mining problem in large databases and give an illustration. Then we explain the goals and techniques of Web Usage Mining with sequential patterns.

2.1 Sequential Pattern Mining

The problem of mining sequential patterns from static databases is defined as follows [2]:

Definition 1. *Let $I = \{i_1, i_2, ..., i_m\}$, be a set of m literals (items). I is a k-itemset where k is the number of items in I. A sequence is an ordered list of itemsets denoted by $< s_1 s_2 \dots s_n >$ where s_j is an itemset. The data-sequence of a customer c is the sequence in D corresponding to customer c. A sequence $< a_1 a_2 \dots a_n >$ is a subsequence of another sequence $< b_1 b_2 \dots b_m >$ if there exist integers $i_1 < i_2 < \dots < i_n$ such that $a_1 \subseteq b_{i_1}, a_2 \subseteq b_{i_2}, \dots, a_n \subseteq b_{i_n}$.*

Example 1. Let C be a client and S=< (c) $(d\ e)$ (h) >, be that client's purchases. S means that "C bought item c, then he bought d and e at the same moment (i.e. in the same transaction) and finally bought item h".

Definition 2. *The support of a sequence s, also called supp(s), is defined as the fraction of total data-sequences that contain s. If supp(s) $\geq$ minsupp, with a minimum support value minsupp given by the user, s is considered as a frequent sequential pattern.*

The problem of sequential pattern mining is thus to find all the frequent sequential patterns as stated in definition 2.

2.2 From Web Usage Mining to Data Stream Mining

For classic Web usage mining methods, the general idea is similar to the principle proposed in [12]. Raw data is collected in access log files by Web servers. Each input in the log file illustrates a request from a client machine to the server (*http daemon*).

Definition 3. *Let Log be a set of server access log entries. An entry g, $g \in Log$, is a tuple $g =< ip_g, ([l_1^g.URL, l_1^g.time]$ ... $[l_m^g.URL, l_m^g.time]) >$ such that for $1 \leq k \leq m$, $l_k^g.URL$ is the item asked for by the user g at time $l_k^g.time$ and for all $1 \leq j < k$, $l_k^g.time > l_j^g.time$.*

The structure of a log file, as described in definition 3, is close to the "`Client-Time-Item`" structure used by sequential pattern algorithms. In order to extract frequent behaviors from a log file, for each g in the log file, we first have to transform ip_g into a client number and for each record k in g, $l_k^g.time$ is transformed into a time number and $l_k^g.URL$ is transformed into an

item number. Table 1 gives a file example obtained after that pre-processing. To each client corresponds a series of times and the URL requested by the client at each time. For instance, the client 2 requested the URL "f" at time $d4$. The goal is thus, according to definition 2 and by means of a data mining step, to find the sequential patterns in the file that can be considered as frequent. The result may be, for instance, <(a)(c)(b)(c)> (with the file illustrated in table 1 and a minimum support given by the user: 100%). Such a result, once mapped back into URLs, strengthens the discovery of a frequent behavior, common to n users (with n the threshold given for the data mining process) and also gives the sequence of events composing that behavior.

Client	d1	d2	d3	d4	d5
1	a	c	d	b	c
2	a	c	b	f	c
3	a	g	c	b	c

Table 1. File obtained after a pre-processing step

Nevertheless, most methods which were designed for mining patterns from access log files cannot be applied to a data stream coming from web usage data (such as clickstreams). In our context, we consider that large volumes of usage data are arriving at a rapid rate. Sequences of data elements are continuously generated and we aim at identifying representative behaviours. We assume that the mapping of URLs and clients as well as the data stream management are performed simultaneously. Furthermore, as stated by [13], sequential pattern extraction, when applied to Web access data, is effective only if the support is very low. A low support means long response time and the authors proposed a divisive approach to extract sequential patterns on similar navigations (in order to get highly significant patterns). Our goal with this work is close to that of [13] since we will provide a navigation clustering scheme designed to facilitate the discovery of interesting sequences, while meeting the needs for rapid execution times involved in data stream processing.

3 Related Work

In recent years, many contributions have been proposed for mining patterns in data streams [6, 3, 5, 8, 16]. [1, 15] also consider the problem of mining sequences in streaming data. In this section, we give an overview of [8] and [16].

3.1 FP-Streaming: Frequent Itemset Mining

The authors of [8] describe an approach based on a batch environment and introduce the FP-stream structure for storing frequent patterns and the evolution of their frequency. The authors propose to consider batches of transactions (the update is done only when enough incoming transactions have arrived to form a

new batch). For each batch, the frequent patterns are extracted by means of the FP-Growth algorithm applied on a FP-tree structure representing the sequences of the batch. Once the frequent patterns are extracted, the FP-stream structure stores the frequent patterns and their tilted time windows. The tilted time windows give a logarithmic overview on the frequency history of each frequent pattern.

3.2 FTP-DS: Temporal Pattern Mining

In [16] a regression based scheme is given for temporal pattern mining from data streams. The authors propose to record and monitor the frequent temporal patterns extracted. The frequent patterns are represented by a regression-based method. The FTP-DS method introduced in [16] processes the transactions time slot by time slot. When a new slot has been reached, FTP-DS scans the data of the new slot with the previous candidates, proposes a set of new candidates and will scan the data in the next slot with those new candidates. This process is repeated while the data stream is active. FTP-DS is designed for mining inter-transaction patterns. The patterns extracted in this framework are itemsets and this work do not adress the extraction of sequences as we propose to do. The authors claim that any type of temporal pattern (causality rules, episodes, sequential patterns) can be handled with proper revisions. However, we discuss the limits of mining sequential patterns from data streams in Section 4.1.

4 The SMDS Algorithm: Motivation and Principle

Our method relies on a batch environment (widely inspired from [8]) and the prefix tree structure of PSP [11] (for managing frequent sequences). We first study the limitations of a sequential pattern mining algorithm that would be integrated in a data stream context. Then, we propose our framework, based on a sequences alignment principle.

4.1 Sequential Pattern Mining in a Batch Environment

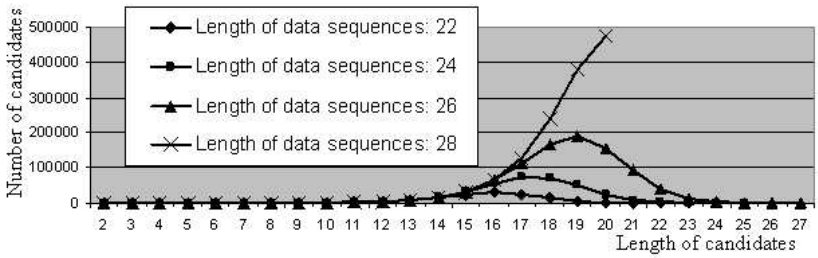

Fig. 1. Limits of a batch environment involving PSP

Our method will process the data stream as batches of fixed size. Let $B_1, B_2, ...B_n$ be the batches, where B_n is the most recent batch of transactions. The principle of SMDS will be to extract frequent sequential patterns from each batch

b in $[B_1..B_n]$ and to store the frequent approximate sequences in a prefix tree structure (inspired from [11]). Let us consider that the frequent sequences are extracted with a classic exhaustive method (designed for a static transaction database). We argue that such a method will have at least one drawback leading to a blocking operator. Let us consider the example of the PSP [11] algorithm. We have tested this algorithm on databases containing only two sequences (s_1 and s_2). Both sequences are equals and contain itemsets having length one. The first database contains 11 repetitions of the itemsets (1)(2) (*i.e.* $s_1 =< (1)(2)(1)(2)...(1)(2) >$, lentgh($s_1$)=22 and $s_2 = s_1$). The number of candidates generated at each scan is reported in figure 1. Figure 1 also reports the number of candidates for databases of sequences having length 24, 26 and 28. For the base of sequences having length 28, the memory was exceeded and the process could not succeed. We made the same observation for PrefixSpan[2] [14] where the number of intermediate sequences was similar to that of PSP with the same mere databases. If this phenomenon is not blocking for methods extracting the whole exact result (one can select the appropriate method depending on the dataset), the integration of such a method in a data stream process is impossible because the worst case can appear in any batch[3].

4.2 Principle

The outline of our method is the following: for each batch of transactions, discovering clusters of users (grouped by behavior) and then analyzing their navigations by means of a sequences alignment process. This allows us to obtain clusters of behaviours representing the current usage of the Web site. For each cluster having size greater than $minSize$ (specified by the user) we store only the summary of the cluster. This summary is given by the aligned sequence obtained on the sequences of that cluster.

Clustering Web Usage Sequences: a Greedy Approach

The clustering scheme we have developed is a straight forward, naive algorithm. It is based on the fact that navigations on a Web site are usually very similar or very different from each other. Basically, users interested in the pages related to job opportunities are usually not likely to request pages related to the next seminar organized by the Inria's unit of Sophia-Antipolis. In order to cluster the navigations as fast as possible, our greedy approach is thus based on the following scheme: the algorithm is initialized with one cluster containing the first navigation. Then, for each navigation n in the the batch, n is compared to each cluster c. As soon as n is found to be similar to at least one sequence of c then s is inserted in c. If s has been inserted in no cluster, then a new cluster is created and s is inserted in this new cluster. The similarity between

[2] Downloaded from http://www-sal.cs.uiuc.edu/~hanj/software/prefixspan.htm

[3] In a web usage pattern, for instance, numerous repetitions of requests for pdf or php files are usual

two sequences is given in definition 4 (s is inserted in c if the following condition holds: $\exists s_c \in c / d(s, s_c) \leq minSim$ with $minSim$ given by the user).

Definition 4. Let s_1 and s_2 be two sequential patterns. Let $LCS(s_1, s_2)$ the length of the longest common subsequences between s_1 and s_2. The similarity $d(s_1, s_2)$ between s_1 and s_2 is defined as follows: $d = \frac{LCS(s_1,s_2)}{max(length(s_1),length(s_2))}$.

Sequences Alignment

Step 1 :				
S_1:	<(a,c)	(e)	()	(m,n)>
S_2:	<(a,d)	(e)	(h)	(m,n)>
SA_{12}:	(a:2, c:1, d:1):2	(e:2):2	(h:1):1	(m:2, n:2):2
Step 2 :				
SA_{12}:	(a:2, c:1, d:1):2	(e:2):2	(h:1):1	(m:2, n:2):2
S_3:	<(a,b)	(e)	(i,j)	(m)>
SA_{13}:	(a:3, b:1, c:1, d:1):3	(e:3):3	(h:1, i:1, j:1):2	(m:3, n:2):3
Step 3 :				
SA_{13}:	(a:3, b:1, c:1, d:1):3	(e:3):3	(h:1, i:1, j:1):2	(m:3, n:2):3
S_4:	<(b)	(e)	(h,i)	(m)>
SA_{14}:	(a:3, b:2, c:1, d:1):4	(e:4):4	(h:2, i:2, j:1):3	(m:4, n:2):4

Fig. 2. Different steps of the alignment method with sequences from example 2

The clustering algorithm ends with clusters of similar sequences, which is a key element for sequences alignment. The alignment of sequences leads to a weighted sequence represented as follows: $SA =< I_1 : n_1, I_2 : n_2, ..., I_r, n_r >: m$. In this representation, m stands for the total number of sequences involved in the alignment. I_p $(1 \leq p \leq r)$ is an itemset represented as $(x_{i_1} : m_{i_1}, ...x_{i_t} : m_{i_t})$,where m_{i_t} is the number of sequences containing the item x_i at the p^{th} position in the aligned sequences. Finally, n_p is the number of occurrences of itemset I_p in the alignment. Example 2 describes the alignment process on 4 sequences. Starting from two sequences, the alignment begins with the insertion of empty items (at the beginning, the end or inside the sequence) until both sequences contain the same number of itemsets.

Example 2. Let us consider the following sequences: $S_1 =<$ (a,c) (e) (m,n) $>$, $S_2 =<$ (a,d) (e) (h) (m,n) $>$, $S_3 =<$ (a,b) (e) (i,j) (m) $>$, $S_4 =<$ (b) (e) (h,i) (m) $>$. The steps leading to the alignment of those sequences are detailed in Figure 2. At first, an empty itemset is inserted in S_1. Then S_1 and S_2 are aligned in order to provide SA_{12}. The alignment process is then applied to SA_{12} and S_3. The alignment method goes on processing two sequences at each step.

At the end of the alignment process, the aligned sequence (SA_{14} in figure 2) is a summary of the corresponding cluster. The approximate sequential pattern

can be obtained by specifying k: the number of occurrences of an item in order for it to be dispayed. For instance, with the sequence SA_{14} from figure 2 and $k = 2$ the filtered aligned sequence will be: <(a,b)(e)(h,i)(m,n)> (corresponding to items having a number of occurrences greater or equal to k).

Frequent Sequences Storage and Management

The aligned sequences obtained from the previous step are stored in a prefix tree similar to that of [11]. If a new sequence s has been discovered, then the tree is modified to store this new sequence. Otherwise, if s is already in the tree, then the support of s is updated. Figure 3 gives an example of a prefix tree where transaction cutting is captured by using labelled edges. Each path from the root to any node in the tree stands for an extracted sequence. The tree from figure 3 contains 6 sequences (<(a c)>, <(a d)>, <(b)>, <(c d)>, <(c)(e)>, <(d)(a)>). Any path, from the root to a leaf stands for a sequence and considering a single branch each node at depth l ($k \geq l$) captures the l^{th} item of the sequence. Transaction cutting is captured by using labelled edges. For instance, the dashed link between nodes c and e in figure 3 illustrates the fact that e is not in the same itemset as c. Each node is provided with the support of the sequence represented by the path from the root to this node. Furthermore, depending on the required level of details, the real support of each sequence can be obtained at the end of the batch processing, by scanning the sequences of the batch with the sequences stored in the tree[4]. Then each node can be provided on the one hand with k, the filter used to obtain this aligned sequence from the corresponding cluster and on the other hand with the real support of the sequence. Example 3 gives an illustration of the sequences support management.

Example 3. Let us consider the sequence s_1 =<(a)> from figure 3. The real support of s_1 is 10, but the support of the aligned sequence s_1 is unknown (-1). This means that s_1 has been extracted in more than one cluster. Let us consider the sequence s_2 =<(d)(a)>. s_2's real support is 2, and the support of the aligned sequence s_2 is 3 (meaning that the corresponding cluster contains this aligned sequence with a filter $k = 2$).

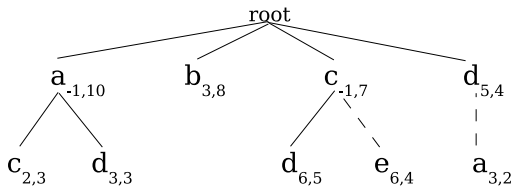

Fig. 3. Example of a prefix tree for frequent sequences management

The SMDS algorithm described in this paper is given below.

[4] This process can be achieved efficiently by using the candidates valuation algorithm given by [11]

Algorithm 1 (SMDS)
Input : $B = \cup_{i=0}^{\infty} B_i$: an infinite set of batches of transactions ; $minSize$: the minimum size of a cluster that has to be summarized ; $minSim$: the minimum similarity between two sequences in order to consider growing a cluster ; k : the filter for the sequences alignment method.
Output : The updated prefix tree structure of approximate frequent sequences.
while (B) **do**
  $b \leftarrow$ NextBatch();
  // 1) Obtain clusters of size $> minSize$
  $C \leftarrow$ Clustering(b, $minSize$, $minSim$);
  // 2) Summarize each cluster with filter k;
  Foreach $(c \in C)$ **do**
    $SA_c \leftarrow$ Alignment(c, k);
    //3) Store frequent sequences
    If (SA_c) **Then** PrefixTree $\leftarrow$ PrefixTree+SA_c **Endif**
  Done
  // 4) Get the real support of sequences stored in the tree (optional)
  GetValuation(PrefixTree, b);
  // 5) Update Tilted Time Windows and delete obsolete sequences
  TailPruning(PrefixTree);
Done (end Algorithm SMDS);

As we wrote in section 1, the first challenge of mining data streams was to extract patterns as fast as possible in order to get adapted to the speed of the streams. Then the history of frequencies has been considered and tilted time windows were proposed [8, 4]. However, no particular effort has been made for extracting temporal relationships between items in data streams (sequences, sequential patterns). Even if our main goal was to show that such patterns could be extracted with SMDS, we have provided our method with logarithmic tilted time windows. Let $f_S(i,j)$ denote the frequency of a sequence S in $B_{(i,j)} = \cup_{(k=i)}^{j} B_k$, with B_k the k^{th} batch of transactions. Let B_n be the current batch, the logarithmic tilted time windows allow to store the set of frequencies $[f(n,n); f(n-1,n-1); f(n-2,n-3); f(n-4,n-7), ...]$ and to save main memory. Frequencies are shifted in the tilted time window when updating with a new batch B. For this purpose, $f_S(B)$ replaces $f(n,n)$, $f(n,n)$ replaces $f(n-1,n-1)$ and so on. An intermediate windows system allows to merge windows when needed in order to follow the logarithmic repartition of frequencies. Tail pruning is also implemented. Actually, in our version, tail frequencies (oldest records) are dropped when their timestamp is greater than a fixed timestamp given by the user (*e.g.* only store frequencies for the last 100,000 batches, which will require $log_2(100,000) \approx 17$ units of time).

Complexity

In the worst case, the sequences in the batch have the same length: m. The LCS algorithm, involved in the similarity of definition 4 has a time complexity of $O(m^2)$. In the worst case, the clustering algorithm has a time complexity of $O(m^2.n^2)$ with n the number of sequences. Actually, in the worst case, LCS is

called once for the first sequence, twice for the second, and so on. The complexity is thus $O(\frac{n.(n+1)}{2}m^2) = O(m^2.n^2)$. It is well suited for Web navigation patterns and the results obtained (see Section 5) on real datasets (access logs of Inria Sophia-Antipolis) show its effectiveness. The complexity of the alignment algorithm for a batch is $O(n.m^2)$.

5 Experiments

The SMDS algorithm is written in Java on a Pentium (2.1 Ghz) PC running a Linux Fedora system. We evaluated our proposal on both real and synthetic data (available at http://www.almaden.ibm.com/cs/quest).

5.1 Feasibility and Scalability of the SMDS algorithm

In order to show the efficiency of the SMDS algorithm, we report in figure 4 the time needed to extract the longest approximate sequential pattern on each batch corresponding to the Web usage data (left part in figure 4) and the synthetic data (right part in figure 4). For the Inria's web site, the data were collected over a period of 14 months for a size of 14 Gb. The total amount of navigations is 3.5 millions and the total number of items is $300,000$. We cut down the log into batches of 4500 transactions (an average amount of 1500 navigation sequences). For those experiments, the filter k was fixed to 30 % (please note that this filter has an impact on time response, since the sequences managed in the prefix tree will be longer when k is low). In our experiment we have injected "parasitic" navigations into the batches. The first batch was not modified. The second batch was added with ten sequences containing repetitions of 2 items and having length 2 (as s_1 and s_2 described in Section 4.1). The third batch was added with ten such sequences having length 3 and so on up to ten sequences having length 30 in batch number 30. The goal is to show that a classic method (PSP, prefixSpan) will block the data stream whereas SMDS will go on performing the mining task. We can observe that the time response of SMDS varies from 1800 ms to 3100 ms. PSP performs very well for the first batches and finally is penalized by the noise added to the data stream (*i.e.* batch 19). The test has also been conducted with prefixSpan. The execution times were greater than 6000 ms and prefixSpan had the same exponential behaviour because of the noise injected in the data streams. For both PSP and prefixSpan the specified minimum support was just enough to find the sequences of repetitions (10 sequences). We added to figure 4 the number of sequences involved in each batch in order to explain the different execution times of SMDS. We can observe, for instance, that batch number 1 contains 1500 sequence and SMDS needs 2700 ms in order to extract the approximate sequential patterns. For the synthetic data we generated batches of $10,000$ transactions (corresponding to 500 sequences in average). The average length of sequences was 10 and the number of items was 200,000. The filter k was fixed to 30 %. We report in figure 4 (right) the time responses and the number of sequences corresponding to each batch. We can observe that SMDS is able to handle $10,000$ transactions in less than 4 seconds (*e.g.* batch number 2).

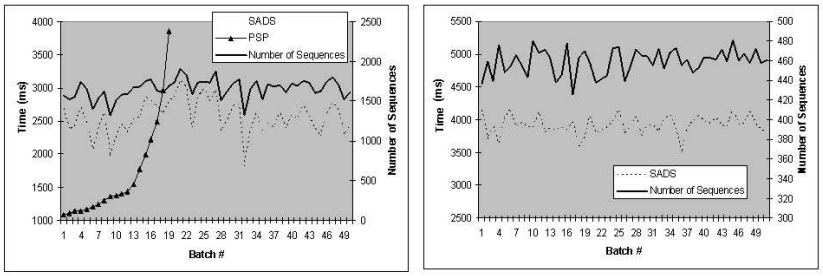

Fig. 4. SMDS execution time for real and synthetic datasets

5.2 Usage Patterns Extracted on Real Access Logs

The list of behaviours discovered by SMDS covers more than 100 navigation goals (clusters of navigation sequences) on the Web site of Inria Sophia-antipolis. Most of the discovered patterns can be considered as "rare" but very "confident" (their support is low with respect to the global number of sequences in the batch, but the filter k used for each cluster is high). We report here a sample of two discovered behaviours:

- $k = 30\%$, cluster size = 13, prefix="http://www-sop.inria.fr/omega/"
  < (MC2QMC2004) (personnel/Denis.Talay/moi.html)
  (MC2QMC2004/presentation.html) (MC2QMC2004/dates.html)
  (MC2QMC2004/Call_for_papers.html)>
  This sequence has been found on batches corresponding to june 2004, when the conference MCQMC has been organized by a team of Inria Sophia Antipolis. This behaviour was shared by up to 13 users (cluster size).
- $k = 30\%$, cluster size = 10,
  prefix="http://www-sop.inria.fr/acacia/personnel/itey/Francais/Cours/"
  < (programmation-fra.html) (PDF/chapitre-cplus.pdf)
  (cours-programmation-fra.html) (programmation-fra.html) >
  This behaviour corresponds to requests that have been made for a document about programming lessons written by a member of a team from Inria Sophia Antipolis. It has been found on a batch corresponding to april 2004.

For the usage sequences of Inria sophia Antipolis, we also observed that SMDS is able to detect the parasitic sequences added to the batches (sequences containing repetitions of 2 items) in a cluster dedicated to those sequences.

6 Conclusion

In this paper, we proposed the SMDS algorithm for extracting sequential patterns in data streams. Our method has two major features. First, batches of transactions are summarized by means of a sequences alignment method. This alignment process relies on a greedy clustering algorithm that considers the main characteristics of Web usage sequences in order to provide distinct clusters of sequences. Second, frequent sequences obtained by SMDS are stored in a prefix tree structure which also allows to detect the real support of each proposed sequence. Thanks to this mining scheme, SMDS is able to detect frequent behaviours shared by very little amounts of users (*e.g.* 13 users, or 0.5%) which

is close to the difficult problem of mining sequential patterns with a very low support. Furthermore, our experiments have shown that SMDS performs fast enough to be integrated in a data stream environment at a negligible cost and extracts significant patterns in a Web usage analysis.

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