

FREQUENT UTILITY SEQUENCE PATTERN MINING USING PTREE+

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Abstract :Sequential pattern mining has various forms in data mining like sequential pattern, constraint-based sequential pattern mining, frequent sequential mining, long sequential pattern mining, utility based sequential mining etc. Among this, recently utility based sequential mining has attracted many researchers. This is because utility based sequence mining considers semantic importance of the sequence, which was not considered in frequent based sequence mining. In this paper a novel algorithm was proposed which considers both frequency and utility of sequence. This algorithm was based on prefix tree structure to retrieve high utility sequences. The algorithm uses the prefix tree to store both support and utility information of sequences. Experimental results were conducted using BMS sequence datasets. Execution time, Memory space and number of patterns retrieved are analyzed in a dataset.

Index Terms: Sequence mining, Utility sequence mining, High Utility sequences, Frequent high utility sequences, Minimum utility threshold.

I. INTRODUCTION

Sequential pattern mining plays an important role in many applications like sales of items in retail marketing, purchasing behavior of customers, web log sequence analysis, analysis in protein sequences, analysis in XML query access patterns etc [1]. But traditional frequent based sequential mining considers only the occurrence of sequence, not the semantic importance of the sequence. Hence utility based sequence mining was introduced, to consider the significance of the sequences [2] [3]. This mining results the sequences whose utility value is greater than minimum utility threshold value.

In real time applications, there is need to retrieve patterns both with high utility and high occurrences. For example in retail marketing to promote cross marketing, we need to identify such high utility and frequent sequences. It can also be applicable in web log sequence analysis to identify which websites that was most frequently visited with high utility value. For such cases we need to retrieve patterns by considering both support and utility values. These types of patterns are termed as frequent high utility patterns. These patterns must satisfy two properties: one is , the support of the pattern must be greater than the minimum support threshold and the other is, the utility of the pattern must be greater than minimum utility threshold.

The remaining section of the paper is organized as follows: Section 2 describes related works, proposed work was given under section 3, Section 4 illustrates experimental results and section 5 concludes the work.

II. RELATED WORKS

In 2006, H. Yao et al. proposed UMining [6] algorithm to find almost all the high utility itemsets from an original database. The drawback of this algorithm was that it could not retrieve complete set of high utility itemsets. Later many algorithms were proposed in utility mining to retrieve high utility itemsets.

Yin et al [3] proposed USPAN algorithm to mine high utility sequential patterns. The authors introduced the lexicographic quantitative sequence tree to extract the complete set of high utility sequences. They also introduced two effective pruning strategies. Experimental results on both synthetic and real datasets show that USpan works efficiently, even in a large scale data.

Zihayat et al. [4] proposed an algorithm to retrieve high utility sequence in data streams. The authors proposed two efficient data structures namely ItemUtilLists (Item Utility Lists) and HUSP-Tree (High Utility Sequential Pattern Tree). In addition, a novel utility model called Sequence- Suffix Utility is proposed for effectively pruning the search space in HUSP mining. The authors named the algorithm as HUSP-Miner (High Utility Sequential Pattern Miner) to find HUSPs in static databases efficiently. Then, a one-pass algorithm namely HUSP-Stream (High Utility Sequential Pattern mining over Data Streams) was proposed to incrementally update ItemUtilLists and HUSP-Tree online and find HUSPs over data streams. Experimental results on both real and synthetic datasets show that HUSP-Miner performs well.

Dave[12] proposed an algorithm to retrieve high utility sequences in from Incremental Sequential Dataset. In the process of mining HUS, when new sequences are added into the existing database the whole procedure of mining HUS starts from the

scratch, in spite of mining HUS only from incremental sequences. This result in excess of time as well as efforts. So the authors proposed an incremental algorithm to mine high utility sequences from the Incremental Database.

III. PROPOSED WORK

This section illustrates the proposed algorithm to retrieve frequent high utility sequences. The algorithm adopted existing prefix tree structure to retrieve frequent high utility patterns. The tree stores both support and utility information about the item. Using depth first search tree traversal, frequent high utility sequences are retrieved. Initially transaction weighted utility and occurrence of the items are calculated [5] [6] [7]. Then the tree is constructed for high utility items. The items whose utility is greater than transaction weighted utility is known as high utility items [8] [9] [10]. Last depth first search is employed for high utility sequences. This can be illustrated with the following example.

Example:

Table 1. An Example transaction

Table2. Profit table

Table3.TWU, support

Item	Unit profit
A	2
B	3
C	4
D	5
E	2

From the example, if minimum utility is taken as 80, the items B, C, D is termed as high transaction weighted utility itemsets. Now a prefix tree is constructed with these items. After the construction of prefix tree, frequent high utility sequences, based on minimum threshold values are retrieved directly from the tree.

Item	TWU	Support
A	68	3
B	89	4
C	110	5
D	81	3
E	60	2

Trans. id	Transactions	TU
T1	(A,1) (B,3) (C,2)	19
T2	(A,2) (C,3) (D,1)	21
T3	(B,2) (C,1)	10
T4	(B,3) (C,1) (D,3) (E,2)	32
T5	(A,1) (B,3) (C,2) (D,1) (E,2)	28

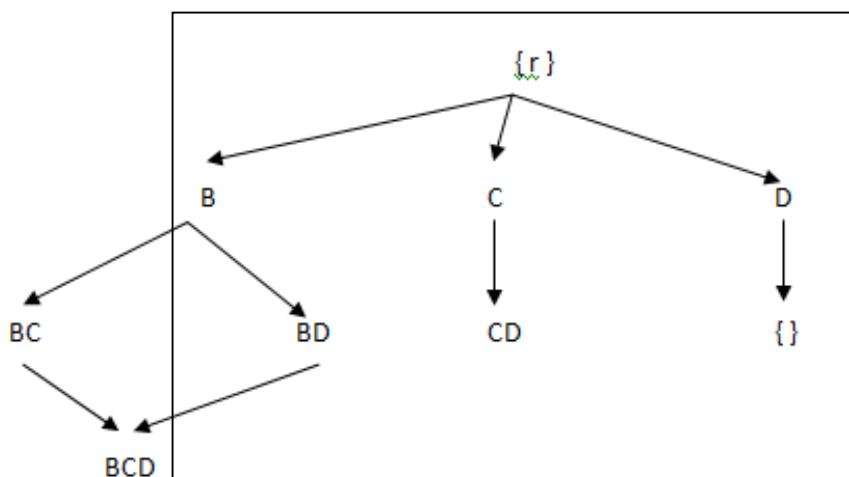


Fig 1.Prefix tree

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Frequent Utility Sequence Mining – Ptree+
Input: sequence database DB, minimum utility threshold min_util, mecum support threshold min_sup
Output: set of frequent utility sequences, FUS
1: FUS = ∅;
2: Transaction Weighted Utility  $TWU = \sum TU$ ; TU = Trasanction Utility;
3: If (TWU > min_util) return HTWU;
4: Construct Prefix tree(HTWU)
5: for itemsets in HTWU
6: If (HTWU.itemset > min_util && HTWU.itemset > min_sup)
7: FUS = itemset;
8: End for;
9: End if;
    
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Pseudocode for Frequent Utility Sequence Mining

IV. EXPERIMENTAL RESULTS

The algorithm is implemented in Java language. The software tool used is NetBeans IDE 8.0. The dataset used in the experiment is BMS sequence dataset. This dataset contains 59,601 sequences of clickstream data from an e-commerce. It contains 497 distinct items. The average length of sequences is 2.42 items with a standard deviation of 3.22. In this dataset, there are some long sequences. For example, 318 sequences contain more than 20 items. This dataset has been taken from SPMF repository. The experiment is conducted with various minimum support threshold and minimum utility threshold. Also in retrieving sequences, the length of sequence is also taken as input. This is because, sequence mining takes more space and time complexity, so if maximum sequence pattern is mentioned in advance, the required patterns can be retrieved efficiently. Table 1 shows the execution time, memory space and number of patterns retrieved with different support and utility values. This result displays the number of sequences with maximum length 2. Table 2 shows the same for different length of patterns.

Table 1. Performance of proposed algorithm with different support and utility values

Min_support	Min_utility	Exe. Time in ms	Memory space in MB	No. of patterns retrieved
20	30	33	9.48	1359
	40	24	11.34	914
	50	11	15.47	565
	60	9	16.24	353
30	30	29	8.54	1047
	40	21	10.5	748
	50	10	13.2	389
	60	9	14.2	281
40	30	25	7.5	854
	40	19	9.58	587
	50	10	12.5	256
	60	9	12.1	148

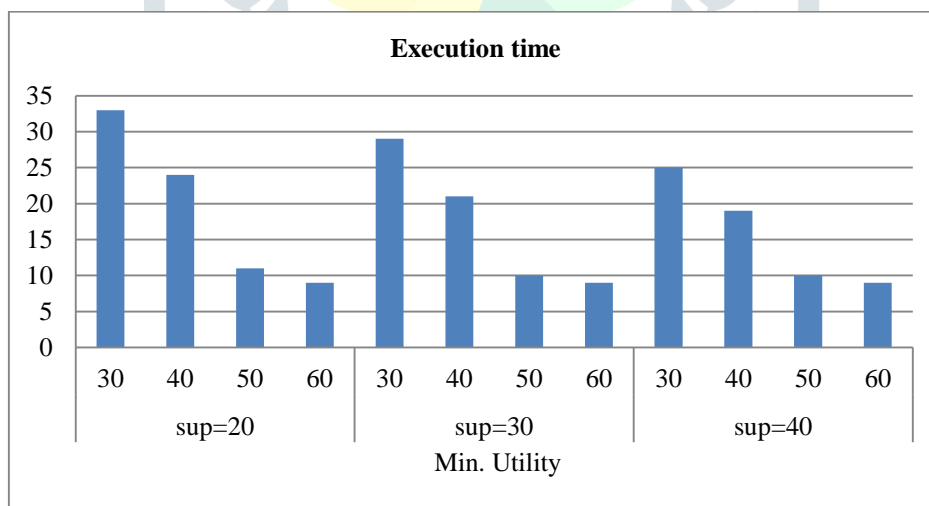


Fig 2. Comparison of Execution time

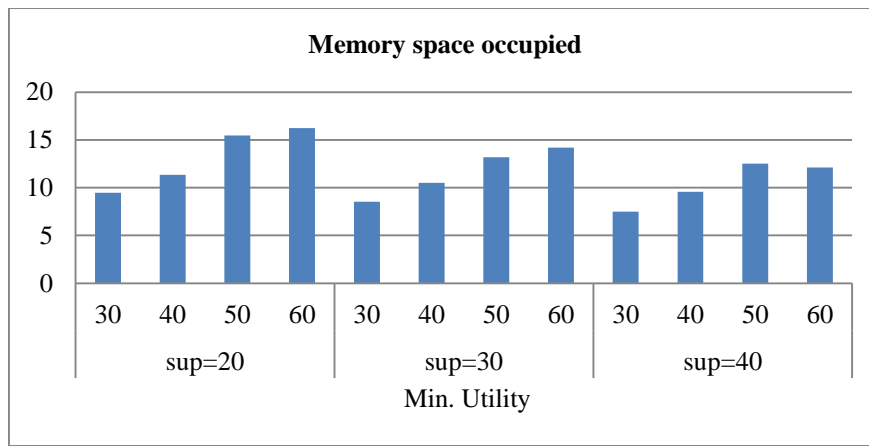


Fig 3.Comparison of Memory space occupied

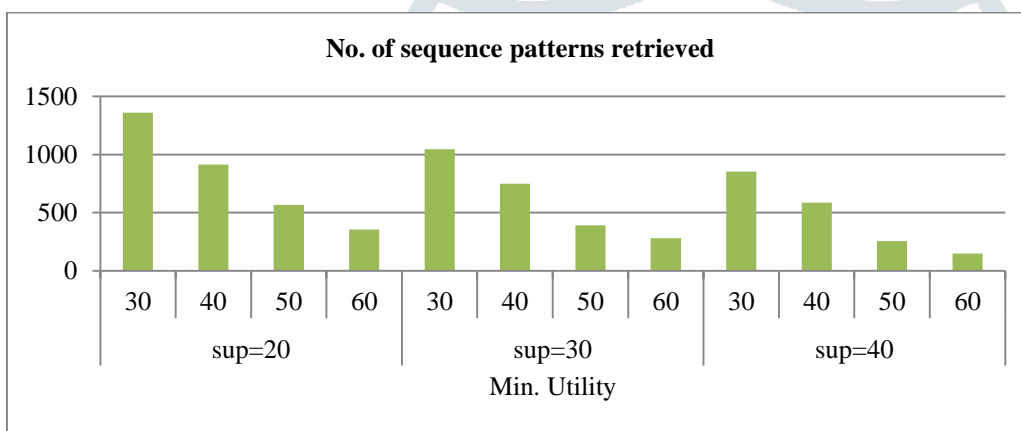


Fig 4.Comparison of Number of patterns retrieved

Table 2 Performance of proposed algorithm with different length of patterns

Length of pattern	Exe. Time in ms	Memory space in MB	No. of sequence patterns retrieved
2	45	9.58	5874
3	84	13.99	10005
4	1125	16.22	205306
5	10240	247.49	2667199

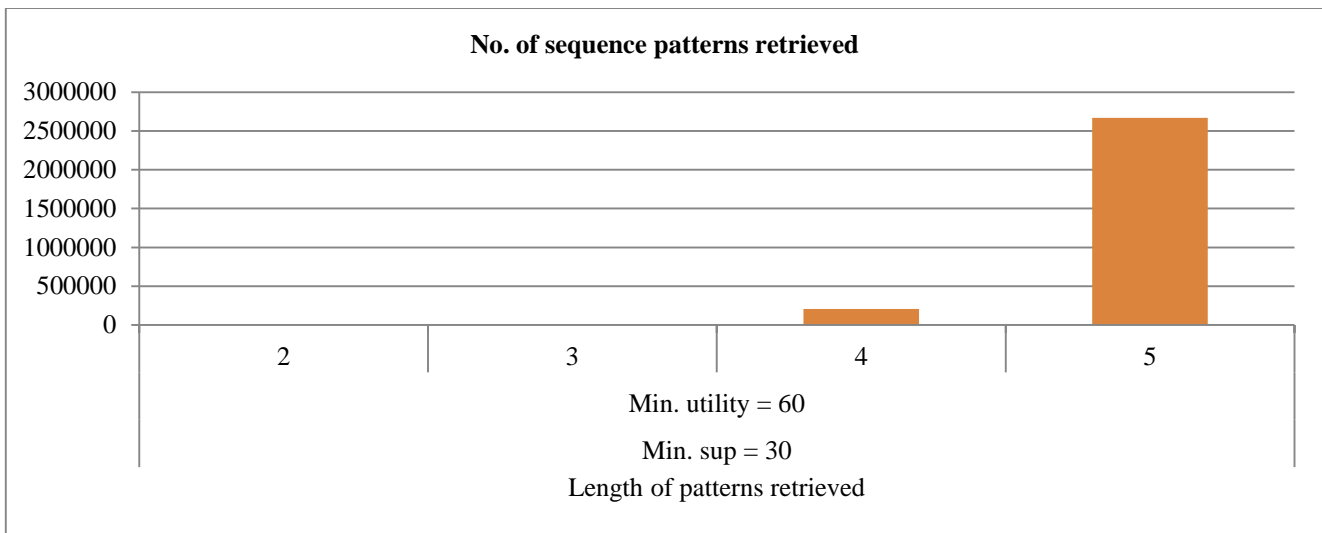


Fig 5.Number of patterns retrieved

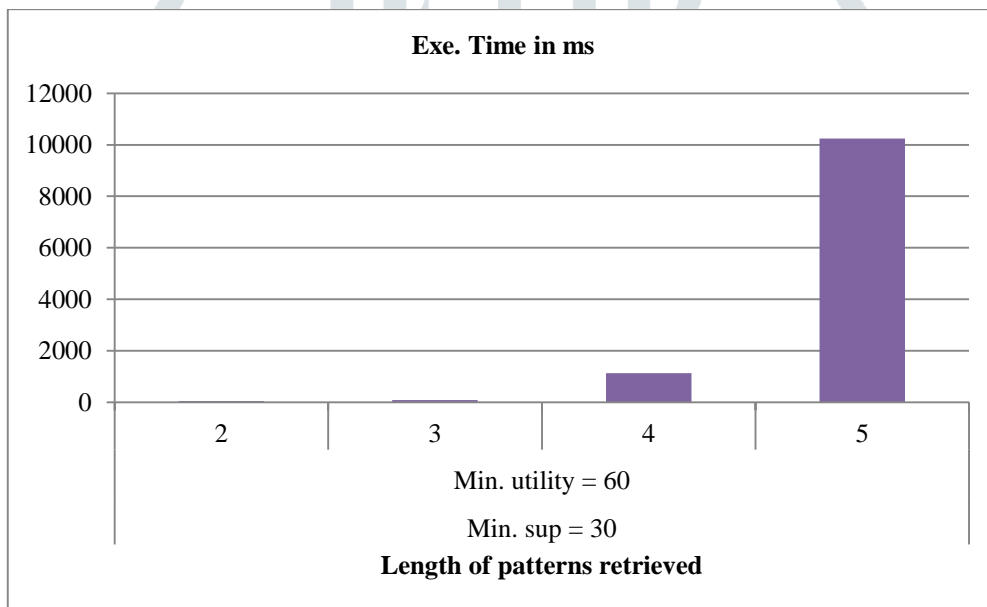


Fig 6.Execution time based on the length of patterns

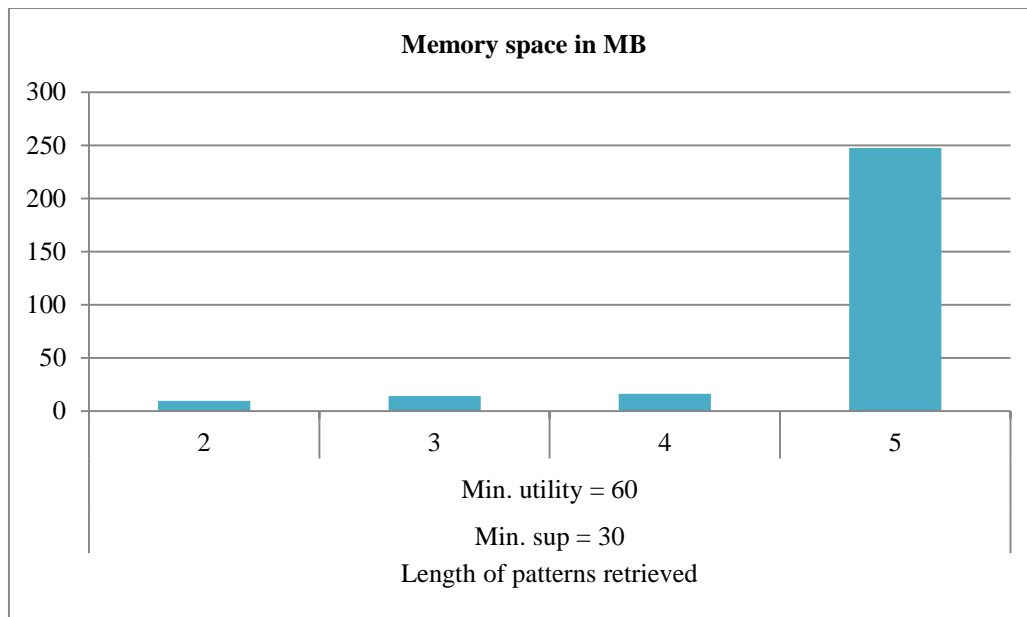


Fig 7.Memory space occupied based on the length of patterns

V. CONCLUSION

In recent years utility based sequential mining has emerged as an interesting research area. This is because utility based sequence mining considers semantic significance of the sequence, which was not considered in frequent based sequence mining. In this paper a novel algorithm was proposed which considers both frequency and utility of sequence. This algorithm was based on prefix tree structure to mine high utility sequence pattern mining algorithm. Experimental results were conducted using BMS sequence datasets. Execution time, Memory space and number of patterns retrieved are analyzed with different support and utility values. Also the same are retrieved using different length of sequence.

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