

# Mining compact high utility sequential patterns

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## Abstract

High utility sequential pattern mining (HUSPM) aims to mine all patterns that yield a high utility (profit) in a sequence dataset. HUSPM is useful for several applications such as market basket analysis, marketing, and website clickstream analysis. In these applications, users may also consider high utility patterns frequently appearing in the dataset to obtain more fruitful information. However, this task is high computation since algorithms may generate a combinatorial explosive number of candidates that may be redundant or of low importance. To reduce complexity and obtain a compact set of frequent high utility sequential patterns (FHUSPs), this paper proposes an algorithm named CHUSP for mining closed frequent high utility sequential patterns (CHUSPs). Such patterns keep a concise representation while preserving the same expressive power of the complete set of FHUSPs. The proposed algorithm relies on a CHUS data structure to maintain information during mining. It uses three pruning strategies to eliminate early low-utility and non-frequent patterns, thereby reducing the search space. An extensive experimental evaluation was performed on six real-life datasets to evaluate the performance of CHUSP in terms of execution time, memory usage, and the number of generated patterns. Experimental results show that CHUSP can efficiently discover the compact set of CHUSPs under different user-defined thresholds.

**Keywords:** data mining, high utility sequential patterns, closed high utility sequential patterns

## 1. Introduction

Frequent high utility sequential pattern mining (FHUSPM) finds sequential patterns with high utility and frequently appear in sequence datasets. Such patterns appear commonly in various real-life applications such as market basket analysis, website clickstream analysis, customer behavior analysis, and stock market analysis. In market basket analysis, when analyzing customer transactions, a retail store manager may be interested in finding the high utility patterns that appear regularly and have a high sale volume. Detecting these purchase patterns is useful for understanding customers' behavior and thus adopting effective sales and marketing strategies. For example, high-end electronic devices and jewelry may generate more profit than many daily-life products. However, they may be sold infrequently, and their

sales volumes may greatly fluctuate. Suppose retailers know that some products yield a high profit and are frequently purchased; they can change business strategies for these items to increase sales and improve inventory management. In marketing, marketers want to know some sets of products frequently sold with high revenue. They can better understand customers' preferences and then design efficient marketing strategies. In website clickstream analysis, the number of clicks or time spent on each web page or user interface (UI) element can be viewed as the quantities of items in sequences. Thus, administrators can discover the elements where users spend most of their time. Based on that, administrators can improve functions and UI to suit these important behaviors better.

Although the problem of HUSPM and its extensions have been studied in several previous

studies [1–7], these algorithms discover a full set of HUSPs requiring exponential complexity. Therefore, in this paper, we extend the concept of closed patterns from frequent sequential pattern mining [8] for HUSPM. A closed (frequent) high utility sequential pattern (CHUSP) is a HUSP having no proper super-sequences that are HUSPs and appear in the same number of sequences. Such patterns are also meaningful for real-life applications since they are the largest FHUSPs common to groups of customers. Detecting the largest sets of items yielding high profit and frequently sold supports sellers to understand better what customers need, adapt their business and marketing strategies, and improve their services. There is a work [9] focusing on this topic in literature. However, the computational complexity of this algorithm is still high. In addition, the experimental evaluation was conducted on small-scale datasets which a few differences in characteristics. Last, this work did not provide the application accompanying its proposed algorithms.

The above observations motivated the design of an efficient algorithm that can mine CHUSPs. Generally, we highlighted the major contributions and innovations of this paper as follows:

- We proposed an efficient pattern-growth-based algorithm named CHUSP to discover the set of CHUSPs interesting for some tasks. CHUSP mines the patterns from the dataset in a divide-and-conquer approach. It first derives the set of size-1 quantitative sequences, and for each sequence  $p$ , it derives  $p$ 's conditional (or projected) dataset by partitioning it and recursively mining the projected dataset. An innovation of the CHUSP is that the algorithm checks the “closed” property of the generated pattern at each round of the mining process. Thanks to this property, at the end of the mining process, we obtain a small set of CHUSPs. The algorithm uses three pruning strategies to eliminate early low-utility and non-frequent patterns. Thus, the algorithm achieves good performances on large-scale datasets.
- An extensive experiment was conducted on real datasets to evaluate the performance of CHUSP in terms of runtime, memory usage, and the number of generated patterns. Experimental results show

that CHUSP can efficiently discover all CHUSPs. In addition, its performance is independent of the datasets' characteristics if they contain utility information, i.e., it can work on both quantitative transaction and quantitative sequence datasets.

- We provide the application of CHUSP. The application can be used for any dataset if its format matches the input requirement.

The rest of this paper is organized as follows. Section 2 reviews related work; section 3 introduces the preliminaries; section 4 describes the proposed CHUSP algorithm; section 5 shows a comparative experiment; section 6 concludes and outlines the direction for future work.

## 2. Related Work

High utility sequential patterns mining aims to find all sequential patterns with a utility greater than or equal to a minimum utility threshold  $\text{minUtil}$  in a sequence dataset. HUSPM is quite challenging as the utility measure is neither monotone nor anti-monotone, unlike the support measure traditionally used in SPM. Numerous algorithms have been proposed for HUSPM, and its extension [1–7, 10–20]. A thorough survey of HUSPM can be found in this work [21]. Yin et al. [1] proposed an algorithm named USpan for HUSPM. This algorithm builds a lexicographic  $q$ -sequence tree (LQS-Tree) to maintain all generated sequences during the mining process. In addition, it uses two concatenation mechanisms: I-Concatenation and S-Concatenation, in combination with two pruning strategies: width and depth pruning. Wang et al. [2] proposed an algorithm named HUS-Span. The algorithm uses a utility-chain structure to represent the search space of HUSPM. It also introduces two tight utility upper bounds: prefix extension utility (PEU) and reduced sequence utility (RSU), as well as two companion pruning strategies to identify HUSPs. The experimental evaluation showed that HUS-Span outperforms USpan in terms of execution time. The reason is that by using PEU and RSU, HUS-Span can generate fewer candidates than USpan.

Le et al. [3] proposed two algorithms, AHUS and

AHUS-P. The algorithms use a pure array structure (PAS) to represent sequences. This data structure is very compact and contains sufficient information on sequences. Thus, it can reduce memory usage and effectively support the mining process. Moreover, the two algorithms use two upper bounds to prune the search space. AHUS-P uses a parallel mining strategy to discover patterns concurrently by sharing the search space with multiple processors. Each processor independently performs its mining task and does not wait for other tasks. AHUS-P is more efficient than the serial AHUS algorithm for large-scale datasets. Lin et al. [22] proposed a sequence-utility (SU)-Chain algorithm for HUSPM. A lexicographic enumeration (LE)-tree is used in the algorithm to represent the search space for promising candidates. The projecting approach is used to accelerate the progress of generating promising candidates. In addition, multiple pruning strategies are used to identify information not relevant to the mining progress.

For frequent high utility sequential pattern mining, Gupta et al. [23] proposed a hybrid pattern growth-based algorithm named HUFTI-SPM to mine sequential patterns satisfying both frequency and utility thresholds. It uses support-utility table to maintain information on support and utility at various time intervals. It uses sequence support as the downward closure property to reduce the search space. Ni et al. [24] proposed an algorithm named FHUSOM to mine the architecture design requirements from the operational scenario data. The algorithm uses a data structure called FHUDES to keep all patterns and combines four pruning strategies called SWU, PEU, RSU, and MFP to reduce the search space. The algorithm supports the design of an integrated multi-platform mission system (MPMS) architect and is efficient in the process of integrated architecture design.

For closed high utility sequential pattern mining, Truong et al. [9] proposed an algorithm named FMaxCloHUSM to mine the set of frequent maximal and closed high utility sequences. The algorithm uses width and depth pruning strategies to remove low utility sequences and a novel local pruning strategy named LPCHUS to remove non-closed and non-maximal high utility sequences. FMaxCloHUSM uses

a data structure called SIDUL to represent the dataset in a vertical format and calculate utility information of sequences and their extensions.

### 3. Preliminaries

Given a set of  $m$  distinct items  $I = \{i_1, i_2, \dots, i_m\}$ . A quantitative item (q-item) is a pair of the form  $(i, q)$  where  $i \in I$  and  $q$  is a positive number representing how many units of this item were purchased (internal utility). The quantity of a q-item  $i$  in  $s$  is denoted as  $q(i, s)$ . Each item  $i_k \in I$  ( $1 \leq k \leq m$ ) is associated with a weight denoted as  $p(i_k)$  representing the unit profit or importance (external utility) of  $i_k$ . A quantitative itemset (q-itemset)  $X = [(i_1, q_1)(i_2, q_2) \dots (i_k, q_k)]$  is a set of one or more q-items where  $(i_j, q_j)$  is a q-item ( $1 \leq j \leq k$ ). In the following, brackets are omitted for brevity if a q-itemset contains only one q-item. In addition, without loss of generality, assume that q-items in a q-itemset are sorted according to the lexicographical order such as  $a < b < c < d < e < f < g$ . A quantitative sequence (q-sequence)  $s$  is an ordered list of q-itemsets  $s = \langle I_1 I_2 \dots I_l \rangle$  where  $I_j$  ( $1 \leq j \leq l$ ) is a q-itemset. A quantitative sequence dataset is a set of  $n$  q-sequences  $SDB = \{s_1, s_2, \dots, s_n\}$ , where each sequence  $s_{sid} \in S$  ( $1 \leq sid \leq n$ ) is a subset of  $I$ , and  $sid$  is its unique identifier.

For example, Table 1 shows the items and their respective unit profits appearing in an online retail store. In this example, the external utility of each item  $a, b, c, d, e, f, g$  are 2, 5, 3, 4, 6, 1, 7, respectively. Table 2 shows five shopping q-sequences with quantities, having the sequence identifiers (sid) 1 to 5 (denoted  $s_1$  to  $s_5$ ). Each q-sequence comprises one or more transactions (q-itemsets). Each transaction in a q-sequence has a unique transaction identifier  $tid$ , and consists of one or many q-items.

The q-sequence  $s_4$  contains three q-itemsets  $[(b, 1)c(1)(e, 2)(g, 5)]$ ,  $[(a, 3)(b, 2)(e, 4)(f, 2)]$  and  $[(b, 2)(c, 1)(e, 2)]$  in which the internal utility of q-item  $e$  in the first, second and third q-itemsets are 2, 4 and 2, respectively. We use the notation  $i_{tid}$  to refer to the occurrence of the item  $i$  in the  $tid$ -th transactions of a q-sequence. In  $s_2$ , the notation  $c_1$  means that the q-item  $c$  appears in the first q-itemset

of  $s_2$ , that is  $(c, 2)$ , while  $c_3$  represents  $(c, 1)$  in the third q-itemset of  $s_2$ , and  $c_1 < c_3$  in  $s_2$ .

Table 1: External utility values

item	a	b	c	d	e	f	g
unit profit	2	5	3	4	6	1	7

Table 2: External utility values

sid	tid	transactions	tu	su
1	1	$(a, 5)(c, 2)(g, 5)$	51	108
	2	$(a, 3)(b, 1)(c, 3)(f, 2)$	22	
	3	$(b, 3)(d, 2)(e, 2)$	35	
2	1	$(c, 2)(e, 1)$	12	110
	2	$(a, 2)(b, 2)(f, 5)$	19	
	3	$(b, 2)(c, 1)(e, 4)(g, 6)$	79	
3	1	$(a, 1)(b, 1)(e, 3)$	25	91
	2	$(c, 3)(d, 2)(g, 3)$	38	
	3	$(b, 2)(e, 1)$	16	
	4	$(d, 3)$	12	
4	1	$(b, 1)(c, 1)(e, 2)(g, 5)$	55	122
	2	$(a, 3)(b, 2)(e, 4)(f, 2)$	42	
	3	$(b, 2)(c, 1)(e, 2)$	25	
5	1	$(a, 4)(d, 2)(f, 2)(g, 10)$	88	88

**Definition 1 (The size and length of a q-sequence)** The size of  $s$  is the number of q-itemsets it contains. The length of  $s$  is the number of q-items in  $s$ . In other words,  $s$  is called  $k$ -sequence if and only if there are  $k$  q-items in  $s$ , i.e.,  $|s| = k$ , where  $|s| = \sum_{I_j \in s} |I_j|$  and  $|I_j|$  is the total number of q-items in the q-itemset  $I_j$ . For example, the size and length of  $s_4$  in Table 1 are 3 and 11, respectively.

**Definition 2 (q-itemset containment)**

Let  $X_a = [(i_{a_1}, q_{a_1})(i_{a_2}, q_{a_2}) \dots (i_{a_m}, q_{a_m})]$  and  $X_b = [(i_{b_1}, q_{b_1})(i_{b_2}, q_{b_2}) \dots (i_{b_{m'}}, q_{b_{m'}})]$  be two q-itemsets, where  $i_{a_k} \in I(1 \leq k \leq m)$  and  $i_{b_{k'}} \in I(1 \leq k' \leq m')$ . If there exist positive integers  $1 \leq j_1 \leq j_2 \leq \dots \leq j_m \leq m'$ , such that  $i_{a_1} = i_{b_{j_1}} \wedge q_{a_1} = q_{b_{j_1}}, i_{a_2} = i_{b_{j_2}} \wedge q_{a_2} =$

$q_{b_{j_2}}, \dots, i_{a_m} = i_{b_{j_m}} \wedge q_{a_m} = q_{b_{j_m}}$  then  $X_b$  is said to contain  $X_a$ , denoted as  $X_a \subseteq X_b$ . For example, q-itemset  $[(a, 1)(b, 1)(e, 3)]$  in  $s_3$  contains  $(a, 1), (b, 1), (e, 3)$ ,  $[(a, 1)(b, 1)]$ ,  $[(a, 1)(e, 3)]$ ,  $[(b, 1)(e, 3)]$ ,  $[(a, 1)(b, 1)(e, 3)]$ .

**Definition 3 (q-subsequence)**

Given q-sequences  $A = \langle A_1 A_2 \dots A_n \rangle$  and  $B = \langle B_1 B_2 \dots B_{n'} \rangle (n \leq n')$ , where  $A_\alpha, B_\beta$  are q-itemsets ( $1 \leq \alpha \leq n, 1 \leq \beta \leq n'$ ). If there exists positive integers  $1 \leq j_1 \leq j_2 \leq \dots \leq j_n \leq n'$ , such that  $A_1 \subseteq B_{j_1}, A_2 \subseteq B_{j_2}, \dots, A_n \subseteq B_{j_n}$ , then  $A$  is a q-subsequence of  $B$  and  $B$  is a q-supersequence of  $A$ , denoted as  $A \subseteq B$ . For example,  $\langle [(a, 5)(c, 2)(g, 5)] \rangle$  and  $\langle [(a, 3)(b, 1)(c, 3)(f, 2)] \rangle$  are q-subsequences of  $s_1$ .

**Definition 4 (Utility of a q-sequence)**

The utility of an  $(i, q)$  in  $s$  is denoted and defined as  $u(i, q) = p(i) \times q(i)$ . The utility of a q-itemset  $X$  in  $s$  is denoted and defined as  $u(X) = \sum_{k=1}^m u(i_k, q_k)$ . The utility of  $s$  is denoted and defined as  $u(s) = \sum_{j=1}^n u(X_j)$ .

For example, the utility of  $g$  in  $s_1$  is  $u(g, 5) = 7 \times 5 = 35$ . The utility of  $[(a, 5)(c, 2)(g, 5)]$  in  $s_1$  is  $u([(a, 5)(c, 2)(g, 5)]) = u(a, 5) + u(c, 2) + u(g, 5) = 2 \times 5 + 3 \times 2 + 7 \times 5 = 51$ . The utility of  $s_1$  is  $u(s_1) = u([(a, 5)(c, 2)(g, 5)]) + u([(a, 3)(b, 1)(c, 3)(f, 2)]) + u([(b, 3)(d, 2)(e, 2)]) = 51 + 22 + 35 = 108$ .

**Definition 5 (Utility matrix)**

A utility matrix of  $s$  is  $m \times n$  matrix, where  $m$  and  $n$  are the number of q-items and q-itemsets (transactions) in  $s$ , respectively. The element at the position  $(k, j)$  ( $0 \leq k < m, 0 \leq j < n$ ) of the utility matrix stores the utility  $u(i_k, q)$  of the q-item  $(i_k, q)$  in the q-itemset  $j$ . Table 3 shows the utility matrix of  $s_3$  for the sequence dataset  $SDB$  depicted in Table 2.

**Definition 6 (Remaining utility)**

Given a sequence  $s = \langle X_1 X_2 \dots X_n \rangle$  where  $X_k = [(i_{k_1}, q_{k_1})(i_{k_2}, q_{k_2}) \dots (i_{k_m}, q_{k_m})]$  is a q-itemset of  $s$ . The remaining utility of q-item  $i_{k_m}$  in  $s$  is denoted and

defined as  $ru(i_{k_m}, s) = \sum_{i' \in s \wedge i_{k_m} < i'} u(i')$ . For example, the values  $ru(a_1, s_3)$ ,  $ru(b_1, s_3)$  and  $ru(b_3, s_3)$  are respectively equal to 89, 84 and 18.

Table 3: The utility matrix of  $s_3$

item	tid <sub>1</sub>	tid <sub>2</sub>	tid <sub>3</sub>	tid <sub>4</sub>
a	2	0	0	0
b	5	0	10	0
c	0	9	0	0
d	0	8	0	12
e	18	0	6	0
g	0	21	0	0

Table 4: The remaining utility matrix of  $s_3$

item	tid <sub>1</sub>	tid <sub>2</sub>	tid <sub>3</sub>	tid <sub>4</sub>
a	89	0	0	0
b	84	0	18	0
c	0	57	0	0
d	0	49	0	0
e	66	0	12	0
g	0	28	0	0

#### Definition 7 (Remaining utility matrix)

The remaining utility matrix of  $s$  is  $m \times n$  matrix, where  $m$  and  $n$  are the number of q-items and q-itemsets (transactions) in  $s$ . The element at the position  $(k, j)$  ( $0 \leq k < m, 0 \leq j < n$ ) of the remaining utility matrix stores the  $ru(i_k, q)$  of q-item  $(i_k, q)$  in q-itemset  $j$ . For example, Table 4 shows the remaining utility matrix of  $s_3$ .

#### Definition 8 (Matching)

Given  $s = \langle (i_1, q_1)(i_2, q_2) \dots (i_n, q_n) \rangle$  and a sequence  $t = \langle t_1 t_2 \dots t_m \rangle$ ,  $s$  is said to match  $t$  if and only if  $n = m$  and  $i_k = t_k$  for  $1 \leq k \leq n$ , denoted as  $t \sim s$ . For example, sequence  $\langle (acg)(abcf)(bde) \rangle$  matches  $s_1$ . Note that because of quantities, two q-items may be considered different, although they contain the same item. Hence there could be multiple q-subsequences of a q-sequence matching a given

sequence. For instance, sequence  $\langle (e) \rangle$  matches respectively the q-subsequence  $\langle (e, 3) \rangle$  and  $\langle (e, 1) \rangle$  in the first and third q-itemsets of  $s_3$ . Sequence  $\langle [ac] \rangle$  matches both the q-subsequences  $\langle [(a, 5)(c, 2)] \rangle$  and  $\langle [(a, 3)(c, 3)] \rangle$  of  $s_1$ .

#### Definition 9 (Ending q-item maximum utility)

Given a sequence  $s = \langle X_1 X_2 \dots X_n \rangle$  where  $X_j$  ( $1 \leq j \leq n$ ) is a q-itemset and a sequence  $t = \langle t_1 t_2 \dots t_m \rangle$ . If any q-subsequence  $s_a = \langle X_{a_1} X_{a_2} \dots X_{a_m} \rangle$  ( $s_a \subseteq s \wedge s_a \sim t$ ) where  $X_{a_m} = [(i_{a_1}, q_{a_1})(i_{a_2}, q_{a_2}) \dots (i_{a_m}, q_{a_m})]$ , then

$(i_{a_m}, q_{a_m})$  is called the ending q-item of sequence  $t$  in

$s$ . The ending q-item maximum utility of a sequence  $t$  in  $s$  is denoted and defined as  $u(t, i, s) = \max \{ u(s') | s' \sim t \wedge s' \subseteq s \wedge i \in s' \}$ .

For example, the ending q-items of  $t = \langle bd \rangle$  in  $s_3$  are  $d_2, d_4$  and their ending q-item maximum utility are  $u(\langle bd \rangle, d_2, s_3) = \max(13) = 13$  and  $u(\langle bd \rangle, d_4, s_3) = \max(17, 22) = 22$ , respectively.

#### Definition 10 (Sequence utility)

The sequence utility of a sequence  $t = \langle t_1 t_2 \dots t_m \rangle$  in  $s = \langle X_1 X_2 \dots X_n \rangle$  is denoted and defined as  $v(t, s) = \bigcup_{s' \sim t \wedge s' \subseteq s} u(s')$ . The utility of  $t$  in the dataset  $SDB$  is denoted and defined as a utility set:  $v(t) = \bigcup_{s \in S} v(t, s)$ . For example, the utility of  $t = \langle cb \rangle$  in  $s_1$  is  $v(t, s_1) = \{ u(\langle (c, 2)(b, 1) \rangle), u(\langle (c, 2)(b, 3) \rangle), u(\langle (c, 3)(b, 3) \rangle) \} = \{11, 21, 24\}$ . The utility of  $t$  in  $SDB$  is  $v(t) = \{ v(t, s_1), v(t, s_2), v(t, s_3), v(t, s_4) \} = \{11, 21, 24, 16, 16, 19, 13, 13\}$ .

#### Definition 11 (Sequence maximum utility)

Given a sequence  $t$ , the maximum utility of  $t$  in  $s$  is denoted and defined as  $u_{max}(t, s) = \max \{ u(t, i, s) : \forall i \in s' \wedge s' \sim t \wedge s' \subseteq s \}$ .

The maximum utility of a sequence  $t$  in a q-sequence dataset  $SDB$  is denoted and defined as  $u_{max}(t) = \sum u_{max}(t, s) : \forall s \in S$ .

For example, the maximum utility of the sequence  $t = \langle cb \rangle$  in the sequence dataset  $SDB$  is  $u_{max}(t) = u_{max}(\langle cb \rangle, s_1) + u_{max}(\langle cb \rangle, s_2) + u_{max}(\langle cb \rangle, s_3) + u_{max}(\langle cb \rangle, s_4) = 24 + 16 + 19 + 13 = 72$ .

**Definition 12 (High utility sequential pattern)**

A sequence  $t$  is said to be a high utility sequential pattern if  $u_{max}(t) \geq minUtil$ , where  $minUtil$  is a given user-specified minimum utility threshold. For example, given  $minUtil = 154$ , the complete set of HUSPs in the sequence dataset  $SDB$  is shown in Table 5.

Table 5: The set of HUSPs for  $minUtil = 154$

HUSP	utility	HUSP	utility
$\langle (cg) \rangle$	154	$\langle (cg)(be) \rangle$	186
$\langle (cg)(abf)(be) \rangle$	159	$\langle (g) \rangle$	203
$\langle (cg)(ab)(be) \rangle$	155	$\langle (g)(be) \rangle$	168

**Definition 13 (Support of a pattern)**

Given a sequence  $t$  and the dataset  $SDB = \{s_1, s_2, \dots, s_n\}$ , the support (or absolute support or support.count) of the sequence  $t$  in  $SDB$  is defined as the number of q-sequences that contain  $t$  and is denoted by  $supp(t)$ . Mathematically, the support of  $t$  is defined as  $supp(t) = |\{s | s \sim t \wedge s \in SDB\}|$ .

For example,  $supp(\langle (cg) \rangle) = |\{s_1, s_2, s_3, s_4\}| = 4$   
 $supp(\langle (cg)(be) \rangle) = |\{s_1, s_3, s_4\}| = 3$ .

**Definition 14 (Frequent high utility sequential patterns)**

Given a sequence  $t$  and the dataset  $SDB = \{s_1, s_2, \dots, s_n\}$ ,  $t$  is said to be a frequent high utility sequential pattern (FHUSP) if and only if  $t$  is a HUSP and  $supp(t) \geq minSup$ , for a threshold  $minSup$  set by the user.

**Definition 15 (Closed frequent high utility sequential patterns)**

Given a sequence  $t$  and the dataset  $SDB = \{s_1, s_2, \dots, s_n\}$ ,  $t$  is said to be a closed frequent high utility sequential pattern (CHUSP) if and only if  $t$  is a FHUSP and there exists no FHUSP that is a proper super-sequence of  $t$  and has the same support. Mathematically, the set of all CHUSPs is defined by

$$CHUSP = \{s \in FHUSP | s' \notin FHUSP: s \subseteq s' \wedge supp(s) = supp(s')\}$$

The goal of CHUSPM is to discover the set of CHUSPs that satisfies Definition 15. For example, given

$minUtil=154, minSup=50\%$ , the set of CHUSPs is shown in Table 6.

Table 6: CHUSP for  $minUtil = 130, minSup = 50\%$

CHUSP	utility	support
$\langle (abf)(be) \rangle$	133	2
$\langle (ab)(be) \rangle$	147	4
$\langle (bceg) \rangle$	134	2
$\langle (cg) \rangle$	154	4
$\langle (cg)(abf)(be) \rangle$	159	2
$\langle (cg)(be) \rangle$	186	3
$\langle (c)(abf)(be) \rangle$	148	3
$\langle (c)(be) \rangle$	138	4

**Definition 16 (ULS: utility list structure)**

Assume that a sequence  $t$  has  $k(k > 0)$  ending q-items  $i$  in a q-sequence  $s$  where  $i_1 < i_2 < \dots < i_k$ . The ULS of  $t$  in  $s$  is a list of  $k$  elements, where the  $\alpha^{th}$  ( $1 \leq \alpha \leq k$ ) element in the ULS contains:

$$\begin{cases} tid: \text{the itemset ID of } i_\alpha \text{ of } t \text{ in } s \\ acu: \text{the maximum utility of } i_\alpha \text{ in } t \\ link: \text{a pointer pointing to either the } (\alpha + 1)^{th} \text{ element or null} \end{cases}$$

**Definition 17 (UCS: utility chain structure)**

Given a sequence  $t$  and q-sequence  $s$ . The UCS of  $t$  in  $s$  is denoted and defined as

$$UCS(t, s) = \begin{cases} peuts: \text{is the prefix extension utility of } t \text{ in } s \\ ULS: \text{is the ULS of sequence } t \text{ in } s \end{cases}$$

**Definition 18 (CHUS: node structure)**

Given a sequence  $t$ , the CHUS of  $t$  in  $SDB$  is denoted and defined as

$$CHUS(t) = \begin{cases} sidSet: \text{the set of sequence IDs containing } t \text{ in } SDB \\ ucpSet = \bigcup_{s \in S} (UCS(t, s)) \end{cases}$$

**Definition 19 (Concatenation)**

Given a sequence  $t$ , there are two types of concatenation of  $t$ :

{I – Extension: insert an item into the last itemset of  $t$   
 {S – Extension: add a new 1 – itemset at the end of  $t$   
 For example,  $\langle\langle acg \rangle\rangle$  and  $\langle\langle ac \rangle\langle a \rangle\rangle$  is generated by performing an I-Extension and an S-Extension of the sequence  $\langle\langle ac \rangle\rangle$ , respectively.

**Definition 20 (SWU: weighted sequence utilization)**

SWU of a sequence  $t$  in  $SDB$  is defined as

$$SWU(t) = \sum_{s' \sim t \wedge s' \subseteq s \wedge s \subseteq SDB} u(s)$$

For example,  $SWU(\langle\langle a \rangle\langle be \rangle\rangle) = u(s_1) + u(s_2) + u(s_3) + u(s_4) = 91 + 96 + 82 + 114 = 383$ .

**Theorem 1 (Sequence weighted downward closure property)**

Given  $t_1$  and  $t_2$ , if  $t_2$  contains  $t_1$ , then  $SWU(t_2) \leq SWU(t_1)$ . Theorem 1 can be used to evaluate whether an item is promising [5, 11, 14]. The CHUSP algorithm also uses this theorem to prune all items with an  $SWU < minUtil$ .

**Definition 21 (PEU: prefix extension utility)**

Given a sequence  $t$  and  $s$ . The  $PEU$  of  $t$  in  $s$  is denoted and defined as

$$PEU(t, s) = \max\{PEU(t, i_k, s) : \forall i_k \text{ that is an ending } q\text{-item of } t \text{ in } s\}$$

$$PEU(t, i_k, s) = \begin{cases} u(t, i_k, s) + ru(i_k, s), & \text{if } ru(i_k, s) > 0 \\ 0, & \text{otherwise} \end{cases}$$

The  $PEU$  of  $t$  in  $SDB$  is denoted and defined as:

$$PEU(t) = \sum_{s' \sim t \wedge s' \subseteq s \wedge s \subseteq SDB} PEU(t, s)$$

Given  $t_1$  and  $t_2$ , if  $t_2$  contains  $t_1$  then  $u(t_2) \leq PEU(t_1)$ .

**Definition 22 (RSU: reduced sequence utility)**

Given a sequence  $t$  and  $s$ . The  $RSU$  of  $t$  in  $s$  is denoted and defined as:

$$RSU(t, s) = \begin{cases} PEU(t') & | t' \subseteq t \wedge s_1 \sim t \wedge s_1 \subseteq s \wedge s_2 \sim t \wedge s_2 \subseteq s \\ 0, & \text{otherwise} \end{cases}$$

The  $RSU$  of the sequence  $t$  in  $SDB$  is denoted and defined as:

$$RSU(t) = \sum_{s' \sim t \wedge s' \subseteq s \wedge s \subseteq SDB} RSU(t, s)$$

Given  $t_1$  and  $t_2$ , if  $t_2$  contains  $t_1$  then  $u(t_2) \leq RSU(t_1)$ .

**Theorem 2 (Pruning strategy by PEU and RSU [2])**

Given a pattern  $t$ ,  $PEU(t)$  and  $RSU(t)$  are considered as upper bounds on the utility of  $t$  and its descendants. If  $PEU(t) < minUtil$  or  $RSU(t) < minUtil$ , then  $t$  and its descendants can be pruned from the search space without affecting the result of the mining process.

**Theorem 3 (MSP: minimum support-based pruning)**

Given a sequence  $t$ , if  $supp(t) < minSup$ , then the sequence  $t$  and its descendants are not CHUSP.

**4. Proposal Algorithm**

**Algorithm 1: The CHUSP algorithm**

---

**input** :  $SDB$ : a  $q$ -sequence dataset,  $t$ : a sequence with its CHUS,  $minUtil$ ,  $minSup$   
**output**:  $CHUSP\_Set$ : The set of CHUSPs

- 1  $CHUSP\_Set \leftarrow \emptyset$
- 2  $\neg CHUSP\_Set \leftarrow \emptyset$
- 3 Scan  $SDB$  to calculate  $SWU$  for all items
- 4 Remove all items that have  $SWU < minUtil$
- 5 **if** ( $PEU(t) < minUtil$ ) **then**
- 6      $\perp$  return
- 7 Scan the projected dataset to:
  - a. put I-Extension items into  $iExts$ ,
  - b. put S-Extension items into  $sExts$
- 8 Remove low  $RSU$  items from  $iExts$  and  $sExts$
- 9 **foreach**  $item\ i \in iExts$  **do**
- 10      $(t', v(t')) \leftarrow I\text{-Extension}(t, i)$
- 11     Construct the  $CHUS$  structure of  $t'$
- 12     **if** ( $supp(t') \geq minSup$ ) **then**
- 13         **if** ( $u_{max}(t') \geq minUtil$ ) **then**
- 14              $\perp$  checkClosedPatterns( $t, t'$ )
- 15              $CHUSP(t', minUtil, minSup)$
- 16 **foreach**  $item\ i \in sExts$  **do**
- 17      $(t', v(t')) \leftarrow S\text{-Extension}(t, i)$
- 18     Construct the  $CHUS$  structure of  $t'$
- 19     **if** ( $supp(t') \geq minSup$ ) **then**
- 20         **if** ( $u_{max}(t') \geq minUtil$ ) **then**
- 21              $\perp$  checkClosedPatterns( $t, t'$ )
- 22              $CHUSP(t', minUtil, minSup)$
- 23 Remove non-CHUSPs from  $CHUSP\_Set$
- 24 **return**  $CHUSP\_Set$ ;

---

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**Algorithm 2:** checkClosedPatterns procedure

---

```
input : previous pattern  $t$ , current pattern  $t'$  ( $t \subseteq t'$ ),  
         $CHUSP\_Set$ ,  $\neg CHUSP\_Set$   
1 /* In this case:  $t$  is not a CHUSP,  $t'$   
   is a candidate */  
2 if  $supp(t) == supp(t')$  then  
3   Remove  $t$  from  $CHUSP\_Set$   
4   Add  $t$  into  $\neg CHUSP\_Set$   
5   Add  $t'$  into  $CHUSP\_Set$   
6 /* In this case: both  $t$  and  $t'$  are  
   candidates */  
7 else  
8   Add  $t'$  into  $CHUSP\_Set$   
9   if  $t \notin \neg CHUSP\_Set$  then  
10  Add  $t$  into  $CHUSP\_Set$ 
```

---

The pseudo-code of the CHUSP algorithm is shown in Algorithm 1. The input is a q-sequence dataset  $SDB$ , a sequence  $t$  with its  $CHUS$  structure, and two predefined parameters:  $minUtil$ ,  $minSup$ . First, a set called  $CHUSP\_Set$  is initialized to keep all CHUSPs. We also use the  $\neg CHUSP\_Set$  to track all but not closed high utility sequential patterns. The algorithm scans  $SDB$  to calculate the  $SWU$  of all items in  $SDB$  (line 3). It then selects all items with an  $SWU$  of greater than  $minUtil$  and builds the initial  $CHUS$  structure and the lexicographic tree required by the mining process. It also removes all items with an  $SWU$  value less than  $minUtil$  (line 4). The topmost node in that tree is the root node, where its children are q-sequences that contain a single item. Each node other than the root stores a sequence  $t$ , the  $CHUS$  structure of  $t$ , utility matrices, remaining utility matrices, and the list that contains sequence IDs called  $seqIdList$  of 1 q-items in q-sequences of  $SDB$ .

If  $PEU(t)$  is less than  $minUtil$ , then the algorithm will consider  $t$  as a leaf and will not expand the lexicographic tree using node  $t$ , i.e., all its descendants will be pruned (lines 5-6). In the next step, the algorithm scans the projected dataset that includes the  $CHUS$  of  $t$  in  $SDB$  to collect all items that can be combined with  $t$  to form a new sequence by I-Extension or S-Extension (line 7). Each item with an  $RSU$  value lower than  $minUtil$  is discarded from the mining process (line 8). Then, the algorithm performs a loop over all items in the iExts (lines 9-15) and sExts (lines 16-22). For each item  $i$  in the iExts, the algorithm performs an I-Extension with this item to

form a new sequence  $t'$  by inserting  $i$  in the last itemset of  $t$ . In addition, the  $CHUS$  structure,  $seqIdList$ , and the maximum utility of  $t'$  are constructed and calculated by extending the  $CHUS$  of  $t$  (lines 10-11). To reduce the search space and enhance the mining process, CHUSP applies the MSP strategy (Theorem 3) to discard non-frequent patterns (line 12). If the condition returns true, CHUSP stops considering these patterns and backtracks to the previous step. Otherwise, the algorithm checks if the pattern's utility value is greater than  $minUtil$ . If yes, the pattern is a high utility sequential pattern (line 13). CHUSP calls the *checkClosedPatterns* procedure to check if that HUSP is closed (line 14).

The inputs of *checkClosedPatterns* procedure are two patterns  $t$ ,  $t'$ ,  $CHUSP\_Set$  and  $\neg CHUSP\_Set$ . Note that the sequence  $t'$  is a super-sequence of  $t$  by performing the I-Extension or S-Extension concatenation. We consider  $t$  and  $t'$  as the previous and current sequences since  $t'$  is generated from  $t$ . The procedure checks if the previous sequence  $t$  is a CHUSP by comparing its support count with the support count of the current sequence  $t'$ . If the two support values are equal, it means that  $t$  is not a CHUSP because it has a super-sequence with the same support (break the Def. 15), then the procedure checks if  $t$  is in  $CHUSP\_Set$ , if yes then removes  $t$  from this set (line 3). The procedure also checks if  $t$  is in  $\neg CHUSP\_Set$ ; if No, add  $t$  into this set (line 4). The purpose of this action is to track all non-candidate sequences. During mining,  $t$  may be extended to other  $t'$  by doing other concatenations. In this case,  $t$  involves in other checking procedures. The procedure then inserts the current sequence  $t'$  into the  $CHUSP\_Set$  (line 5). It is worth noting that CHUSP is a recursive algorithm. Thus, the current sequence  $t'$  will be later called in other rounds of the algorithm to extend itself. In other words, the sequence  $t'$  is the super-sequence of a sequence  $t$  at this stage, but it will be the sub-sequence of another sequence in another stage. Thus, any sequences in the  $CHUSP\_Set$  are candidates and may be removed from the set when the algorithm detects super-sequences having the same support. If the supports of  $t$  and  $t'$  are different, the two patterns become candidates. The procedure adds the current pattern  $t'$  to the  $CHUSP\_Set$  as a

candidate (line 8). Next, the procedure checks if the previous sequence  $t$  is in the  $\neg CHUSP\_Set$ . If yes, then it will not be a CHUSP candidate. Otherwise,  $t$  is inserted into  $CHUSP\_Set$ .

The CHUSP recursively calls itself to expand  $t'$  (line 15). A similar process is performed for all items in  $sExts$ . It passes a sequence and its projected dataset to each recursive call as input parameters. The sequence dataset  $SDB$  and lines 1-4 are used only for initializing the algorithm and are not performed during recursive calls. For each item in  $sExts$ , a new pattern is generated by performing an S-Extension (lines 16 to 22). When the algorithm completes recursive calls, the algorithm traverses all patterns in the  $CHUSP\_Set$  to remove non-CHUSPs from this list (line 23). Finally, it returns all CHUSPs as the output.

## 5. Experimental Results

Experiments were performed to evaluate the performance of CHUSP on a computer with a 64-bit Intel(R) Xeon(R) Gold 6330 CPU @ 2.00GHz, 12 GB of RAM, running Windows 10 Enterprise LTSC. The source code is publicly available on GitHub. All the algorithms were implemented in C#. Fig. 1 shows the user interface of the CHUSP algorithm. The proposed algorithm was compared with two algorithms. The first algorithm is the HUS-Span algorithm [2] for mining HUSPs. The second algorithm is FHUSP, an extension of HUS-Span for mining FHUSPs. The performance of the three algorithms has been compared on six real datasets. The characteristics of these datasets are shown in Table 7. They are six real-life datasets. They have varied characteristics, such as sparse and dense datasets, short and long sequences.

For each dataset, the  $minUtil$  was decreased until a clear winner was observed, or algorithms became too long to execute. In some cases, a constraint on the maximum length of CHUSP ( $maxLength$ ) was used to speed up the experiments. For  $minSup$ , a suitable empirical value was chosen for each dataset to ensure that the algorithms discovered a certain number of CHUSPs. The  $minSup$  values for Sign, Kosarak10k, BMSWebView1, BMSWebView2, Fifa and Bible were set to 50%, 5%, 20%, 20%, 0.5%, 0.5%, respectively.

Table 7: Characteristics of the datasets

Dataset	#Sequence	#Item	Avg. seq length
Sign	800	310	51.99
Kosarak10k	10,000	10,094	8.14
BMSWebView1	59,601	497	2.51
BMSwebview2	77,512	3,340	4.62
Fifa	20,450	2,990	34.74
Bible	36,369	13,905	21.64

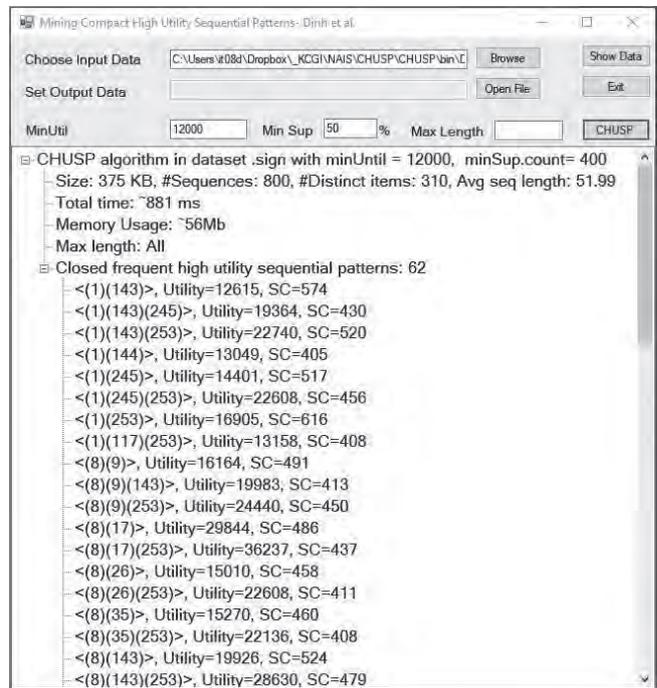


Figure 1: The CHUSP application

First, the execution time of CHUSP is compared with HUS-Span and FHUSP. Fig. 2 shows that CHUSP outperforms the compared algorithms on all datasets. Each subfigure's vertical and horizontal axes represent the execution time (milliseconds) and minimum utility threshold values, respectively. In general, for all datasets, when the minimum utility threshold is decreased or when datasets contain more sequences or longer sequences, the running time of the algorithms increases. In that case, CHUSP can be much more efficient than the two algorithms, especially on Sign, Bible, BMSWebview1, and FIFA

datasets. On Sign ( $minSup = 50\%$ ) CHUSP is respectively up to 295.7, 250.3, 222.7, 188.9, 156.6, 125.9, 116.2, 75.8, 50.9, and 37.5 times faster than HUS-Span for  $minUtil$  from 12,000 to 35,000. Compare with FHUSP, it is up to 292.72, 245.01, 215.88, 188.51, 154.50, 118.80, 111.47, 73.24, 50.24, and 35.94. On BMSWebView2 ( $minSup = 50\%$ ) CHUSP is respectively up to 12.2, 8.9, 7.6, 6.3, 4.7, 3.4, 3.2, 2.1, 1.9, and 1.7 times faster than HUS-Span for  $minUtil$  from 10,000 to 100,000. It is respectively up to 11.5, 8.0, 7.1, 5.8, 4.1, 3, 2.3, 1.8, 1.5, and 1.3 times faster than FHUSP. Similar results can be observed for other datasets. The results indicate that the MSP pruning strategy of CHUSP is effective and can prune many non-frequent patterns. In addition, the CHUS structure and pruning strategies are suitable for mining CHUSPs. Thus, the algorithm can facilitate the mining process and prune more non-candidates than HUS-Span and FHUSP algorithms.

Second, the algorithms have also been compared in terms of memory performance for the six datasets for the same  $minUtil$ ,  $minSup$ , and  $maxLength$  values as in the runtime experiment. Results are shown in Fig. 3 in terms of memory usage (vertical axes) for various  $minUtil$  values (horizontal axes). CHUSP consumes less memory than HUS-Span in all cases. It means that the CHUSP structure is more effective than the structure used by the HUS-Span algorithm. In addition, the MSP strategy can filter many non-frequent candidates. CHUSP is also better than FHUSP in most cases, although they are very close in some cases. On FIFA and Bible, we can observe that CHUSP performs much better than FHUSP. Except for the BMSWebview1 dataset, FHUSP consumes less memory than CHUSP on large  $minUtil$  values. However, for low  $minUtil$  values, when the algorithms need more time to mine patterns, CHUSP outperforms FHUSP. Generally, for each dataset, the memory usage increases when the  $minUtil$  is decreased, and it is also greater for larger datasets.

Finally, the number of patterns was measured for various  $minUtil$  threshold values on each dataset. In

Fig. 4, vertical axes denote the number of patterns, and horizontal axes indicate the corresponding maximum threshold values. The number of patterns generated by CHUSP is much less than that of HUS-Span and FHUSP for each dataset. On Sign ( $minSup = 50\%$ ), for  $minUtil$  from 12,000 to 35,000, CHUSP found 62, 58, 51, 48, 41, 35, 31, 13, 5, and 3, respectively. It can be observed that the number of patterns by CHUSP is respectively up to 169.1, 121.2, 93.7, 68.2, 37.7, 21.5, 16.5, 7.3, 3.4, and 1.3 times less than those found by HUS-Span. In addition, the number of patterns by CHUSP is respectively up to 1.13, 1.09, 1.1, 1.04, 1.02, 1.03, 1.03, 1.08, 1.00, and 1.00 times less than those found by FHUSP. On Kosarak10k ( $minSup = 5\%$ ), the  $maxLength$  was set to 3 for the  $minUtil$  values of 10,000 and 20,000 for HUS-Span and FHUSP; for CHUSP, this parameter was set to full. For  $minUtil$  from 10,000 to 100,000, CHUSP found 21, 14, 10, 5, 3, 2, 2, 2, 1, and 1 CHUSPs, respectively. It can be observed that the number of patterns by CHUSP is respectively up to 3.9, 1.9, 1.4, 1.2, 1.3, 1.5, 1.5, 1.5, 2.0, and 2.0 times less than those by HUS-Span. In addition, the number of patterns by CHUSP is up to 1.4, 1.4, 1.2, 1.2, 1.3, 1.5, 1.5, 1.5, 2.0, and 2.0 times less than those by FHUSP. On BMSwebview1 ( $minSup = 0.5\%$ ). The  $maxLength$  was set to 3 for HUS-Span and FHUSP; for CHUSP, this parameter was set to full. For  $minUtil$  from 5,000 to 35,000, CHUSP found 45, 42, 39, 38, 31, 18, 10, 3, 2, and 2 CHUSPs, respectively. It can be observed that the number of patterns by CHUSP is respectively up to 3.6, 3.5, 3.5, 3.2, 3.0, 3.3, 3.4, 6, 7, and 5.5 times less than those by HUS-Span. In addition, the number of patterns by CHUSP is up to 3.6, 3.5, 3.5, 3.2, 3.0, 3.3, 3.4, 6, 7, and 5.5 times less than those by FHUSP. Similar results can be observed for the BMSwebview1, FIFA, and BIBLE datasets. These results indicate that the CHUSP algorithm can eliminate many non-candidate patterns from the search space and reduce the number of patterns from the mining process.

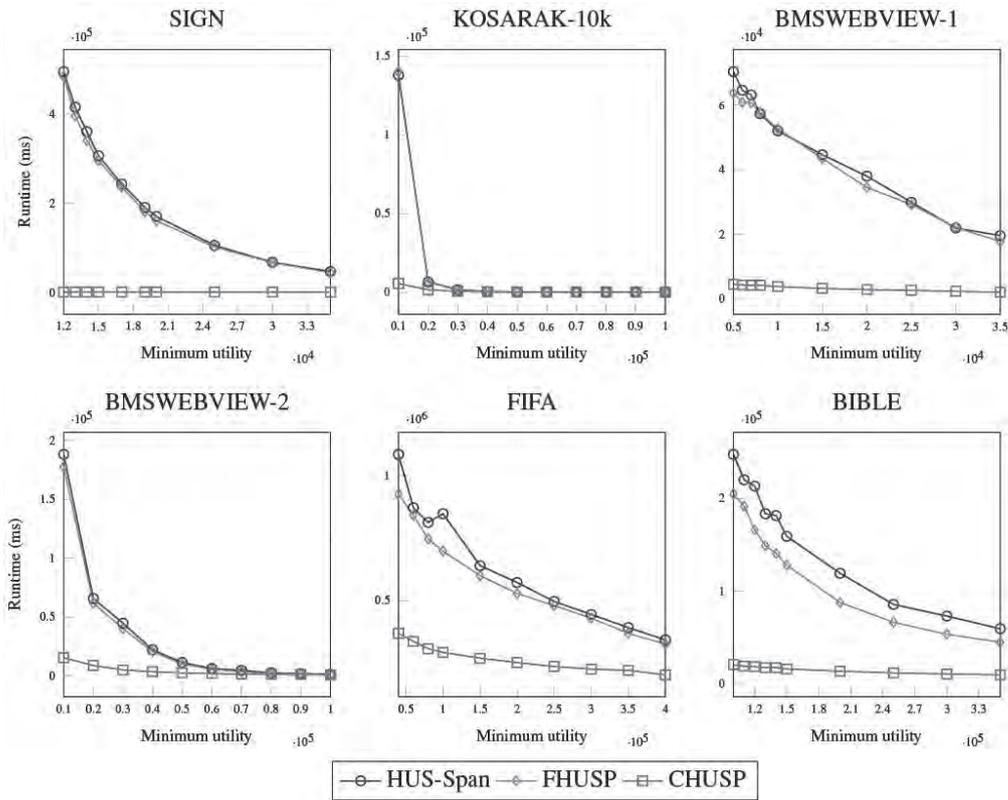


Figure 2: Runtimes for various minimum utility threshold values

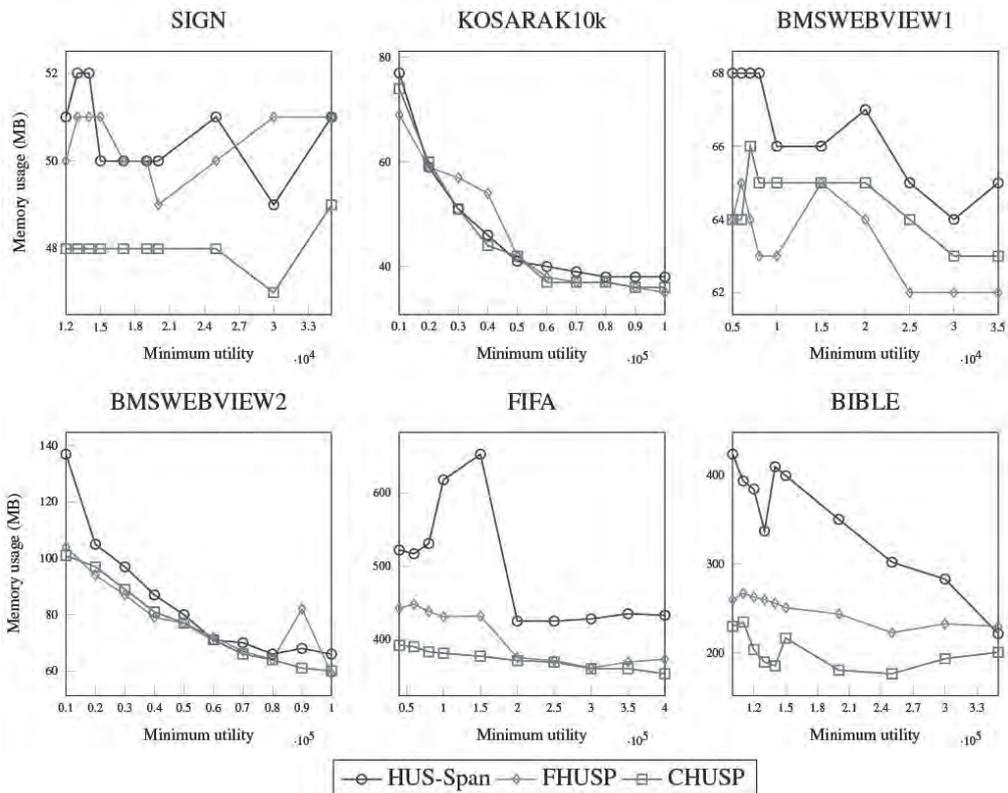


Figure 3: Memory usage for various minimum utility threshold values

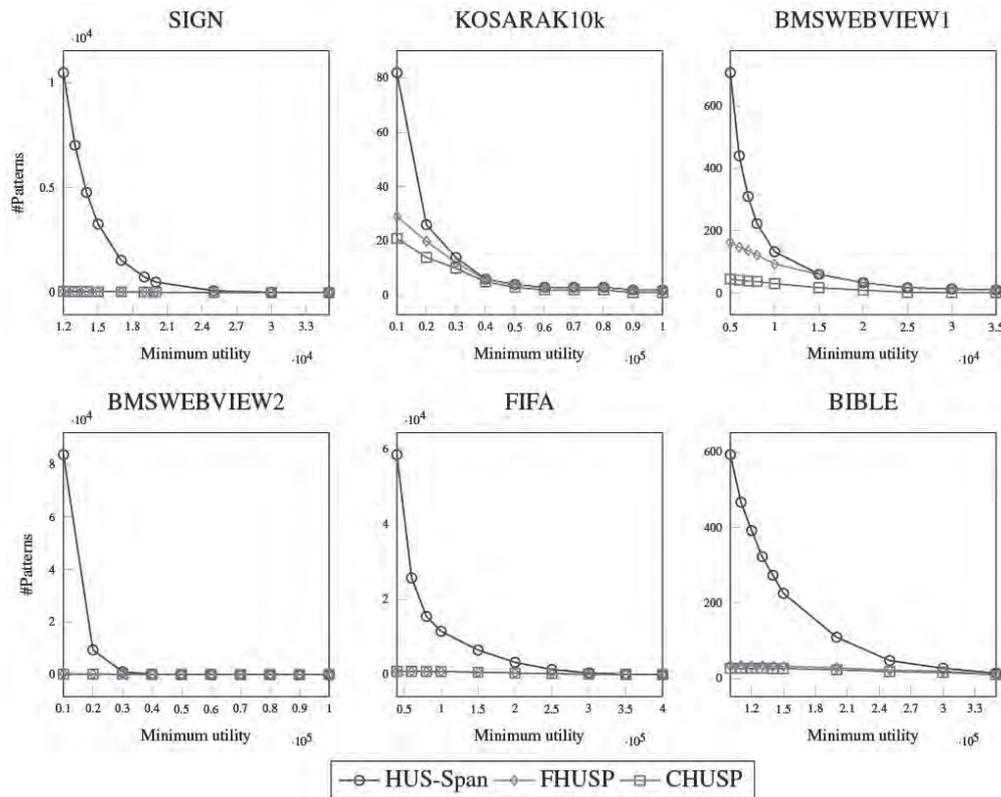


Figure 4: Number of patterns for various minimum utility threshold values

## 6. Conclusion

This paper proposed an algorithm named CHUSP for mining closed high utility sequential patterns. The proposed algorithm uses the CHUS structure for efficiently mining CHUSP. Experimental results indicate that CHUSP outperforms HUS-Span and FHUSP algorithms in terms of execution time and memory usage. The number of patterns generated by the three algorithms was also measured for various minimum utility threshold values. The results show that all the pruning strategies used in CHUSP can eliminate many non-CHUSP and thus speed up the mining process. In future work, we will design a parallel framework that can enhance the computational cost of CHUSP and extend the pattern mining framework for other tasks [14, 19, 25–27].

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