Mining Uncertain Data with Probabilistic Guarantees

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ABSTRACT

Data uncertainty is inherent in applications such as sensor monitoring systems, location-based services, and biological databases. To manage this vast amount of imprecise information, probabilistic databases have been recently developed. In this paper, we study the discovery of *frequent patterns* and *association rules* from probabilistic data under the *Possible World Semantics*. This is technically challenging, since a probabilistic database can have an exponential number of possible worlds. We propose two efficient algorithms, which discover frequent patterns in *bottom-up* and *top-down* manners. Both algorithms can be easily extended to discover maximal frequent patterns. We also explain how to use these patterns to generate association rules. Extensive experiments, using real and synthetic datasets, were conducted to validate the performance of our methods.
Source codes and data are available at:
http://www.cs.hku.hk/~lwsun/codes/kdd10/

Categories and Subject Descriptors

H.2.8 [**Information Systems**]: Database applications—*Data Mining*

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Algorithms, Experimentation, Performance, Theory

Keywords

uncertain data, frequent pattern, association rule

1. INTRODUCTION

The data managed in many emerging applications is often uncertain. Integration and record linkage tools, for example, associate confidence values to the output tuples according to the quality of matching [11]. In structured information extractors, confidence values are appended to rules for extracting patterns from unstructured data [28]. In habitat monitoring systems, data collected from sensors like temperature and humidity are noisy [1]. The locations of users obtained through RFID and GPS systems are also imprecise [25, 16]. To handle these problems, *probabilistic databases* have been recently proposed, where uncertainty is treated as a "first-class citizen" [8, 11, 21, 10, 15].

Due to its simplicity in database design and query semantics, the *tuple-uncertainty* model is commonly used in probabilistic databases. Conceptually, each tuple carries an *existential probability* attribute, which denotes the confidence that the tuple exists. Figure 1 illustrates this model, which records traffic violation events due to red-light running. The details of each event (e.g., location, and traffic volume) are captured by a red-light camera system, which contains sensors and cameras mounted in road intersections. Each tuple is annotated by a probability that a true violation happens. The probability that a violation occurs is determined by sensor measurement errors, as well as the uncertainty caused by automatic information extraction of the photographs taken by the system [30].

Figure 1: A probabilistic database example.

ID	location	time	speed	traffic	weather	prob.
t_1	x	8-9pm	30-40	high	Rain	0.1
t_2	x	7-8am	80-90	low	*null*	1.0
t_3	x	8-9pm	80-90	low	Foggy	0.5
t_4	x	8-9pm	30-40	high	Rain	0.2
t_5	y	2-3pm	50-60	low	Sunny	1.0

To interpret tuple uncertainty, the *Possible World Semantics* (or PWS in short) is often used [11]. Conceptually, a database is viewed as a set of deterministic instances (called *possible worlds*), each of which contains a set of zero or more tuples. A possible world for Figure 1 consists of the tuples $\{t_2, t_3, t_5\}$, existing with a probability of $(1-0.1) \times 1.0 \times 0.5 \times (1-0.2) \times 1.0 = 0.036$. Any query evaluation algorithm for a probabilistic database has to be correct under PWS. That is, the results produced by the algorithm should be the same as if the query is evaluated on every possible world [11].

Although PWS is intuitive and useful, evaluating queries under this notion is costly. This is because a probabilistic database has an exponential number of possible worlds. For example, the table in Figure 1 has $2^3 = 8$ possible worlds. Performing query evaluation or data mining under PWS can thus be technically challenging. In fact, the mining of uncertain or probabilistic data has recently attracted research attention [3]. In [18], efficient clustering algorithms were developed to group uncertain objects that are close to each

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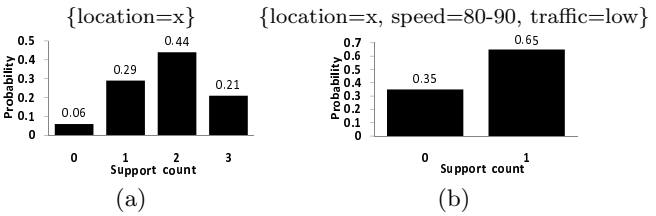


Figure 2: Sample p-FPs derived from Figure 1

other. Recently, a Naïve Bayes classifier has been developed [26]. The goals of this paper are: (1) propose a definition of frequent patterns and association rules for the tuple uncertainty model; and (2) develop efficient algorithms for mining patterns and rules that are correct under PWS.

Figure 3: Sample p-ARs derived from Figure 1

Association rule	Probability
r_1: {location=x} ⇒ {time=8-9pm}	0.15
r_2: {location=x} ⇒ {speed=80-90,traffic=low}	0.49

The frequent patterns discovered from probabilistic data are also probabilistic, to reflect the confidence placed on the mining results. Figure 1 shows two *probabilistic frequent patterns* (or *p-FP*) extracted from the database in Figure 1. A *p-FP* is a set of attribute values that occur frequently with sufficiently-high probabilities. In Figure 1, the *support probability mass function* (or *support pmf*) for each *p-FP* is shown. This is the pmf of the number of tuples (or *support count*) that contains a pattern. Under PWS, a database is a set of possible worlds, each of which records a (different) support of the same pattern. Hence, the support of a frequent pattern is a pmf. In Figure 1, if we consider all possible worlds where pattern {location=x} occurs three times, the pmf of {location=x} with a support of 3 is 0.49. For the *p-FP*s shown, Figure 3 displays their related *probabilistic association rules* (or p-ARs). Here, rule r_2 suggests that with a 0.49 probability, 1) red-light violations occur frequently at location x and 2) when this happens, the involved vehicle is likely driving at a high speed amid low traffic. We will later explain more about the semantics of p-FP and p-AR.

A simple way of finding p-FPs is to extract frequent patterns from every possible world. This is practically infeasible, since the number of possible worlds is exponentially large. We present simple and effective methods to prune infrequent patterns. We also adopt dynamic programming (DP) to compute the support pmf of a pattern. This method, also used by [31, 27] to derive p-FPs for other probabilistic models, has a complexity of $O(n^2)$. We further develop a divide-and-conquer (DC) approach, which achieves $O(n \log^2 n)$ time. Based on these methods, we propose the *p-Apriori* algorithm to retrieve p-FPs in a *bottom-up* manner. We further observe that, given patterns X and Y, if X is a subset of Y, the support pmf of X can be efficiently derived from that of Y. We realize this by proposing the *TODIS* algorithm, which extracts p-FPs in a *top-down* fashion. We extend p-Apriori and TODIS to retrieve *maximal* p-FPs, i.e., those that are not the subsets of other p-FPs. Our experiments on real and synthetic datasets showed that DC is more scalable than DP, and TODIS is generally faster than p-Apriori. When TODIS is used with DC together, it can outperform p-Apriori by an order of magnitude.

In exact databases, deriving association rules from frequent patterns is not difficult. Given two frequent patterns X and XY, the confidence of $X \Rightarrow Y$ can be calculated with an arithmetic division on their supports. This is no longer true for probabilistic data. Here, the support of X and XY become *correlated* random variables. It is not clear how to define and compute the "confidence" of $X \Rightarrow Y$. We propose the concept of p-AR, which naturally extends the association rule semantics. We also study an efficient method, which uses deconvolution operations, to evaluate the probability of p-AR based on the support pmfs of p-FPs. We further develop a new algorithm for generating p-ARs, which exploits the anti-monotonicity property of p-ARs, and attain a 80% performance gain in our experiments.

Prior work. [7] studied approximate frequent patterns on noisy data, while [19] examined association rules on fuzzy sets. The notion of a "vague association rule" was developed in [20]. These solutions were not developed on probabilistic data models. For probabilistic databases, [9, 2] derived patterns based on their expected support counts. [31, 27] found that the use of expected support may render important patterns missing. They discussed the computation of the probability that a pattern is frequent. While [31] handled the mining of *single* items, our solution can discover patterns with more than one item. The data model used in [27] assumes that for each tuple, each attribute value has a probability of being correct. This is different from the tuple-uncertainty model, which describes the joint probability of attribute values within a tuple. Moreover, our DC algorithm is asymptotically faster than the DP algorithms used in [31, 27], and is thus more scalable for large and dense datasets. To our best knowledge, none of the above works considered the important problem of generating association rules on probabilistic databases.

This paper is organized as follows. Section 2 introduces the notions of p-FPs and p-ARs. Sections 3 and 4 present two algorithms for mining p-FPs. In Section 5, we develop an algorithm for generating p-ARs. Section 6 presents our experimental results. We conclude in Section 7.

2. PROBLEM DEFINITION

We first review frequent patterns and association rules in Sections 2.1. Then, we discuss the uncertain data model in Section 2.2. We present the problems of mining p-FPs and p-ARs, in Sections 2.3 and 2.4.

2.1 Frequent Patterns and Association Rules

A transaction is a set of *items* (e.g., goods bought by a customer in a supermarket). A set of items is also called an *itemset* or a *pattern*. Given a transaction database of size n and a pattern X, we use $sup(X)$ to denote the *support* of X, i.e., the number of times that X appears in the database. A pattern X is *frequent* if:

$$sup(X) \geq \texttt{minsup} \tag{1}$$

where $\texttt{minsup} \in \mathcal{N} \cap [1, n]$ is the *support threshold* [4]. Given patterns X and Y (with $X \cap Y = \emptyset$), if pattern XY is frequent, then X is also frequent (called the anti-monotonicity property). Also, $X \Rightarrow Y$ is an association rule if the follow-

ing conditions hold:

$$sup(XY) \geq \texttt{minsup} \tag{2}$$

$$\frac{sup(XY)}{sup(X)} \geq \texttt{minconf} \tag{3}$$

where $\frac{sup(XY)}{sup(X)}$, denoted by $conf(X \Rightarrow Y)$, is the *confidence* of $X \Rightarrow Y$, and $\texttt{minconf} \in \mathcal{R} \cap (0, 1]$ is the *confidence threshold*. To verify Equation 3, the values of $sup(XY)$ and $sup(X)$ have to be found first.

We remark that a transaction database is essentially a relational table with asymmetric binary attribute values. For example, the existence of item "apple" in a transaction is equivalent to a binary attribute of a tuple with a value of 1. This kind of attributes, assumed in this paper, is also considered by some mining algorithms (e.g., [4, 5]). To handle other attribute types (e.g., continuous and categorical), discretization and binarization techniques can be used to convert them to binary attributes [29].

2.2 The Possible World Semantics

We assume that each transaction has an *existential probability*, which specifies the chance that the transaction exists. Figure 4(a) illustrates this database, in which each transaction is a set of items represented by letters. This model has been used to capture uncertainty in many applications, including data streams [10] and geographical services [22]. Now, let $P(E)$ be the probability that an event E occurs, and $\mathcal{PDB}$ be a probabilistic database of size n. Also, let T_i (where $i = 1, \ldots, n$) be the ID of each tuple in $\mathcal{PDB}$. Suppose $T_i.S$ is the set of items contained in T_i, and $T_i.p$ is the existential probability of T_i.

ID	set of items	prob.
T_1	$\{a, c, e, g, i\}$	0.6
T_2	$\{a, c, f, h\}$	0.5
T_3	$\{a, d, e, g, j\}$	0.7
T_4	$\{b, d, f, h, i\}$	1.0

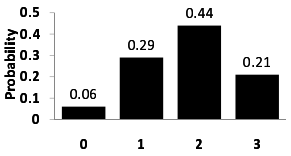


Figure 4: (a) $\mathcal{PDB}$ example; and (b) $f_{\{a\}}$

Figure 5: Possible worlds for Figure 4(a)

$\mathcal{W}$	Tuples in W	Prob.	$\mathcal{W}$	Tuples in W	Prob.
W_1	T_4	0.06	W_5	T_1, T_2, T_4	0.09
W_2	T_1, T_4	0.09	W_6	T_1, T_3, T_4	0.21
W_3	T_2, T_4	0.06	W_7	T_2, T_3, T_4	0.14
W_4	T_3, T_4	0.14	W_8	T_1, T_2, T_3, T_4	0.21

Under PWS, $\mathcal{PDB}$ is a set of possible worlds $\mathcal{W}$. Figure 5 lists all possible worlds for Figure 4(a). Each world $W_i \in \mathcal{W}$ exists with probability $P(W_i)$. For example, $P(W_2) = T_1.p \times (1 - T_2.p) \times (1 - T_3.p) \times T_4.p$, or 0.09. The sum of possible world probabilities is one. Also, the number of possible worlds is exponentially large, i.e., $|\mathcal{W}| = O(2^n)$. Our goal is to discover patterns and rules *without* expanding $\mathcal{PDB}$ into possible worlds. Table 1 summarizes the symbols used.

Table 1: Summary of Notations

Notation	Meaning
Prob. Database	
$\mathcal{PDB}$	a probabilistic database of size n
T_i	ID of a tuple in $\mathcal{PDB}$, where $i = 1, \ldots, n$
$T_i.S$	set of items contained in T_i
$T_i.p$	existential probability of T_i
$\mathcal{W}$	set of possible worlds expanded from $\mathcal{PDB}$
W_i	a possible world, where $W_i \in \mathcal{W}$
$P(E)$	probability of event E
Prob. Frequent Patterns	
`minsup`	support threshold
`minprob`	probability threshold
$sup(X)$	support count of pattern X
$f_X(k)$	support pmf of X in $\mathcal{PDB}$
$cnt(X)$	No. of tuples for which $p_i^X > 0$
$esup(X)$	expected support of pattern X
p_i^X	prob. that X occurs in T_i
L^X	inverted probability list of X
X`.exItem`	exclusive item of X
X`.cnt`	length of L^X
Prob. Association Rules	
`minconf`	confidence threshold
$conf(X \Rightarrow Y)$	confidence of $X \Rightarrow Y$

2.3 Probabilistic Frequent Patterns

We first explain the concept of "support" for probabilistic data. Given a pattern X, we denote its support in each world W_i as $sup_i(X)$. Note that $sup_i(X)$ is obtained by counting the number of times X appears in W_i. Since each W_i exists with a probability, the support of X in $\mathcal{PDB}$, i.e., $sup(X)$, is a random variable. We denote by $f_X(k)$ that the probability mass function (pmf) of $sup(X)$, where k is a non-negative integer that $sup(X)$ can take. Specifically, $f_X(k)$ is the probability that $sup(X) = k$, and $f_X(k) = 0$ for any $k \notin [0, n]$. We use an array to store the non-zero values of f_X, where $f_X[k] = P(sup(X) = k)$. Figure 4(b) depicts the support pmf of $\{a\}$ for Figure 5. The probability that $sup(\{a\}) = 1$ is 0.29.

Definition 1. *A pattern X is a probabilistic frequent pattern (or p-FP) in $\mathcal{PDB}$ if*

$$P(sup(X) \geq \texttt{minsup}) \geq \texttt{minprob} \tag{4}$$

where $\texttt{minprob} \in \mathcal{R} \cap (0, 1]$ is the *probability threshold*.

Problem 1 (p-FP Mining). *Given $\mathcal{PDB}$,* `minsup` *and* `minprob`*, return a set of $\{X, f_X(k)\}$, where X is a p-FP.*

As we will discuss, the pmfs obtained with *p-FP*s are essential to generating probabilistic association rules. There are methods to approximating and compressing pmfs (e.g., see [12]). Here we assume that the pmf is exact, but our solutions can be extended to support these schemes. Next, we present a useful lemma.

Lemma 1 (Anti-monotonicity). *If pattern X is a p-FP, then any pattern $X' \subset X$ is also a p-FP.*

Proof. Let X' be a sub-pattern of X. Suppose that $\mathcal{W}^X$ and $\mathcal{W}^{X'}$ are the sets of possible worlds where X and X' are frequent respectively. For each possible world $W_i \in \mathcal{W}^X$, if X is frequent in W_i, then X' is also frequent. Hence, we have $\mathcal{W}^X \subseteq \mathcal{W}^{X'}$. Then $P(sup(X) \geq \texttt{minsup}) = \sum_{W_i \in \mathcal{W}^X} P(W_i)$,

and $P(sup(X') \geq \texttt{minsup}) = \sum_{W_i \in \mathcal{W}^{X'}} P(W_i)$. Since X is a p-FP, we have: $P(sup(X') \geq \texttt{minsup}) \geq P(sup(X) \geq \texttt{minsup}) \geq \texttt{minprob}$. Therefore, X' is also a p-FP. □

The anti-monotonicity property is true for frequent patterns in exact data [4]. Lemma 1 allows us to stop examining a pattern, if any of its sub-pattern is not a p-FP. A p-FP X is said to be *maximal* if we cannot find another p-FP Y such that $X \subset Y$. A maximal p-FP can succinctly represent a set of p-FPs when their supports are not concerned. Since the mining of maximal frequent patterns is an important problem [5] for exact data, we also study maximal p-FPs:

PROBLEM 2 (MAXIMAL P-FP MINING). *Given a database $\mathcal{PDB}$,* `minsup` *and* `minprob`*, return all maximal p-FPs.*

2.4 Probabilistic Association Rules

In a probabilistic database, the support counts of patterns are random variables. Let $P(X \Rightarrow Y)$ be the probability that $X \Rightarrow Y$ is an association rule. By Equations 2 and 3, we have:

$$P(X \Rightarrow Y) = P\,[sup(XY) > \texttt{minsup} \wedge conf(X \Rightarrow Y) \geq \texttt{minconf}] \quad (5)$$

DEFINITION 2. *$X \Rightarrow Y$ is a probabilistic association rule (p-AR in short) if*

$$P(X \Rightarrow Y) \geq \texttt{minprob} \quad (6)$$

The problem of *p-AR* mining is defined as follows.

PROBLEM 3 (P-AR MINING). *Given* `minsup`*,* `minprob`*,* `minconf`*, and the p-FPs and their support pmfs obtained from Problem 1, derive all p-ARs and their probabilities.*

A simple way of solving Problems 1, 2 and 3 is to expand $\mathcal{PDB}$ into all possible worlds, compute patterns and rules from each world, and then combine the results. If `minsup` = 2, `minconf` = 0.5, and `minprob` = 0.2, for Figure 4(a), $\{a\} \Rightarrow \{c\}$ is an association rule only in worlds W_5 and W_8 (Figure 5), with $P(\{a\} \Rightarrow \{c\}) = Pr(W_5) + Pr(W_8) = 0.09 + 0.21 = 0.3$. Since this is larger than 0.2, $\{a\} \Rightarrow \{c\}$ is a *p-AR*. This method is not practical, due to the large number of possible worlds. To tackle Problems 1 and 2, we propose two efficient algorithms, namely *p-Apriori* and *TODIS*, in respectively Sections 3 and 4. Then we address Problem 3 in Section 5.

3. THE P-APRIORI ALGORITHM

To solve Problem 1, we propose the *p-Apriori* algorithm, which is an adaptation of the *Apriori* algorithm [4] for probabilistic databases. Specifically, p-Apriori uses the *bottom-up* framework [4]: each item is tested to see whether it is a p-FP. All probabilistic frequent singletons then have their support pmfs computed, and are used to generate size-2 patterns (called candidate patterns). These patterns are examined to see which are frequent patterns. The size-2 p-FPs again have their support pmfs evaluated, and are used to create size-3 candidate patterns. The process is repeated until no more frequent patterns are found. In general, to create a size-(m+1) candidate patterns from size-m p-FPs, we use the anti-monotonicity property (Lemma 1), which implies that a size-(m+1) pattern can be a candidate only if all its size-m sub-patterns are frequent. Finally, the p-FPs and their support pmfs are returned.

The p-Apriori can also solve Problem 2, by returning only the maximal p-FPs that appear in p-Apriori's mining result.

For p-Apriori to work well, we have to efficiently check whether a given pattern X is frequent. When the database is exact, we can scan the database once, find the support count of X, and test it with Equation 1. For p-Apriori, we have to (1) find X's support pmf; (2) derive $P(sup(X) \geq \texttt{minsup})$ and test against Equation 4. To find X's support pmf, we may consider its support from all possible worlds; however, this is practically infeasible. In Sections 3.1, we discuss how to prune infrequent patterns *without* deriving support pmfs. For patterns that cannot be pruned, we discuss two efficient methods for generating support pmfs, in Sections 3.2 and 3.3. We present a data structure to improve our algorithms, in Section 3.4.

3.1 Pruning Infrequent Patterns

Let $cnt(X)$ be the number of tuples that contain pattern X regardless of the tuple probabilities (i.e., $T_i.p$). Also, let $esup(X)$ be the expected support of X, which can be found by summing up all $T_i.p$'s in $\mathcal{PDB}$ [9]. The lemmas below describe how to prune X without knowing its support pmf.

LEMMA 2. *If $cnt(X) < \texttt{minsup}$, then X is not a p-FP.*

PROOF. The maximum possible value of $sup(X)$ is $cnt(X)$, which happens when all tuples that contain X exist. Hence, $P[sup(X) > cnt(X)] = 0$. Since $cnt(X) < \texttt{minsup}$, we have $P[sup(X) \geq \texttt{minsup}] \leq Pr[sup(X) > cnt(X)] = 0$. Therefore, for any $\texttt{minprob} > 0$, X cannot be a p-FP according to Equation 4. □

LEMMA 3. *Let $\mu = esup(X)$, and $\sigma = \frac{\texttt{minsup} - \mu - 1}{\mu}$. Then X is not a p-FP if:*

- *$\sigma \geq 2e - 1$ and $2^{-\sigma\mu} < \texttt{minprob}$, or*
- *$0 < \sigma < 2e - 1$ and $e^{\frac{-\sigma^2\mu}{4}} < \texttt{minprob}$*

PROOF. Notice that the probability $P[sup(X) \geq \texttt{minsup}]$ is equal to $Pr[sup(X) > \texttt{minsup} - 1]$, or $Pr[sup(X) > (1 + \sigma)\mu]$. Using the Chernoff Bound [23], we have:

$$Pr[sup(X) > (1+\sigma)\mu] \quad < \quad \begin{cases} 2^{-\sigma\mu}, & \text{if } \sigma \geq 2e - 1 \\ e^{\frac{-\sigma^2\mu}{4}}, & \text{if } 0 < \sigma < 2e - 1 \end{cases}$$

which is less than `minprob`. Hence, according to Equation 4, X is not a p-FP. □

To prune X, we first scan the database once and obtain the values of $cnt(X)$ and $esup(X)$, in $O(n)$ time. Then, the lemmas are used to prune away X, in $O(1)$ time. For patterns that cannot be pruned, we next present two efficient techniques to derive their support pmfs.

3.2 The Dynamic-Programming Algorithm

Algorithm 1 (`DP`) finds support pmf by dynamic programming. The pmf f_X of pattern X is initialized to $\{1, 0, \ldots, 0\}$ in Step 2 (i.e., $sup(X)$ is zero before $\mathcal{PDB}$ is visited). Then, each $f_X[k]$ is updated by the information of every tuple T_i (Steps 3-7). Here, p_i^X is the probability that X occurs in tuple T_i, where $p_i^X = T_i.p$ if $X \subseteq T_i.S$, or zero otherwise. The array f'_X is a temporary buffer. Step 6 is a recursive equation. It means that $sup(X)$ can be i when either 1) X occurs in the current tuple and had $(i-1)$ occurrences in visited tuples, or 2) X does not occur in the current tuple

Algorithm 1: DP

Input: probabilistic database $\mathcal{PDB}$, pattern X
Output: support pmf f_X

```
1 begin
2   Initialize f_X ← {1, 0, ..., 0}
3   for each tuple T_i in PDB do
4     f'_X[0] ← (1 − p_i^X) × f_X[0]
5     for k ← 1 to n do
6       f'_X[k] ← p_i^X × f_X[k-1] + (1 − p_i^X) × f_X[k]
7     f_X ← f'_X
8   return f_X;
9 end
```

but occurred in visited tuples for exactly i times. This step is repeated until all tuples have been processed. The time and space complexity of DP are $O(n^2)$ and $O(n)$ respectively.

3.3 The Divide-and-Conquer Algorithm

Algorithm 2: DC

Input: probabilistic database $\mathcal{PDB}$, pattern X
Output: support pmf f_X

```
1 begin
2   if n = 1 then
3     f_X[0] ← 1 − p_1^X, f_X[1] ← p_1^X
4     return f_X
5   Horizontally partition PDB into D_1 and D_2, where
    |D_1| = ⌊n/2⌋ and |D_2| = ⌈n/2⌉
6   f_X^1 ← DC (D_1, X)
7   f_X^2 ← DC (D_2, X)
8   f_X ← Convolution (f_X^1, f_X^2)
9   return f_X;
10 end
```

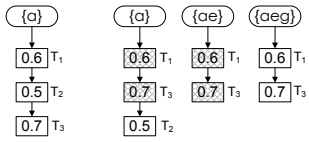
Algorithm 2 (DC) is another way of evaluating support pmf. Given a pattern X, Steps 2-4 compute the pmf for the case where $\mathcal{PDB}$ has only one tuple. Otherwise, $\mathcal{PDB}$ is horizontally partitioned into two databases ($\mathcal{D}_1$ and $\mathcal{D}_2$) in Step 5. Then, DC is recursively invoked on $\mathcal{D}_1$ and $\mathcal{D}_2$ to obtain X's pmf for each database (Steps 6-7). The two pmfs are used to generate the support pmf of X (Step 8).

To understand Step 8, let $sup_{D1}(X)$ and $sup_{D2}(X)$ be the support of X in $\mathcal{D}_1$ and $\mathcal{D}_2$ respectively. Since $sup_{D1}(X)$ and $sup_{D2}(X)$ are independent random variables, $sup(X) = sup_{D1}(X) + sup_{D2}(X)$. Let f_X^1 and f_X^2 be the pmfs of $sup_{D1}(X)$ and $sup_{D2}(X)$ respectively. Then,

$$f_X[k] = \sum_{i=0}^{k} f_X^1[i] \times f_X^2[k-i] \tag{7}$$

In fact, f_X is the convolution of f_X^1 and f_X^2, denoted by $f_X = f_X^1 * f_X^2$ [14]. While a naïve way of evaluating Equation 7 requires $O(n^2)$ time, this can be improved by applying Discrete Fourier Transform (DFT) on f_1^X and f_2^X, computing the pairwise products of the two transformed sequences, and performing an inverse DFT on the product. With the use of the Fast Fourier Transform (FFT) algorithm, Equation 7 can be evaluated in $O(n \log n)$ time [24].

Complexity. Let $c(n)$ be the time cost of Algorithm 2 with database size n. Steps 6 and 7 both need $c(n/2)$ time, and Step 8 takes $O(n \log n)$ time with the use of the FFT algorithm. Then, $c(n) = 2c(n/2) + O(n \log n)$, which yields $O(n \log^2 n)$. Thus, DC is more efficient and scalable than DP for large datasets. The space complexity is $O(n)$.



(a) $L^{\{a\}}$ (b) $L^{\{a\}}$, $L^{\{ae\}}$, and $L^{\{aeg\}}$

Figure 6: Inverted Probability List (ip-list)

3.4 Inverted Probability List

So far, all tuples in $\mathcal{PDB}$ are used to prune a pattern X, or to find X's support pmf. This is not always necessary. Consider a tuple T_i, where X does not appear in $T_i.S$. Since T_i does not contribute to the values of $cnt(X)$ and $esup(X)$, the absence of T_i will not affect the correctness of Lemmas 2 and 3. Since $p_i^X = 0$, Algorithms 1 and 2 also work without T_i. In fact, our pruning lemmas and support pmf algorithms can be used on only the list of tuples which contain X. We call this the *inverted probability list* (or *ip-list*) of X, denoted by L^X. Figure 6(a) shows $L^{\{a\}}$ for pattern $\{a\}$. Now let $l = |L^X|$. If (1) $\mathcal{PDB}$ is sparse, and (2) X is long, then l can be much smaller than n. In this case, the algorithms executed on L^X can be faster than $\mathcal{PDB}$. From now on, we assume that L^X is used in our algorithms.

Let us summarize the process of handling a pattern X in p-Apriori. We first scan the database to obtain L^X, $cnt(X)$ and $esup(X)$. Then, Lemmas 2 and 3 are used to check whether X can be pruned. If not, either Algorithm 1 or 2 is used to find the support pmf, which is passed to Equation 4 for checking the frequentness of X. Finally, L_X is discarded, so that the memory can be reused to store other lists.

Complexity. Let $l = |L^X|$. We can generate L^X by scanning the database in $O(n)$ time. Notice that $cnt(X) = l$, and $esup(X)$ can be found by summing up all the tuple probabilities on L^X. Afterwards, Lemmas 2 and 3 can be evaluated in $O(l)$ time. If X cannot be pruned, and Algorithm 1 (DP) is used on L^X, then $O(l^2)$ operations are needed. If Algorithm 2 (DC) is used instead, a $O(l \log^2 l)$ cost is required. Finally, we discard L^X. Hence, the overall cost of evaluating a pattern in p-Apriori is $O(n+l^2)$ when Algorithm DP is used, or $O(n+l \log^2 l)$ when Algorithm DC is used. The space complexity is $O(n)$.

While Lemmas 2 and 3 can prune infrequent patterns effectively, our experiments revealed that p-Apriori spends a lot of time to compute pmfs for the remaining patterns. Moreover, to extract maximal p-FPs, p-Apriori cannot avoid deriving the pmfs of all their sub-patterns. We next study a novel algorithm that alleviates these problems.

4. THE TODIS ALGORITHM

We call the second p-FP mining algorithm *TODIS*, which stands for "TOp-Down Inheritance of Support pmf". It involves the execution of two phases: (1) extract patterns that are supersets of p-FPs; and (2) derive p-FPs in a *top-down* manner (i.e., in descending order of pattern size).

We first explain the intuition behind TODIS. Let X' be a sub-pattern of X. Then, any tuple that consists of X

must also contain X'. Hence, the ip-list of X, i.e., L^X, is a subset of $L^{X'}$. In Figure 6(b), for instance, $L^{\{aeg\}} \subseteq L^{\{ae\}} \subseteq L^{\{a\}}$. Notice that these ip-lists, with their common entries shadowed, are quite similar. Since ip-lists are used to generate support pmfs, these pmfs should be similar too. We exploit this observation by *incrementally* deriving support pmfs. For example, $L^{\{aeg\}}$ is first used to generate $f_{\{aeg\}}$. We next use $f_{\{aeg\}}$ to derive $f_{\{ae\}}$, which then produces $f_{\{a\}}$. This new approach, as we will explain, is faster than generating each pmf from scratch. In Section 4.1, we discuss how TODIS makes use of this technique. We explain how to adapt TODIS to solve Problem 2 (i.e., find maximal p-FPs) in Section 4.2.

4.1 Algorithm Design

Phase 1: Generate candidate patterns. We first swiftly identify a set of patterns which contains all p-FPs. This is done by slightly modifying p-Apriori. Specifically, for patterns that cannot be pruned by lemmas 2 and 3, we assume that they are candidate p-FPs, without evaluating their exact support pmfs. All these candidate p-FPs generated are then passed to the next phase for verification.

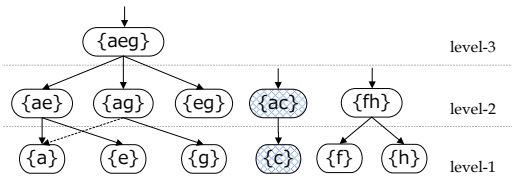


Figure 7: Illustrating the TODIS algorithm.

Phase 2: Top-down support inheritance. To illustrate this step, we suppose that the patterns in Figure 7 are those generated by Phase 1. Since TODIS examines patterns in descending order of their lengths, the longest pattern, i.e., $\{aeg\}$, is considered first. Specifically, the support pmf of $\{aeg\}$, or $f_{\{aeg\}}$, is created "from scratch", by Algorithms DP or DC. Then $f_{\{aeg\}}$ is *inherited* by its three sub-patterns: $\{ae\}$, $\{ag\}$ and $\{eg\}$. That is to say, we use $f_{\{aeg\}}$ to derive the pmf for these sub-patterns. For other size-2 patterns, $\{ac\}$ and $\{fh\}$, we also generate their pmfs from scratch. After all the support pmfs for size-2 patterns are generated, the pmfs are inherited by size-1 patterns that are subsets of them. For example, $\{a\}$ inherits the pmf of $\{ae\}$. All patterns that are true p-FPs (Equation 4) are returned. In this example, all patterns except $\{ac\}$ and $\{c\}$ are p-FPs.

How to use the "inherited support pmf" to generate a pmf of a given pattern X? We define the *exclusive item* of X, denoted by X.exItem, to be the set difference between X and the pattern from which X inherits the pmf. In Figure 7, for example, $\{ae\}$ is a sub-pattern of $\{aeg\}$ and inherits $f_{\{aeg\}}$. Then, $\{ae\}$.exItem is $\{aeg\} - \{ae\}$, or $\{g\}$. To derive $f_{\{ae\}}$ given $f_{\{aeg\}}$ and $\{g\}$, we first evaluate the pmf $f_{\{ae\overline{g}\}}$, with algorithms DP or DC. Since the sets of tuples that contain $\{aeg\}$ and $\{ae\overline{g}\}$ are disjoint, $sup(\{aeg\})$ and $sup(\{ae\overline{g}\})$ are independent. As discussed in Section 3.3, $f_{\{ae\}}$ is the convolution $f_{\{aeg\}}$ and $f_{\{ae\overline{g}\}}$. We call the above procedure the *update* of support pmf. Observe that list $L^{\{ae\overline{g}\}}$ is empty, and is shorter than $L^{\{ae\}}$ that contains T_1 and T_3 (Figure 6(b)). Hence, with the efficient convolution of $f_{\{aeg\}}$ and $f_{\{ae\overline{g}\}}$, updating $f_{\{ae\}}$ is generally faster than computing it from scratch.

Inheriting from the "best" pmf. A pattern may be able to inherit pmf from two or more patterns. In Figure 7, for instance, $\{a\}$ can inherit the support pmf from either $\{ae\}$ and $\{ag\}$, since $\{a\}$ is a sub-pattern of both of them. Which pmf should $\{a\}$ inherit then? We make the decision based on the lengths of the ip-lists. To understand, let X'' be a parent of pattern X. Then, $X'' = X \cup X.\texttt{exItem}$. Also, let L be the ip-list where $X \subseteq T_i.S$ but $X.\texttt{exItem} \notin T_i.S$. Then, L is used by the support pmf update operation to compute X. For example, $L = L^{\{ae\overline{g}\}}$ in the previous paragraph. Notice that $|L| = |L^X| - |L^{X''}|$. If $L^{X''}$ is longer, then L is shorter and the pmf update is more efficient. For example, suppose $|L^{\{ag\}}| > |L^{\{ae\}}|$, then $\{a\}$ inherits $f_{\{ag\}}$ instead of $f_{\{ae\}}$. Hence, a pattern should choose to inherit from the parent whose ip-list is the *longest*, in order to minimize the cost of updating its pmf.

Algorithm 3: TODIS

Input: $\mathcal{PDB}$, minsup, minprob
Output: Set of p-FP Sets: $\mathcal{F} = \{F_1, F_2, \ldots, F_m\}$

```
1  begin
2    F ← FindCandidatePFP(PDB, minsup, minprob)
3    ▷ F_k ∈ F is the set of patterns of length k
4    ▷ X.exItem is initialized as null for every X ∈ F_k
5    ▷ X.cnt is initialized as 0 for every X ∈ F_k
6    for k ← m to 1 do
7      for each X ∈ F_k do
8        X ← UpdateSupPMF(PDB, X, f_X)
9        for each (k-1)-subpattern X' of X do
10         if X'.cnt < X.cnt then
11           f_X' ← f_X                          ▷ search X' in F_{k-1}
12           X'.exItem ← X − X'
13           X'.cnt ← X.cnt
14       if isPFP(X.pmf, minsup, minprob) = FALSE then
15         remove X from F_k
16   return F
17 end
```

Algorithms. Based on the above discussions, we propose Algorithm 3. Let $F_k (k = 1, \ldots, m)$ be the set of p-FPs of length k, where m is the size of the largest p-FP. Also, let $\mathcal{F}$ be the set of all F_k's. For each pattern $X \in F_k$, let X.cnt be the length of L^X. In Step 2, we execute Phase 1 and store all candidate p-FPs in $\mathcal{F}$. Then, Steps 6-15 execute Phase 2, by examining each pattern in F_k in descending order of k. Step 8 updates X's support pmf, based on X.exItem and the pmf inherited from its parent. Steps 11-13 select the best support pmf for X to inherit, where a pattern's inherited pmf is replaced by another one if there exists a longer ip-list. In Steps 14-15, X is removed from F_k if it is not a p-FP (Equation 4). The final result, $\mathcal{F}$, is returned in Step 16.

Algorithm 4 shows the routine for updating support pmf. Steps 3-5 generate L, the ip-list used by the support pmf update operation. If X has no exclusive item, X is not a subset of any candidate p-FP. Then $L = L^X$, and we evaluate f_X with the DP or DC algorithm (Steps 6-7). Otherwise, we compute the support pmf on L, perform convolution with the inherited pmf of X (i.e., f'), in order to generate f_X. Step 11 updates the length of L^X. Finally, L is discarded and X is returned (Steps 12-13).

Complexity. In Algorithm 3, evaluating a maximal p-FP's pmf requires executing DP/DC alone, and so the cost

Algorithm 4: `UpdateSupPMF`

Input: $\mathcal{PDB}$, pattern X, inherited pmf f
Output: support pmf of X

```
1  begin
2  |  Set L as an empty list
3  |  for each tuple T_i ∈ PDB do
4  |  |  if X ⊆ T_i.S ∧ X.exItem ∉ T_i.S then
5  |  |  |  Add T_i.p to L
6  |  if X.exItem = NULL then
7  |  |  f_X ← CompSupPMF(L)            ▷ invoke Algo. 1 or Algo. 2
8  |  else
9  |  |  f' ← CompSupPMF(L)             ▷ invoke Algo. 1 or Algo. 2
10 |  |  f_X ← Convolution(f, f')
11 |  X.cnt ← X.cnt + |L|
12 |  Discard(L)
13 |  return X
14 end
```

is the same as that of `DP`/`DC`. For a non-maximal p-FP X, its pmf is obtained by updating the inherited pmf, with a cost of $O(n + l'^2)$ (for `DP`) or $O(n + l' \log^2 l')$ (for `DC`). Here, $l' = |L^X| - max\{|L^{X''}| \mid X \subseteq X''\}$. When $l' \ll |L^X|$, TODIS computes pmfs much faster than p-Apriori. To facilitate searching of sub-patterns for inheritance (Step 9) and deletion of patterns (Step 15), we build a *trie* [17] of depth k for each F_k, in which each non-leaf node uses a hash map to store the addresses of its child nodes. The cost of a pattern retrieval and deletion in F_k is $O(k)$.

Since we only need the maximal candidates for top-down generation in Phase 2, we remark that it is possible to adapt existing algorithms of maximal FP mining (e.g., [6, 13]) to achieve a faster candidate generation in Phase 1.

4.2 Finding Maximal p-FPs

To discover only maximal p-FPs, TODIS can be modified as follows. First, the same Phase 1 is used to find the candidate patterns. In Phase 2, once we have identified a p-FP, we do not compute the support pmf of its sub-patterns. Finding maximal p-FPs with TODIS is generally faster than p-Apriori, since (1) long patterns that are potentially maximal p-FPs can be quickly yielded in Phase 1; and (2) to obtain a maximal pattern, there is no need to generate the support pmf for any of its sub-patterns. Next, we examine how association rules can be generated from p-FPs.

5. PROBABILISTIC ASSOCIATION RULES

We now discuss efficient techniques for tackling Problem 3. In Section 5.1 we present an algorithm to compute the probability of an association rule. Then, Section 5.2 explains how p-ARs can be obtained.

5.1 Computing Association Rule Probability

Let X and Y be disjoint patterns, i.e., $X \cap Y = \emptyset$. To check whether $X \Rightarrow Y$ is a p-AR, we have to compute the probability $P(X \Rightarrow Y)$, and compare it against `minprob` (Equation 6). As discussed, computing this probability by expanding possible worlds is not practical. Given that X and XY are p-FPs, and their support pmfs are f_X and f_{XY}, we now explain how to efficiently evaluate $P(X \Rightarrow Y)$.

Step 1. Find $f_{X\overline{Y}}$. Notice that the sets of tuples that contain XY and $X\overline{Y}$ are disjoint. Hence, $sup(XY)$ and $sup(X\overline{Y})$ are independent random variables. Since $sup(X) = sup(XY) + sup(X\overline{Y})$, f_X is the convolution of f_{XY} and $f_{X\overline{Y}}$. Conversely, $f_{X\overline{Y}}$ is the *deconvolution* of f_X and f_{XY}. By using Fast Fourier Transform methods, deconvolution can also be implemented in $O(n \log n)$ time. The details can be found in [24].

Step 2. Compute $P(X \Rightarrow Y)$ by using the values of f_{XY} and $f_{X\overline{Y}}$, based on the following lemma:

LEMMA 4. *The probability of $X \Rightarrow Y$ is:*

$$P(X \Rightarrow Y) = \sum_{i=\texttt{minsup}}^{n} f_{XY}[i] \sum_{j=0}^{\frac{(1-\texttt{minconf})i}{\texttt{minconf}}} f_{X\overline{Y}}[j] \qquad (8)$$

PROOF.

$$\begin{aligned}
& P(X \Rightarrow Y) \\
= \; & P\left[sup(XY) \geq \texttt{minsup} \wedge \frac{sup(XY)}{sup(X)} \geq \texttt{minconf}\right] \\
= \; & P\left[sup(XY) \geq \texttt{minsup} \wedge \frac{sup(XY)}{sup(XY) + sup(X\overline{Y})} \geq \texttt{minconf}\right] \\
= \; & P\left[sup(XY) \geq \texttt{minsup} \wedge sup(X\overline{Y}) \leq \frac{1-\texttt{minconf}}{\texttt{minconf}} sup(XY)\right] \\
= \; & \sum_{i=\texttt{minsup}}^{n} \sum_{j=0}^{\frac{(1-\texttt{minconf})i}{\texttt{minconf}}} P[sup(XY) = i \wedge sup(X\overline{Y}) = j]
\end{aligned}$$

Since XY and $X\overline{Y}$ are disjoint, the above becomes:

$$\begin{aligned}
& \sum_{i=\texttt{minsup}}^{n} \sum_{j=0}^{\frac{(1-\texttt{minconf})i}{\texttt{minconf}}} P[sup(XY) = i] P[sup(X\overline{Y}) = j] \\
= \; & \sum_{i=\texttt{minsup}}^{n} f_{XY}[i] \sum_{j=0}^{\frac{(1-\texttt{minconf})i}{\texttt{minconf}}} f_{X\overline{Y}}[j]
\end{aligned}$$

Hence, Lemma 4 is correct. □

Algorithm 5: Computing prob. of a p-AR

Input: support pmf f_{XY} and f_X
Output: $Pr[X \Rightarrow Y]$

```
1  begin
2  |  f_{XȲ} ← Deconvolution(f_XY, f_X)
3  |  ▷ f_XY = {f_XY[0], f_XY[1], ..., f_XY[h_1]} (h_1 ≤ n)
4  |  ▷ f_{XȲ} = {f_{XȲ}[0], f_{XȲ}[1], ..., f_{XȲ}[h_2]} (h_2 ≤ n)
5  |  Initialize prAR and prCum to be 0
6  |  Initialize j to be 0
7  |  for i ← minsup to h_1 do
8  |  |  while j < h_2 do
9  |  |  |  if j > ((1−minconf)/minconf) × i then
10 |  |  |  |  break loop
11 |  |  |  else
12 |  |  |  |  prCum ← prCum + f_{XȲ}
13 |  |  |  |  j ← j + 1
14 |  |  prAR ← prCum + prCum × f_XY[i]
15 |  return prAR
16 end
```

Algorithm 5 implements the above procedures. We first evaluate the deconvolution $f_{X\overline{Y}}$ (Step 2). Then, Steps 7-14 compute $P(X \Rightarrow Y)$ with Equation 8. While a basic implementation of Equation 8 requires $O(n^2)$ time, we use a variable, $prCum$, to accumulate the temporary sum of $f_{X\overline{Y}}[j]$. Then Equation 8 can be evaluated in $O(n)$ time. Hence, Algorithm 5 has a $O(n \log n)$ cost.

5.2 Deriving Association Rules

We now explain how to obtain the p-ARs from the p-FPs generated by p-FP mining algorithms. We first present the following lemma.

LEMMA 5 (ANTI-MONOTONICITY). *Let X be a p-FP, X' and X'' be non-empty patterns where $X'' \subset X' \subset X$. If $X - X' \Rightarrow X'$ is a p-AR, then $X - X'' \Rightarrow X''$ is a p-AR.*

PROOF. Let X be a p-FP, and X' and X'' be non-empty sub-patterns of X, where $X'' \subseteq X'$. Suppose that $\mathcal{W}'$ and $\mathcal{W}''$ are the set of possible worlds where $X - X' \Rightarrow X'$ and $X - X'' \Rightarrow X''$ are association rules respectively. For each possible world $W_i \in \mathcal{W}$, if $X - X' \Rightarrow X'$ is an association rule, then so is $X - X'' \Rightarrow X''$, based on the anti-monotonicity property of association rules for exact data [4]. We know that $P(X - X' \Rightarrow X') = \sum_{W_i \in \mathcal{W}'} P(W_i)$, and $P(X - X'' \Rightarrow X'') = \sum_{W_i \in \mathcal{W}''} P(W_i)$. Since $X - X' \Rightarrow X'$ is an association rule, we have: $P(X - X'' \Rightarrow X'') \geq P(X - X' \Rightarrow X') \geq$ `minprob`. By Equation 6, $X - X'' \Rightarrow X''$ is therefore also a p-AR. □

This lemma implies that if XYZ is a p-FP and $X \Rightarrow YZ$ is a p-AR, then so is $XY \Rightarrow Z$ and $XZ \Rightarrow Y$.

To generate p-ARs, we adopt the framework of the Apriori algorithm [4], which was developed for exact data. Specifically, let X_i be a size-i sub-pattern of X. For a p-FP X, we enumerate all X_1's as the consequent of the rule. Then we check whether $X - X_1 \Rightarrow X_1$ is a p-AR by computing its probability with Algorithm 5. If $X - X_1 \Rightarrow X_1$ is not a p-AR, then for any X_i where $X_1 \in X_i$, $X - X_i \Rightarrow X_i$ cannot be a p-AR (by Lemma 5). Hence, we can stop examining the rules that contain the superset of X_1 as the consequent. Otherwise, we check the validity of $X - X_2 \Rightarrow X_2$, for every X_2 such that $X_1 \subset X_2$. The checking goes on with larger X_is, until we find that $X - X_i \Rightarrow X_i$ is not a p-AR, or $X_i = X$. We repeat this for every p-FP X.

6. EXPERIMENTAL RESULTS

We evaluated the performance of our solutions on two datasets. The first one, called $T25I10D500$, is provided by the IBM data generator[1]. The average length of a transaction is 25, the average length of a frequent pattern is 10, and the dataset size n is $500k$. The existential probability of each tuple is randomly drawn between $[0, 1]$. Since no item has support larger than 10% of n, this dataset is sparse, and we set `minsup` to be $0.65\% \cdot n$.

The second dataset, called *Accident*, comes from the Frequent Itemset Mining (FIMI) Dataset Repository [2]. It contains $340k$ transactions, which record traffic accidents in the Flanders-Belgium region during 1991-2000. Each transaction stores the attributes (e.g., time, place and car type) of an accident. The average length of a frequent pattern is 45, and the number of items is 572. The existential probability of each transaction is a random variable, drawn from a Gaussian distribution with mean 0.5 and variance 0.02. The default value of `minsup` is 35% of n.

For both datasets, the default values of `minprob` and `minconf` are 0.5 and 0.9 respectively. All the experiments were carried out on the Windows XP operating system, on a machine with a 2.66 GHz Intel Core Duo processor and 2GB memory. The programs were written in C++ and compiled on Microsoft Visual Studio 2005. We next present the results for the two datasets in Sections 6.1 and 6.2.

[1] `http://www.almaden.ibm.com/cs/disciplines/iis/`
[2] `http://fimi.cs.helsinki.fi/data/`

6.1 Results on the Synthetic Dataset

(a)Basic solution. We compared the running time of p-Apriori and the "basic" solution, which finds p-FP by expanding possible worlds. For p-Apriori, we used `DP` to compute support pmf. Figure 8(a) shows that the performance of the basic solution degrades sharply with a slight increase of n, due to the exponential growth of the number of possible worlds. p-Apriori does not expand possible worlds, and so its performance is much better. In fact, all our solutions (i.e., p-Apriori and TODIS) significantly outperform the basic solution. Next, we focus on our solutions.

(b)ip-list. We then studied the benefit of using the ip-list in p-Apriori. We used `DP-n` and `DC-n` to denote the versions of `DP` and `DC` that do not use the ip-list. Figure 8(b) shows that `DP` (`DC`) perform better than `DP-n` (correspondingly `DC-n`). Hence, it is worthwhile to build and maintain the ip-list. For example, when $n = 8k$, `DC` is two order of magnitudes faster than `DC-n`. We next assume that the ip-list is used.

(c)Scalability. We compared p-Apriori and TODIS over a wide range of n in Figure 8(c). For both algorithms, we examined `DP` and `DC`. The four variants scale well with n. Also, `DC` is always better than `DP`. When TODIS and DC are used together, the best result is yielded. At $n = 1000k$, `TODIS-DC` is more than one order of magnitude faster than `pApriori-DP`.

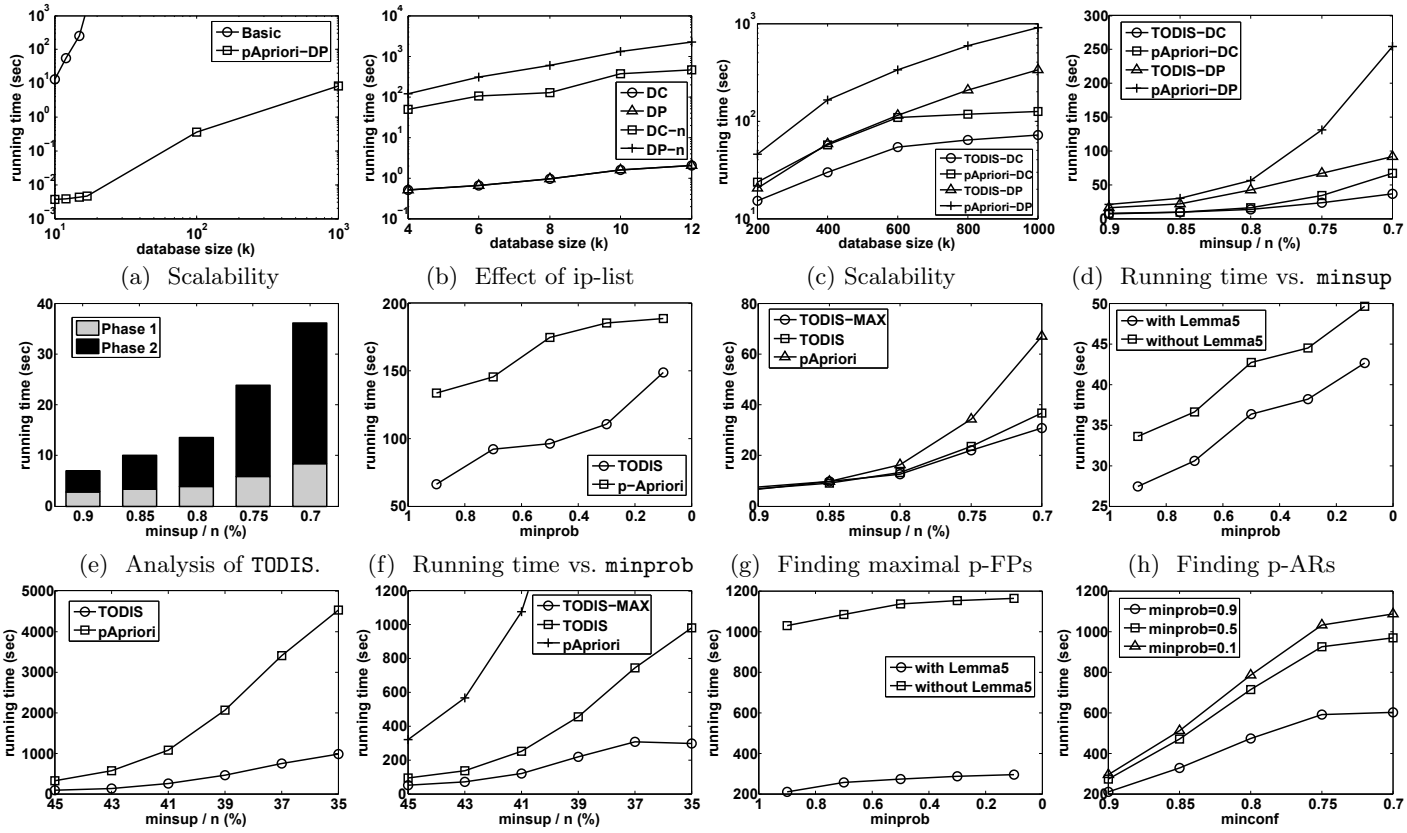
(d)Effect of `minsup`. Figure 8(d) compared p-Apriori and TODIS under different `minsup` values. When `minsup` decreases, the performance gap between `pApriori-DP` and `TODIS-DP` increases. With a smaller `minsup`, longer patterns have to be tested, and so computing their pmf from scratch is more expensive. `TODIS`, which updates pmfs instead, benefits more in handling long patterns. The same can be said for `pApriori-DC` and `TODIS-DC`. Again `TODIS-DC` is the best.

(e)Analysis of TODIS. Recall that TODIS spends some effort (in Phase 1) to generate candidate patterns, so that they can be used to identify p-FPs in Phase 2. Over different values of `minsup`, the time spent on Phase 1 is a small fraction of that of Phase 2 (Figure 8(e)). The effort of finding candidate patterns in Phase 1 is thus worthwhile, since this facilitates the top-down pmf update in Phase 2. Hence TODIS outperforms p-Apriori. We also investigate the effectiveness of pruning lemmas used in Phase 1. Let r be the number of true p-FPs. The number of candidates generated in Phase 1 is less than $2r$ under different `minsup` settings.

(f)Effect of `minprob`. Figure 8(f) showed that the running times of p-Apriori and TODIS increase with a lower `minprob`. A lower `minprob` implies that more patterns can become p-FPs. Hence both algorithms spend more time to compute their pmfs. Again, TODIS outperforms p-Apriori.

(g)Maximal p-FPs. Figure 8(g) studied algorithms for finding maximal p-FPs. Since the results produced by TODIS and p-Apriori contain the maximal p-FPs, these p-FPs can be obtained from their results. We also see that `TODIS-MAX` (Section 4.2) is faster than `TODIS`, since not all p-FPs have their pmfs evaluated. At `minsup` $= 0.7\% \cdot n$, `TODIS-MAX` is 20% faster than `TODIS`.

(h)Finding p-ARs. In Figure 8(h), we examined the use of the anti-monotonicity property (Lemma 5) for generating p-ARs. The running time increases with smaller `minprob`,



(a) Scalability (b) Effect of ip-list (c) Scalability (d) Running time vs. `minsup`

(e) Analysis of `TODIS`. (f) Running time vs. `minprob` (g) Finding maximal p-FPs (h) Finding p-ARs

(i) Running time vs. `minsup` (j) Finding maximal p-FPs (k) Finding p-ARs (l) Running time vs. `minconf`

Figure 8: Performance Evaluation

since more rules become p-ARs. Under a wide range of `minprob`, Lemma 5 prunes a lot of rules without computing their probabilities. Hence, the speed of generating p-ARs increases significantly.

6.2 Results on the Real Dataset

Since most experiments on the real dataset show a similar trend as the synthetic data, we only present the most representative ones.

(i)Effect of `minsup`. Figure 8(i) compared p-Apriori and TODIS using `DC`. We do not show the results for `DP`, since they take more than three hours to complete. TODIS substantially outperforms p-Apriori; at `minsup` $= 35\% \cdot n$, TODIS is 75% faster than p-Apriori. This big difference is due to the fact that the real dataset is dense – regardless of the tuple probability, 11 singletons have a support of more than 80%. This results in long ip-lists, which benefits TODIS more than p-Apriori.

(j)Maximal p-FPs. As shown in Figure 8(j), `TODIS-MAX` is much better than `TODIS`. When `minsup` is $35\% \cdot n$, `TODIS-MAX` is 70% faster than `TODIS`. The dense dataset implies that the maximal p-FPs can be large. A maximal p-FP contains many subpatterns. While `TODIS` has to compute pmfs for all subpatterns, `TODIS-MAX` does not do so. Hence `TODIS-MAX` is better than `TODIS`.

(k)Finding p-ARs. From Figure 8(k), we observed that Lemma 5 effectively reduces its running time under different `minprob` values. Finally, Figure 8(l) showed that the p-AR algorithm needs more time to complete with a lower `minconf`. When `minconf` decreases, more rules can become p-ARs, and so more time is spent on computing their probabilities. The running time flattens when `minconf` ≤ 0.75. We found that most rules generated have confidence higher than 0.75, and so a decrease of `minconf` does not have much effect on the performance.

7. CONCLUSIONS

We studied efficient algorithms for extracting frequent patterns from probabilistic databases. The TODIS algorithm, when used together with DC, yields the best performance. We examined the efficient mining of p-ARs, which, to our knowledge, has not been studied before. We plan to study the discovery of association rules for other uncertain data models. We will also consider to extend existing mining methods on exact databases, to handle probabilistic data.

8. ACKNOWLEDGMENTS

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