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Article

Finding Negative Associations from Medical Data Streams Based on Frequent and Regular Patterns

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Abstract: Medical data flows in streams as the data related to clinical tests and administered drugs by the doctors flows continuously. The doctors must be immediately alerted if negative associations are found among the drugs they prescribe. Data streams are to be processed in single scans as it is not possible to re-scan the data for any iterative processing. To detect negative drug connections, regular and frequent drug patterns must be processed. Negative correlations between disease-curing medications might create adverse responses that kill patients. This paper proposes an algorithm that finds the negative associations among regular and frequent patterns mined from medical data streams. The negative associations mined are the most effective and reduce the negative associations, which are more critical by 50%.

Keywords: data streams; negative associations; adverse effects; side reactions; frequent and regular patterns

1. Introduction

Association rule mining is a prominent data mining method for object or item set relationships [1–3]. Today, association rule mining requires massive data. The popular association rule mining method is Apriori [4].

Most of the medical data is generated continuously and moves in streams. Doctors carry diagnoses and prognoses. Continuously prescribes the medicines. The doctors need to be altered instantly when negative associations are found among the drugs prescribed by them.

Many Applications in modern days require capturing continuous data generated by man-held wearable devices. The data flowing through those streams must be processed, and any negative associations must be reported to the people concerned. Since data is detected and transported quickly, instream data is huge. Unlike databases, since instream data is never kept raw, it can only be scanned once.

Sensors and other streaming devices collect data now. The processed findings are briefly kept for analysis and decision-making, not the instream data. The instream data must be processed sequentially to uncover regular and frequent patterns with negative relationships.

Positive association rule mining is used for online log data, census data, biological data, fraud detection, and more. The number of negative associations decreases as the frequency of the Item set increases. Negative association rule mining can help improve healthcare crime data analysis decision support systems [5]]. A basic technique mines too many patterns, creating too many association rules in which consumers may not be interested [6].

Di-Sets helps a vertical data presentation, which helps in comparing candidate patterns and reduces vertical table entry memory Mohammed J. Zaki [7].

Although FP-Tree [8] and RP-Tree are more stable and effective, many algorithms have been described. Several methods were developed to find sequential, irregular, unusual, etc. patterns. There's

little focus on uncovering rare negative patterns. Real-time settings are important for finding negative patterns, such as penguins being birds but not flying.

Patterns are item sets that occur in multiple transactions. Processing enormous numbers of patterns will take time. As the database grows, so do patterns. Frequent patterns matter more. Selecting patterns that fulfil the user-specified minimum threshold value finds frequent patterns. The user-selected support value is intriguing. The pattern frequency is how often it appears in the database. No timeframe is set here. Sporadic frequent patterns may not have a regular occurrence behavior.

Regular patterns can be inconsistent with frequent ones. Sometimes, both must be considered. Association between mined patterns is crucial. Positive connections between regular or regular-frequent, regular-frequent-maximal-closed patterns are commonly considered.

Some patterns are negatively correlated, meaning they conflict. When dealing with a medicine with a different chemical composition or weather forecast, one pattern contradicts another, leading to incorrect conclusions and actions. Negative associations are sometimes more essential than good ones and require clear examinations.

Based on the data to be processed, pattern discovery varies substantially. Streamed data must be handled as it flows and is not stored, although non-streamed data can be processed multiple times. Data flows are recognized, and actions are taken when recognized. Data streams are dynamic, with many variables and complicated objects. Such an environment benefits from the sliding window technique.

Mining common items and favorable relationships dominated the research. In addition to item set frequency, item regularity is significant. Negative associations show patterns of enemies, whereas positive relationships are desirable. Stream data flow is important, especially for medical data.

Problem Definition

Negative associations among chemicals of various drugs are dangerous as they lead to adverse effects on the patients. Medical data moves in streams continuously from the hospitals, which needs to be processed soon after the data is captured, and the negative associations are to be found and reported immediately. The item sets which are frequent and regular, which meet threshold criteria, must be found, and see if the item sets form any negative associations.

Objectives of the Research

- Create a database and example set to investigate negative associations between regular, frequent, closed, and maximal items.
- 2. To create a mechanism for processing medical institution data streams.
- 3. Develop an algorithm to identify frequent, regular item sets and negative correlations among them.
- Determine optimal frequency and regularity thresholds for accurate negative connections.

2. Related work

Many techniques for mining frequent data sets from static databases are published. Data flows in streams with the internet, especially from remote sensors to cloud storage. Dynamic mining follows data streams. To satisfy the user, respond quickly to constant requests. Time-sensitive sliding windowing was utilized by Chih-Hsiang Lin et al. [9] for frequent data stream mining. Their algorithm stores all frequent items in memory and a database containing expired data items. Based on storage space, the table can hold fewer expired data items.

One confidence threshold is typically used to identify positive and negative association rules $(A \Rightarrow B, A \Rightarrow \neg B, \neg A \Rightarrow B, \text{ and } \neg A \Rightarrow \neg B)$. In this method, the user must choose between positive and negative connections. X. Dong et al. [(CH4 \Rightarrow CH8).[10] compared confidence criteria for four positive and three negative associations. The linkages between the four confidences showed that four confidence intervals should focus on the four types of associations. Considering the four confidences

helps create deceptive rules. They explained how the chi-squared test mines association rules. They suggested a chi-squared test-based PNARMC algorithm with four confidence thresholds.

Many data-gathering technologies have allowed every organization to store data on every activity. Large amounts of data make it hard to mine relevant information. Large data sets allow for more realistic and informative patterns. Sequential patterns give intriguing data insights. Existing sequential mining approaches focus on positive pattern behavior to anticipate the next event after a series. Fahad Anwar et al. [11] mine negative sequential patterns that contradict each other. Their technique finds patterned events/event sets.

Due to internet application migration, most data flows in streams. Streamed data is difficult to find fascinating. Support metric-based streamed data pattern mining is successful. However, pattern occurrence frequency is not a good measure for finding significant patterns. However, temporal regularity is best for online data stream mining for stock market applications. A pattern is regular if it appears within the user-defined period. None of the methods mine frequent patterns from online application stream data. Regular Pattern Stream tree (RPS tree) and an effective mining method for detecting interesting patterns in streamed data were developed by Syed Khairuzzaman Tanbeer et al. [12]. They recorded stream data in the RPS tree using a sliding window approach. The tree has been updated with the current data using an efficient approach.

Shirin Mirabedini et al. [13] reviewed all data stream pattern mining algorithms. Frequent item mining helps cluster and classify data. As network data volume has expanded, so needs to mine data streams for interesting patterns. Regular itemset mining is needed for static and streaming data. Frequent patterns might reveal business trends, scientific phenomena, etc. Pattern finding is the foundation for machine learning activities like association rule induction. Data has been scanned several times to uncover intriguing patterns. Only one scan of streamed data is possible; therefore, pattern-finding is performed in one scan. Since the stream length is unknown, such data has no closure. Before processing streaming data, an initial data set is collected and kept temporarily. VE: A review of online frequent pattern mining methods by Lee et al. [14]. They categorised approaches by pattern, data, and time window.

DSM-Miner by Juni Yang et al. [15] mines maximal common patterns effectively. Shirin Mirabedini et al. [13] examined all data stream pattern mining techniques. Frequent item mining clusters and classifies data. Mining network data streams for intriguing patterns has increased as data volume has grown. Static and streaming data require consistent itemset mining. Frequent patterns may reflect business, scientific, etc., trends. Machine learning operations like association rule induction start with pattern detection. Data was scanned multiple times to find unusual patterns. Only one streamed data scan is possible; therefore, pattern-finding is done there. No closure exists for such data because the stream length is uncertain. A temporary data set is collected before processing streaming data. VE Lee et al. present a structured review of online frequent pattern mining [14]. By pattern, data, and period, they classed approaches. Included the transaction sliding window mechanism that leverages each processing phase's transaction count. Decaying distinguishes old and new transactions. SWM trees (Sliding window maximum frequent pattern trees) are suggested for retaining frequent patterns. SWM tree root is used as an enumerated tree root for searching.

Low interest or great confidence can make association rules stand out. The Daly et al. [16] method assessed exceptional mining rules. They explored negative and exceptional association rules. Negative association rules generate exceptions. Also, they created a metric for anomalous rule interest. Candidate rules analyze patterns and decisions using exceptional rules and metrics.

Most literature-based tactics cut desirable decision-making patterns utilizing fascinating criteria. However, choosing an interest measure is tricky and may need trial and error. No accurate method exists for determining interesting metrics. Thiruvady 2004[17] suggested using user inputs to determine rules and limitations. The GRD algorithm finds the most intriguing rules.

Statistical correlations determine data set connectivity. Maria-Luiza and Antonie [18] used a correlation between two item sets to identify negative association rules. Negative rules are retrieved if item sets correlate negatively, and confidence is strong.

Negative rules are retrieved if item sets are negatively correlated, and confidence is strong. Chris Cornelis [19] examined many algorithms that mine negative and positive association rules and identified various failures. These characteristics were used to classify and catalogue mining algorithms and identify gaps. A confidence framework-based modified Apriori mining method can find negative correlations with intriguing ones. They used upward closure to match validity definitions' support-based negative connection interest. Dataset entries frequently have the intriguing "Support" parameter. Each level of data records has support values. Each level has multiple support values. The authors devised an Apriori-based upward closure method (PNAR) to find negative association rules. If \neg X passes the minimal support condition, so do $Y \subseteq I$, $X \cap Y = \phi$, and $\neg(XY)$.

Interesting negative and positive association rules (PNAR) and mining multiple-level support approaches have been developed. Their method mines positive and negative association rules from fascinating frequent and infrequent item sets using varying support levels. Based on item set regularity, Pavan et al. [20] found positive and negative associations using vertical table mining.

Bagui and Dhar et al. [21] demonstrated how to mine positive and negative association rules from MAP REDUCE data. They utilised the Apriori approach to mine several item sets, which was efficient but required much computation time.

None of the negative association rule mining studies [22,23] used big data. Positive and negative association rules were found in uncommon item sets. The positive association rule mining identifies commonalities. This could reject many important or low-support items. Rare commodities or item sets can trigger negative association rules despite low support. Significant negative association rule mining requires more search space than positive rule mining for low-support objects. It would make sequential Apriori algorithm implementations easier and harder on big data. Few times has negative association rule mining been used.

Simarjeet Kauri et al. [24] reviewed AI-based illness diagnosis. However, no review has examined the medications' effects on heart disease prediction. Jianxiong et al. [25] developed a machine learning-based drug response risk prediction algorithm. They anticipated disease-treatment drug risks. They have not considered patient risk when administering adversely related medications.

Lu Yuwen, Shuyu et al. [26] suggested "Prefix-Span" sequential data mining and "Proportional Report Ratio" disproportionality-based technique to detect major adverse drug responses based on casual relationships, drugs, and drug reactions. They tested single drug-to-drug reactions. Restricting adverse pharmaceutical responses has not been studied.

Yifeng Lu et al. [27] found predicted patterns in frequent item set mining. Negative correlations between suggested medicines are discovered. However, an uncommon item collection with negative drug connections is also important. The authors used bi-directional traversal to mine uncommon, closed item sets. However, negative relationships between infrequent or frequent item sets have not been studied.

Jingzhuo Zhang et al. [28] developed a system to obtain drug interactions for patients with various conditions. They compiled a drug–drug interaction database from medical sources. Distance monitoring was used to extract drug–drug interactions. A transformer-based bidirectional encoder representation was employed to extract drug interactions. There is no modelling to classify positive or negative interactions.

Generalised tensor decomposition was used to create drug-gene-disease connections by Yoonbee Kim et al. [29]. Chemical structure and ATC code drug feature networks predicted drug-gene-disease relationships. They learned drug, gene, and sickness using a multi-layer perceptron neural network. They emphasised positive connections and disregarded unfavourable ones, especially among drugs.

Aan Ahmed Toor etc al., [30] have presented a data stream mining method that includes enforcing Privacy before the same is disseminated. The data is mined from the data streams, and privacy is

preserved. They primarily focussed on the drift in data Flowing in the streams due to changes in the data flow context.

U. H. W. A. Hewage et al. [31] have conducted a literature survey of the methods used for privacy-preserving data streaming mining methods. They focus primarily on the accuracy of privacy-preserving accuracy and data stream mining accuracy. They have not considered the issue of response time.

In his thesis, Aref [32] focused on developing a data stream association rule mining algorithm among co-occurring events, which means the kind of data stream varies occasionally. The proposed algorithm incrementally mines association rules over data streams that carry varied data.

Nannan Zhang et al. [33] have recommended a method to mine sequential patterns from data streams. They have used the sliding window method to arrive at the latest data by updating the old data with new data. A Prefix tree generates sequential patterns. They contended that Negative associations can be mined using the Prefix tree.

Most of the presentation in the thesis concentrated on mining drift privacy preservation of the data structure variations flowing in the data streams. The sliding window technique is used to store the current state of the data and ignore the continuous data flowing in the data stream. The main drawback is the inability to process data streams as they appear, find negative associations considering even the historical data and report the same to the destination to take control of false treatments.

3. Establishing data streams

A medical database is created out of registrations and prescriptions and fetching the details from pharmaceutical companies regarding the chemical compositions of the drugs. 100,000 records have been used to create the database.

Ninety thousand records were stored into a flat file, then 10,000 were placed into another flat file using streamed data. The same server holds both flat files. This implies that a 90,000-record static database and a 10,000-record streamed database are examined. Updates to the streamed database consider one window.

The data collected over the WEB is placed. Into a window (Buffer slot at a time), while the nearest is filled with the data, the rarest window is copied into a database. The size of Each window is designed to hold 1000 records. 10 such widow slots are used to hold the instream data.

Figure 1 shows the data streaming method used to process ongoing and continuous data flow from medical establishments.

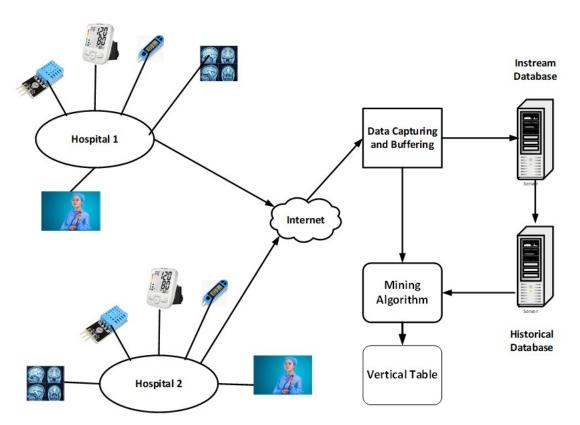


Figure 1. Capturing, buffering and creating a database representing the data streams.

4. Streamed database algorithms for negative association finding based on item set regularity and frequency

Algorithm-A This technique generates negative patterns using sliding windowing. Data is scanned as received, and the initial data is copied into 10 windows, each window of size 1000 records. 10 such windows are buffered, after which, while the latest window is received, the oldest window is written to a database.

A concurrent process accesses window database data. The Horizontal table, which lists item details and sales transactions, is updated. The pattern generation algorithm finds transaction data in instream data and writes it to a memory buffer. A buffer large enough to hold 1000 transactions is allocated. After round-robin buffer scanning, the horizontal table was updated based on transaction table data.

From a historical database, algorithm A creates an inverted table. Instream processing and Inverted Table updates are done in algorithm B. Process C creates negative linkages between medications and their development chemicals.

Algorithm-Process-A

- 1. Read the support value to set pattern frequency and user-defined regularity thresholds.
- 2. Read historical DBMS data into memory, as indicated in Table 1.
- 3. Convert Table 2 data to vertical format; see Table 2.

Table 1. Sample Medical Data Extracted from Historical Database (P - Patient, DE - Disease, DR = Drug, CH -

P.SL. No.	Transaction ID	Patient Number	Disease	Drug	Chem	icals				Drug	(
1	T2	P100	DE2	DR3	CH4	CH5	CH6	NA	NA	DR4	
2	T4	P223	DE4	DR7	CH5	CH8	CH10	NA	NA	DR8	
3	T6	P749	DE6	DR10	CH4	CH5	CH16	CH19	NA	NA	N
5	Т8	P119	DE8	DR13	CH5	CH8	CH11	NA	NA	DR14	(
	T10	P119	DE10	DR17	CH2	CH3	CH7	CH8	NA	DR18	
	T12	P11	DE12	DR21	CH4	CH5	CH6	NA	NA	DR22	-
7	T13	P11	DE13	DR23	CH2	CH3	CH7	CH8	NA	DR24	(
	T14	P11	DE14	DR25	CH5	CH8	CH11	CH15	NA	DR26	N
	T16	P4573	DE16	DR29	CH4	CH5	CH6	NA	NA	DR30	(
	T17	P8765	DE17	DR31	CH2	CH3	CH6	CH7	NA	DR32	(
	T18	P8765	DE18	DR33	CH5	CH8	CH11	CH12	NA	DR34	(
9	T20	P10987	DE20	DR37	CH4	CH5	CH6	NA	NA	DR38	-
	T21	P10987	DE21	DR39	CH2	CH3	CH4	NA	NA	DR40	_
	T22	P10987	DE22	DR41	CH5	CH8	CH11	NA	NA	DR42	
	T23	P10987	DE23	DR43	CH1	CH3	CH5	NA	NA	DR44	_

Table 2. Inverted Table along with filled-up frequency and Regularity.

Chemical Code	Trans	action	tion Ids Maximum Regularity (4)											
CH1		TT5		TT13	TT17	TT21								
CH3			TT5				TT13		TT17	TT19	TT21			
CH4		TT2	TT6	TT10	TT14	TT18								
CH5		TT2	TT4		TT6	TT8		TT10	TT12	TT13	TT14	TT16	TT17	TT18
CH6	TT2		TT6	TT10	TT14		TT17	TT18						
CH7	TT3													
CH8	TT4	TT8			TT12	TT16	TT20							
CH9		TT5		TT13	TT17	TT21								
CH10		TT2	TT4	TT10	TT17									
CH11	TT4		TT8	TT12	TT13	TT16	TT20							
CH12		TT8		TT16	TT18	TT20								
CH13	TT3													
CH14			TT8		TT14	TT16	TT18	TT21						
CH15	TT2		TT4	TT6	TT8	TT10	TT12	TT14	TT16	TT18	TT20			

}

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```
Algorithm Process-B
 While (TRUE)
  While there is an instream Transaction
      If the Temp buffer is not full
      {
           Raise the pointer.
           Read the data and store it in the Temp Buffer using the pointer.
      }
      else
      {
           If the Window Buffer is full
           {
                Write the last window to the Stream Database, as shown Table 3
                For each of the records in the Last Window
                     Find the frequent and regular item set.
                     If the item set satisfies the threshold values
                          Add to inverted Table 4
                         If the Item set is in the Inverted Table 2
                              Update the Transaction Table 5
                         Update the Inverted table as shown in Table 6.
                         else
                              Add to the Inverted Table 6
                     Move the windows to the left.
                     Write the temp-Buffer to the first window of the window buffer.
                {
                else
                {
                     Move the Temp-Buffer to the first window of the stream Buffer.
           Prune the updated Inverted Table comparing with the threshold implies
           deleting such records from Table 7.
```

Table 3. Records from the Data stream into the window buffer

P.SL. No.	Transaction ID	Patient Number	Disease	Drug	Chem	icals				Drug	(
	T1	P100	DE1	DR1	CH1	CH2	СНЗ	NA	NA	DR2	(
1	Т3	P100	DE3	DR5	CH2	СНЗ	CH7	NA	NA	DR6	(
	T5	P223	DE5	DR9	CH1	СНЗ	CH5	CH16	CH19	NA	N
4	T7	P937	DE7	DR11	CH2	СНЗ	CH7	CH11	NA	DR12	(
5	Т9	P119	DE9	DR15	CH1	СНЗ	CH5	NA	NA	DR16	C
6	T11	P1235	DE11	DR19	CH5	CH8	CH11	CH15	NA	DR20	N
8	T15	P4573	DE15	DR27	CH1	СНЗ	CH5	NA	NA	DR28	(
10	T19	P10987	DE19	DR35	CH1	СНЗ	CH5	NA	NA	DR36	(

Table 4. Inverted Table for Instream Data

Chemical Code			Trai	nsaction	Ids		
CH1	TT1	TT5	TT9	TT15	TT19		
CH2	TT1	TT3	TT7				
СНЗ	TT1	TT3	TT5	TT7	TT9	TT15	TT19
CH4	TT1						
CH5	TT1	TT5	TT9	TT11	TT15	TT19	
CH6	TT19						
CH7	TT3	TT7					
CH8	TT6						
CH9	TT1	TT9	T15	T19			
CH10	TT1	TT19					
CH11	TT11	TT15					
CH12	TT7						
CH13	TT3	TT7					
CH14	TT3						
CH15	TT3	TT11					
CH16	TT5						
CH19	TT5						

Table 5. Updated Medical Data (Historical Data + Instream data) (P - Patient, DE - Disease, DR = Drug, CH - G

P.SL. No.	Transaction ID	Patient Number	Disease	Drug	Chem	icals				Drug	(
	T1	P100	DE1	DR1	CH1	CH2	СНЗ	NA	NA	DR2	(
1	T2	P100	DE2	DR3	CH4	CH5	CH6	NA	NA	DR4	(
	T3	P100	DE3	DR5	CH2	СН3	CH7	NA	NA	DR6	(
2	T4	P223	DE4	DR7	CH5	CH8	CH10	NA	NA	DR8	(
_	T5	P223	DE5	DR9	CH1	CH3	CH5	CH16	CH19	NA	N
3	T6	P749	DE6	DR10	CH4	CH5	CH16	CH19	NA	NA	N
4	T7	P937	DE7	DR11	CH2	CH3	CH7	CH11	NA	DR12	C
	T8	P119	DE8	DR13	CH5	CH8	CH11	NA	NA	DR14	(
5	T9	P119	DE9	DR15	CH1	CH3	CH5	NA	NA	DR16	C
	T10	P119	DE10	DR17	CH2	CH3	CH7	CH8	NA	DR18	(
6	T11	P1235	DE11	DR19	CH5	CH8	CH11	CH15	NA	DR20	N
	T12	P11	DE12	DR21	CH4	CH5	CH6	NA	NA	DR22	
7	T13	P11	DE13	DR23	CH2	CH3	CH7	CH8	NA	DR24	(
	T14	P11	DE14	DR25	CH5	CH8	CH11	CH15	NA	DR26	N
8	T15	P4573	DE15	DR27	CH1	CH3	CH5	NA	NA	DR28	
	T16	P4573	DE16	DR29	CH4	CH5	CH6	NA	NA	DR30	
9	T17	P8765	DE17	DR31	CH2	CH3	CH6	CH7	NA	DR32	(
	T18	P8765	DE18	DR33	CH5	CH8	CH11	CH12	NA	DR34	_
	T19	P10987	DE19	DR35	CH1	CH3	CH5	NA	NA	DR36	
10	T20	P10987	DE20	DR37	CH4	CH5	CH6	NA	NA	DR38	
10	T21	P10987	DE21	DR39	CH2	CH3	CH4	NA	NA	DR40	(
	T22	P10987	DE22	DR41	CH5	CH8	CH11	NA	NA	DR42	(
	T23	P10987	DE23	DR43	CH1	CH3	CH5	NA	NA	DR44	(

Table 6. Updated Inverted Table along with filled-up frequency and Regularity.

Chemical Code								Transa	action Ic	ls					
CH1	TT1	TT5	TT9	TT13	TT17	TT21									
CH2	TT1	TT3	TT7	TT11	TT5	TT9									
CH3	TT1	TT3	TT5	TT7	TT9	TT11	TT13	TT15	TT17	TT19	TT21				
CH4	TT1	TT2	TT6	TT10	TT14	TT18	TT19								
CH5	TT1	TT2	TT4	TT5	TT6	TT8	TT9	TT10	TT12	TT13	TT14	TT16	TT17	TT18	TT20
CH6	TT2	TT5	TT6	TT10	TT14	TT15	TT17	TT18							
CH7	TT3	TT7	TT11	TT15	TT19										
CH8	TT4	TT8	TT9	TT11	TT12	TT16	TT20								
CH9	TT1	TT5	TT9	TT13	TT17	TT21									
CH10	TT1	TT2	TT4	TT10	TT17										
CH11	TT4	TT7	TT8	TT12	TT13	TT16	TT20								
CH12	TT7	TT8	TT15	TT16	TT18	TT20									
CH13	TT3	TT7	TT11	TT15	TT19										
CH14	TT1	TT3	TT8	TT11	TT14	TT16	TT18	TT21							
CH15	TT2	TT3	TT4	TT6	TT8	TT10	TT12	TT14	TT16	TT18	TT20				

Table 7. Pruned Inverted Table for Maximum Regularity and Minimum Frequency

Chemical Code								Transa	action Id	ls					
CH1	TT1	TT5	TT9	TT13	TT17	TT21									
CH3	TT1	TT3	TT5	TT7	TT9	TT11	TT13	TT15	TT17	TT19	TT21				
CH4	TT1	TT2	TT6	TT10	TT14	TT18	TT19								
CH5	TT1	TT2	TT4	TT5	TT6	TT8	TT9	TT10	TT12	TT13	TT14	TT16	TT17	TT18	TT20
CH6	TT2	TT5	TT6	TT10	TT14	TT15	TT17	TT18							
CH7	TT3	TT7	TT11	TT15	TT19										
CH8	TT4	TT8	TT9	TT11	TT12	TT16	TT20								
CH9	TT1	TT5	TT9	TT13	TT17	TT21									
CH11	TT4	TT7	TT8	TT12	TT13	TT16	TT20								
CH13	TT3	TT7	TT11	TT15	TT19										

Algorithm Process-C

```
While (True) {
```

Find Negatively associated Chemicals Associations

For every Next Record in Table 8

- i. Fetch the intersection of subsequent and current records if the intersection is empty.
- ii. Find the frequency and regularity of the item sets
- iii. Enter the item sets into Table 8, If the frequency and regularity values satisfy the threshold values.

Find Negatively Associated Chemicals

For each adversely correlated chemical in Table 8, discover related medications and indicate their negative correlations.

}

Table 8. Drugs mapped to Chemicals with Negative Association

"Chemical"	"Associated Drugs"	"Chemical"	"Associated Drugs"	"Chemical"	"Associated Drugs"	"Chemical"	"Associated Drugs"
CC4	DH3	CC8	DG7	CC11	DG11		
CC6	DG3	CC8	DG7	CC11	DG11		
CC4	DG3	CC6	DG3	CC8	DG7	CC11	DG11

5. Experimenting and Results

5.1. Creation of data set

A database contains patent registration, diagnostic, patient-diagnosis, chemical, drug-chemical, quantity, and prescription codes. Hospitals have contributed 100,000 patient registrations and medications to the database. Each diagnosis, drug administration, and drug chemical makeup are included in an Example set. Data items in repeating groups are encoded and replaced with codes. We sort the sample set, compute the frequency and regularity of each item set, update the database, and import 100,000 Flat file entries. These records were processed using this paper's algorithm. No standard data set exists with the data items needed to discover negative connections.

5.2. Results

The procedure was applied on the data above, yielding the following results.

Step-1

Read the Historical Data Contained in a Database and add transaction IDs for each transaction. Details of the data fetched from the Database is shown in Table 1.

Step-2

Construct an Inverted Table in vertical format for the Transactions shown in Table 8 and Table 2, along with the frequency of occurrence and the Regularity. Regularity is based on database record placements, and frequency is based on occurrence count.

Step-3

Read the Data from the Input data stream and load the same into a Temporary buffer. After filling the Temporary buffer, transfer the Records to window-1 of the window buffer after the last window is written to the database. The Records are read from the window Buffer. Table 3 shows the records from the data stream

Step 4

Develop an Inverted Table from the buffered data. Table 4 shows the Inverted Table for records read from the window buffer. Here, the issue of frequency and regularity has not been used. The data is retrieved from online transactions.

Step 5

Update the Historical Inverted Table with the data in the inverted table relating to the data stream. The frequencies and the regularity are updated simultaneously. The updated Transaction and Inverted are shown in Tables 5 and 6.

Step-6

Prune the records which do not meet the Maximum Frequency and Minimum regulatory.

Records that do not satisfy the user's criterion are pruned using the maximum regularity and minimum frequency of 4 and 3, respectively. Table 3 reveals that Chemical codes CH2, CH10, CH12, CH14, and CH15 were trimmed because they do not fulfil the Regularity and Frequency criterion. Table 7 lists leftover records. By this criteria, 5 chemicals were pruned. Yellow records are trimmed because they don't meet thresholds.

Step-7

Make adverse chemicals. Find Negative Associations with Records with No Common Transactions (Nill Common Items). Application of record intersection Produces unfavourable associations like

 $(CC4 \Rightarrow CC8, CC11), (CC4 \Rightarrow CC8), (CC6 \Rightarrow CC8), (CC4 \Rightarrow CC11), (ACC6 \Rightarrow CC11), (CC8 \Rightarrow CC4, CC6), (CC6 \Rightarrow CC8, CC11), (CC11 \Rightarrow CC4, CC6), (CC4, CC6), <math>\Rightarrow$ CC8, CC11)

Step 8 Find Negatively Associated Drugs

As stated in Table 8, map back the chemicals connected with the medications to determine the negatively associated pharmaceuticals.

The unfavourable associations show that DG3 should not be used with DG7 or DG11 because they conflict.

6. Discussion

Data Analysis has been conducted considering different sample sizes of 20,000, 50,000 and 80,000 Examples. The analysis is carried out considering thresholds in respect of frequencies and Regularities. While the sample sizes are used for the historical database, the Instream data size is fixed at 10,000 examples. Table 9 shows the number of negative associations considering the sample size of 20000 and data stream size of 10,000 Examples.

Data gathering yielded 100,000 cases evaluated for 30,000 sample sizes. 50,000, and 70,000). We set regularity and support thresholds and the number of unfavorable Associations observed. Table 9 shows frequent, regular, negative connections from 30,000 samples varying in regularity between 2.0 and 3.0 and frequency between 1.5 and 2.0.

Table 10 displays the number of negative Associations with frequency 1.75 and regularity 2–3 for 20,000 and 10,000 data stream instances. Negative associations respond to regularity modifications in Figure 1, with frequency fixed at 1.75. Figure 2 demonstrates the variation in negative correlations with regularity varying and Frequency set at 1.75.

Table 9. Negative Frequent Regular Associations (20,000 Historical and 10000 Data Stream Examples) Vs Varying Regularity + Frequency

Total Transactions	"%Max Regularity"	"%Support Count"	"Number of Negative Frequent Regular assertions"
	3	2	3
30,000	3	1.75	21
	3	1.625	77
	3	1.5	230
	2.5	1.75	20
30,000	2.5	1.625	77
	2.5	1.5	176
	2.5	1.125	490
	2	1.75	18
30,000	2	1.625	59
	2	1.5	90
	2	1.1.25	334

Table 10. Negative Associations vs. Frequency @ 1.75 and varying Regularity (20,000 historical + 10,000 data stream examples).

"Regularity"	"Negative Frequent Regular Item Sets"	% of Negative Associations * 1000
3.00	3	3 / 30,000 = 0.10
2.50	20	20/30,000 = 0.66
2.00	18	18/30,000=0.60
The average pe	rcentage of Negative association per 1000 Examples	0.45

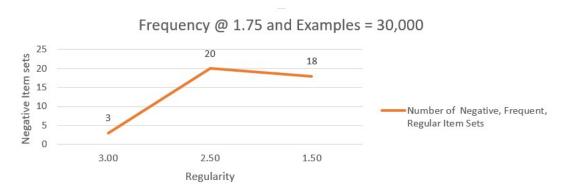


Figure 2. Negative association Item sets @ Frequency (1.75) and (30000 Examples) and varying Regularity.

Table 11 illustrates the number of negative connections with Frequency 1.5 and Regularity 2-3 in 30,000 cases. The line graph of negative associations with 1.5 frequency and variable regularity is shown in Figure 2. Figure 3 shows the variation in negative associations with regularity varying and frequency set at 1.50.

Table 11. Negative Associations @ Frequency at 1, (30000 Examples) Varying Regularity

"Regularity"	"Negative Frequent Regular Item Sets"	% of Negative Associations * 1000
3.00	230	230/30000 =7.6
2.50	176	176/30000 = 5.8
2.00	90	90/30000= 3.0
Average Nega	tive Associations per 1000 Examples	5.4

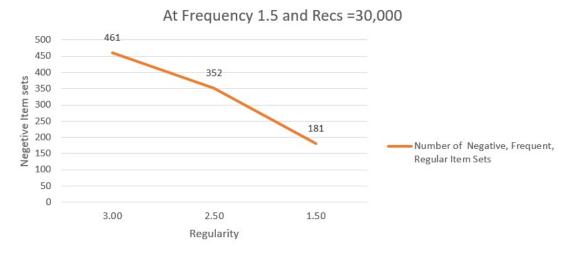


Figure 3. association Item sets @ Frequency (1.50) and (30000 Examples) varying Regularity

The larger example set was analysed further. Table 12 illustrates the percentage of negative correlations per 1000 Examples for sample sizes (20,000, 50,000, 80,000), including 10,000 DataStream instances. Frequency varies.

Table 12. % reduction in negative relationships with larger samples and appropriate frequency and support

"Total Transactions"	"%Max Regularity"	"%Support Count"	"Number of Negative Frequent Regular"	% of Negative Associations * 1000	Average % of Negative Associations per 1000 samples
	1.50	1.750	18	18/30=0.60	
30,000	1.50	1.625	59	59/30=1.96	1.85
	1.50	1.500	90	90/30=3.0	
	1.65	1.65	7	7/50=0.14	
50,000	1.65	1.25	20	20/50=0.40	0.60
	1.65	1.00	75	75/50=1.25	
	1.35	1.65	18	18/80=0.22	
80,000	1.35	1.35	59	59/80=0.73	0.70
	1.35	1.00	90	90/80=1.13	

From the above Table, it can be inferred that Considering a sample size of 50,000 examples, fixing the regularity 1.65 and frequency 1.25 gives the least and most effective negative associations 20 out of 50,000 could be identified.

Further analysis examines the effects of fixing regularity, altering frequency, and different sample sizes. Table 13 lists unfavourable relationships with Regularity = 1.50 and Sample Size = 30,000. Figure 4 exhibits negative association variation.

Table 13. Negative associations @ Regularity 1.50 (30000 Examples) Varying frequency

"Frequency"	"Negative Frequent Regular Item Sets"	"% of Negative Associations * 1000"
1.750	18	18/30=0.60
1.625	59	59/30=1.97
1.500	90	90/30=3.00
Average		1.85

At Regularity fixed @ 1.50 and varying frequency for sample size 30,000

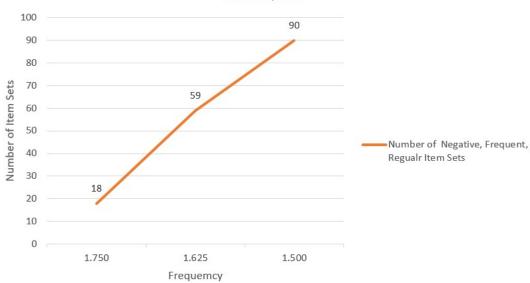


Figure 4. Negative association @ regularity (1.50) (30000 Examples) varying the Frequency

Table ?? lists negative relationships with a regularity 1.65 and a sample size of 50,000. Negative connections dropped 73%. Figure 5 shows variances.

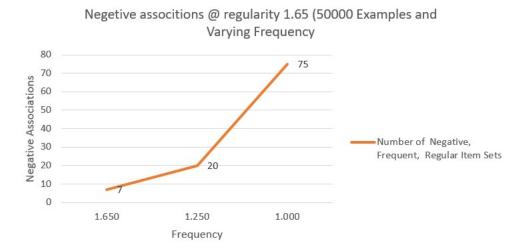


Figure 5. Negative association Item sets @ Regularity (1.65) (Examples 50,000) varying the Frequency

7. Conclusions and Future Scope

Medical data moves in streams, and doctors must be warned soon after prescription if any negative associations exist among drugs prescribed by them, or else there could be a devastating effect on the patients. Many patients died during the coronavirus time as no system existed at that time that warned doctors not to use some drugs in combination. The use of humidifier drugs killed many due to many side reactions that affected the human organs.

Finding minimum and effective negative correlations is critical when medical data is rapidly shared online. Critical items are emphasised. Minifying regular and common item sets from historical databases and data streams yields the most effective negative associations. Since the complete data set is unavailable for study, finding the maximal and closed data sets is impossible. Regularity at 1.5 and frequency at 1.75 yields the last and most effective negative associations.

This research identifies all negative correlations with a collection of medications given to patients. Finding positive associations can be challenging due to many negative ones. Every medicine is chemically made. Chemical mixtures can be harmful. Consider negative correlations among chemicals and decode them into medications to determine the most important ones. This research is mainly limited by the chemical composition of medications doctors give to treat disorders.

Research medication administration limits and large trends. Rare and new medicinal item sets must be investigated. Further research may reveal intriguing elements beyond frequency and support that directly fit to uncover effective negative associations. The method may find negative links in remote or incremental medical databases and streaming data.

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