Unit-V Mining sequence patterns







Dr. K.RAGHAVA RAO

Professor of CSE

Dept. of MCA

KL University
krraocse@gmail.com
http://datamining.blog.com

Sequence Databases & Sequential Patterns

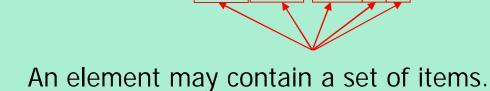
- Transaction databases, time-series databases vs. sequence databases
- Frequent patterns vs. (frequent) sequential patterns
- Applications of sequential pattern mining
 - Customer shopping sequences:
 - First buy computer, then CD-ROM, and then digital camera, within 3 months.
 - Medical treatments, natural disasters (e.g., earthquakes), science & eng. processes, stocks and markets, etc.
 - Telephone calling patterns, Weblog click streams
 - Program execution sequence data sets
 - DNA sequences and gene structures

What Is Sequential Pattern Mining?

 Given a set of sequences, find the complete set of frequent subsequences

A <u>sequence database</u>

SID	sequence
10	<a(<u>abc)(a<u>c</u>)d(cf)></a(<u>
20	<(ad)c(bc)(ae)>
30	<(ef)(<u>ab</u>)(df) <u>c</u> b>
40	<eg(af)cbc></eg(af)cbc>



A <u>sequence</u>: < (ef) (ab) (df) c b >

An element may contain a set of items. Items within an element are unordered and we list them alphabetically._

Given <u>support threshold</u> min_sup = 2, < (ab)c> is a <u>sequential pattern</u>

Challenges on Sequential Pattern Mining

- A huge number of possible sequential patterns are hidden in databases
- A mining algorithm should
 - find the complete set of patterns, when possible, satisfying the minimum support (frequency) threshold
 - be highly efficient, scalable, involving only a small number of database scans
 - be able to incorporate various kinds of user-specific constraints

Sequential Pattern Mining Algorithms

- Concept introduction and an initial Apriori-like algorithm
 - Agrawal & Srikant. Mining sequential patterns, ICDE'95
- Apriori-based method: GSP (Generalized Sequential Patterns: Srikant & Agrawal @ EDBT'96)
- Pattern-growth methods: FreeSpan & PrefixSpan (Han et al.@KDD'00; Pei, et al.@ICDE'01)
- Vertical format-based mining: SPADE (Zaki@Machine Leanining'00)
- Constraint-based sequential pattern mining (SPIRIT: Garofalakis, Rastogi, Shim@VLDB'99; Pei, Han, Wang @ CIKM'02)
- Mining closed sequential patterns: CloSpan (Yan, Han & Afshar @SDM'03)

The Apriori Property of Sequential Patterns

- A basic property: Apriori (Agrawal & Sirkant'94)
 - If a sequence S is not frequent
 - Then none of the super-sequences of S is frequent
 - E.g, <hb> is infrequent → so do <hab> and <(ah)b>

Seq. ID	Sequence
10	<(bd)cb(ac)>
20	<(bf)(ce)b(fg)>
30	<(ah)(bf)abf>
40	<(be)(ce)d>
50	<a(bd)bcb(ade)></a(bd)bcb(ade)>

Given <u>support threshold</u> min_sup =2

GSP—Generalized Sequential Pattern Mining

- GSP (Generalized Sequential Pattern) mining algorithm
 - proposed by Agrawal and Srikant, EDBT'96
- Outline of the method
 - Initially, every item in DB is a candidate of length-1
 - for each level (i.e., sequences of length-k) do
 - scan database to collect support count for each candidate sequence
 - generate candidate length-(k+1) sequences from length-k frequent sequences using Apriori
 - repeat until no frequent sequence or no candidate can be found
- Major strength: Candidate pruning by Apriori

Finding Length-1 Sequential Patterns

- Examine GSP using an example
- Initial candidates: all singleton sequences

Scan database once, count support for candidates

mi	in	SU	D	=2
	· ·—		~	

Seq. ID	Sequence		
10	<(bd)cb(ac)>		
20	<(bf)(ce)b(fg)>		
30	<(ah)(bf)abf>		
40	<(be)(ce)d>		
50	<a(bd)bcb(ade)></a(bd)bcb(ade)>		

Cand	Sup
<a>>	3
	5
<c></c>	4
<d>></d>	3
<e></e>	3
<f></f>	2
>g>	1
>h>	1

GSP: Generating Length-2 Candidates

51 length-2 Candidates

	<a>>		<c></c>	<d>></d>	<e></e>	<f></f>
<a>>	<aa></aa>	<ab></ab>	<ac></ac>	<ad></ad>	<ae></ae>	<af></af>
	<ba></ba>	>	<pc></pc>	<bd></bd>	<be></be>	<bf></bf>
<c></c>	<ca></ca>	<cp></cp>	<cc></cc>	<cd></cd>	<ce></ce>	<cf></cf>
<d></d>	<da></da>	<db></db>	<dc></dc>	<dd></dd>	<de></de>	<df></df>
<e></e>	<ea></ea>	<eb></eb>	<ec></ec>	<ed></ed>	<ee></ee>	<ef></ef>
<f></f>	<fa></fa>	<fb></fb>	<fc></fc>	<fd></fd>	<fe></fe>	<ff></ff>

	<a>>		<c></c>	<d></d>	<e></e>	<f></f>
<a>>		<(ab)>	<(ac)>	<(ad)>	<(ae)>	<(af)>
			<(bc)>	<(bd)>	<(be)>	<(bf)>
<c></c>				<(cd)>	<(ce)>	<(cf)>
<d>></d>					<(de)>	<(df)>
<e></e>						<(ef)>
<f></f>						

Without Apriori property, 8*8+8*7/2=92 candidates

Apriori prunes 44.57% candidates

The GSP Mining Process

5th scan: 1 cand. 1 length-5 seq. pat.

4th scan: 8 cand. 6 length-4 seq. pat.

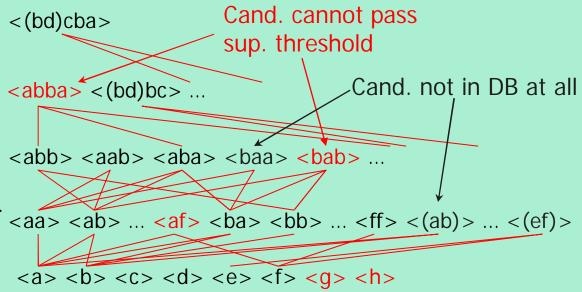
3rd scan: 46 cand. 19 length-3 seq. pat. 20 cand. not in DB at all

2nd scan: 51 cand. 19 length-2 seq.

pat. 10 cand. not in DB at all

1st scan: 8 cand. 6 length-1 seq.

pat.



Seq. ID	Sequence
10	<(bd)cb(ac)>
20	<(bf)(ce)b(fg)>
30	<(ah)(bf)abf>
40	<(be)(ce)d>
50	<a(bd)bcb(ade)></a(bd)bcb(ade)>

Candidate Generate-and-test: Drawbacks

- A huge set of candidate sequences generated
 - Especially 2-item candidate sequence
- Multiple Scans of database needed
 - The length of each candidate grows by one at each database scan
- Inefficient for mining long sequential patterns
 - A long pattern grow up from short patterns
 - The number of short patterns is exponential to the length of mined patterns

The SPADE Algorithm

- SPADE (<u>Sequential PAttern Discovery using Equivalent</u> Class) developed by Zaki 2001
- A vertical format sequential pattern mining method
- A sequence database is mapped to a large set of
 - Item: <SID, EID> sequence id and eventid
- Sequential pattern mining is performed by
 - growing the subsequences (patterns) one item at a time by Apriori candidate generation

The SPADE Algorithm

SID	EID	Items
1	1	a
$ \begin{array}{c c} 1 \\ 1 \\ 1 \\ 2 \\ 2 \\ 2 \\ 3 \\ \end{array} $	2	abc
1	3	ac
1	4	d
1	5	cf
2	1	ad
2	2	c
2	3	bc
2	4	ae
3	1	ef
3	2	ab
3 3	3	df
3	4	c
3	5	b
4	1	e
4	2	g
4 4 4 4	3	af
4	4	c
4	$ \begin{array}{c} 1 \\ 2 \\ 3 \\ 4 \\ 5 \\ 1 \\ 2 \\ 3 \\ 4 \\ 5 \\ 6 \end{array} $	b
4	6	c

	a	1)	
SID	EID	SID	EID	
1	1	1	2	
1	2	2	3	
1	3	3	2	
2	1	3	5	
2	4	4	5	
3	2			
4	3			

	ab			ba		• • •
SID	EID (a)	EID(b)	SID	EID (b)	EID(a)	
1	1	2	1	2	3	
2	1	3	2	3	4	
3	2	5				
4	3	5				

aba				
SID	EID (a)	EID(b)	EID(a)	
1	1	2	3	
2	1	3	4	

Bottlenecks of GSP and SPADE

- A huge set of candidates could be generated
 - 1,000 frequent length-1 sequences generate s huge number of length-2 candidates! $1000 \times 1000 + \frac{1000 \times 999}{2} = 1,499,500$
- Multiple scans of database in mining
- Breadth-first search
- Mining long sequential patterns
 - Needs an exponential number of short candidates
 - A length-100 sequential pattern needs 10^{30} $\sum_{i=1}^{100} \binom{100}{i} = 2^{100} 1 \approx 10^{30}$ candidate sequences!

Prefix and Suffix (Projection)

- <a>, <aa>, <a(ab)> and <a(abc)> are <u>prefixes</u> of sequence <a(abc)(ac)d(cf)>
- Given sequence <a(abc)(ac)d(cf)>

Prefix	Suffix (Prefix-Based Projection)
<a>	<(abc)(ac)d(cf)>
<aa></aa>	<(_bc)(ac)d(cf)>
<ab></ab>	<(_c)(ac)d(cf)>

Mining Sequential Patterns by Prefix Projections

- Step 1: find length-1 sequential patterns
 - <a>, , <c>, <d>, <e>, <f>
- Step 2: divide search space. The complete set of seq. pat. can be partitioned into 6 subsets:
 - The ones having prefix <a>;
 - The ones having prefix ;
 - **.** . . .
 - The ones having prefix <f>

SID	sequence
10	<a(abc)(ac)d(cf)></a(abc)(ac)d(cf)>
20	<(ad)c(bc)(ae)>
30	<(ef)(ab)(df)cb>
40	<eg(af)cbc></eg(af)cbc>

Finding Seq. Patterns with Prefix <a>

- Only need to consider projections w.r.t. <a>
 - <a>-projected database:
 - <(abc)(ac)d(cf)>
 - <(_d)c(bc)(ae)>
 - <(_b)(df)cb>
 - < <(_f)cbc>

SID	sequence
10	<a(abc)(ac)d(cf)></a(abc)(ac)d(cf)>
20	<(ad)c(bc)(ae)>
30	<(ef)(ab)(df)cb>
40	<eg(af)cbc></eg(af)cbc>

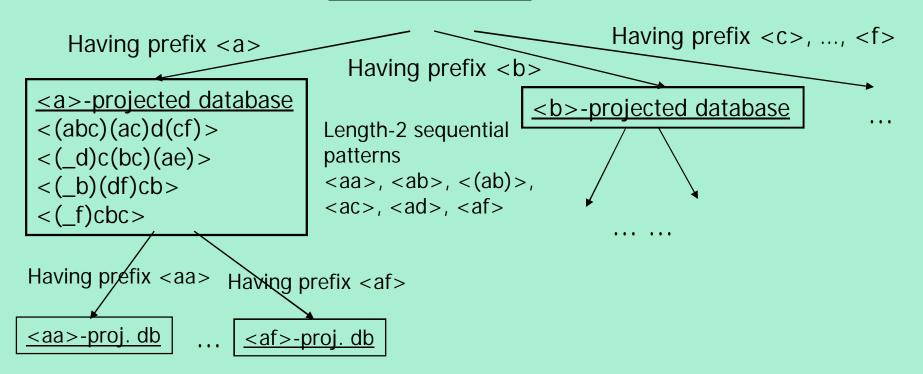
- Find all the length-2 seq. pat. Having prefix <a>: <aa>, <ab>, <(ab)>, <ac>, <ad>, <af></ar>
 - Further partition into 6 subsets
 - Having prefix <aa>;
 - **...**
 - Having prefix <af>

Completeness of PrefixSpan

SDB

SID	sequence
10	<a(abc)(ac)d(cf)></a(abc)(ac)d(cf)>
20	<(ad)c(bc)(ae)>
30	<(ef)(ab)(df)cb>
40	<eg(af)cbc></eg(af)cbc>

Length-1 sequential patterns <a>, , <c>, <d>, <e>, <f>



Efficiency of PrefixSpan

- No candidate sequence needs to be generated
- Projected databases keep shrinking
- Major cost of PrefixSpan: Constructing projected databases
 - Can be improved by pseudo-projections

Speed-up by Pseudo-projection

- Major cost of PrefixSpan: projection
 - Postfixes of sequences often appear
 repeatedly in recursive projected databases
- When (projected) database can be held in main memory, use pointers to form projections
 - Pointer to the sequence
 - Offset of the postfix

Pseudo-Projection vs. Physical Projection

- Pseudo-projection avoids physically copying postfixes
 - Efficient in running time and space when database can be held in main memory
- However, it is not efficient when database cannot fit in main memory
 - Disk-based random accessing is very costly
- Suggested Approach:
 - Integration of physical and pseudo-projection
 - Swapping to pseudo-projection when the data set fits in memory

CloSpan: Mining Closed Sequential Patterns

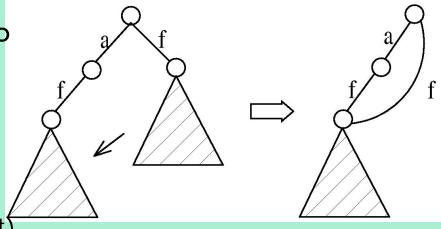
A closed sequential pattern s: there exists no superpattern s' such that s' > s, and s' and s have the same support

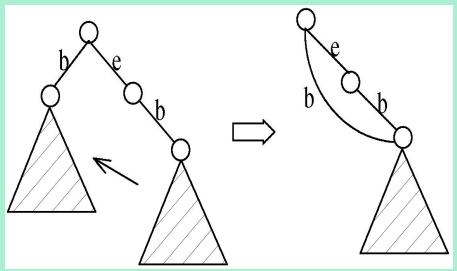
Which one is closed? <abc>: 20, <abcd>: 15

Why mine close seq. patterns?

Reduces the number of (redundant)
 patterns but attains the same
 expressive power

- Property: If s' > s, closed iff two project DBs have the same size
- Using Backward Subpattern and Backward Superpattern pruning to prune redundant search space





Constraint-Based Seq.-Pattern Mining

- Constraint-based sequential pattern mining
 - Constraints: User-specified, for focused mining of desired patterns
 - How to explore efficient mining with constraints? Optimization
- Classification of constraints
 - Anti-monotone: E.g., value_sum(S) < 150, min(S) > 10
 - Monotone: E.g., count (S) > 5, S ⊇ {PC, digital_camera}
 - Succinct: E.g., length(S) ≥ 10, S ∈ {Pentium, MS/Office, MS/Money}
 - Convertible: E.g., value_avg(S) < 25, profit_sum (S) > 160, max(S)/avg(S) < 2, median(S) min(S) > 5
 - Inconvertible: E.g., avg(S) median(S) = 0

