

Sequence Databases & Sequential Patterns

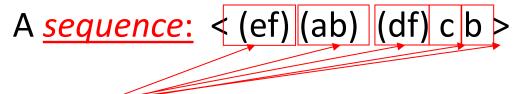
- Sequential pattern mining has broad applications
 - Customer shopping sequences
 - Purchase a laptop first, then a digital camera, and then a smartphone,
 within 6 months
 - Medical treatments, natural disasters (e.g., earthquakes), science & engineering processes, stocks and markets, ...
 - Weblog click streams, calling patterns, ...
 - Software engineering: Program execution sequences, ...
 - Biological sequences: DNA, protein, ...
- ☐ Transaction DB, sequence DB vs. time-series DB
- Gapped vs. non-gapped sequential patterns
 - Shopping sequences, clicking streams vs. biological sequences

Sequential Pattern and Sequential Pattern Mining

Sequential pattern mining: Given a set of sequences, find the complete set of frequent subsequences (i.e., satisfying the min_sup threshold)

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>



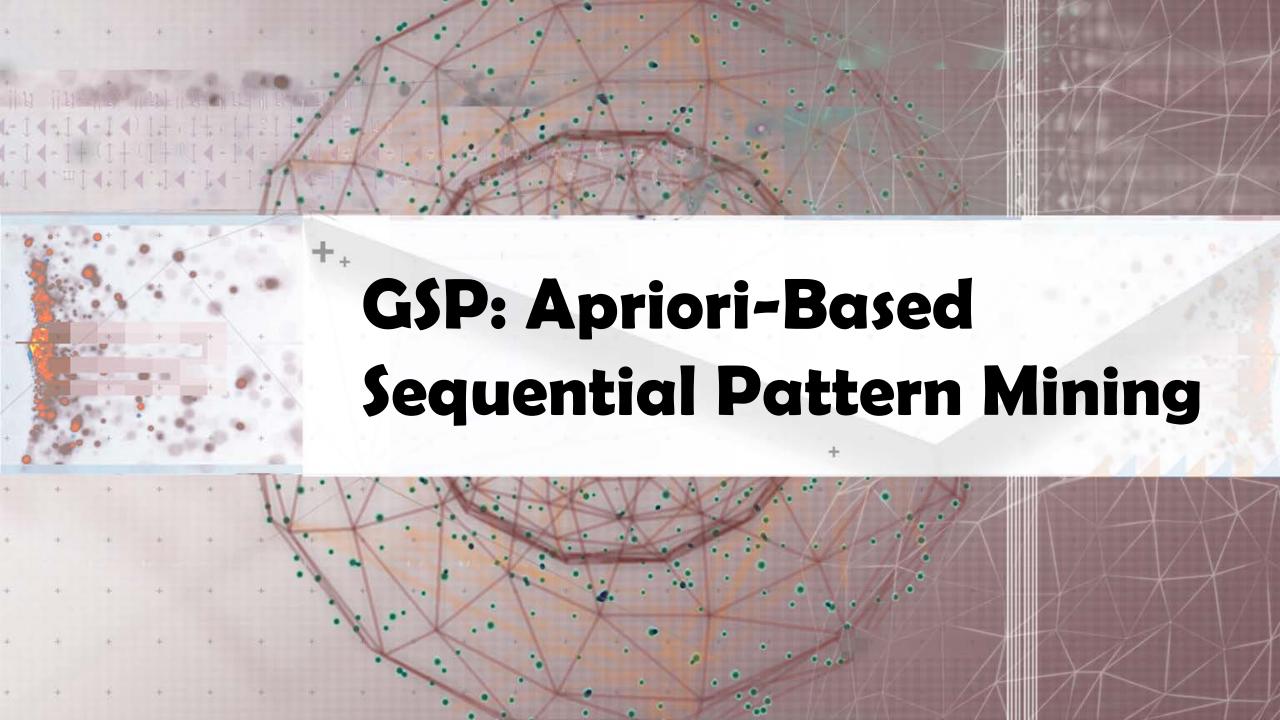
- → An <u>element</u> may contain a set of *items* (also called events)
- □ Items within an element are unordered and we list them alphabetically

 $<a(bc)dc>is a <u>subsequence</u> of <math><\underline{a(abc)(ac)\underline{d(cf)}}>$

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

Sequential Pattern Mining Algorithms

- Algorithm requirement: Efficient, scalable, finding complete set, incorporating various kinds of user-specific constraints
- The Apriori property still holds: If a subsequence s_1 is infrequent, none of s_1 's super-sequences can be frequent
- Representative algorithms
 - GSP (Generalized Sequential Patterns): Srikant & Agrawal @ EDBT'96)
 - Vertical format-based mining: SPADE (Zaki@Machine Leanining'00)
 - Pattern-growth methods: PrefixSpan (Pei, et al. @TKDE'04)
- Mining closed sequential patterns: CloSpan (Yan, et al. @SDM'03)
- Constraint-based sequential pattern mining



GSP: Apriori-Based Sequential Pattern Mining

- Initial candidates: All singleton sequences
- <a>, , <c>, <d>, <e>, <f>, <g>, <h>
- Scan DB once, count support for each candidate
- Generate length-2 candidate sequences

$$min_sup = 2$$

Cand.	sup
<a>	3
	5
<c></c>	4
<d></d>	3
<e></e>	3
<f></f>	2
785	1

	<a>		<c></c>	<d></d>	<e></e>	<f></f>
<a>	<aa></aa>	<ab></ab>	<ac></ac>	<ad></ad>	<ae></ae>	<af></af>
	<ba></ba>	<bb></bb>	<bc></bc>	<bd></bd>	<be></be>	<bf></bf>
<c></c>	<ca></ca>	<cb></cb>	<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>						

SID	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)>

■ Length-2 candidates:

$$36 + 15 = 51$$

■ Without Apriori pruning: 8*8+8*7/2=92 candidates

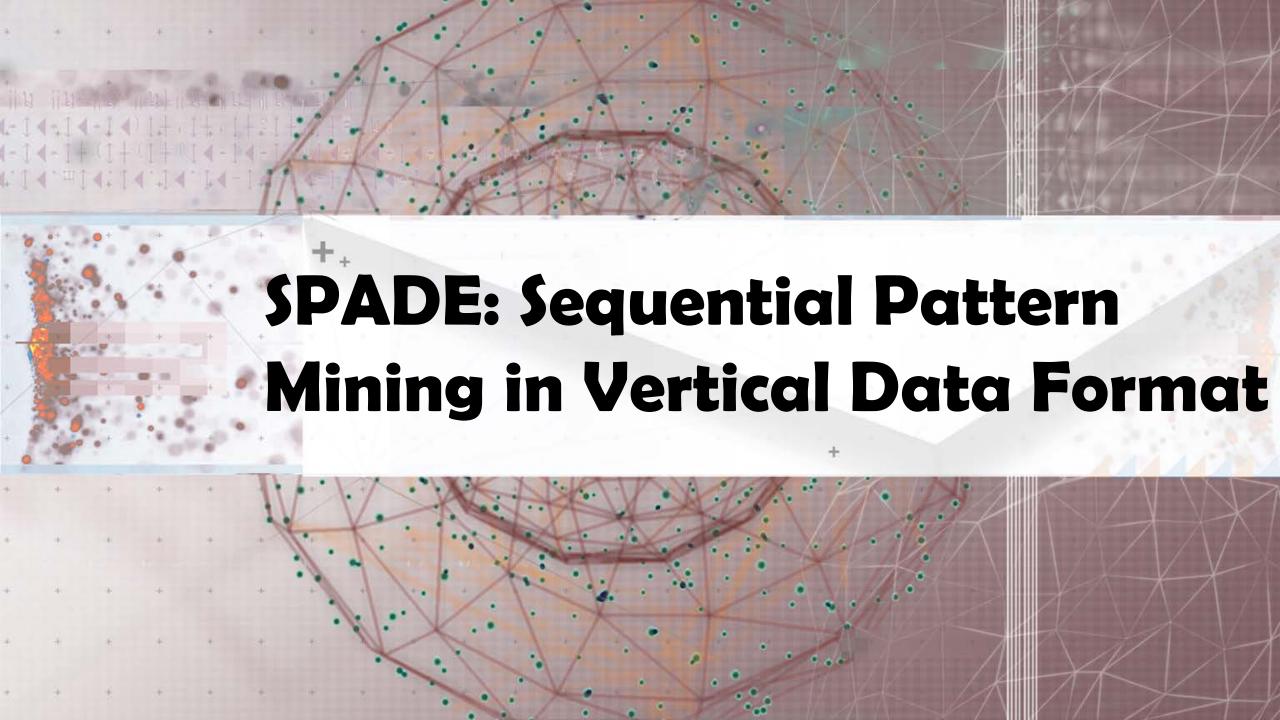
GSP (Generalized Sequential Patterns): Srikant & Agrawal @ EDBT'96)

GSP Mining and Pruning

Candidates cannot pass min_sup 5th scan: 1 cand. 1 length-5 seq. pat. <(bd)cba> threshold 4th scan: 8 cand. 7 length-4 seq. pat. Candidates not in DB <abba> <(bd)bc> ... 3rd scan: 46 cand. 20 length-3 seq. pat. 20 <abb> <aab> <aba> <bab> ... cand, not in DB at all 2nd scan: 51 cand. 19 length-2 seq. pat. <aa> <ab> ... <af> <ba> <bb> ... <ff> <(ab)> ... <(ef)> 10 cand. not in DB at all <a> <c> <d> <e> <f> <g> <h> $min_sup = 2$ 1st scan: 8 cand. 6 length-1 seq. pat.

- Repeat (for each level (i.e., length-k))
- Scan DB to find length-k frequent sequences
- ☐ Generate length-(k+1) candidate sequences from length-k frequent sequences using Apriori
- \square set k = k+1
- Until no frequent sequence or no candidate can be found

SID	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)>



Sequential Pattern Mining in Vertical Data Format: The SPADE Algorithm

- A sequence database is mapped to: <SID, EID>
- ☐ Grow the subsequences (patterns) one item at a time by Apriori candidate generation

SID	Sequence	
1	<a(<u>abc)(a<u>c</u>)d(cf)></a(<u>	
2	<(ad)c(bc)(ae)>	
3	<(ef)(<u>ab</u>)(df) <u>c</u> b>	
4	4 <eg(af)cbc></eg(af)cbc>	
min_sup = 2		

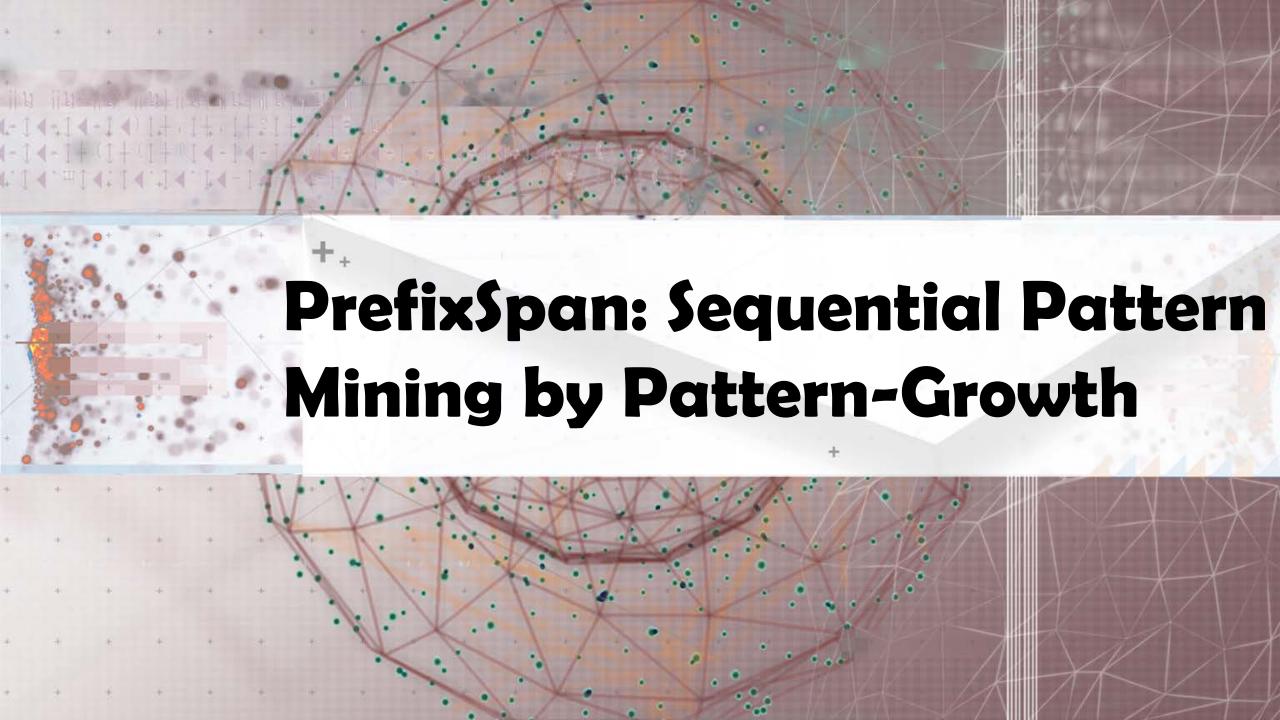
Ref: SPADE (<u>Sequential</u>
<u>PAttern Discovery</u>
using <u>Equivalent Class</u>)
[M. Zaki 2001]

SID	EID	Items
1	1	a
1	2	abc
1	3	\mathbf{ac}
1 1 2 2 2 2 2 3	4	d
1	5	cf
2	1	ad
2	2	\mathbf{c}
2	3	\mathbf{bc}
2	4	ae
	$\frac{1}{2}$	$\mathbf{e}\mathbf{f}$
3	2	ab
3	3	$\mathrm{d}\mathrm{f}$
3	4	\mathbf{c}
3	5 1	b
4		\mathbf{e}
4	2	g
4	3	af
4	4	\mathbf{c}
4	5	b
4	6	\mathbf{c}

i	a	1	о	
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			
	, 			

	$^{\mathrm{ab}}$			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				

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



PrefixSpan: A Pattern-Growth Approach

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>

Prefix	Suffix (Projection)
<a>	<(abc)(ac)d(cf)>
<aa></aa>	<(_bc)(ac)d(cf)>
<ab></ab>	<(_c)(ac)d(cf)>
1	

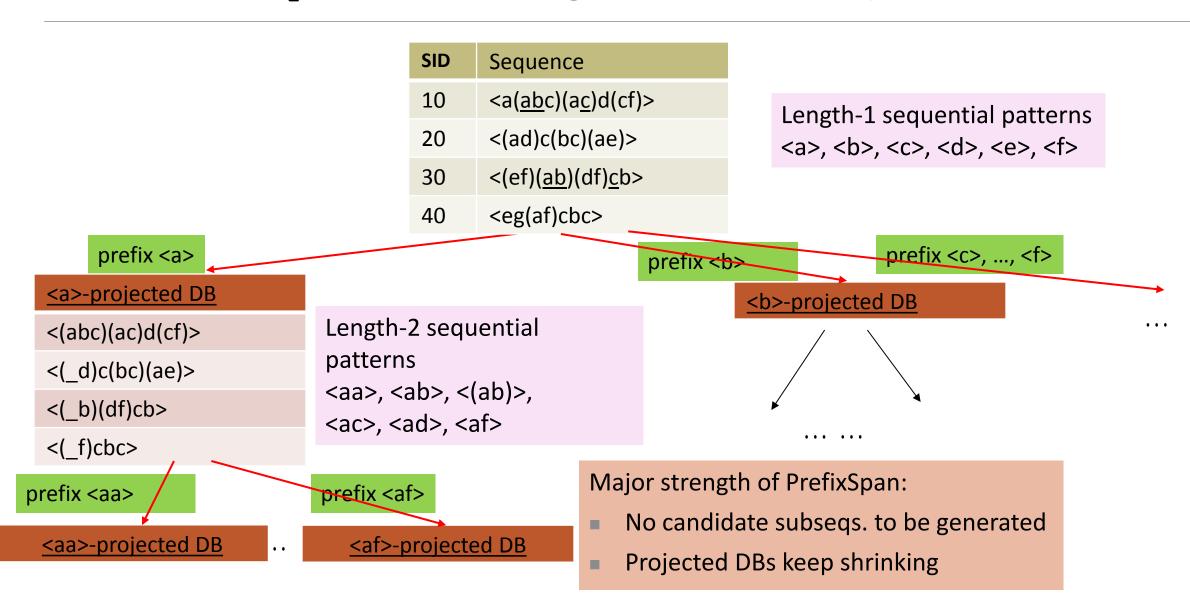
- Prefix and suffix
 - ☐ Given <a(abc)(ac)d(cf)>
 - Prefixes: <a>, <aa>,
 <a(ab)>, <a(abc)>, ...
 - Suffix: Prefixes-based projection

- PrefixSpan Mining: Prefix Projections
 - Step 1: Find length-1 sequential patterns
 - <a>, , <c>, <d>, <e>, <f>
 - Step 2: Divide search space and mine each projected DB
 - <a>-projected DB,
 - -projected DB,

 - <f>-projected DB, ...

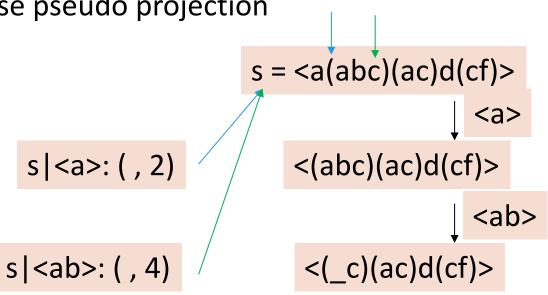
PrefixSpan (Prefix-projected Sequential pattern mining) Pei, et al. @TKDE'04

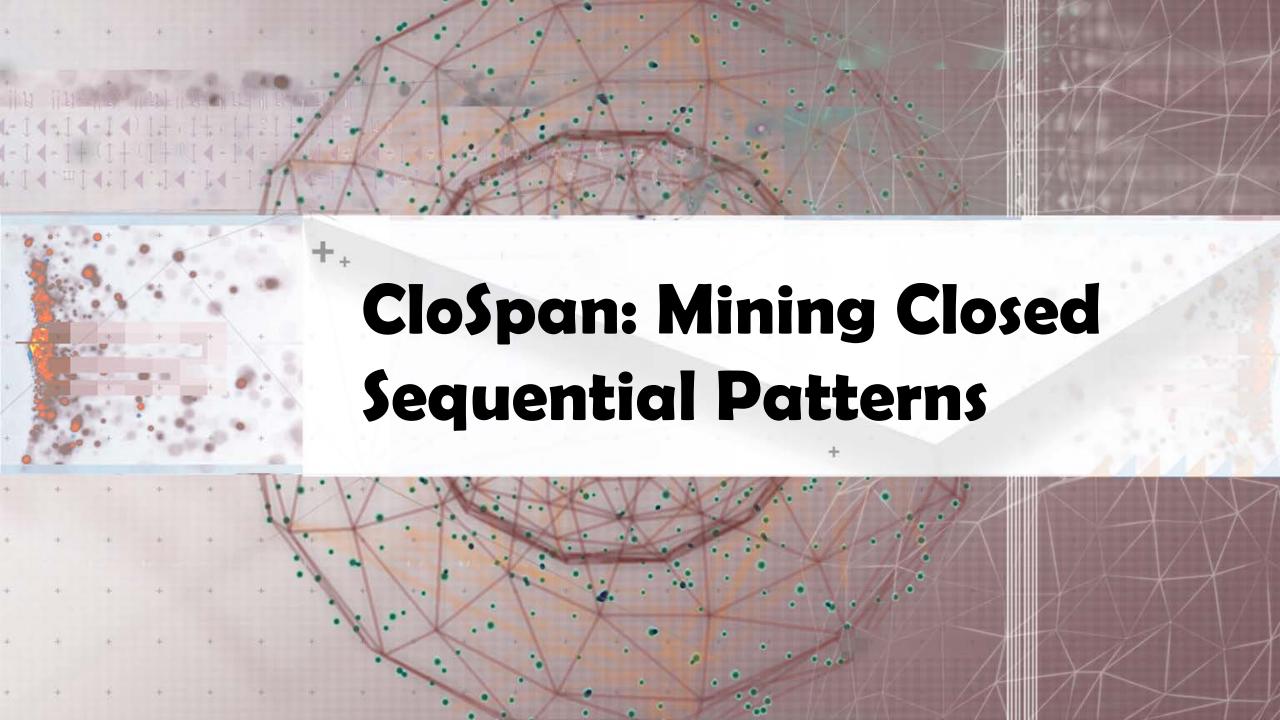
PrefixSpan: Mining Prefix-Projected DBs



Implementation Consideration: Pseudo-Projection vs. Physical Projection

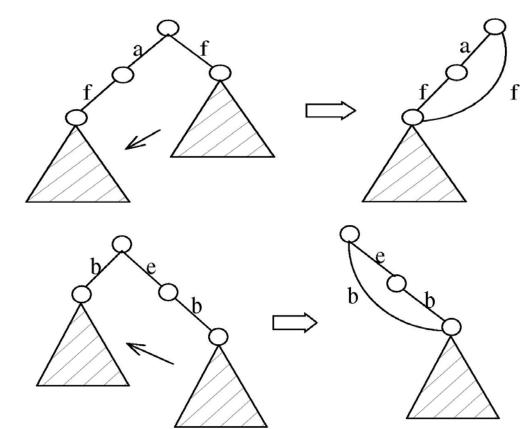
- Major cost of PrefixSpan: Constructing projected DBs
 - Suffixes largely repeating in recursive projected DBs
- When DB can be held in main memory, use pseudo projection
 - No physically copying suffixes
 - Pointer to the sequence
 - Offset of the suffix
- But if it does not fit in memory
 - Physical projection
- Suggested approach:
 - Integration of physical and pseudo-projection
 - Swapping to pseudo-projection when the data fits in memory





CloSpan: Mining Closed Sequential Patterns

- \square A closed sequential pattern s: There exists no superpattern s' such that $s' \supset s$, and s' and s have the same support
- □ Which ones are closed? <abc>: 20, <abcd>:20, <abcd>: 15
- Why directly mine closed sequential patterns?
 - Reduce # of (redundant) patterns
 - Attain the same expressive power
- □ Property P_1 : If $s \supset s_1$, s is closed iff two project DBs have the same size
- Explore Backward Subpattern and Backward Superpattern pruning to prune redundant search space
- ☐ Greatly enhances efficiency (Yan, et al., SDM'03)





Summary: Sequential Pattern Mining

- Concepts of Sequential Pattern Mining
- Sequential Pattern Mining Algorithms
 - GSP (Generalized Sequential Patterns)
 - Vertical Format-Based Mining: SPADE
 - Pattern-Growth Methods: PrefixSpan
- Mining Closed Sequential Patterns: CloSpan

Recommended Readings

- R. Srikant and R. Agrawal, "Mining sequential patterns: Generalizations and performance improvements", EDBT'96
- M. Zaki, "SPADE: An Efficient Algorithm for Mining Frequent Sequences", Machine Learning, 2001
- J. Pei, J. Han, B. Mortazavi-Asl, J. Wang, H. Pinto, Q. Chen, U. Dayal, and M.-C. Hsu, "Mining Sequential Patterns by Pattern-Growth: The PrefixSpan Approach", IEEE TKDE, 16(10), 2004
- X. Yan, J. Han, and R. Afshar, "CloSpan: Mining Closed Sequential Patterns in Large Datasets", SDM'03