Data Mining & Knowledge Discovery

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Chapter 3: Sequential Pattern Analysis

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Course Content

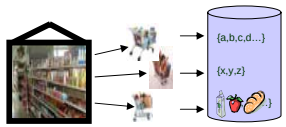
- Introduction to Data Mining
- Association Analysis
- Sequential Pattern Analysis
- Classification and prediction
- Contrast Sets
- Data Clustering
- Outlier Detection
- Web Mining
- Other topics if time permits (spatial data, biomedical data, etc.)

Chapter 3 Objectives

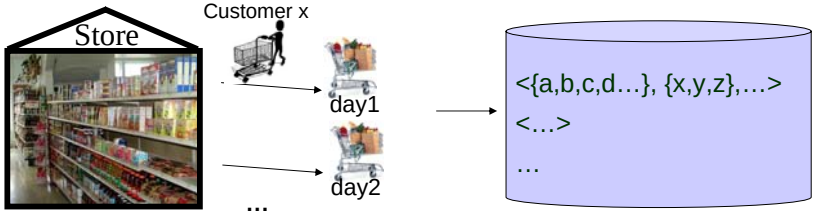
Understand Sequential Pattern Analysis in the context of transactional data and get a brief introduction to the different algorithms for sequential pattern discovery

Sequence of Transactions

- Association rule mining searches for relationships between items in a dataset where time is irrelevant.



- Sequential Pattern Analysis considers time (or order of transactions).



Data: sequences of evidences in time order
Target: sub-sequences that happened frequently

Sequence Pattern Examples

- Examples 1
  - 60% of customers typically rent “Star Wars”, then “Empire Strikes Back”, and then “Return of Jedi”.
  - Note: these rentals need not to be consecutive.
  - <SW>,…,<ESB>,…,<RJ>
- Example 2
  - 60% of customers buy “Fitted Sheet and flat sheet and pillow”, followed by “comforter”, followed by “drapes and ruffles”
  - Note: elements of a sequential pattern need not to be simple items.
  - <FittedSheet, FaltSheet, Pillow>, …,<Comforter>,…,<Drapes, Ruffles>

Lecture Outline

Part I: Concepts *(30 minutes)*

- **Basic concepts**

Part II: Apriori-based Approaches *(45 minutes)*

- **Apriori-all**
- **GSP**

Part III: Pattern-Growth-based Approaches *(45 minutes)*

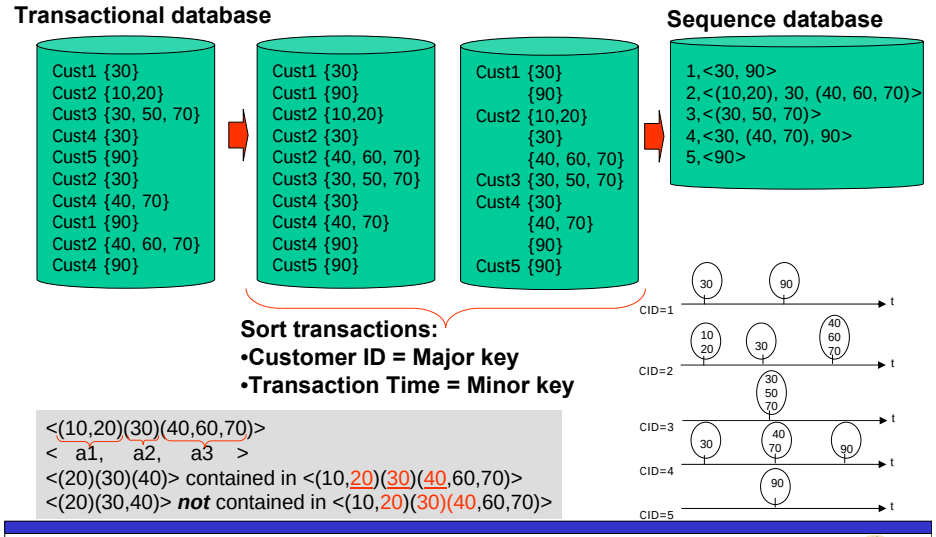
- **Free-Span**
- **Prefix-Span**

Why **sequential pattern** mining?

- Time or order in which actions appear or happen can be relevant in decision making.
- Many applications of sequential pattern mining
  - Customer shopping sequences (idem for book/video rental):
    - First buy computer, then CD-ROM, and then digital camera, within 3 months.
  - Medical treatment (e.g., symptoms and diseases)
  - Serial crime solving
  - Natural disasters (e.g., earthquakes),
  - Science & engineering processes,
  - Stocks and markets,
  - Telephone calling patterns,
  - Web access log click streams,
  - DNA sequences and gene structures, etc.

Sequence Database

Converts the original transaction database into a database of customer sequences.



<(10,20)(30)(40,60,70)>
< a1, a2, a3 >
<(20)(30)(40)> contained in <(10,20)(30)(40,60,70)>
<(20)(30,40)> ***not*** contained in <(10,20)(30)(40,60,70)>

What Is Sequential Pattern Mining?

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

A *sequence* : <(ef)(ab)(df)cb>

A *sequence database*

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

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

<a(bc)dc> is a *subsequence* of <a(abc)(ac)d(cf)>

Given *support threshold* *min_sup* =2, <(ab)c> is a *sequential pattern* (cf. SID 10 & 30)

Sequential Patterns

- Given
  - a set of sequences, where each sequence consists of a list of elements and each element consists of set of items
  - user-specified min_support threshold

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

<a(abc)(ac)d(cf)> - 5 elements, 9 items

<a(abc)(ac)d(cf)> - 9-sequence

<a(abc)(ac)d(cf)> = <a(cba)(ac)d(cf)>
<a(abc)(ac)d(cf)> ≠ <a(ac)(abc)d(cf)>

Order doesn't Matter (list)

Order matters (sequence)

Sequential Pattern Mining

- Find all the frequent subsequences, i.e. the subsequences whose occurrence frequency in the set of sequences is no less than min_support

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

min_support = 2

Solution – 53 frequent subsequences

<a><aa> <ab> <a(bc)> <a(bc)a> <aba> <abc> <(ab)> <(ab)c> <(ab)d> <(ab)f> <(ab)dc> <ac> <aca> <acb> <acc> <ad> <adc> <af>

<b> <ba> <bc> <(bc)> <(bc)a> <bd> <bdc> <bf>

<c> <ca> <cb> <cc>

<d> <db> <dc> <dcb>

<e> <ea> <eab> <eac> <eacb> <eb> <ebc> <ec> <ecb> <ef> <efb> <efc> <efcb>

<f> <fb> <fbc> <fc> <fcb>

Subsequence vs. super sequence

- Given two sequences $\alpha=<a_1a_2\ldots a_n>$ and $\beta=<b_1b_2\ldots b_m>$
- α is called a subsequence of β, denoted as $\alpha \subseteq \beta$, if there exist integers $1\leq j_1<j_2<\ldots<j_n \leq m$ such that $a_1\subseteq b_{j1}, a_2 \subseteq b_{j2},\ldots, a_n\subseteq b_{jn}$
- β is a super sequence of α
- A sequence *s* is maximal if it is not contained in any other sequence.

β =<a(abc)(ac)d(cf)>

α_1=<aa(ac)d(c)>

α_2=<(ac)(ac)d(cf)>

α_3=<ac>

β =<a(abc)(ac)d(cf)>

α_4=<df(cf)>

α_5=<(cf)d>

α_6=<(abc)dcf>

Sequence Support Count

- A sequence database is a set of tuples <sid, s>
- A tuple <sid, s> is said to contain a sequence α, if α is a subsequence of s, i.e., $\alpha \subseteq s$
- The support of a sequence α is the number of tuples containing α

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

α_1=<a> support(α_1) = 4

α_2=<ac> support(α_2) = 4

α_3=<(ab)c> support(α_3) = 2

Counting Sequences (An example)

<(7)(3,8)(9)(4,5,6)(8)>	Contained
<(8)(3,8)(9)(4,5)(6)(7)>	
<(3)(5,4)>	
<(3)(5,4)(6)(9,8)>	Contained
<(10)(3)(5,4)(9,8)>	Contained
<(5,4)(6,6)(9,8)>	
<(3)(5,4)(6)(9,8)>	Contained
<(3)(5)(4)(6)(9,8)>	
<(3)(5,2,1)(6)(9,8)>	
<(3)(5,4)(6)(9,8)>	Contained

A Generated Candidate Pattern

<(3)(4,5)(8)>

Support count 5

Not Contained → Not Counted

IF Min_Support ≤ 50% THEN <(3)(4,5)(8)> is Frequent

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
- Comparison of association rules and sequence mining
  - Mining for association rules
    - Purpose: Discovery of frequent unordered itemsets.
    - Complexity: With n items there are $\binom{n}{k} = \frac{n!}{k!(n-k)!}$ k-itemsets (sets with k items).
  - Mining for Sequential Patterns
    - Purpose: Discovery of frequent *sequences of* (unordered) itemsets.
    - Complexity: With n items there are n^k k-sequences (sequences with k items).

Association mining algorithms discover *isolated* item sets (*intra*-event patterns).
Sequence mining algorithms discover *series of* item sets (*inter*-event patterns).

Studies on Sequential Pattern Mining

- Concept introduction and an initial Apriori-like algorithm
  - R. Agrawal & R. Srikant. "Mining sequential patterns," ICDE'95
- GSP—An Apriori-based, influential mining method (developed at IBM Almaden)
  - R. Srikant & R. Agrawal. "Mining sequential patterns: Generalizations and performance improvements," EDBT'96
- From sequential patterns to episodes (Apriori-like + constraints)
  - H. Mannila, H. Toivonen & A.I. Verkamo. "Discovery of frequent episodes in event sequences," Data Mining and Knowledge Discovery, 1997
- Data Projection-based approaches
  - FreeSpan (Han et al. "frequent pattern-projected sequential pattern mining" SIGKDD 2000)
  - PrefixSpan (Pei et al. "Prefix-projected pattern growth" ICDE 2001)
- Mining sequential patterns with constraints
  - M.N. Garofalakis, R. Rastogi, K. Shim: SPIRIT: Sequential Pattern Mining with Regular Expression Constraints. VLDB 1999

Lecture Outline

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AprioriAll: The idea

- Basic method to mine sequential patterns
  - Based on the Apriori algorithm
  - Count all the large sequences, including non-maximal sequences
  - Use Apriori-generate function to generate candidate sequences: get candidates for a pass using only the large sequences found in the previous pass and make a scan over the data to find their support

AprioriAll: The big picture

Five-phase algorithm

1. Sort phase:

   Create the sequence database from transactions.

2. Large itemset phase

   Find all frequent itemsets using Apriori

3. Transformation phase:

   Do integer mapping for large itemsets

4. Sequence phase:

   Find all frequent sequential patterns using Apriori.

5. Maximal phase:

   Eliminate non maximal sequences.

AprioriAll Algorithm(1)

- **AprioriAll Algorithm**

  C_k: Candidate sequence of size k
  L_k : frequent or large sequence of size k

  L_1 = {large 1-sequence}; //result of litemset phase
  for (k = 2; L_{k-1} !=∅; k++) **do begin**
  C_k = candidates generated from L_{k-1};
  for each customer-sequence c in database do
  Increment the count of all candidates in C_k that are contained in c
  L_k =Candidates in C_k with minimum support
  end
  Answer=Maximal sequences in $\cup_k L_k$;

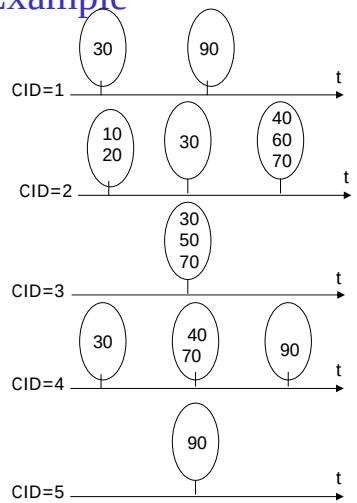
- **Candidate Generation --Join Step**:

  C_k is generated by joining $L_{k-1}$with itself
  Insert into C_k,
  Select p.litemset$_1$, …, p.litemset$_{k-1}$, q.litemset$_{k-1}$
  From L_{k-1} p, L_{k-1} q
  Where p.litemset$_1$= q.litemset$_1$,...,
  p.litemset$_{k-2}$= q.litemset$_{k-2}$

For example:
{1,2,3} X {1,2,4}
=
{1,2,3,4}
and
{1,2,4,3}

Sequence Database Example

Customer ID	TransactionTime	Items
1	1	30
1	2	90
2	1	10,20
2	2	30
2	3	40,60,70
3	1	30,50,70
4	1	30
4	2	40,70
4	3	90
5	1	90



MinSupport =40%, i.e. 2 customers

Answer: (<30><90>) (CID1,4) (<30><40,70>) (CID2,4)

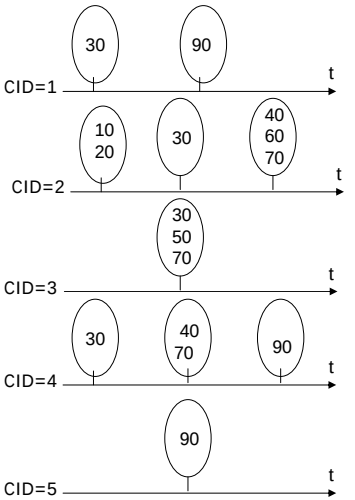
Not Answer: <30> <40><70><90>(<30><40>)(<30><70>)(<40 70>) **Why?**

Sort Phases

- **Sort Phases**

  CID: major key, TID: secondary key

Customer ID	TransactionTime	Items
1	1	30
1	2	90
2	1	10,20
2	2	30
2	3	40,60,70
3	1	30,50,70
4	1	30
4	2	40,70
4	3	90
5	1	90



Litemset Phase

- **Litemset Phase:**
  - Find all large itemset

    (Why? Because each itemset in a large sequence has to be a large itemset.)
  - To get large (frequent) itemsets → Use Apriori algorithm
  - Need to modify support counting. (For sequential patterns, support is measured by fraction of customers.)

Customer ID	TransactionTime	Items
1	1	30
1	2	90
2	1	10,20
2	2	30
2	3	40,60,70
3	1	30,50,70
4	1	30
4	2	40,70
4	3	90
5	1	90

MinSupport =40%, i.e. 2 customers

Litemset Result:

{30} {40} {70} {40 70}{90}

Difference from Apriori:

- the support count should be incremented only once per customer

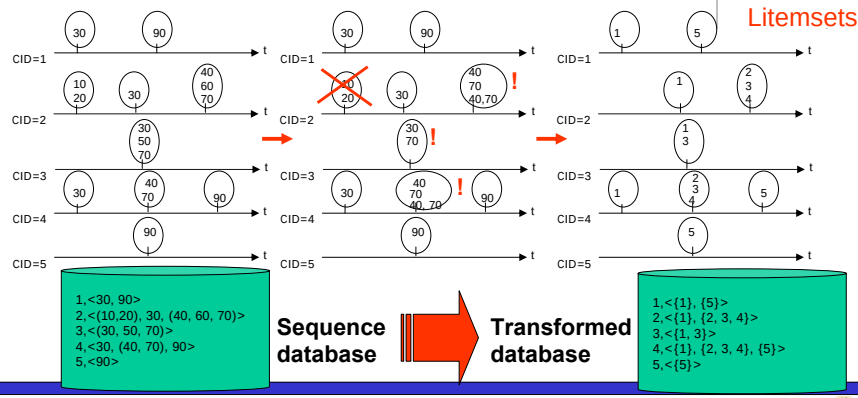
Transformation Phase

- **Transformation Phase:**
  - Each large itemset is then mapped to a set of contiguous integers

    (Why? to be able to compare two frequent itemsets in constant time)
  - Represent transactions as sets of large itemsets.

itemset	Map
{30}	1
{40}	2
{70}	3
{40 70}	4
{90}	5

Litemsets

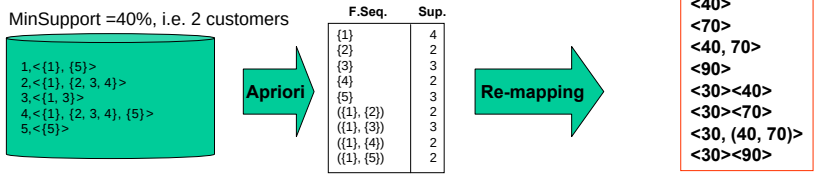


Sequence Phase

- Sequence Phase:
  - Use set of large itemsets to find the desired sequences.
  - Similar structure to Apriori algorithms used to find large itemsets.
    - Use seed set to generate candidate sequences.
    - Count support for each candidate.
    - Eliminate candidate sequences which are not large.

itemset	Map
{30}	1
{40}	2
{70}	3
{40 70}	4
{90}	5

Litemsets



Maximal phase

- **Maximum Phase:**
  - Find the maximal sequences among the set of frequent sequences

    delete all sequences that are sub-sequences of other frequent sequences.

for (k=n; k>1; k--) do
 for each k-sequence s_k do
  Delete from all subsequences of s_k

~~<30>~~
~~<40>~~
~~<70>~~
~~<40, 70>~~
~~<90>~~
~~<30><40>~~
~~<30><70>~~
<30, (40, 70)>
<30><90>

Summary for AprioriAll

- Algorithm wastes much time in counting non-maximal sequences, which can not be sequential patterns
- There are other variations of AprioriAll that reduce the candidates that are not maximals: **AprioriSome** and **DynamicSome**
- Absence of time window constraints
- *AprioriALL* is the basis of many efficient algorithm developed later. GSP is among them.

GSP—A Generalized Sequential Pattern Mining Algorithm

- 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

A Basic Property of Sequential Patterns: Apriori

- 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)>

Given *support threshold*
min_sup =2

The GSP Algorithm

- Take sequences in form of <x> as length-1 candidates
- Scan database once, find F_1, the set of length-1 sequential patterns
- Let k=1; while F_k is not empty do
  - Form C_{k+1}, the set of length-(k+1) candidates from F_k;
  - If C_{k+1} is not empty, scan database once, find F_{k+1}, the set of length-(k+1) sequential patterns
  - Let k=k+1;

Finding Length-1 Sequential Patterns

- Examine GSP using an example
- Initial candidates: all singleton sequences
  - <a>, <b>, <c>, <d>, <e>, <f>, <g>, <h>
- Scan database once, count support for candidates

min_sup =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)>

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

Generating Length-2 Candidates

36

51 length-2 Candidates

15

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

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

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

Apriori prunes 44.57% candidates

Generating Length-2 Candidates

min_sup = 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>	<b>	<c>	<d>	<e>	<f>
<a>	**<aa>:2**	**<ab>:2**	**<ac>:1**	**<ad>:1**	**<ae>:1**	**<af>:1**
<b>	<ba>	<bb>	<bc>	<bd>	<be>	<bf>
<c>	<ca>	<cb>	<cc>	<cd>	<ce>	<cf>
<d>	<da>	<db>	<dc>	<dd>	<de>	<df>
<e>	<ea>	<eb>	<ec>	<ed>	<ee>	<ef>
<f>	<fa>	<fb>	<fc>	<fd>	<fe>	<ff>

SID: 30, 50

	<a>	<b>	<c>	<d>	<e>	<f>
<a>		<(ab)>	<(ac)>	<(ad)>	<(ae)>	<(af)>
<b>			**<(bc)>:0**	**<(bd)>:2**	**<(be)>:1**	**<(bf)>:2**
<c>				<(cd)>	<(ce)>	<(cf)>
<d>					<(de)>	<(df)>
<e>						<(ef)>
<f>						

SID: 20, 30

Generating Length-2 Candidates

min_sup = 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>	<b>	<c>	<d>	<e>	<f>
<a>	**<aa>:2**	**<ab>:2**	<ac>:1	<ad>:1	<ae>:1	<af>:1
<b>	**<ba>:3**	**<bb>:4**	**<bc>:4**	**<bd>:2**	**<be>:3**	**<bf>:2**
<c>	**<ca>:2**	**<cb>:3**	<cc>:1	**<cd>:2**	<ce>:1	<cf>:1
<d>	**<da>:2**	**<db>:2**	**<dc>:2**	<dd>:0	<de>:1	<df>:0
<e>	<ea>:0	<eb>:1	<ec>:0	<ed>:1	<ee>:1	<ef>:1
<f>	<fa>:1	**<fb>:2**	<fc>:1	<fd>:0	<fe>:1	**<ff>:2**

	<a>	<b>	<c>	<d>	<e>	<f>
<a>		<(ab)>:0	<(ac)>:1	<(ad)>:1	<(ae)>:1	<(af)>:0
<b>			<(bc)>:0	**<(bd)>:2**	<(be)>:1	**<(bf)>:2**
<c>				<(cd)>:0	**<(ce)>:2**	<(cf)>:0
<d>					<(de)>:1	<(df)>:0
<e>						<(ef)>:0
<f>						

Length-2 Sequential Patterns

- After scanning the database to collect support count for each length-2 candidate
- There are 19 length-2 candidates which pass the minimum support threshold
  - They are length-2 sequential patterns
    - 16 of them in the pattern of <*xy*>
    - 3 of them in the pattern of <(*xy*)>

Generating Length-3 Candidates and Finding Length-3 Patterns

- Generate Length-3 Candidates
  - Self-join length-2 sequential patterns
    - Based on the Apriori property
    - <ab>, <aa> and <ba> are all length-2 sequential patterns → <aba> is a length-3 candidate
      - 54 candidates are generated
    - <(bd)>, <bb> and <db> are all length-2 sequential patterns → <(bd)b> is a length-3 candidate
      - 27 candidates are generated

a(bd), (bd)a, b(bd), (bd)b, (bd)c, (bd)d, (bd)e, (bd)f, c(bd), d(bd), f(bd), a(bf), (bf)a, (bf)b, b(bf), (bf)c, (bf)d, (bf)e, (bf)f, c(bf), d(bf), f(bf), b(ce), (ce)a, (ce)b, (ce)d, d(ce)

- Find Length-3 Sequential Patterns
  - Scan database once more, collect support counts for candidates
  - 19 out of 81 candidates pass support threshold

Generating Length-3 Candidates

	<a>	<b>	<c>	<d>	<e>	<f>
<a>	**<aa>:2**	**<ab>:2**	<ac>:1	<ad>:1	<ae>:1	<af>:1
<b>	**<ba>:3**	**<bb>:4**	**<bc>:4**	**<bd>:2**	**<be>:3**	**<bf>:2**
<c>	**<ca>:2**	**<cb>:3**	<cc>:1	**<cd>:2**	<ce>:1	<cf>:1
<d>	**<da>:2**	**<db>:2**	**<dc>:2**	<dd>:0	<de>:1	<df>:0
<e>	<ea>:0	<eb>:1	<ec>:0	<ed>:1	<ee>:1	<ef>:1
<f>	<fa>:1	**<fb>:2**	<fc>:1	<fd>:0	<fe>:1	**<ff>:2**

Example of generating <*xyz*> pattern for <aa>:
- Need to concatenate another Length-2 frequent itemset
- Concatenating another frequent itemsets that **start with a** to form <aaa> and <aab>

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)>

min_sup = 2

- <aaa>:0, <aab>:0
- <aba>:2, <abb>:2, <abc>:1, <abd>:1, <abe>:1, <abf>:1
- <baa>, <bab>
- <bba>, <bbb>, <bbc>, <bbd>, <bbe>, <bbf>
- <bca>, <bcb>, <bcd>
- <bda>, <bdb>, <bdc>
- <bfb>, <bff>
- <caa>, <cab>
- <cba>, <cbb>, <cbc>, <cbd>, <cbe>, <cbf>
- <cda>, <cdb>, <cdc>
- <daa>, <dab>
- <dba>, <dbb>, <dbc>, <dbd>, <dbe>, <dbf>
- <dca>, <dcb>, <dcd>
- <fba>, <fbb>, <fbc>, <fbd>, <fbe>, <fbf>
- <ffb>, <fff>

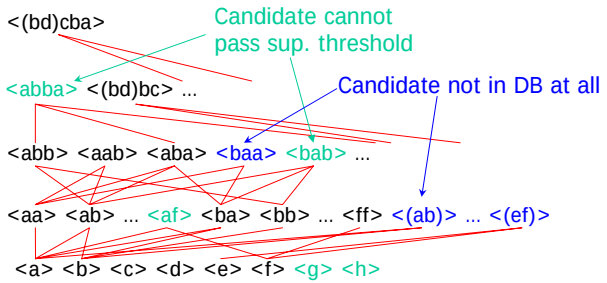
Generating Length-3 Candidates

	<a>	<b>	<c>	<d>	<e>	<f>
<a>	**<aa>:2**	**<ab>:2**	<ac>:1	<ad>:1	<ae>:1	<af>:1
<b>	**<ba>:3**	**<bb>:4**	**<bc>:4**	**<bd>:2**	**<be>:3**	**<bf>:2**
<c>	**<ca>:2**	**<cb>:3**	<cc>:1	**<cd>:2**	<ce>:1	<cf>:1
<d>	**<da>:2**	**<db>:2**	**<dc>:2**	<dd>:0	<de>:1	<df>:0
<e>	<ea>:0	<eb>:1	<ec>:0	<ed>:1	<ee>:1	<ef>:1
<f>	<fa>:1	**<fb>:2**	<fc>:1	<fd>:0	<fe>:1	**<ff>:2**

<c>	<d>	<e>	<f>
<(ac)>:1	<(ad)>:1	<(ae)>:1	<(af)>:0
<(bc)>:0	**<(bd)>:2**	<(be)>:1	**<(bf)>:2**
	<(cd)>:0	**<(ce)>:2**	<(cf)>:0
		<(de)>:1	<(df)>:0
			<(ef)>:0

Example of generating <(*xy*)*z*> pattern for <(bd)>:
- Need to concatenate another Length-2 frequent itemset
- Concatenating those patterns that **end with b or d** to form something like
  <a(bd)>, <b(bd)>, <c(bd)>, <d(bd)>, <f(bd)>
- Concatenating those patterns that **starts with b or d** to form something like
  <(bd)a>, <(bd)b>, <(bd)c>, <(bd)d>, <(bd)e>, <(bd)f>

The GSP Mining Process



min_sup = 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)>

Bottlenecks of GSP

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

Lecture Outline

Part I: Concepts *(30 minutes)*

- **Basic concepts**

Part II: Apriori-based Approaches *(45 minutes)*

- **Apriori-All**
- **GSP**

Part III: Pattern-Growth-based Approaches *(45 minutes)*

- **Free-Span** (Frequent Pattern-Projected Sequential Pattern Mining)
- **Prefix-Span** (Prefix-Projected Sequential Pattern)

FreeSpan (Generalities)

- J. Han, J. Pei, B. Mortazavi-Asl, Q. Chen, U. Dayal, and M.-C. Hsu. FreeSpan: Frequent pattern-projected sequential pattern mining. KDD'00, pages 355-359.

- A divide-and-conquer approach
  - Recursively project a sequence database into a set of smaller databases
  - Mine each projected database to find the subset of patterns

FreeSpan (example)

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

- Given a sequence database S and min_support = 2
- Step 1: find length-1 sequential patterns and list them in support descending order
  - f_list = a:4,b:4,c:4,d:3,e:3,f:3; ~~g:1~~
- Step 2: divide search space. The complete set of seq. patterns can be partitioned into 6 disjoint subsets (move down the f_list):
  - ones only contain item a
  - ones contain item b but no items after b in f_list
  - ones contain item c but no items after c in f_list
  - ones contain item d but no items after d in f_list
  - ones contain item e but no items after e in f_list
  - ones contain item f

  find subsets of sequential patterns. They can be mined by constructing projected databases and mining each recursively

FreeSpan (con't)

- Finding Seq. Patterns containing item b but no items after b in f_list
  - <b>-projected database:
    - 10:<a(ab)a>, 20:<aba>, 30:<(ab)b>, 40:<ab>
  - Find all the length-2 seq. patterns containing item b but no items after b in f_list :
    - <ab>:4, <ba>:2, <(ab)>:2
  - Further partition and mining

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

f_list = a:4,b:4, c:4,d:3,e:3,f:3

From FreeSpan to PrefixSpan

- Freespan:
  - Projection-based: No candidate sequence needs to be generated
  - But, projection can be performed at any point in the sequence, and the projected sequences may not shrink much. For example, the size of f-projected database is the same as the original sequence database
- PrefixSpan
  - Projection-based
  - But only prefix-based projection: less projections and quickly shrinking sequences

• J. Pei, J. Han, H. Pinto, Q. Chen, U. Dayal, and M.-C. Hsu, "PrefixSpan: Mining Sequential Patterns Efficiently by Prefix-Projected Pattern Growth", Proc. 2001 Int. Conf. on Data Engineering (ICDE'01), Heidelberg, Germany, April 2001.

Prefix of a Sequence

- Given two sequences $\alpha=<a_1a_2\ldots a_n>$ and $\beta=<b_1b_2\ldots b_m>$, $m\leq n$
- Sequence β is called a prefix of α if and only if:
  - $b_i = a_i$ for $i \leq m-1$;
  - $b_m \subseteq a_m$;
  - All the items in $(a_m - b_m)$ are alphabetically after those in b_m

Given an alphabetical order of items in each itemset (element)

α =<a(abc)(ac)d(cf)>

β =<a(abc)a>

β=<a>

β =<a(ab)>

~~α =<a(abc)(ac)d(cf)>~~

~~β =<a(ab)a>~~

~~β =<a(abc)c>~~

Projection

- Given sequences α and β, such that β is a subsequence of α.
- A subsequence α' of sequence α is called a projection of α w.r.t. β prefix if and only if
  - α' has prefix β;
  - There exist no proper super-sequence α'' of α' such that α'' is a subsequence of α and also has prefix β

α =<a(abc)(ac)d(cf)>

β =<(bc)a>

α' =<(bc)(ac)d(cf)>

Postfix

- Let $\alpha'=<a_1a_2\ldots a_n>$ be the projection of α w.r.t. prefix $\beta=<a_1a_2\ldots a_{m-1}a'_m>$ $(m \leq n)$
- Sequence $\gamma=<a''_m a_{m+1}\ldots a_n>$ is called the postfix of α w.r.t. prefix β, denoted as $\gamma = \alpha/\beta$, where $a''_m=(a_m-a'_m)$
- We also denote $\alpha = \beta\cdot\gamma$

α' =<a(abc)(ac)d(cf)>

β =<a(abc)a>

γ=<(_c)d(cf)>

PrefixSpan – Algorithm

- **Input**: A sequence database S, and the minimum support threshold min_sup
- **Output**: The complete set of sequential patterns
- **Method**: Call PrefixSpan(<>,0,S)
- **Subroutine** PrefixSpan(α, l, $S|_\alpha$)
- **Parameters**:
  - α: sequential pattern,
  - l: the length of α;
  - $S|_\alpha$: the α-projected database, if $\alpha \neq <>$; otherwise; the sequence database S.

PrefixSpan – Algorithm (2)

- **Method**

1. Scan $S|_\alpha$ once, find the set of frequent items b such that:
   a) b can be assembled to the last element of α to form a sequential pattern; or
   b) <b> can be appended to α to form a sequential pattern.
2. For each frequent item b, append it to α to form a sequential pattern α', and output α';
3. For each α', construct α'-projected database $S|_{\alpha'}$, and call PrefixSpan(α', l+1, $S|_{\alpha'}$).

PrefixSpan - Example

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

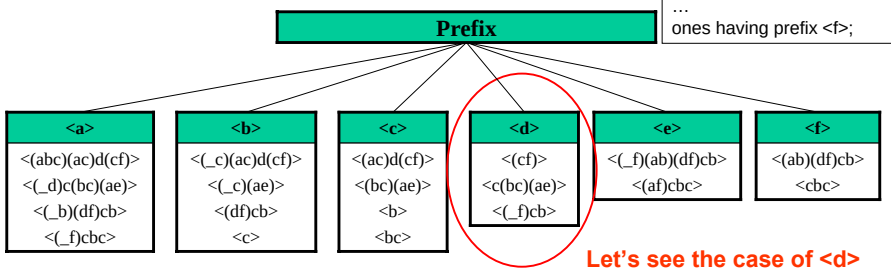
min_support = 2

1. Find length-1 sequential patterns

<a>	<b>	<c>	<d>	<e>	<f>	<g>
4	4	4	3	3	3	1

2. Divide search space

Partition search space into 6 subsets:
ones having prefix <a>;
ones having prefix <b>;
…
ones having prefix <f>;

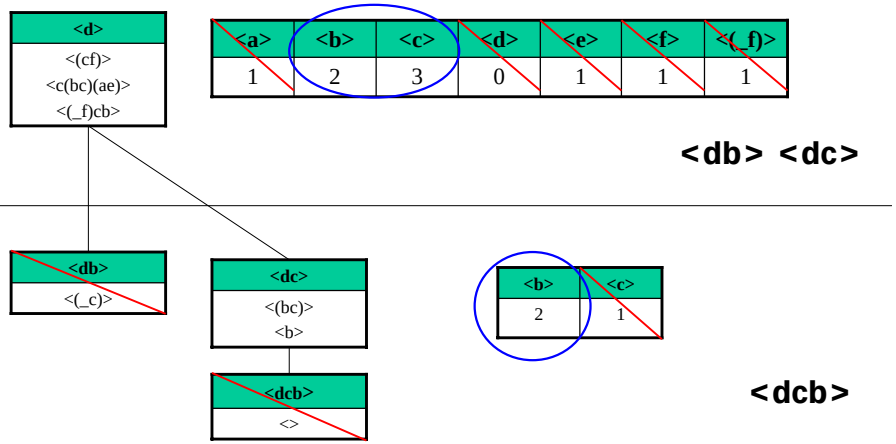


Let's see the case of <d>

PrefixSpan – Example (2)

Projected database for <d>

3. Find subsets of sequential patterns



PrefixSpan - characteristics

- No candidate sequence needs to be generated by PrefixSpan
- Projected databases keep shrinking
- The major cost of PrefixSpan is the construction of projected databases
  - ***How to reduce this cost?***

Different projection methods

- Bi-level projection
  - reduces the number and the size of projected databases
- Pseudo-Projection
  - reduces the cost of projection when projected database can be held in main memory

Bi-level Projection

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

min_support = 2

- Scan to get 1-length sequences
- Construct a triangular matrix instead of projected databases for each length-1 patterns

	a	b	c	d	e	f
a	2					
b	(4,2,2)	1				
c	(4,2,1)	(3,3,2)	3			
d	(2,1,1)	(2,2,0)	(1,3,0)	0		
e	(1,2,1)	(1,2,0)	(1,2,0)	(1,1,0)	0	
f	(2,1,1)	(2,2,0)	(1,2,1)	(1,1,1)	(2,0,1)	1

ALL length-2 sequential pattern

Support(<**ac**>) = 4
Support(<**ca**>) = 2
Support(<**(ac)**>) = 1

Support(<**cc**>) = 3

Bi-level projection (2)

- For each length-2 sequential pattern α, construct the α-projected database and find the frequent items
- Construct corresponding S-matrix

<ab>
<(_c)(ac)(cf)>
<(_c)a>
<c>

a	b	c	(_c)	d	(_d)	e	(_e)	f	(_f)
2	0	2	2	0	1	0	0	1	0

<aba> <abc> <a(bc)>

	a	c	(_c)
a	0		
c	(1,0,1)	1	
(_c)	(ϕ,2, ϕ)	(ϕ,1, ϕ)	ϕ

<a(bc)a>

Bi-level projection (3) - optimization

- "Do we need to include every item in a postfix in the projected databases?"
- NO! Item pruning in projected database by 3-way Apriori checking

<ac> is not frequent

Any super-sequence of it can never be a sequential pattern

c can be excluded from construction of <ab> - projected database

<a(bd)> is not frequent

To construct <a(bc)>-projected database, sequence <a(bcde)df> should be projected to <(_e)df> instead of <(_de)df>

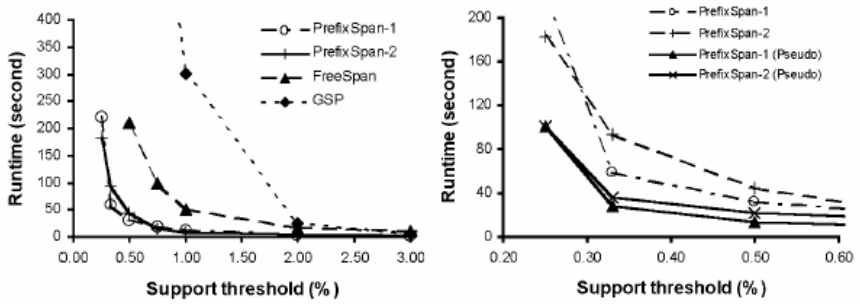
Pseudo-Projection

- **Observation**: postfixes of a sequence often appear repeatedly in recursive projected databases
- **Method**: instead of constructing *physical* projection by collecting all the postfixes, we can use pointers referring to the sequences in the database as a pseudo-projection
- Every projection consists of two pieces of information: pointer to the sequence in database and offset to the postfix in the sequence

s1=<a(abc)(ac)d(cf)>

Pointer	Offset	Postfix
s1	2	<(abc)(ac)d(cf)>
s1	5	<(ac)d(cf)>
s1	6	<(_c)d(cf)>

Efficiency of Prefix-Span and Effect of Pseudo-Projection



PrefixSpan-1 (level-by-level projection
PrefixSpan-2 (bi-level projection)

Summary

- Sequential Pattern Mining is useful in many application, e.g. weblog analysis, financial market prediction, BioInformatics, etc.
- It is similar to the frequent itemsets mining, *but* with consideration of ordering.
- We have looked at different approaches that are descendants from two popular algorithms in mining frequent itemsets
  - Candidates Generation: AprioriAll and GSP
  - Pattern Growth: FreeSpan and PrefixSpan