Lecture 3
Week 4 (March 31)

33459-01 Principles of Knowledge Discovery in Data

# Sequential Pattern Analysis

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# Course Content

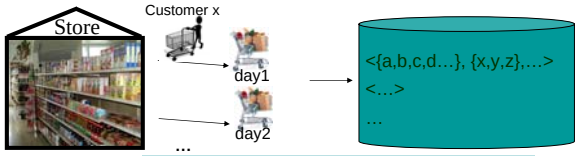
- Introduction to Data Mining
- Association analysis
- Sequential Pattern Analysis
- Classification and prediction
- Contrast Sets
- Data Clustering
- Outlier Detection
- Web Mining



# 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**

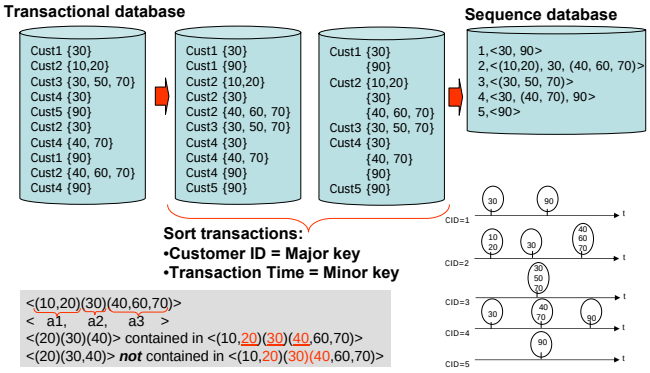


# Why **sequential pattern** mining?

- 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) c b >

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 $\alpha=<a_1 a_2 \ldots a_n>$ and $\beta=<b_1 b_2 \ldots b_m>$
- $\alpha$ is called a subsequence of $\beta$, denoted as $\alpha \subseteq \beta$, if there exist integers $1 \le j_1 < j_2 < \ldots < j_n \le m$ such that $a_1 \subseteq b_{j1}$, $a_2 \subseteq b_{j2}, \ldots, a_n \subseteq b_{jn}$
- $\beta$ is a super sequence of $\alpha$
- A sequence *s* is maximal if it is not contained in any other sequence.

$\beta$ =<a(abc)(ac)d(cf)>

$\alpha_1$=<aa(ac)d(c)>

$\alpha_2$=<(ac)(ac)d(cf)>

$\alpha_3$=<ac>

$\beta$ =<a(abc)(ac)d(cf)>

$\alpha_4$=<df(cf)>

$\alpha_5$=<(cf)d>

$\alpha_6$=<(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 $\alpha$, if $\alpha$ is a subsequence of s, i.e., $\alpha \subseteq s$
- The support of a sequence $\alpha$ is the number of tuples containing $\alpha$

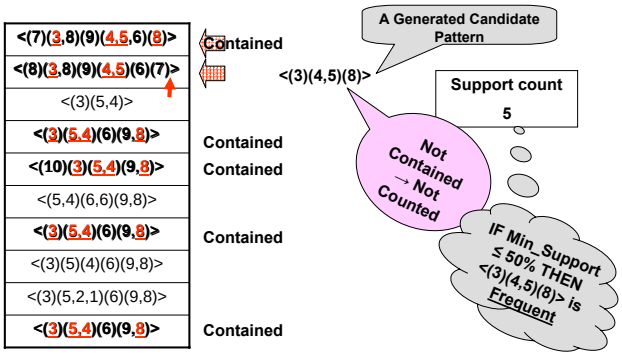
| id | Sequence |
|---|---|
| 10 | <a(abc)(ac)d(cf)> |
| 20 | <(ad)c(bc)(ae)> |
| 30 | <(ef)(ab)(df)cb> |
| 40 | <eg(af)cbc> |

$\alpha_1$=<a> support($\alpha_1$) = 4

$\alpha_2$=<ac> support($\alpha_2$) = 4

$\alpha_3$=<(ab)c> support($\alpha_3$) = 2

## Counting Sequences (An example)






## 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**:

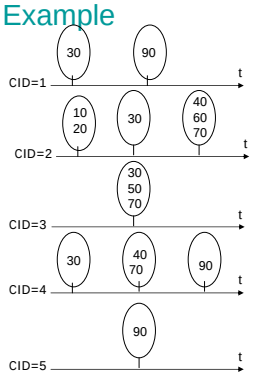
  $C_k$ is generated by joining $L_{k-1}$with itself
  Insert into $C_k$,
  Select p.litemset$_1$, …, p.litemset$_{k-1}$, q.litemset$_{k-1}$
  From $L_{k-1}$ p, $L_{k-1}$ q
  Where p.litemset$_1$= q.litemset$_1$,…,
  p.litemset$_{k-2}$= q.litemset$_{k-2}$

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?**

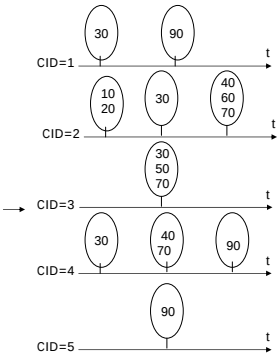


## Sort Phases

- **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

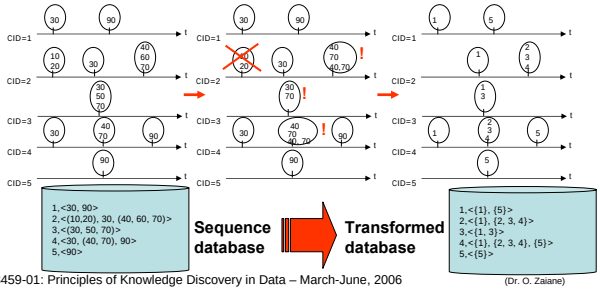


## Transformation Phase

- **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





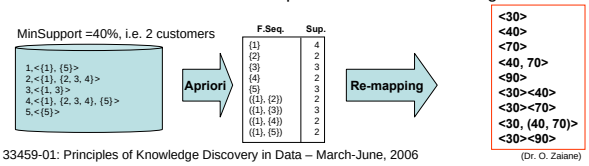

## Sequence Phase

- 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

MinSupport =40%, i.e. 2 customers



## 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 Sk do
    Delete from  all subsequences of Sk
```

~~<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 73 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

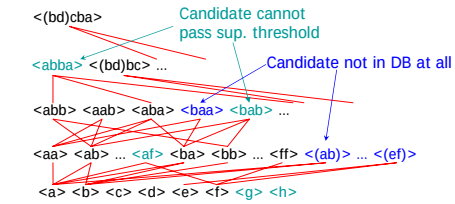
| | <a> | <b> | <c> | <d> | <e> | <f> |
|---|---|---|---|---|---|---|
| <a> | **<aa>:2** | **<ab>:2** | <ac>:1 | <ad>:1 | <ae>:1 | <af>:1 |
| <b> | **<ba>:3** | **<bb>:4** | **<bc>:4** | **<bd>:2** | **<be>:3** | **<bf>:2** |
| <c> | **<ca>:2** | **<cb>:3** | <cc>:1 | **<cd>:2** | <ce>:1 | <cf>:1 |
| <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> |
|---|---|---|---|---|
| <a> | <(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> | | | | |

**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 $\beta$ is called a prefix of $\alpha$ 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)

$\alpha$ =<a(abc)(ac)d(cf)>

$\beta$ =<a(abc)a>

$\beta$=<a>

$\beta$ =<a(ab)>

~~$\alpha$ =<a(abc)(ac)d(cf)>~~

~~$\beta$ =<a(ab)a>~~

~~$\beta$ =<a(abc)c>~~



## Projection

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

$\alpha$ =<a(abc)(ac)d(cf)>

$\beta$ =<(bc)a>

$\alpha'$ =<(bc)(ac)d(cf)>



## Postfix

- Let $\alpha' = <a_1a_2\ldots a_n>$ be the projection of $\alpha$ 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 $\alpha$ w.r.t. prefix $\beta$, denoted as $\gamma = \alpha / \beta$, where $a''_m=(a_m-a'_m)$
- We also denote $\alpha = \beta\cdot\gamma$

$\alpha'$ =<a(abc)(ac)d(cf)>

$\beta$ =<a(abc)a>

$\gamma$=<(_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($\alpha$, l, $S|_\alpha$)
- **Parameters**:
  - $\alpha$: sequential pattern,
  - l: the length of $\alpha$;
  - $S|_\alpha$: the $\alpha$-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 $\alpha$ to form a sequential pattern; or
   b) <b> can be appended to $\alpha$ to form a sequential pattern.
2. For each frequent item b, append it to $\alpha$ to form a sequential pattern $\alpha$', and output $\alpha$';
3. For each $\alpha$', construct $\alpha$'-projected database $S|_{\alpha'}$, and call PrefixSpan($\alpha$', 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> |

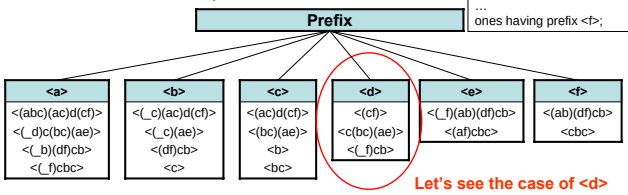
min_support = 2

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

| <d> |
|---|
| <(cf)> |
| <c(bc)(ae)> |
| <(_f)cb> |

| <a> | <b> | <c> | <d> | <e> | <f> | <(_f)> |
|---|---|---|---|---|---|---|
| 1 | 2 | 3 | 0 | 1 | 1 | 1 |

<db> <dc>

| <db> |
|---|
| <(_c)> |

| <dc> |
|---|
| <(bc)> |
| <b> |

| <b> | <c> |
|---|---|
| 2 | 1 |

<dcb>

| <dcb> |
|---|
| <> |



# 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 | 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 |
| | a | b | c | d | e | f |

**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 $\alpha$, construct the $\alpha$-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 | 0 | | |
| c | (1,0,1) | 1 | |
| (_c) | (ϕ,2, ϕ) | (ϕ,1, ϕ) | ϕ |
| | a | c | (_c) |

<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

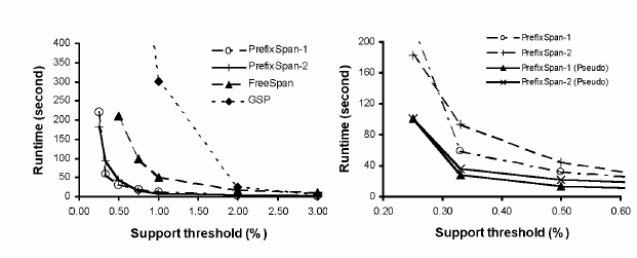
- **Observation**: postfixes of a sequence often appear repeatedly in recursive projected databases
- **Method**: instead of constructing *physical* projection by collecting all the postfixes, we can use pointers referring to the sequences in the database as a pseudo-projection
- Every projection consists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