

Part 2

Mining Patterns in Sequential Data

Sequential Pattern Mining: Definition

"Given a set of sequences, where each sequence consists of a list of elements and each element consists of a set of items, and given a userspecified min_support threshold, sequential pattern mining is to find all of the frequent subsequences, i.e., the subsequences whose occurrence frequency in the set of sequences is no less than min_support."

~ [Agrawal & Srikant, 1995]¹

"Given a set of data sequences, the problem is to discover sub-sequences that are frequent, i.e., the percentage of data sequences containing them exceeds a user-specified minimum support."

~ [Garofalakis, 1999]

Why Sequential Patterns?



Notation & Terminology

- Data:
 - Dataset: set of sequences
 - Sequence: an ordered list of *itemsets (events)* <*e*₁,...,*e*_n>
 - Itemset: an (unordered) set of items $e_i = \{i_{i1}, ..., i_{iz}\}$
- $S_{sub} = \langle s_1, ..., s_n \rangle$ is a *subsequence* of sequence $S_{ref} = \langle r_1, ..., r_n \rangle$ if:

$$\exists i_1 < \cdots < i_n : s_k \subseteq r_{i_k}$$

Example:



is subsequence

More Examples: CJUPyter

Length of a sequence: # items used in the sequence (not unique):
 Example: length (<a,(b,c),a>) = 4

Frequent Sequential Patterns

- Support sup(S) of a (sub-)sequence S in a dataset: Number of sequences in the dataset that have S as a subsequence
- Given a user chosen constant minSupport:
 Sequence S is frequent in a dataset if sup (S) ≥ minSupport
- Task: Find all frequent sequences in the dataset

 If all sequences contain exactly one event: Frequent itemset mining!

Pattern Space

- General approach: enumerate candidates and count
- Problem: "combinatorial explosion": Too many candidates



- Candidates for 100 items:
 - Length 1: 100;
 - Length 2: 100 * 100 * $\frac{100 * 99}{2} = 14,950$
 - Length 3: \sum_{i}^{100} #candidates for length $i = 2^{100} 1 \approx 10^{30}$

Monotonicity and Pruning

- If S is a subsequence of $R \rightarrow$ then sup(S) is at most as large as sup(R)
- Monotonicity: If S is not frequent, then it is impossible that R is frequent! E.g. < a > occurs only 5 times, then <a, b> can occur at most 5 times
- Pruning:

If we know that S is not frequent, we do not have to evaluate any supersequence of S!



Apriori Algorithm (for Sequential Patterns) [Agrawal & Srikant, 1995]

- Evaluate pattern "levelwise" according to their length:
 - Find frequent patterns with length 1
 - Use these to find frequent patterns with length 2
- First find frequent single items
- At each level do:
 - Generate candidates from frequent patterns of the last level
 - For each pair of candidate sequences (A, B):
 - Remove first item of A and the last item of B
 - If these are then equal: generate a new candidate by adding the last item of b at the end of a
 - E.g.: A = <a, (b,c), d>, B = <(b,c), (d,e)> → new candidate <a, (b,c), (d,e)>

- Prune the candidates (check if all subsequences are frequent)
- Check the remaining candidates by counting

Extensions based on Apriori:

- Generalized Sequential Patterns (GSP): [Srikant & Agrawal 1996]
 - Adds max/min gaps,
 - Taxonomies for items,
 - Efficiency improvements through hashing structures
- PSP: [Masseglia et al. 1998]
 Organizes candidates in a prefix tree
- Maximal Sequential Patterns using Sampling (MSPS): Sampling
 [Luo & Choung 2005]
- ...
- See Mooney / Roddick for more details [Mooney & Roddick 2013]

SPaDE: Sequential Pattern Discovery using Equivalence Classes

• Uses a vertical data representation:

SID	Time	Items	a		_	b			С		 d	
1	10	a, b, d	SID	Time		SID	Time		SID	Time	SID	Time
1	15	b, d	1	10		1	10		1	20	1	10
1	20	С	2	15		1	15		2	20	1	15
2	15	а				2	20				2	20
2	20	b, c, d				3	10				3	10
3	10	b, d										

(Original) Horizontal database layout

Vertical database layout

- ID-lists for longer candidates are constructed from shorter candidates
- Exploits equivalence classes:
 and <d> are equivalent → <b, x> and <d, x> have the same support
- Can traverse search space with depth-first or breadth-first search

Extensions based on SPaDE

- SPAM: Bitset representation [Ayres et al. 2002]
- LAPIN: [Yang & et al. 2007]
 Uses last position of items in sequence to reduce generated candidates
- LAPIN-SPAM: combines both ideas [Yang & Kitsuregawa 2005]
- IBM: [Savary & Zeitouni 2005]
 Combines several datastructures (bitsets, indices, additional tables)

PrefixSpan [Pei et al. 2001]

- Similar idea to Frequent Pattern Growth in FIM
- Determine frequent single items (e.g., a, b, c, d, e):
 - First mine all frequent sequences starting with prefix <a...>
 - Then mine all frequent sequences starting with *prefix* <b...>
- Mining all frequent sequences starting with <a...> does not require complete dataset!
- Build projected databases:

...

- Use only sequences containing a
- For each sequence containing a only use the part "after" a

Given Sequence	Projection to a
< b, (c,d), a, (b d), e >	<a, (b,d),="" e=""></a,>
<c, (a,d),="" (d,e)="" b,=""></c,>	<(a,d), b, (d,e)>
<b, (de),="" c=""></b,>	[will be removed]

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PrefixSpan (continued)

- Given prefix a and projected database for a: mine recursively!
 - Mine frequent single items in projected database (e.g., b, c, d)
 - Mine frequent sequences with prefix <a, b>
 - Mine frequent sequences with prefix <a, c>
 - ...
 - Mine frequent sequences with prefix <(a,b)>
 - Mine frequent sequences with prefix <(a,c)>



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Advantages of PrefixSpan

- Advantages compared to Apriori:
 - No explicit candidate generation, no checking of not occuring candidates
 - Projected databases keep shrinking

• Disadvantage:

⊖ Construction of projected database can be costly

So... which algorithm should you use?

- All algorithm give the same result
- Runtime / memory usage varies
- Current studies are inconclusive
- Depends on dataset characteristics:
 - Dense data tends to favor SPaDE-like algorithms
 - Sparse data tends to favor PrefixSpan and variations
- Depends on implementations



The Redundancy Problem

- The result set often contains many and many similar sequences
- Example: find frequent sequences with minSupport = 10
 - Assume <a, (bc), d> is frequent
 - Then the following sequence also MUST be frequent:

<a>, , <c>, <a, b>, <a, c>, <a, d>, <b, d>, <c, d>, <(b,c)>, <a, (b,c)>, <a, b, d>, <a, c, d>, <(b,c), d>

• Presenting all these as frequent subsequences carries little additional information!

Closed and Maximal Patterns

- Idea: Do not use all patterns, but only...
 - ... frequent *closed* sequences:
 all super-sequences have a smaller support
 - ... frequent *maximal* sequences :
 All super-sequences are not frequent
- Example:

Dataset				
<a, b,="" c,="" d,="" e,="" f=""></a,>				
<a, c,="" d=""></a,>				
<c, a="" b,=""></c,>				
<b, (de)="" a,=""></b,>				
<b, a,="" c,="" d,="" e=""></b,>				

sup (<a,c>) = 3 → frequent sup (<a,c,d>) = 3 → frequent, closed sup (<a,c,d,e>) = 2 → frequent, closed, max. sup (<a,c,d,e,f>) = 1 → not frequent

Try this example: Cjupyter

- Set of all frequent sequences can be derived from the maximal sequences
- Count of all frequent sequences can be derived from the closed sequences

Mining Closed & Maximal Patterns

- In principle: can filter resulting frequent itemsets
- Specialized algorithms
 - Apply pruning during the search process
 - Much faster than mining all frequent sequences
- Some examples
 - Closed:
 - CloSpan: PrefixTree with additional pruning [Yan et al. 2003]
 - BIDE: Memory-efficient forward/backward checking [Wang&Han 2007]
 - ClaSP: Based on SPaDE [Gomariz et al. 2013]
 - Maximal:
 - AprioriAdjust: Based on Apriori [Lu & Li 2004]
 - VMSP: Based on vertical data structures [Fournier-Viger et al. 2014]
 - MaxSP: Inpired by PrefixSpan,

maximal backward and forward extensions [Fournier-Viger et al. 2013]

• MSPX: approximate algorithm using samples [Luo & Chung 2005]

Beyond Frequency

- Frequent sequence ≠ interesting sequence
- Example for text sequences: Most frequent sequences in "Adventures from Tom Sawyer"¹:

Sequence	Support (in %)
<and, and=""></and,>	13%
<and, to=""></and,>	9.8%
<to, and<="" td=""><td>9.1%</td></to,>	9.1%
<of, and=""></of,>	8.6%

- Two options:
 - Add constraints (filter)
 - Use interestingness measures

Constraints

- Item constraints: e.g., high-utility items: Sum all items in the sequence > 1000\$
- *Length constraint*: Minimum/maximum number of events/transactions
- *Model-based constraints:* Sub-/supersequences of a given sequence
- Gap constraints: Maximum gap between events of a sequence
- *Time constraints*: Given timestamps, maximum time between events of a sequence
- Closed or maximal sequences only
- ..
- Computation:



Interestingness Measures and top-k Search

- Use interestingness measures
 - Function that assign a numeric value (score) to each sequence
 - Should reflect the "assumed interestingness" for users
 - Desired properties:
 conciseness, generality, reliability, diversity, novelty, surprisingness, applicability
- New goal: search for the *k* sequences that achieve the highest score
- Interestingness measure also implies a ranking of the result
- Simple mining approach:
 - 1. Compute all frequent patterns
 - 2. Compute the score of each pattern

Confidence

- Typical measure for association rule mining
- Can easily be adapted for sequential pattern
- Split sequence into a rule (e.g., with the last event as rule head)
- Confidence = accuracy of this rule



• Can be used as a constraint or as an interestingness measure

Leverage [Petitjean et al. 2015]

- Compare support of a sequence with "expected support":
 Score (S) = sup(S) expectedSupport (S)
- Idea of expected support?



Is also more likely to be frequent then the average 4-sequence It should be reported only, if ist frequency exceeds expectation

• Formalization for 2-sequences:

expectedSupport (< a, b >= $\frac{\sup(< a, b > + \sup < b, a > 2)}{2}$

• Formalization for larger sequences generalizes this

Other Interestingness Measures

- Information theoretic approaches: [Tatti & Vreeken 2012], [Lam et al. 2014]
 - Use minimum description length
 - Find sequence (sets) that best explain/compress the dataset
- Model-based approaches [Gwadera & Crestani 2010], [Lam et al. 2014]
 - Build a reference model (e.g., learn a markov chain model)
 - Determine which sequences are most unlikely given that model
 - (Compute statistical significance)
- Include time information
- ...

Efficient top-k Sequential Pattern Mining [Petitjean et al. 2015]

- Example Algorithm SkOPUS:
- Depth First Search
- Pruning:
 - Interestingness measures like leverage/confidence are not directly monotone (unlike support)
 E.g.: score (<a, b, c>) can be higher then score (<a, b>)
 - Use upper bounds ("optimistic estimates") oe(S)
 For each sequence S this is threshold,
 such that no super-sequence of S has a higher score
 - Has to be determined for each interestingness measure separately
 - Often easy to compute for a single interestingness measure

Case Study Web Log Mining [Soares et al. 2006]

- Portuguese web portal for business executives:
- Data: 3,000 users; 70,000 session; 1.7M accesses
- Navigation patterns found on page level:
 - Too many
 - Not very useful
- On type level ("news", "navigation")
 - More interesting findings

Mining Web logs to Improve Website Organization

[Srikant & Yang 2001]

- Given link structure of a web page, visitor log
- Build sequences for each visitor
- Define target page
- Find frequent paths to the target page
- Identify links that could shorten user paths

Available Software Libraries

- Java:
 - SPMF (most extensive library)
 <u>http://www.philippe-fournier-viger.com/spmf/</u>
 - Basic support in RapidMiner, KNIME
- R
 - arulesSequences package
 - TraMiner package
- Python
 - Multiple basic implementations
 - The implementations for this tutorial (mainly educational, not efficient)
- Spark: PrefixSpan available

What we did not talk about...

- Episode mining [Mannila et al. 1997]
 - Given long sequences: find recurring patterns
 - Mining: candidate generation vs. pattern growth
- Discriminative sequential pattern
- Incremental mining / data streams
- Pattern in time-series



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