T-61.6020 PrefixSpan

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OUTLINE

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PROBLEM

- Sequential pattern mining with subsequences as patterns.
- A sequence database <a(abc)(ac)d(cf)> <(ad)c(bc)(ae)> <(ef)(ab)(df)cb> <eg(af)cbc>
- Inside a subsequence (...) items are listed alphabetically. An item can occur at most once in an subsequence.
- Subsequence with one item is writen without brackets.

METHOD, definition

- PrefixSpan is like APriori but, uses prefix-projection method to reduce a candidate generation.
 - a_i, b_j are items.
 - α_i, β_j are itemsets.
 - α, β are sequences of itemsets.
 - $\alpha = \langle \alpha_1, \alpha_2, ..., \alpha_n \rangle$ and $\beta = \langle \beta_1, \beta_2, ..., \beta_m \rangle$.

METHOD, subsequence

• α is subsequence of β , $\alpha \subseteq \beta$ if, $\exists 1 \leq j_1 < ... < j_n \leq m$, such that $\alpha_2 \subseteq \beta_{j1}, \alpha_2 \subseteq \beta_{j2}, ..., \alpha_n \subseteq \beta_{jn}$.

$$\langle a(ab)c \subseteq a(abc)da(ac) \rangle.$$

METHOD, prefix, postfix

•
$$\pmb{lpha}=\langle \pmb{lpha}_1,\pmb{lpha}_2,...,\pmb{lpha}_n
angle$$
 and $\pmb{eta}=\langle \pmb{eta}_1,\pmb{eta}_2,...,\pmb{eta}_m
angle.$

- α is prefix of β if $\alpha_1 = \beta_1, ..., \alpha_{m-1} = \beta_{m-1}, \alpha_m \subseteq \beta_m$ and items in $\beta_m - \alpha_m$ are alphabtically after those in α_m .
- a(ab)c is prefix of a(ab)(acd)d(ab) .
- Sequence after prefix is postfix. $(_d)d(ab)$ is postfix in a(ab)(acd)d(ab) after a(ab)c.

METHOD, project

- Given $\beta \subseteq \alpha$, $\gamma \subseteq \alpha$, γ is β -project of α if β is prefix of γ and there is no longer subsequence in α so that β is its prefix.
- *c*-project of a(ab)(cd)cd(ab) is $(_d)cd(ab)$

METHOD, y-project.

- Two types of last items, y and $(_y)$.
- With *y*: $xyz... \rightarrow z...$
- With *y*: $(xyz)... \rightarrow (_z)...$
- With $(_y)$: (vyz)... $\rightarrow (_z)$...
- With $(_y)$: $(_xyz)$... $\rightarrow (_z)$...
- Where x, z can be zero, one or more items and v one or more items.

Method, next item from y-project.

- Two types of last items, y and $(_y)$.
- Every item that can be joined with y, (y)
- Items from b-project, <(_c)(abc)d(cf)> (_c),a,b,c,(_c),d,c,f
- Items from (_b)-project, <(_c)(abc)d(cf)> (_c),a,b,c,d,c,f

Method, next item from y-project.

- Two types of last items, y and $(_y)$.
- With y: $xyz \rightarrow x_i, y, z_i$ With y: $(xyz) \rightarrow x_i, y, z_i, (_z_i)$ With y: $(_xyz) \rightarrow (_x_i), (_y), (_z_i).$ with $(_y)$: $xyz \rightarrow x_i, y, z_i.$ with $(_y)$: $(xyz) \rightarrow x_i, y, z_i.$ with $(_y)$: $(_z) \rightarrow (_z_i).$
- Where x,z can be zero,one or more items.

Method, joining items.

- Do projecting and scanning recursively until items can not be scanned any more.
- Join x with every item found from x-project and sequences from next round.

$$x, y \to xy.$$

$$x, (_y) \to (xy).$$

$$(_x), y \to (_x)y.$$

$$(_x), (_y) \to (_xy).$$

EXAMPLE

- Finding sequential patterns startting with {ab}, and with support 2, from the database below.
- <a(abc)(ac)d(cf)><(ad)c(bc)(ae)><(ef)(ab)(df)cb><eg(af)cbc>

- <a(abc)(ac)d(cf)><(ad)c(bc)(ae)><(ef)(ab)(df)cb><eg(af)cbc>
- First we scan all items which have support at least 2. a,b,c,d,e,f
- a-project:
 <(abc)(ac)d(cf)>
 <(_d)c(bc)(ae)>
 <(_b)(df)cb>
 <(_f)cbc>

- a-project:
 <(abc)(ac)d(cf)>
 <(_d)c(bc)(ae)>
 <(_b)(df)cb>
 <(_f)cbc>
- Items with support at least 2: $\{a, b, c, d, f, (_b)\}$
- Items with support less than 2: {e,(_e),(_c),(_d),(_f)}
- Pruned a-project: <(abc)(ac)d(cf)> <c(bc)a> <(_b)(df)cb> <cbc>

From a-project: <(abc)(ac)d(cf)> <c(bc)a> <(_b)(df)cb> <cbc>

b-project:
 <(_c)(ac)d(cf)>
 <(_c)a>
 <</pre>

- b-project:
 <(_c)(ac)d(cf)>
 <(_c)a>
 <</pre>
- Items with support at least 2: {(_c),a,c}
- Items with support less than 2: {d,f}
- Pruned b-project:
 - <(_c)(ac)c> <(_c)a> <c>

- From b-project: <(_c)(ac)c> <(_c)a> <c>
 (_c)-project: <(ac)c>
 - <a>

- (_c)-project:
 <(ac)c>
 <a>
- Items with support at least 2: {a}
- Items with support less than 2: {c}
- Pruned (_c)-project:
 - <a>

<a>

a-project:

<>

- From b-project: <(_c)(ac)c> <(_c)a> <C>
- a-project:
 <(_c)c>

Only one sequence. We can not get anything with support 2.

c-project:

<C>

Only one sequence. We can not get anything with support 2.

EXAMPLE, items form a tree.



From the tree we get sequential patterns startting with ab:

a ab a(bc) a(bc)a aba abc

- Find from database all items which have at least support s. Add them to iList.
- call prefixSpan(Database,iList,s)
- program prefixSpan(Database,iList,s) for all items x in iList:
 - Form x-project;
 - Find supported Items;
 - Prune x-project;
 - If x-project has more than one sequence:
 - nextLewel=prefixspan(x-project,Items,s);
 - IList=join(x,Items+nextLewel);

Return IList;

SOME RESULTS, small support.

abzfghklmpqruvx abcdefghijklmnopqrstuvxyz fghijklmnopqrstuvxyz klmnopqrstuvxyz pqrstuvxyz uvxyz

Support	APriori	PrefixSpan
6	0.001 s	0.003 s
5	0.009 s	0.146 s
4	0.748 s	0.160 s
3	362 s	3.435 s
2	> 5000 s	131 s

SOME RESULTS, scalability.

Good scalability:



- PrefixSpan is faster than FreeSpan and GSP, when support value is small.
- PrefixSpan-2 use pseudo projections and is faster than prefixSpan.
- Pseudo projections: From <a(abc)(ac)d(cf)> a-project <(abc)(ac)d(cf)> ab-project <(_c)(ac)d(cf)> Has lot of redundancy.

Pei, J. Han, B. Mortazavi-Asl, H. Pinto, Q. Chen, U. Dayal and M-C. Hsu. PrefixSpan: Mining Sequential Patterns Efficiently by Prefix-Projected Pattern Growth. In Proceedings of the 17th international Conference on Data Engineering (April 02 - 06, 2001). ICDE '01. IEEE Computer Society, Washington, DC.

http://www-sal.cs.uiuc.edu/ hanj/pdf/span01.pdf