Scalable CP approach for Mining Frequent Sequence with gap constraints http://sites.uclouvain.be/cp4dm/spm/

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Abstract

Sequence mining is an important tool for analyzing large databases of timed events, such as in click stream mining. Recently, constraint programming (CP) approaches for pattern mining are gaining interest, due to the modularity of the framework and flexibility to add additional constraints. While CP systems were less scalable than specialized mining systems, we recently showed this can be overcome by hybridizing advanced CP techniques (trailing) with algorithmic improvements. In this work, we study the more involved task of mining under the restriction that the time gap between two matching events must be smaller then a threshold. We show that this too can benefit greatly from hybridization.

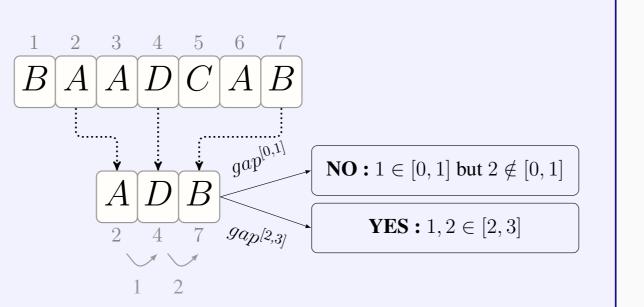
Problem of SPM under $gap^{[M,N]}$

Find all patterns $p = \langle p_1, p_2, \cdots, p_l \rangle$ such that at least θ sequences are matched by the pattern satisfying the gap constraints. A sequence $S \in SDB$ is matched by $p \text{ iff } \exists (e_1, e_2, \cdots, e_l)$ such that:

• $S[e_i] = p_i \land i \in [1 \dots l]$

• $M \le e_{i-1} - e_i - 1 \le N \land i \in [2 \dots l]$

 e_i is thus the matching position of item p_i in a sequence S.



Objective

The main objective of this project is to design new constraint in CP to improve the literature.

Sample of SDB lastPosListlastPosMapsequence $\langle ABDCB \rangle$ [(B,5),(C,4),(D,3),(A,1)] $\{A\rightarrow 1, B\rightarrow 5, C\rightarrow 4, D\rightarrow 3, E\rightarrow 0\}$ $\{A\rightarrow6, B\rightarrow7, C\rightarrow5, D\rightarrow4, E\rightarrow0\}$ $\langle BAADCAB \rangle$ [(B,7),(A,6),(C,5),(D,4)] $\langle ABDDBEC \rangle$ [(C,7),(E,6),(B,5),(D,4),(A,1)] {A \rightarrow 1, B \rightarrow 5, C \rightarrow 7,D \rightarrow 4,E \rightarrow 6} $\{A\rightarrow 1, B\rightarrow 4, C\rightarrow 3, D\rightarrow 0, E\rightarrow 0\}$ $\langle ACCB \rangle$ [(B,4),(C,3),(A,1)]

CP Model

A constraint model consists of variables, domains and constraints.

A CP model over $P = [P_1, P_2, \dots, P_L]$ (P_i is integer variables) represents the frequent sequence pattern with threshold θ , iff the following three conditions are satisfied by every valid assignment to P:

1. $P_1 \neq \epsilon$ (ϵ represents empty character and the end of pattern)

 $2. \forall i \in \{2, \dots, L-1\} : P_i = \epsilon \Rightarrow P_{i+1} = \epsilon$

3. $\#\{(sid, s) \in SDB \ \langle P_1 \dots P_j \rangle \leq s\} \geq \theta, j = \max(\{i \in \{1 \dots L\} | P_i \neq 0\}).$

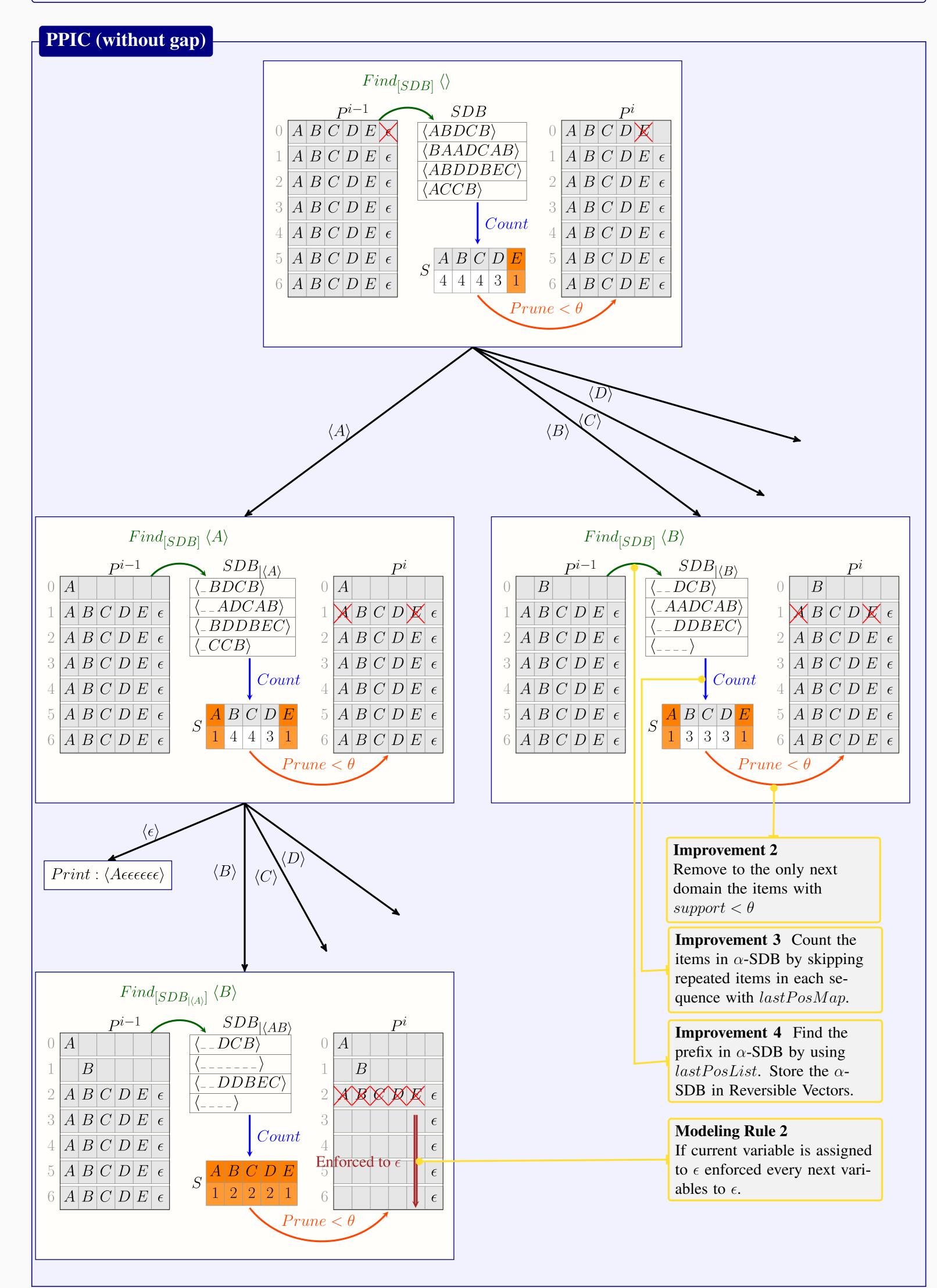
Related Work

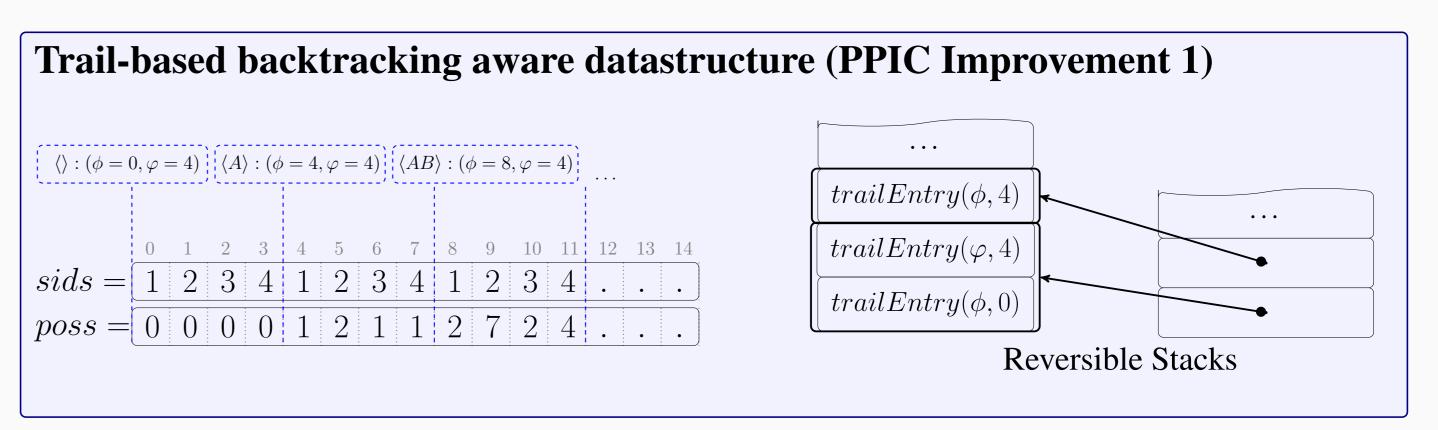
Specialised Methods:

- PrefixSpan [6] : prefix and prefixprojection method with DFS;
- cspade [8] : vertical database with join rules in DFS/BFS;
- LAPIN-SPAM [7] : idea of last position of items;

CP-based Methods:

- CPSM [4] : one constraint per sequence + reified constraints;
- PP and GapSeq [3, 2] : global constraint with filtering inspired of prefixSpan method + maximal gap constraint;
- PPIC [1] : last position of items applied in prefix-projection and Trail-based backtracking aware datastructure.





PPICgap with gap challenge

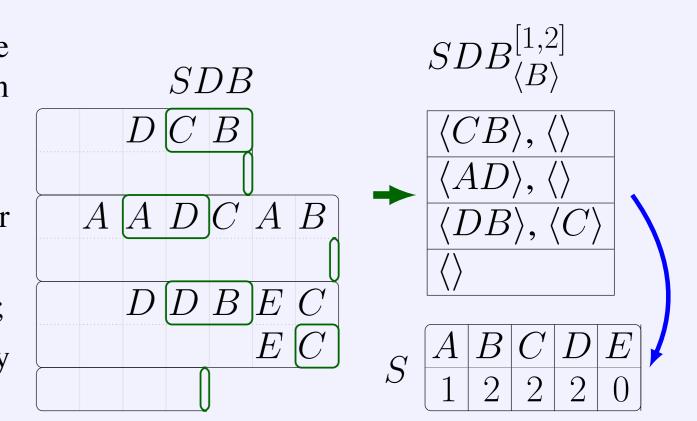
A $qap^{[M,N]}$ constraint changes when a subsequence is included in a sequence, namely iff the gap between two subsequent symbols $\geq M$ and $\leq N$.

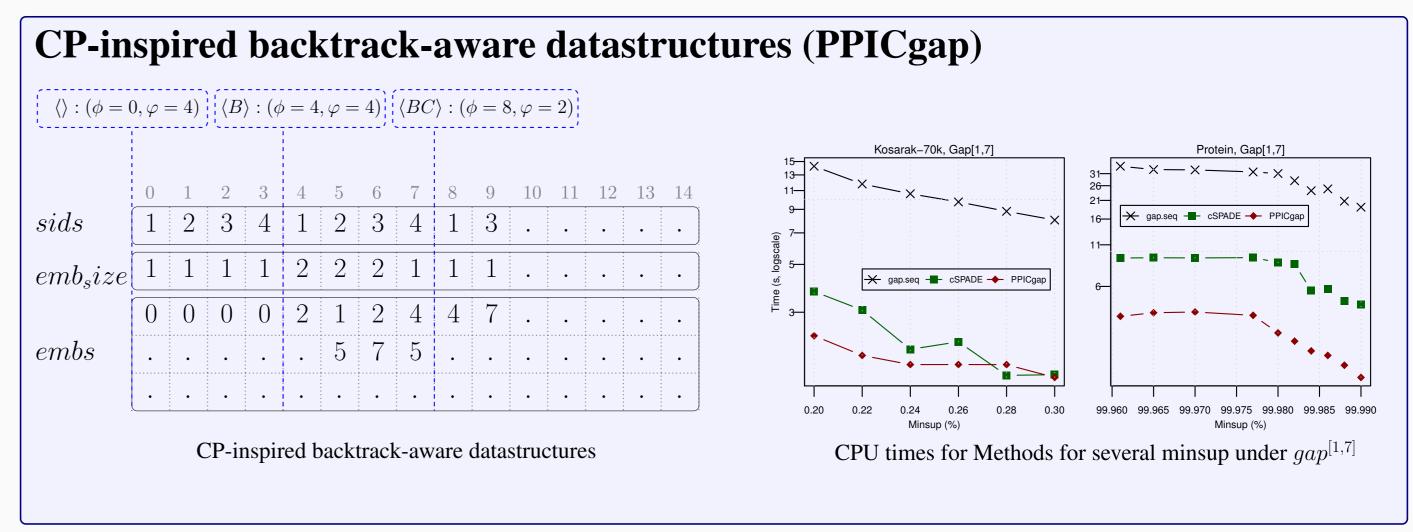
PPICgap compared to PPIC

1. Projected database, keep all possible suffixes for each prefix;

2. Trail-Based backtracking aware datastructure;

3. **Pruning** is based on prefix-antimonotonicity property.





Implementation is done in Scala with OscaR Solver [5].

References

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