CSE 5243 INTRO. TO DATA MINING

Advanced Frequent Pattern Mining
&
Locality Sensitive Hashing

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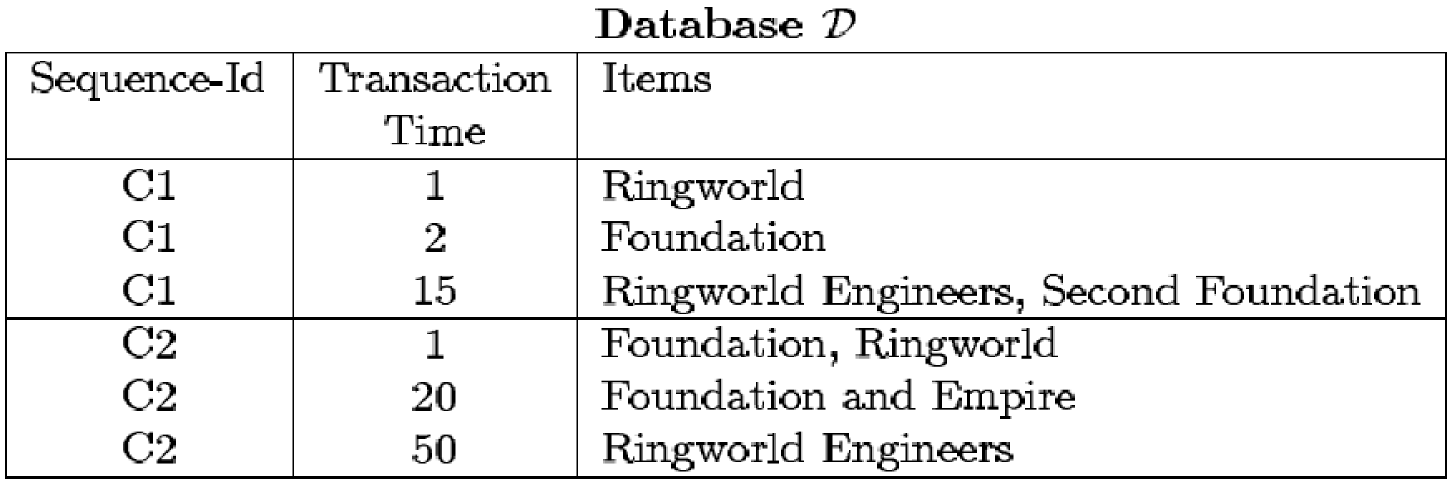
Slides adapted from Prof. Jiawei Han @UIUC, Prof. Srinivasan Parthasarathy @OSU

Sequence Mining: Description

- Input
  - A database ***D*** of sequences called *data-sequences,* in which:
    - $I=\{i_1, i_2,\ldots,i_n\}$ is the set of items
    - each sequence is a list of transactions ordered by transaction-time
    - each transaction consists of fields: sequence-id, transaction-id, transaction-time and a set of items.



Database $\mathcal{D}$

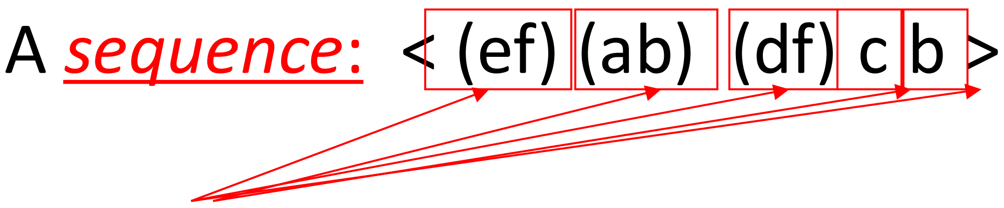
Sequence-Id	Transaction Time	Items
C1	1	Ringworld
C1	2	Foundation
C1	15	Ringworld Engineers, Second Foundation
C2	1	Foundation, Ringworld
C2	20	Foundation and Empire
C2	50	Ringworld Engineers

Sequential Pattern and Sequential Pattern Mining

- Sequential pattern mining: Given a set of sequences, find the complete set of *frequent* subsequences (i.e., satisfying the min_sup threshold)

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>



A *sequence*: < (ef) (ab) (df) c b >

- An element may contain a set of *items* (also called *events*)
- Items within an element are unordered and we list them alphabetically

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

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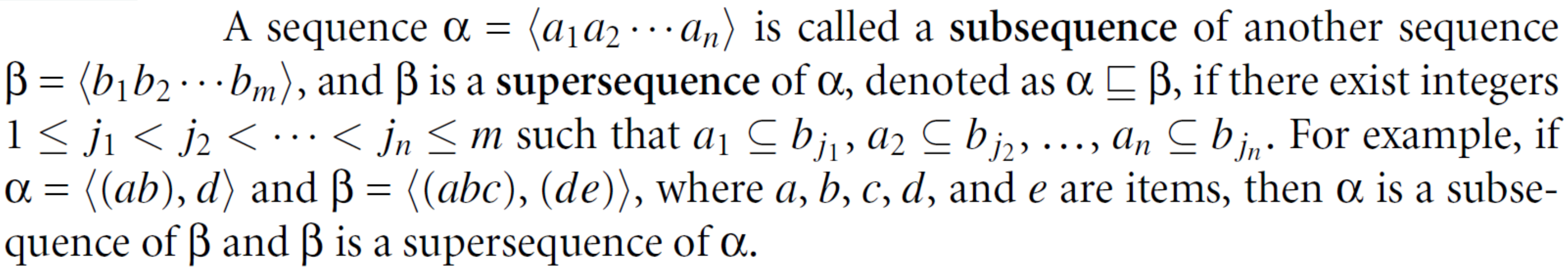
Formal definition:



A sequence $\alpha = \langle a_1 a_2 \cdots a_n \rangle$ is called a **subsequence** of another sequence $\beta = \langle b_1 b_2 \cdots b_m \rangle$, and β is a **supersequence** of α, denoted as $\alpha \sqsubseteq \beta$, if there exist integers $1 \leq j_1 < j_2 < \cdots < j_n \leq m$ such that $a_1 \subseteq b_{j_1}$, $a_2 \subseteq b_{j_2}$, $\ldots$, $a_n \subseteq b_{j_n}$. For example, if $\alpha = \langle (ab), d \rangle$ and $\beta = \langle (abc), (de) \rangle$, where a, b, c, d, and e are items, then α is a subsequence of β and β is a supersequence of α.

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- An element may contain a set of *items* (also called *events*)
- 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*

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>

GSP (Generalized Sequential Patterns): Apriori-Based Sequential Pattern Mining

GSP (Generalized Sequential Patterns): Srikant & Agrawal @ EDBT'96)

SID	Sequence
10	<(bd)cb(ac)>
20	<(bf)(ce)b(fg)>
30	<(ah)(bf)abf>
40	<(be)(ce)d>
50	<a(bd)bcb(ade)>

- Initial candidates: All 8-singleton sequences
  - <a>, <b>, <c>, <d>, <e>, <f>, <g>, <h>
- Scan DB once, count support for each candidate

min_sup = 2

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

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	<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>

Why?

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<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>						

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<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 pruning:

  (8 singletons) 8*8+8*7/2 = 92 length-2 candidates
- With pruning, length-2 candidates: 36 + 15= 51

GSP Mining and Pruning

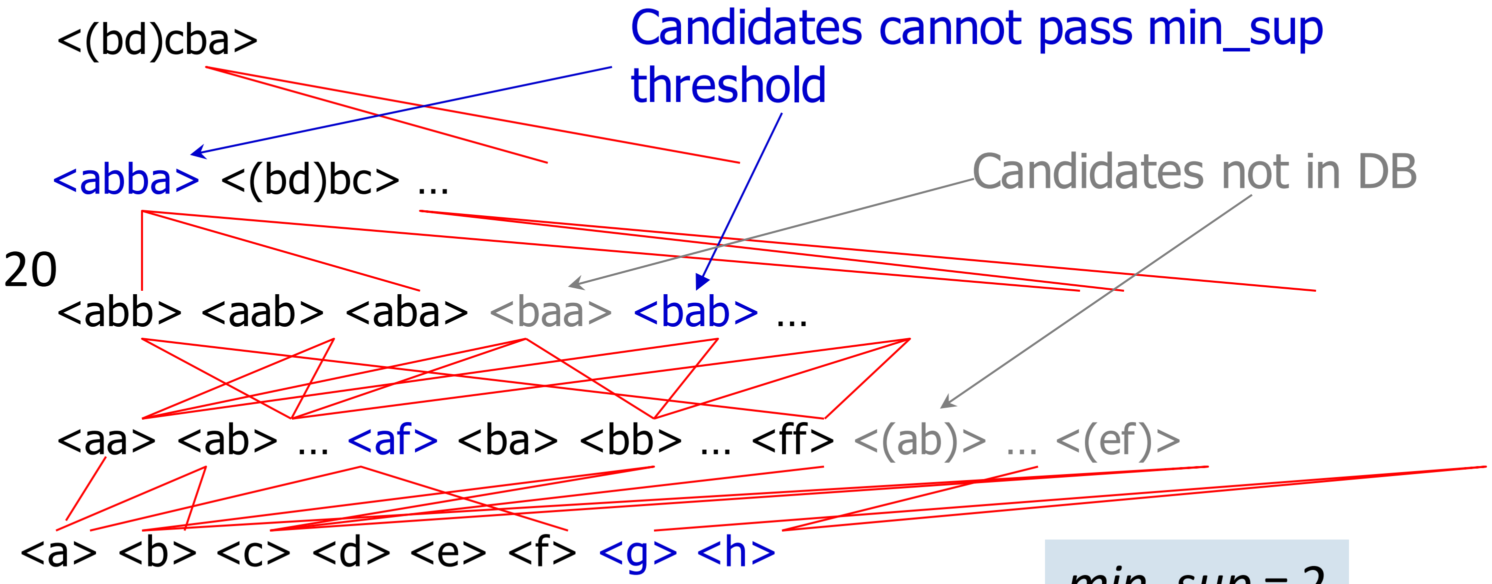
5th scan: 1 cand. 1 length-5 seq. pat.

4th scan: 8 cand. 7 length-4 seq. pat.

3rd scan: 46 cand. 20 length-3 seq. pat. 20 cand. not in DB at all

2nd scan: 51 cand. 19 length-2 seq. pat. 10 cand. not in DB at all

1st scan: 8 cand. 6 length-1 seq. pat.



<(bd)cba>

<abba> <(bd)bc> …

<abb> <aab> <aba> <baa> <bab> …

<aa> <ab> … <af> <ba> <bb> … <ff> <(ab)> … <(ef)>

<a> <b> <c> <d> <e> <f> <g> <h>

Candidates cannot pass min_sup threshold

Candidates not in DB

min_sup = 2

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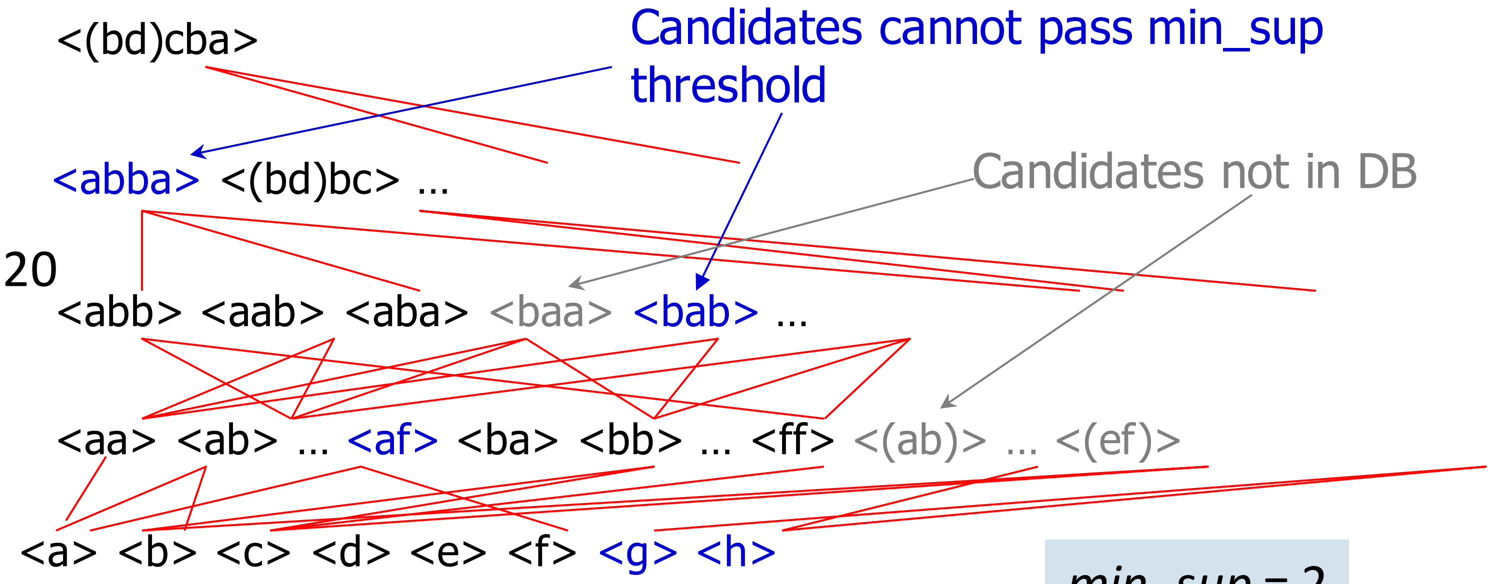

<(bd)cba>

<abba> <(bd)bc> …

<abb> <aab> <aba> <baa> <bab> …

<aa> <ab> … <af> <ba> <bb> … <ff> <(ab)> … <(ef)>

<a> <b> <c> <d> <e> <f> <g> <h>

Candidates cannot pass min_sup threshold

Candidates not in DB

- Repeat (for each level (i.e., length-k))
  - Scan DB to find length-k frequent sequences
  - Generate length-(k+1) candidate sequences from length-k frequent sequences using Apriori
  - set k = k+1
- Until no frequent sequence or no candidate can be found

min_sup = 2

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10	<(bd)cb(ac)>
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Mining Sequential Patterns: Generalizations and Performance Improvements, Srikant and Agrawal et al.
https://pdfs.semanticscholar.org/d420/ea39dc136b9e390d05e964488a65fcf6ad33.pdf

GSP: Algorithm

- **Phase 1:**
  - Scan over the database to identify all the frequent items, i.e., 1-element sequences

- **Phase 2:**
  - Iteratively scan over the database to discover all frequent sequences. Each iteration discovers all the sequences with the same length.
  - In the iteration to generate all *k*-sequences
  - Generate the set of all candidate *k*-sequences, $\mathbf{C}_k$, by joining two (*k-1*)-sequences
    - Prune the candidate sequence if any of its *k-1* subsequences is not frequent
    - Scan over the database to determine the support of the remaining candidate sequences
  - Terminate when no more frequent sequences can be found

A detailed example illustration:

http://simpledatamining.blogspot.com/2015/03/generalized-sequential-pattern-gsp.html

Bottlenecks of GSP

- A huge set of candidates could be generated
  - 1,000 frequent length-1 sequences generate length-2 candidates!

$$1000 \times 1000 + \frac{1000 \times 999}{2} = 1{,}499{,}500$$

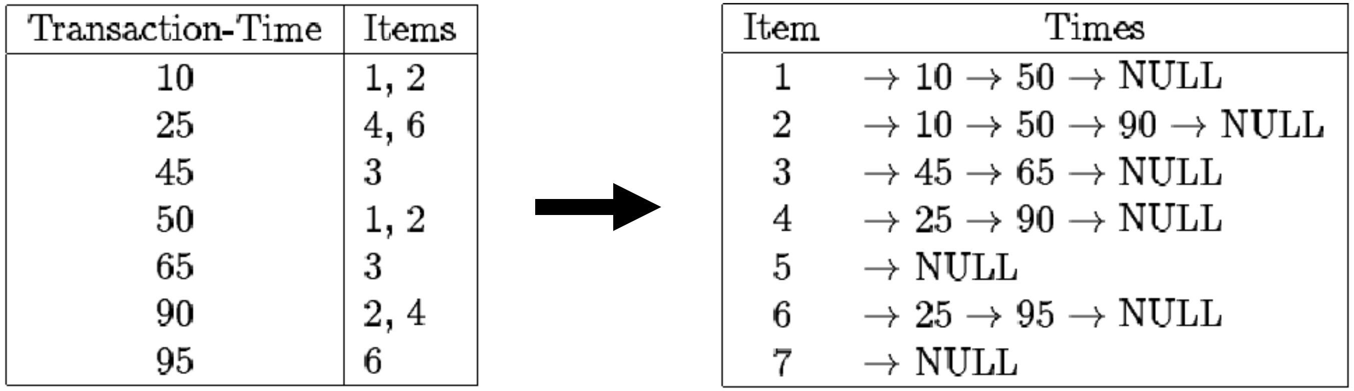
- Multiple scans of database in mining

- Real challenge: mining long sequential patterns
  - An exponential number of short candidates
  - A length-100 sequential pattern needs 10^{30} candidate sequences!

$$\sum_{i=1}^{100} \binom{100}{i} = 2^{100} - 1 \approx 10^{30}$$

GSP: Optimization Techniques

- Applied to phase 2: computation-intensive
- Technique 1: the hash-tree data structure
  - Used for counting candidates to reduce the number of candidates that need to be checked
    - Leaf: a list of sequences
    - Interior node: a hash table
- Technique 2: data-representation transformation
  - From horizontal format to vertical format



Transaction-Time	Items
10	1, 2
25	4, 6
45	3
50	1, 2
65	3
90	2, 4
95	6

Item	Times
1	→ 10 → 50 → NULL
2	→ 10 → 50 → 90 → NULL
3	→ 45 → 65 → NULL
4	→ 25 → 90 → NULL
5	→ NULL
6	→ 25 → 95 → NULL
7	→ NULL

SPADE

- **Problems in the GSP Algorithm**
  - Multiple database scans
  - Complex hash structures with poor locality
  - Scale up linearly as the size of dataset increases

- **SPADE: Sequential PAttern Discovery using Equivalence classes**
  - Use a vertical id-list database
  - Prefix-based equivalence classes
  - Frequent sequences enumerated through simple temporal joins
  - Lattice-theoretic approach to decompose search space

- **Advantages of SPADE**
  - 3 scans over the database
  - Potential for in-memory computation and parallelization

Paper Link:
http://citeseerx.ist.psu.edu/viewdoc/download?doi=10.1.1.113.6042&rep=rep1&type=pdf

MMDS Secs. 3.2-3.4.

Slides adapted from: J. Leskovec, A. Rajaraman, J. Ullman: Mining of Massive Datasets, http://www.mmds.org

FINDING SIMILAR ITEMS

Slides also adapted from Prof. Srinivasan Parthasarathy @OSU

Task: Finding Similar Documents

- **Goal: Given a large number (N in the millions or billions) of documents, find "near duplicate" pairs**
- **Applications:**
  - Mirror websites, or approximate mirrors → remove duplicates
  - Similar news articles at many news sites → cluster

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What are the challenges?

Task: Finding Similar Documents

- **Goal: Given a large number (N in the millions or billions) of documents, find "near duplicate" pairs**
- **Applications:**
  - Mirror websites, or approximate mirrors → remove duplicates
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- **Problems:**
  - Many small pieces of one document can appear out of order in another
  - Too many documents to compare all pairs
  - Documents are so large or so many (scale issues)

Two Essential Steps for Similar Docs

1. ***Shingling:*** Convert documents to sets

2. ***Min-Hashing:*** Convert large sets to short signatures, while preserving similarity

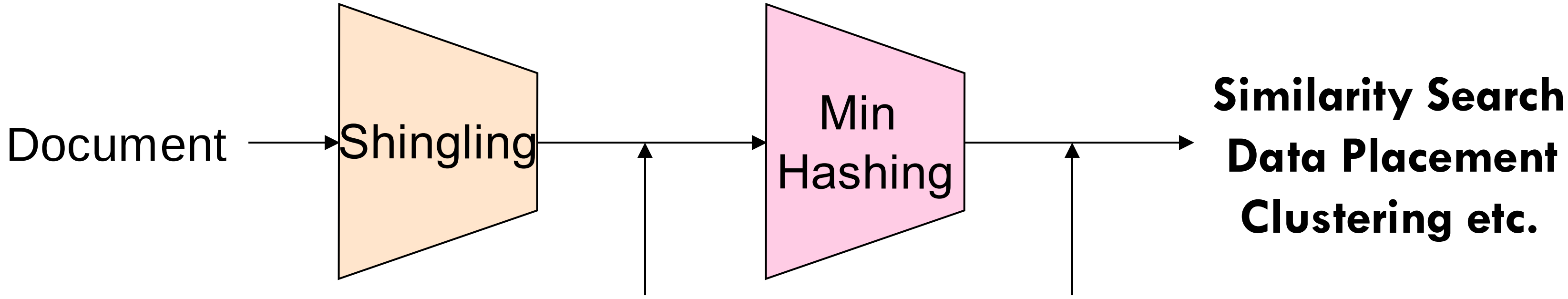
Host of follow up applications

e.g. Similarity Search

Data Placement

Clustering etc.

The Big Picture



Document

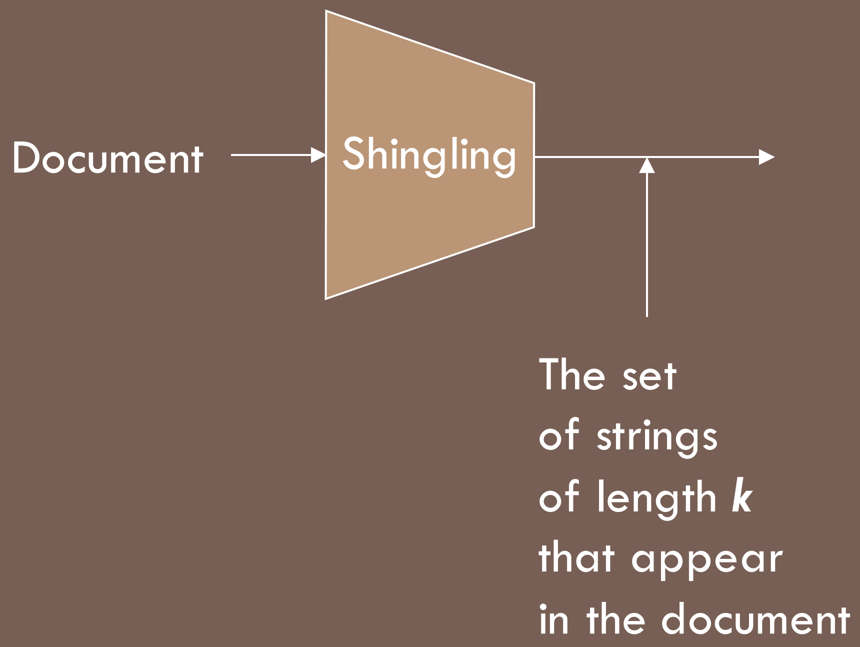
Shingling

Min Hashing

Similarity Search
Data Placement
Clustering etc.

The set of strings of length ***k*** that appear in the document

Signatures: short integer vectors that represent the sets, and reflect their similarity



Document

Shingling

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SHINGLING

Step 1: ***Shingling:*** Convert documents to sets

Documents as High-Dim Data

- **Step 1: *Shingling:* Convert documents to sets**

- **Simple approaches:**
  - Document = set of words appearing in document
  - Document = set of "important" words
  - Don't work well for this application. Why?

- **Need to account for ordering of words!**
- A different way: **Shingles!**

Define: Shingles

- A *k*-shingle (or *k*-gram) for a document is a sequence of *k* tokens that appears in the doc
  - Tokens can be characters, words or something else, depending on the application
  - Assume tokens = characters for examples

Define: Shingles

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- **Example:** **k=2**; document $\mathbf{D_1}$ = abcab
  Set of 2-shingles: $\mathbf{S(D_1)}$ = {ab, bc, ca}

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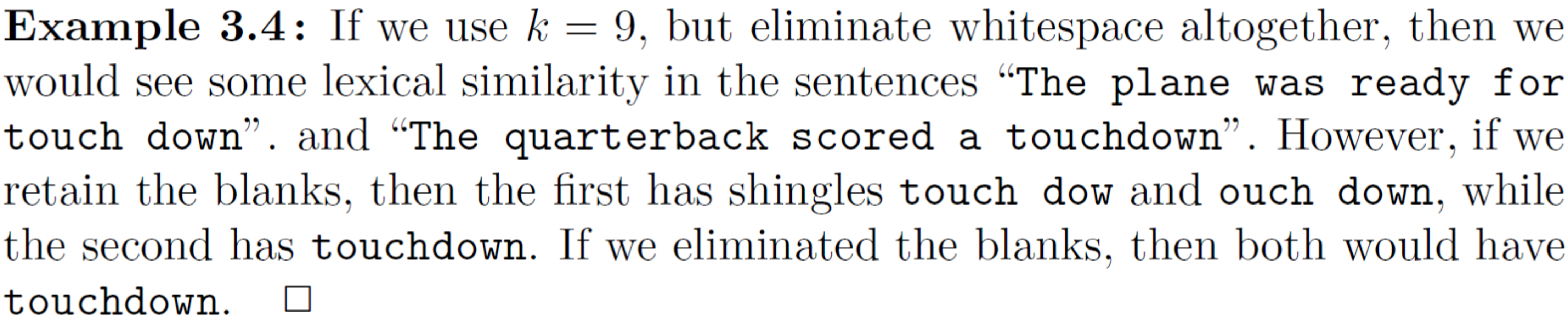
- **Example:** **k=2**; document **D_1** = abcab
  Set of 2-shingles: **$S(D_1)$** = {ab, bc, ca}

  - **Another option:** Shingles as a **bag** (multiset), count ab twice: **$S'(D_1)$ =** {ab, bc, ca, ab}

Shingles: How to treat white-space chars?



Example 3.4: If we use $k = 9$, but eliminate whitespace altogether, then we would see some lexical similarity in the sentences “`The plane was ready for touch down`”. and “`The quarterback scored a touchdown`”. However, if we retain the blanks, then the first has shingles `touch dow` and `ouch down`, while the second has `touchdown`. If we eliminated the blanks, then both would have `touchdown`. □

It makes sense to replace any sequence of one or more white-space characters (blank, tab, newline, etc.) by a single blank.

This way distinguishes shingles that cover two or more words from those that do not.

How to choose K?

- **Documents that have lots of shingles in common have similar text, even if the text appears in different order**

- **Caveat:** You must pick ***k*** large enough, or most documents will have most shingles
  - $\boldsymbol{k}$ = 5 is OK for short documents
  - $\boldsymbol{k}$ = 10 is better for long documents

Compressing Shingles

- To **compress long shingles**, we can **hash** them to (say) 4 bytes
  - Like a Code Book
  - If #shingles manageable → Simple dictionary suffices

e.g., 9-shingle => bucket number [0, 2^32 - 1]

(using 4 bytes instead of 9)

Compressing Shingles

- To **compress long shingles**, we can **hash** them to (say) 4 bytes
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- **Doc represented by the set of hash/dict. values of its *k*-shingles**
  - **Idea:** Two documents could appear to have shingles in common, when the hash-values were shared

Compressing Shingles

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- **Doc represented by the set of hash/dict. values of its *k*-shingles**

- **Example:** **k=2**; document **D_1** = abcab
  Set of 2-shingles: **$S(D_1)$** = {ab, bc, ca}
  Hash the singles: **$h(D_1)$** = {1, 5, 7}

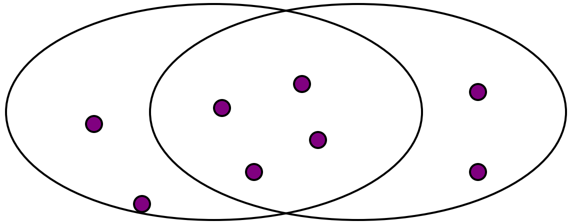
Similarity Metric for Shingles

- **Document D_1 is a set of its k-shingles $C_1=S(D_1)$**

- Equivalently, each document is a 0/1 vector in the space of *k*-shingles
  - Each unique shingle is a dimension
  - Vectors are very sparse

- **A natural similarity measure is the Jaccard similarity:**

$$sim(D_1, D_2) = |C_1 \cap C_2| / |C_1 \cup C_2|$$



Motivation for Minhash/LSH

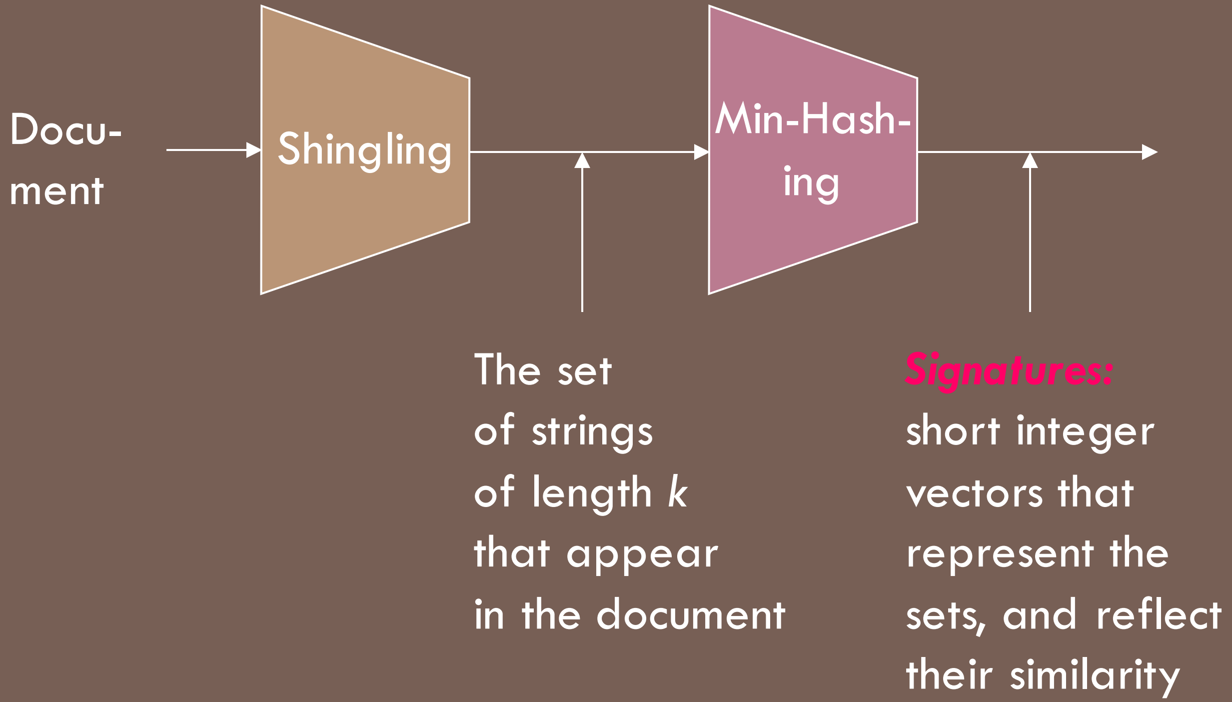
- **Suppose we need to find similar documents among $N = 1$ million documents**

- Naïvely, we would have to compute **pairwise Jaccard similarities** for **every pair of docs**

  - $N(N-1)/2 \approx$ **5*10^{11}** comparisons
  - At 10^5 secs/day and 10^6 comparisons/sec, it would take **5 days**

- For $N = 10$ million, it takes more than a year…

MINHASHING



Docu-ment

Shingling

Min-Hash-ing

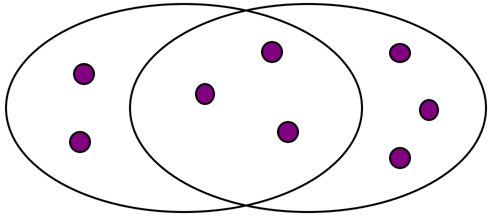
The set
of strings
of length *k*
that appear
in the document

Signatures:
short integer
vectors that
represent the
sets, and reflect
their similarity

Step 2: ***Minhashing:*** Convert **large variable length sets** to **short fixed-length signatures**, while **preserving similarity**

Encoding Sets as Bit Vectors

- Many similarity problems can be formalized as **finding subsets that have significant intersection**



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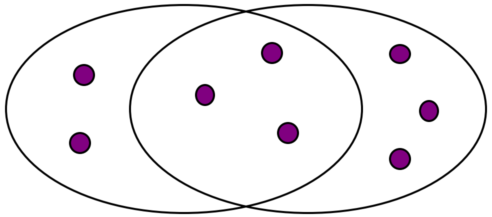

- **Encode sets using 0/1 (bit, boolean) vectors**
  - One dimension per element in the universal set
- Interpret set intersection as bitwise **AND**, and set union as bitwise **OR**

Encoding Sets as Bit Vectors

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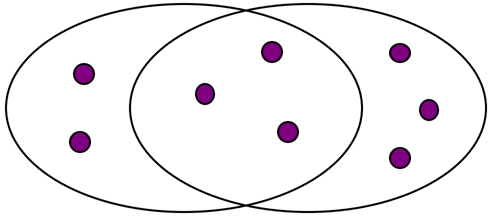

- **Encode sets using 0/1 (bit, boolean) vectors**
  - One dimension per element in the universal set
- Interpret set intersection as bitwise **AND**, and set union as bitwise **OR**
- **Example: C_1** = 10111; **C_2** = 10011
  - Size of intersection **= 3**; size of union **= 4,**
  - **Jaccard similarity** (not distance) **= 3/4**
  - **Distance: $d(C_1,C_2)$ = 1 – (Jaccard similarity) = 1/4**

From Sets to Boolean Matrices

Note: Transposed Document Matrix

- **Rows** = elements (shingles)
- **Columns** = sets (documents)
  - 1 in row **e** and column *s* if and only if **e** is a valid shingle of document represented by s
  - Column similarity is the Jaccard similarity of the corresponding sets (rows with value *1*)
  - **Typical matrix is sparse!**

	Documents			
Shingles	1	1	1	0
	1	1	0	1
	0	1	0	1
	0	0	0	1
	1	0	0	1
	1	1	1	0
	1	0	1	0

Outline: Finding Similar Columns

- **So far:**
  - A documents → a set of shingles
  - Represent a set as a boolean vector in a matrix

$$\begin{array}{c|cccc}
 & \multicolumn{4}{c}{\text{Documents}} \\
\hline
\text{Shingles} & 1 & 1 & 1 & 0 \\
 & 1 & 1 & 0 & 1 \\
 & 0 & 1 & 0 & 1 \\
 & 0 & 0 & 0 & 1 \\
 & 1 & 0 & 0 & 1 \\
 & 1 & 1 & 1 & 0 \\
 & 1 & 0 & 1 & 0
\end{array}$$

Outline: Finding Similar Columns

- **So far:**
  - A documents → a set of shingles
  - Represent a set as a boolean vector in a matrix

- **Next goal: Find similar columns while computing small signatures**
  - **Similarity of columns == similarity of signatures**

Documents

Shingles

1	1	1	0
1	1	0	1
0	1	0	1
0	0	0	1
1	0	0	1
1	1	1	0
1	0	1	0

Outline: Finding Similar Columns

- **Next Goal: Find similar columns, Small signatures**

- **Naïve approach:**
  - **1) Signatures of columns:** small summaries of columns

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Hashing Columns (Signatures) : LSH principle

- **Key idea:** "hash" each column **C** to a small ***signature*** ***h(C)***, such that:
  - (1) ***h(C)*** is small enough that the signature fits in RAM
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J. Leskovec, A. Rajaraman, J. Ullman: Mining of Massive Datasets, http://www.mmds.org

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Min-Hashing

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- **There is a suitable hash function for the Jaccard similarity:** It is called **Min-Hashing**

Min-Hashing

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Zoo example (shingle size k=1)

Universe $\longrightarrow$ { dog, cat, lion, tiger, mouse}

π_1 $\longrightarrow$ [cat, mouse, lion, dog, tiger]

π_2 $\longrightarrow$ [lion, cat, mouse, dog, tiger]

A = { mouse, lion }

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$mh_1(A) = \min(\pi_1\{\text{mouse, lion}\}) = \text{mouse}$

$mh_2(A) = \min(\pi_2\{\text{mouse, lion}\}) = \text{lion}$

Min-Hashing Example

Permutation π

2
3
7
6
1
5
4

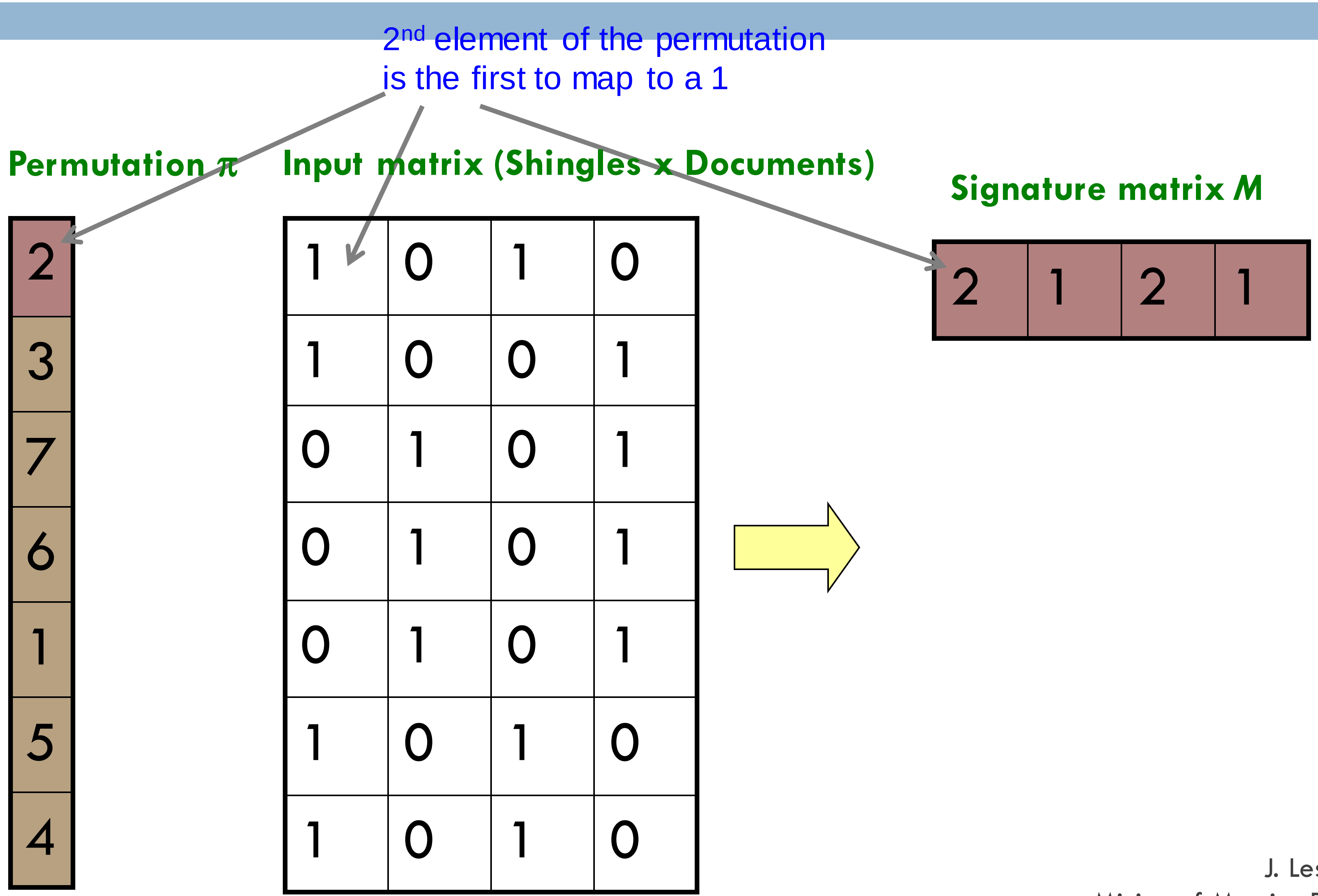
Input matrix (Shingles x Documents)

1	0	1	0
1	0	0	1
0	1	0	1
0	1	0	1
0	1	0	1
1	0	1	0
1	0	1	0

Signature matrix *M*

2	1	2	1

Min-Hashing Example



2nd element of the permutation is the first to map to a 1

Permutation π

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3
7
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5
4

Input matrix (Shingles x Documents)

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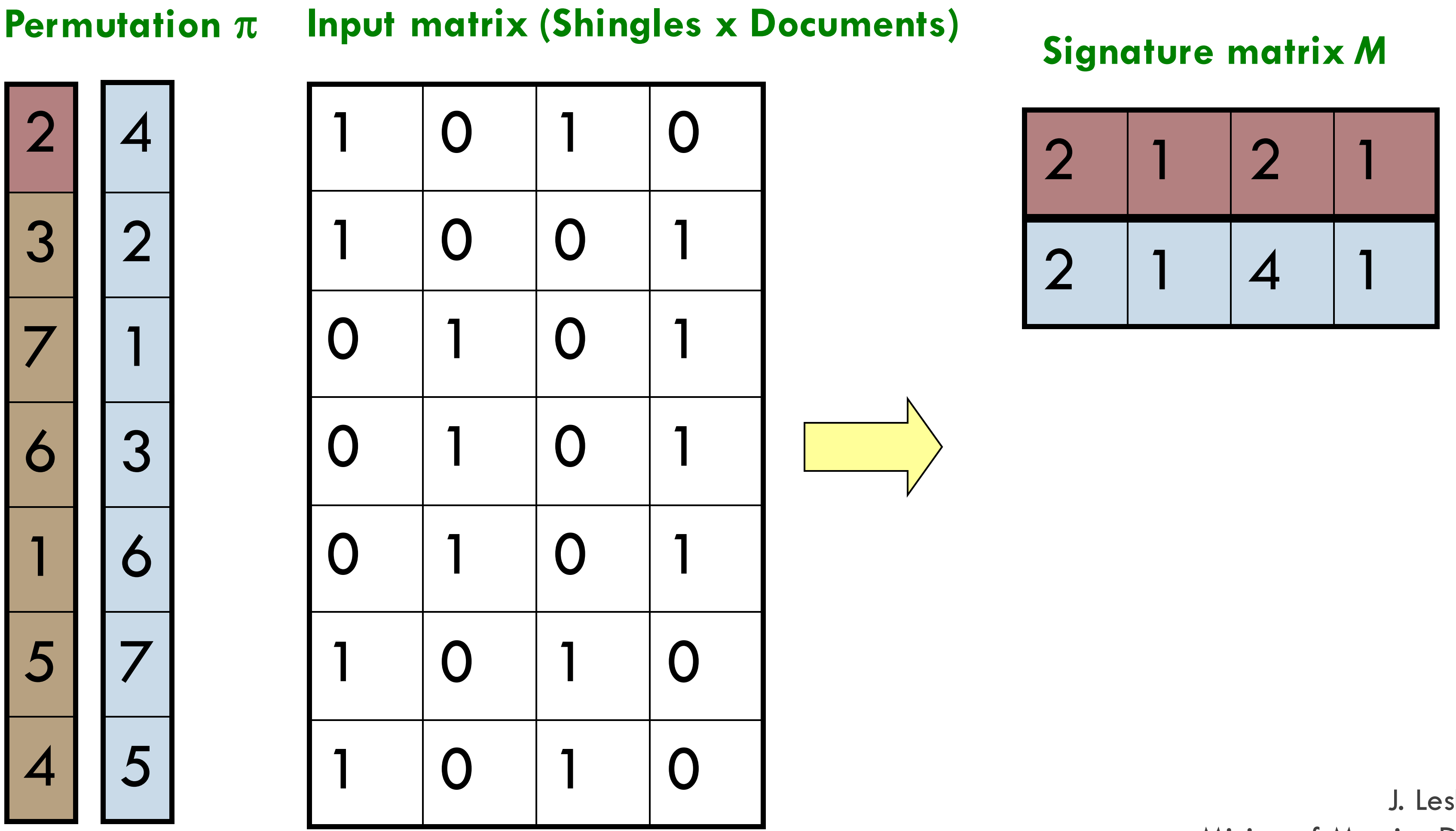


Permutation π

2	4
3	2
7	1
6	3
1	6
5	7
4	5

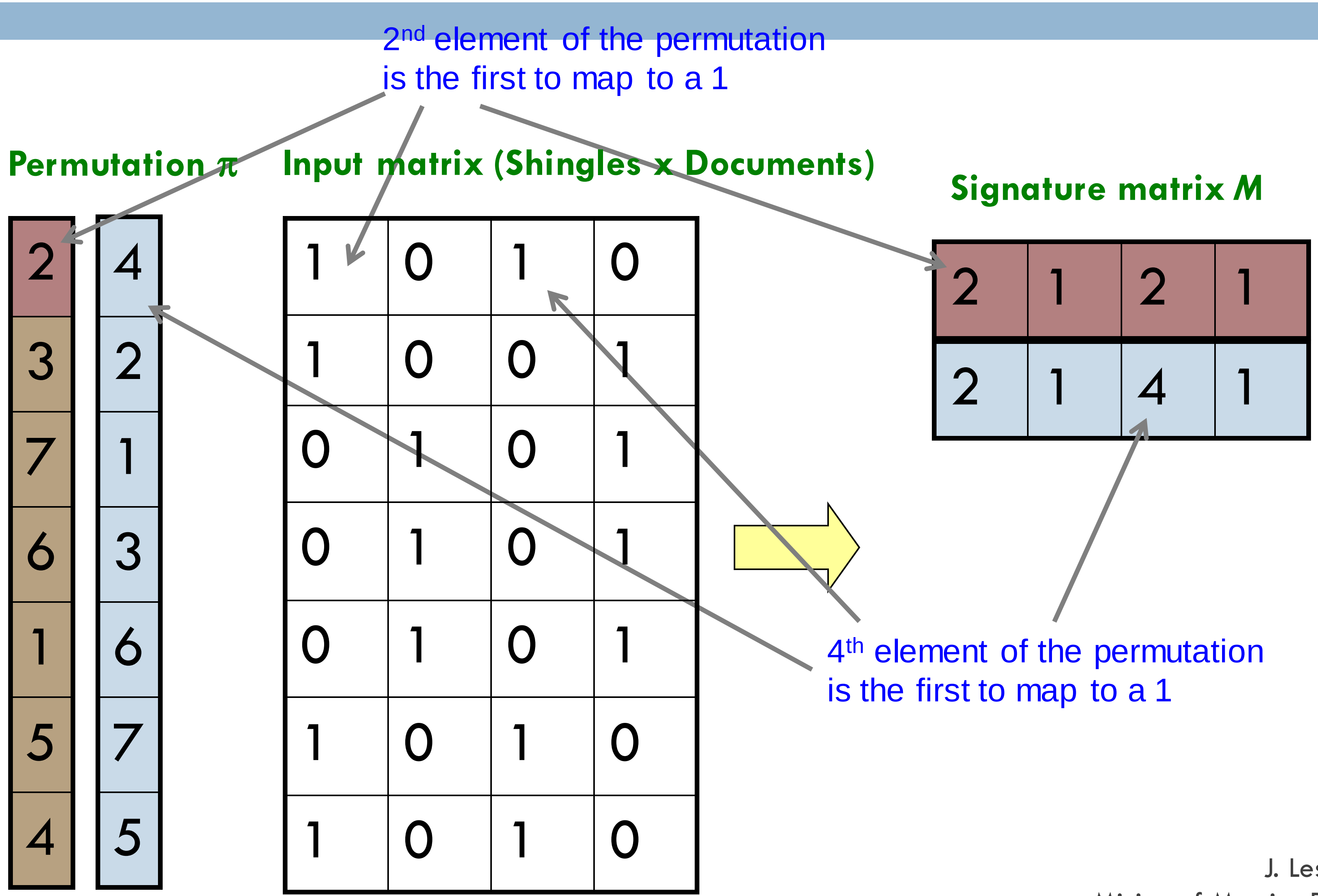
Input matrix (Shingles x Documents)

1	0	1	0
1	0	0	1
0	1	0	1
0	1	0	1
0	1	0	1
1	0	1	0
1	0	1	0

Signature matrix *M*

2	1	2	1
2	1	4	1

Min-Hashing Example



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Permutation π

2	4
3	2
7	1
6	3
1	6
5	7
4	5

Input matrix (Shingles x Documents)

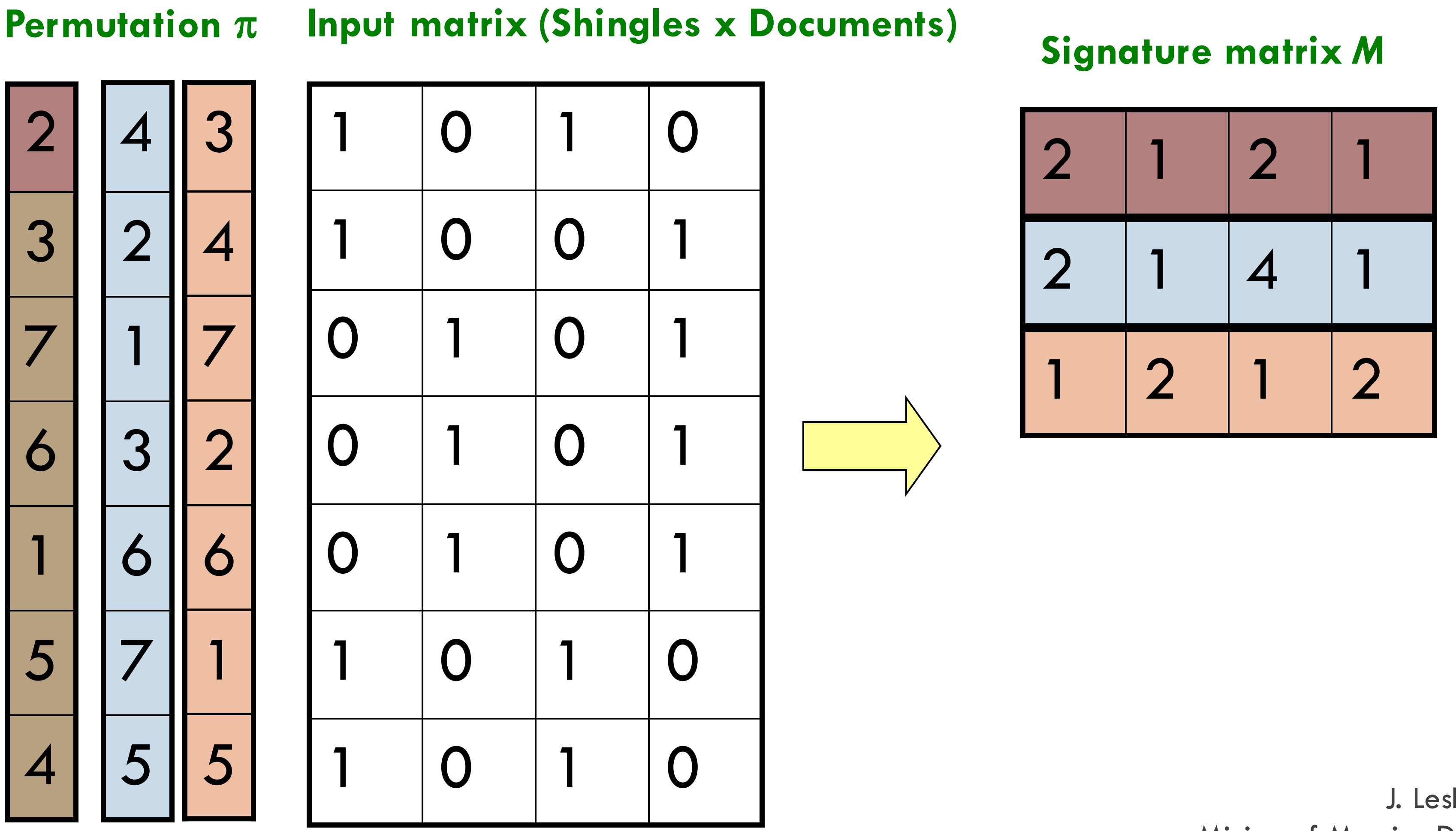
1	0	1	0
1	0	0	1
0	1	0	1
0	1	0	1
0	1	0	1
1	0	1	0
1	0	1	0

Signature matrix *M*

2	1	2	1
2	1	4	1

4th element of the permutation is the first to map to a 1

Min-Hashing Example



Permutation π

2	4	3
3	2	4
7	1	7
6	3	2
1	6	6
5	7	1
4	5	5

Input matrix (Shingles x Documents)

1	0	1	0
1	0	0	1
0	1	0	1
0	1	0	1
0	1	0	1
1	0	1	0
1	0	1	0

Signature matrix *M*

2	1	2	1
2	1	4	1
1	2	1	2

Min-Hashing Example

Note: Another (equivalent) way is to store row indexes or raw shingles (e.g. mouse, lion):

1	5	1	5
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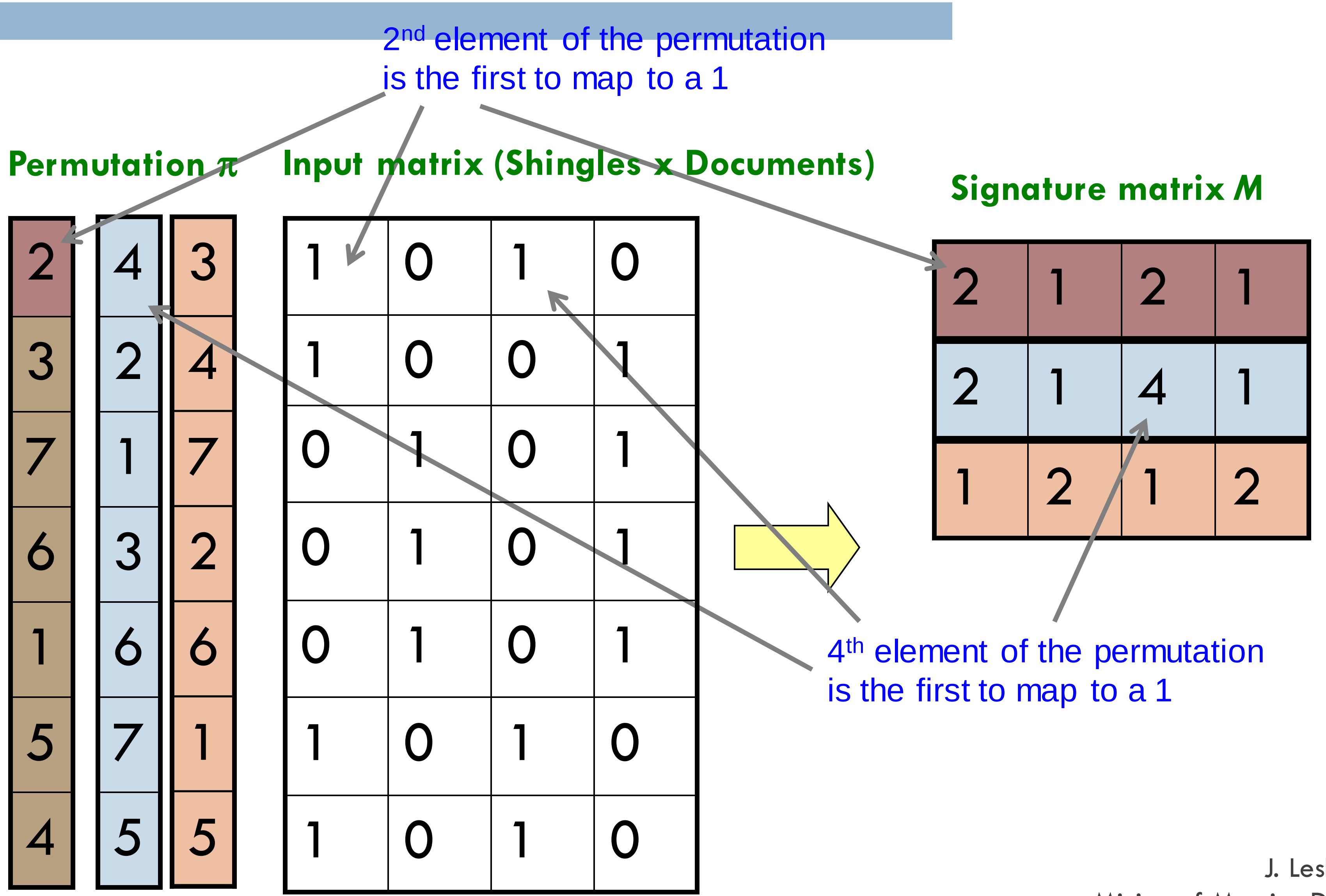

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7	1	7
6	3	2
1	6	6
5	7	1
4	5	5

Input matrix (Shingles x Documents)

1	0	1	0
1	0	0	1
0	1	0	1
0	1	0	1
0	1	0	1
1	0	1	0
1	0	1	0

Signature matrix *M*

2	1	2	1
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Min-Hash Signatures

- **Pick K=100 random permutations of the rows**
- Think of ***sig*(C)** as a column vector
- ***sig*(C)[i] =** according to the *i*-th permutation, the index of the first row that has a 1 in column C

$$sig(C)[i] = \min(\pi_i(C))$$

- **Note:** The sketch (signature) of document C is small **~100 bytes!**
- **We achieved our goal! We "compressed" long bit vectors into short signatures**

Key Fact

For two sets A, B, and a min-hash function $mh_i()$:

$$Pr[mh_i(A) = mh_i(B)] = Sim(A, B) = \frac{|A \cap B|}{|A \cup B|}$$

Unbiased estimator for Sim using *K* hashes (notation policy – this is a different K from size of shingle)

$$S\hat{im}(A, B) = \frac{1}{k} \sum_{i=1:k} I[mh_i(A) = mh_i(B)]$$

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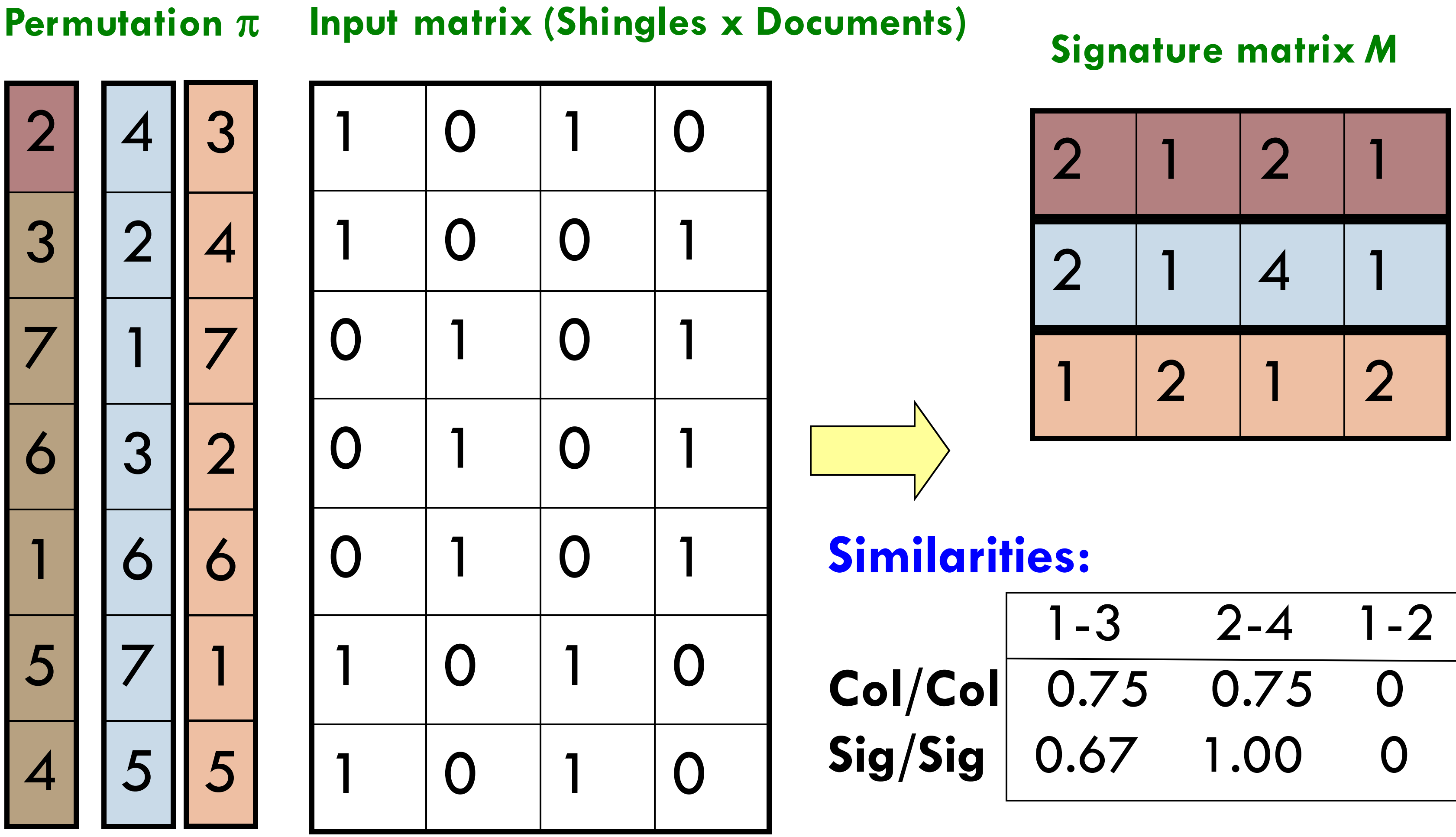

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Signature matrix *M*

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2	1	4	1
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Similarities:

	1-3	2-4	1-2	3-4
Col/Col	0.75	0.75	0	0
Sig/Sig	0.67	1.00	0	0

The Min-Hash Property

- **Choose a random permutation π**
- **Claim:** $\Pr[h_\pi(C_1) = h_\pi(C_2)] = sim(C_1, C_2)$
- **Why?**

0	0
0	0
1	**1**
0	0
0	1
1	0

One of the two cols had to have 1 at position ***y***

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  - Let **X** be a doc (set of shingles), $y \in X$ is a shingle

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- **Why?**
  - Let **X** be a doc (set of shingles), $y \in X$ is a shingle
  - **Then:** $\Pr[\pi(y) = \min(\pi(X))] = 1/|X|$
    - It is equally likely that any $y \in X$ is mapped to the ***min*** element

0	0
0	0
1	**1**
0	0
0	1
1	0

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  - Let ***y*** be s.t. $\pi(y) = \min(\pi(C_1 \cup C_2))$
  - **Then either:** $\pi(y) = \min(\pi(C_1))$ if $y \in C_1$, **or**

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One of the two cols had to have 1 at position y

  - So the prob. that **both** are true is the prob. $y \in C_1 \cap C_2$
  - $\Pr[\min(\pi(C_1)) = \min(\pi(C_2))] = |C_1 \cap C_2| / |C_1 \cup C_2| = sim(C_1, C_2)$

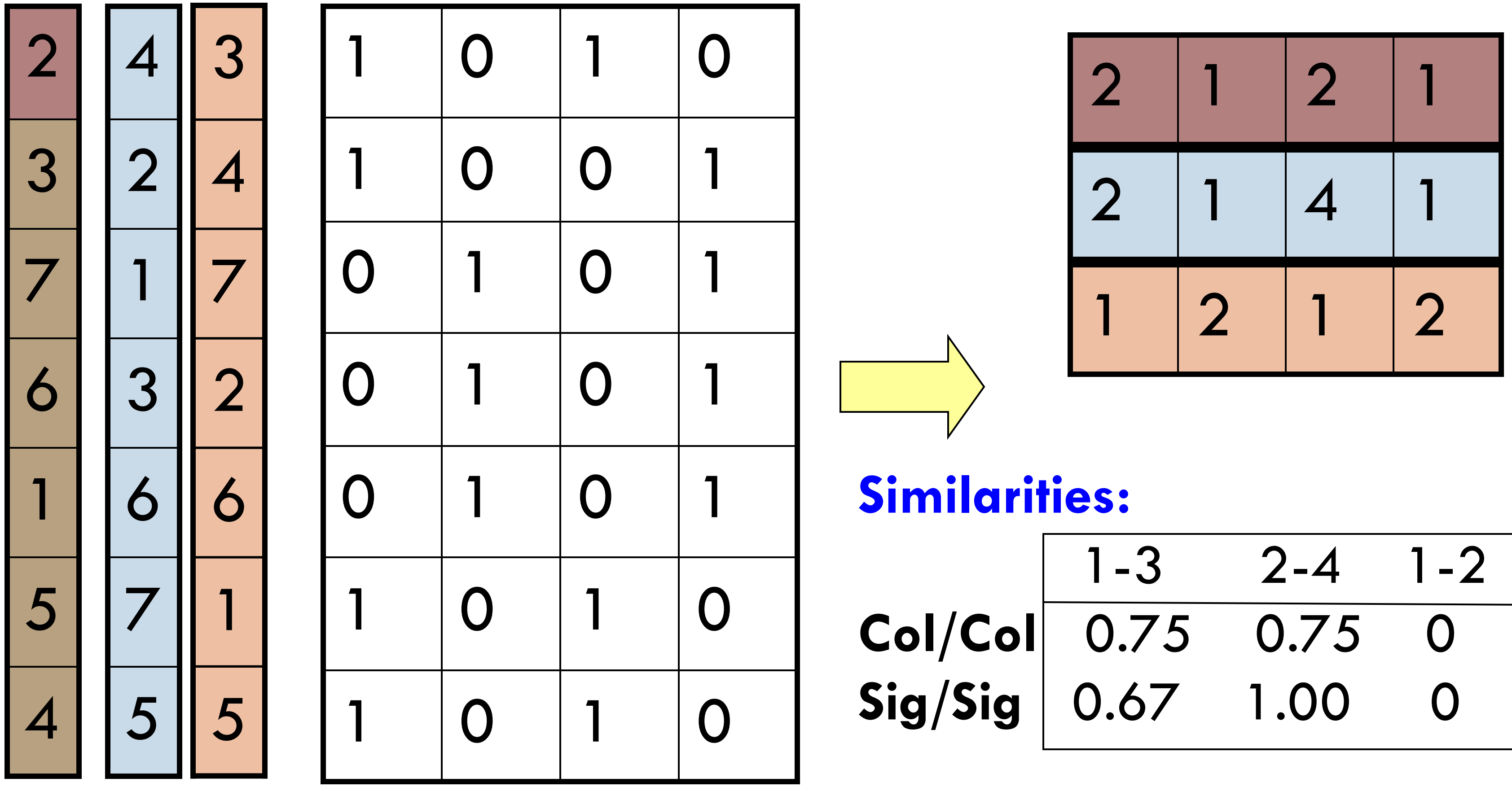
The Min-Hash Property (Take 2: simpler proof)

- **Choose a random permutation π**
- **Claim:** $\Pr[h_\pi(C_1) = h_\pi(C_2)] = sim(C_1, C_2)$
- **Why?**
  - Given a set X, the probability that any one element is the min-hash under π is $1/|X|$ ← (0)
    - It is equally likely that any $y \in X$ is mapped to the ***min*** element
  - Given a set X, the probability that one of any **k** elements is the min-hash under π is $\mathbf{k}/|X|$ ← (1)
  - For $C_1 \cup C_2$, the probability that any element is the min-hash under π is $1/|C_1 \cup C_2|$ (from 0) ← (2)
  - For any C_1 and C_2, the probability of choosing the same min-hash under π is $|C_1 \cap C_2|/|C_1 \cup C_2|$ ← from (1) and (2)

Similarity for Signatures

- We know: $\Pr[h_\pi(C_1) = h_\pi(C_2)] = sim(C_1, C_2)$
- Now generalize to multiple hash functions
- **The *similarity of two signatures* is the fraction of the hash functions in which they agree**
- **Note:** Because of the Min-Hash property, the similarity of columns is the same as the expected similarity of their signatures

Min-Hashing Example



Permutation π

2	4	3
3	2	4
7	1	7
6	3	2
1	6	6
5	7	1
4	5	5

Input matrix (Shingles x Documents)

1	0	1	0
1	0	0	1
0	1	0	1
0	1	0	1
0	1	0	1
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Signature matrix *M*

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Implementation Trick

- **Permuting rows even once is prohibitive**
- **Approximate Linear Permutation Hashing**
- Pick K independent hash functions (use a, b below)
  - Apply the idea on ***each column (document)*** for each hash function and get minhash signature

How to pick a random hash function h(x)?

Universal hashing:

$h_{a,b}(x)=((a\cdot x+b) \bmod p) \bmod N$
where:
a,b … random integers
p … prime number ($p > N$)

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Summary: 3 Steps

- **Shingling:** Convert documents to sets
  - We used hashing to assign each shingle an ID

- **Min-Hashing:** Convert large sets to short signatures, while preserving similarity
  - We used **similarity preserving hashing** to generate signatures with property $\Pr[h_\pi(C_1) = h_\pi(C_2)] = sim(C_1, C_2)$

  - We used hashing to get around generating random permutations

Backup slides

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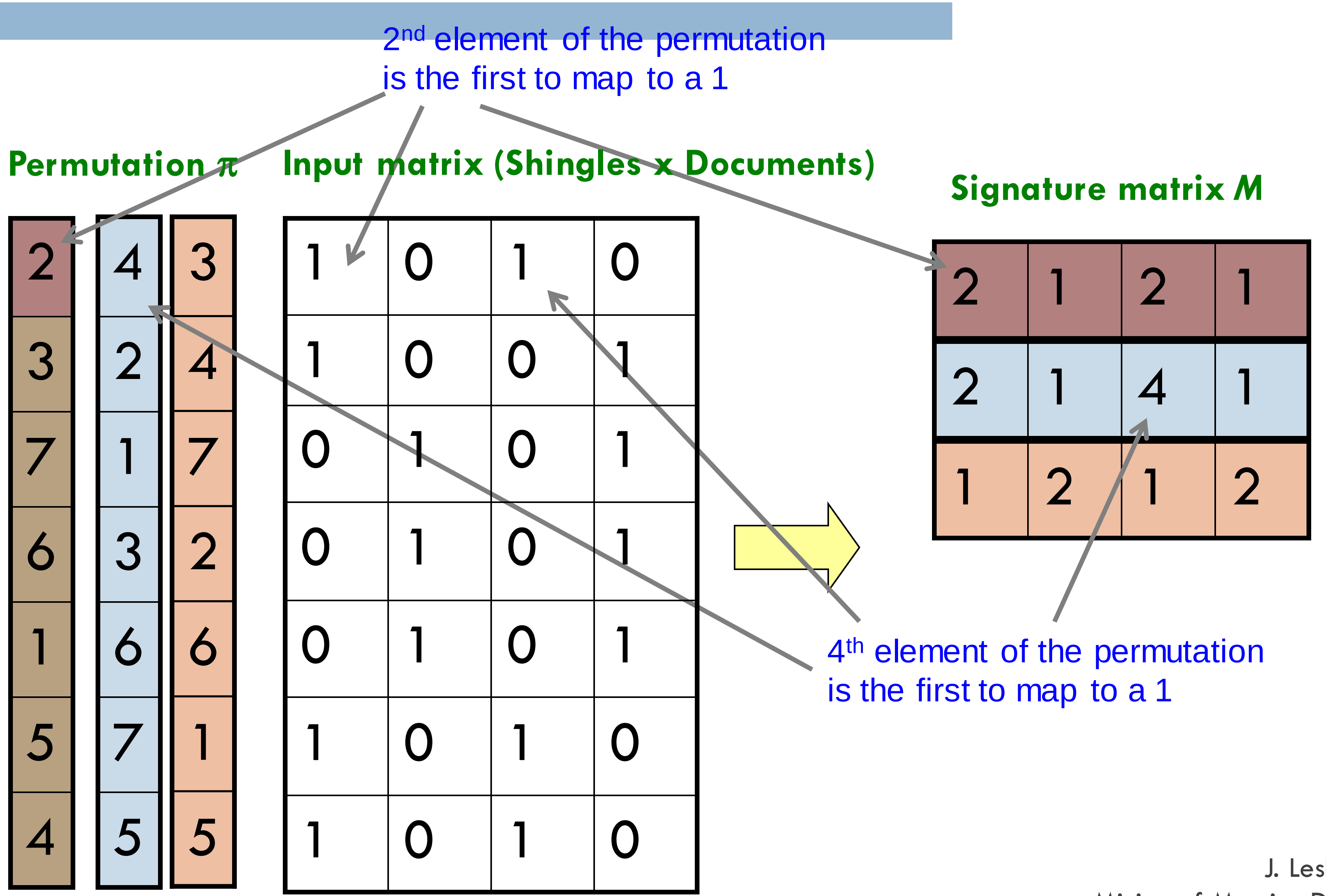

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1	0	0	1
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0	1	0	1
0	1	0	1
1	0	1	0
1	0	1	0

Signature matrix *M*

2	1	2	1
2	1	4	1
1	2	1	2

4th element of the permutation is the first to map to a 1

The Min-Hash Property

- **Choose a random permutation π**
- **<u>Claim:</u>** **$\Pr[h_\pi(C_1) = h_\pi(C_2)] = sim(C_1, C_2)$**
- **Why?**
  - Let **X** be a doc (set of shingles), ***y*** $\in$ ***X*** is a shingle
  - **Then: $\Pr[\pi(y) = \min(\pi(X))] = 1/|X|$**
    - It is equally likely that any ***y*** $\in$ ***X*** is mapped to the ***min*** element
  - Let ***y*** be s.t. $\pi(y) = \min(\pi(C_1 \cup C_2))$
  - **Then either:** $\pi(y) = \min(\pi(C_1))$ if $y \in C_1$ **, or**
    $\pi(y) = \min(\pi(C_2))$ if $y \in C_2$
  - So the prob. that **both** are true is the prob. ***y*** $\in C_1 \cap C_2$
  - **$\Pr[\min(\pi(C_1))=\min(\pi(C_2))]=|C_1 \cap C_2|/|C_1 \cup C_2| = sim(C_1, C_2)$**

0	0
0	0
1	**1**
0	0
0	1
1	0

One of the two cols had to have 1 at position ***y***

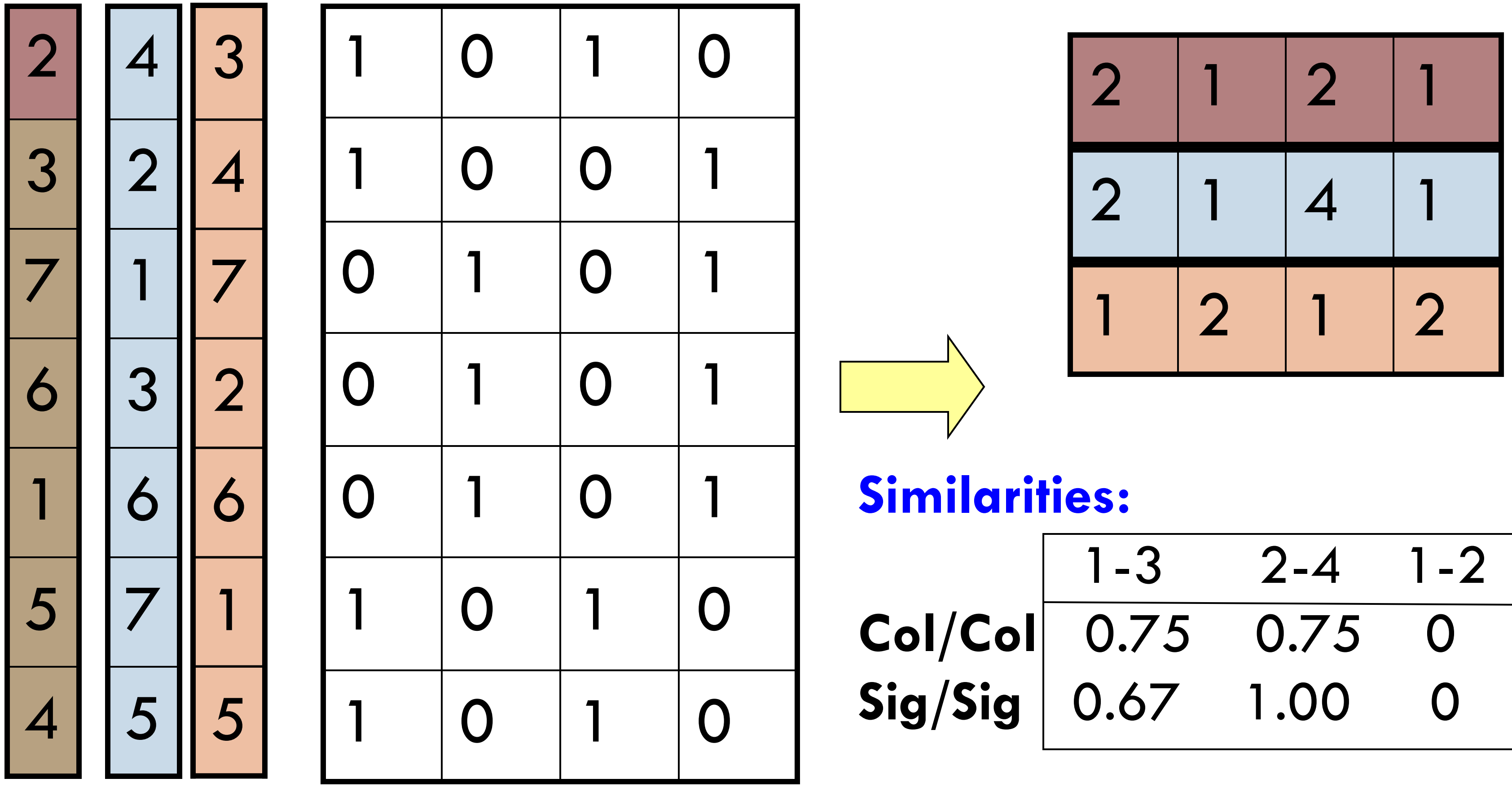
The Min-Hash Property (Take 2: simpler proof)

- **Choose a random permutation π**
- **Claim:** **$\Pr[h_\pi(C_1) = h_\pi(C_2)] = sim(C_1, C_2)$**
- **Why?**
  - Given a set X, the probability that any one element is the min-hash under π is $1/|X|$ ← (0)
    - It is equally likely that any $y \in X$ is mapped to the ***min*** element
  - Given a set X, the probability that one of any **k** elements is the min-hash under π is $\mathbf{k}/|X|$ ← (1)
  - For $C_1 \cup C_2$, the probability that any element is the min-hash under π is $1/|C_1 \cup C_2|$ (from 0) ← (2)
  - For any C_1 and C_2, the probability of choosing the same min-hash under π is $|C_1 \cap C_2|/|C_1 \cup C_2|$ ← from (1) and (2)

Similarity for Signatures

- We know: $\Pr[h_\pi(C_1) = h_\pi(C_2)] = sim(C_1, C_2)$
- Now generalize to multiple hash functions
- **The *similarity of two signatures* is the fraction of the hash functions in which they agree**
- **Note:** Because of the Min-Hash property, the similarity of columns is the same as the expected similarity of their signatures

Min-Hashing Example



Permutation π

2	4	3
3	2	4
7	1	7
6	3	2
1	6	6
5	7	1
4	5	5

Input matrix (Shingles x Documents)

1	0	1	0
1	0	0	1
0	1	0	1
0	1	0	1
0	1	0	1
1	0	1	0
1	0	1	0

Signature matrix *M*

2	1	2	1
2	1	4	1
1	2	1	2

Similarities:

	1-3	2-4	1-2	3-4
Col/Col	0.75	0.75	0	0
Sig/Sig	0.67	1.00	0	0

J. Leskovec, A. Rajaraman, J. Ullman: Mining of Massive Datasets, http://www.mmds.org

Min-Hash Signatures

- **Pick K=100 random permutations of the rows**
- Think of ***sig*(C)** as a column vector
- ***sig*(C)[i] =** according to the *i*-th permutation, the index of the first row that has a 1 in column C

$$sig(C)[i] = \min(\pi_i(C))$$

- **Note:** The sketch (signature) of document C is small **~100 bytes!**
- **We achieved our goal! We "compressed" long bit vectors into short signatures**

Implementation Trick

- **Permuting rows even once is prohibitive**
- **Approximate Linear Permutation Hashing**
- **Pick K independent hash functions (use a, b below)**
    - Apply the idea on ***each column (document)*** for each hash function and get minhash signature

How to pick a random hash function h(x)?

Universal hashing:

$h_{a,b}(x)=((a \cdot x+b) \bmod p) \bmod N$
where:
a,b … random integers
p … prime number ($p > N$)

Summary: 3 Steps

- **Shingling:** Convert documents to sets
  - We used hashing to assign each shingle an ID

- **Min-Hashing:** Convert large sets to short signatures, while preserving similarity
  - We used **similarity preserving hashing** to generate signatures with property $\mathbf{Pr}[h_\pi(C_1) = h_\pi(C_2)] = sim(C_1, C_2)$
  - We used hashing to get around generating random permutations

Backup slides

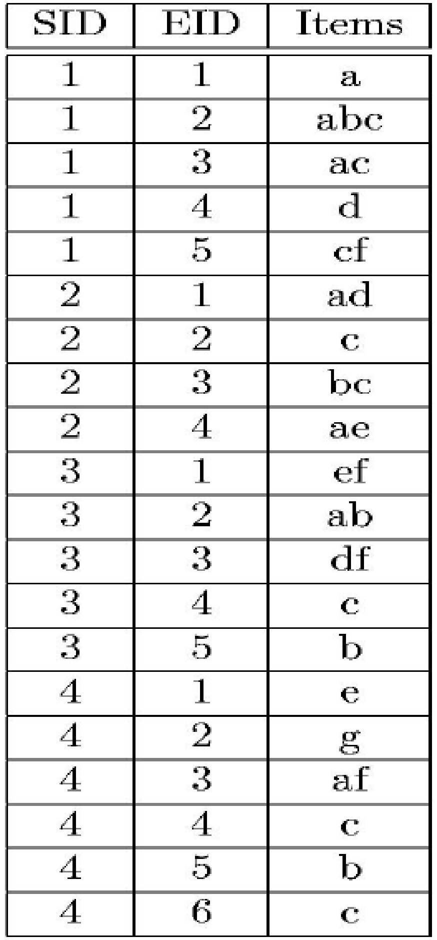
Sequential Pattern Mining in Vertical Data Format: The SPADE Algorithm

- A sequence database is mapped to: <SID, EID>
- Grow the subsequences (patterns) one item at a time by Apriori candidate generation

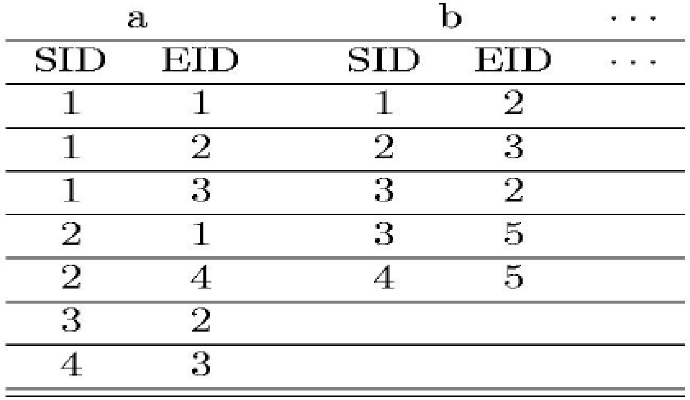
SID	Sequence
1	<a(abc)(ac)d(cf)>
2	<(ad)c(bc)(ae)>
3	<(ef)(ab)(df)cb>
4	<eg(af)cbc>

min_sup = 2

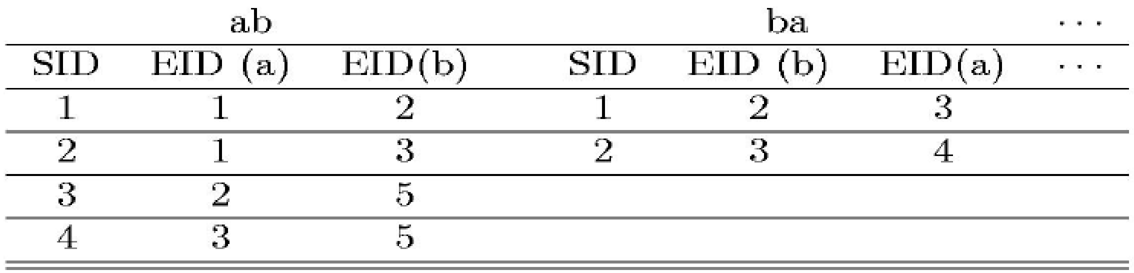
Ref: SPADE (Sequential PAttern Discovery using Equivalent Class) [M. Zaki 2001]



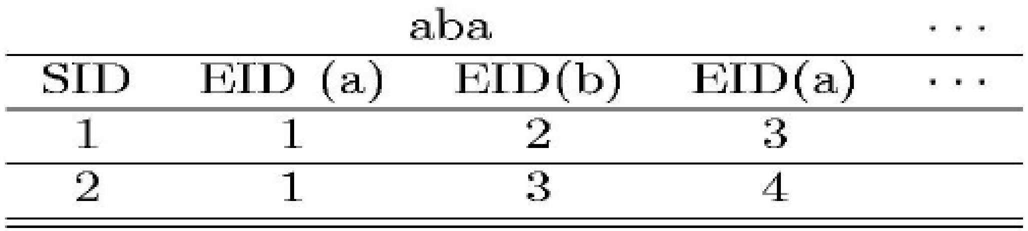
SID	EID	Items
1	1	a
1	2	abc
1	3	ac
1	4	d
1	5	cf
2	1	ad
2	2	c
2	3	bc
2	4	ae
3	1	ef
3	2	ab
3	3	df
3	4	c
3	5	b
4	1	e
4	2	g
4	3	af
4	4	c
4	5	b
4	6	c



a		b		. . .
SID	EID	SID	EID	. . .
1	1	1	2	
1	2	2	3	
1	3	3	2	
2	1	3	5	
2	4	4	5	
3	2			
4	3			



ab			ba			. . .
SID	EID (a)	EID(b)	SID	EID (b)	EID(a)	. . .
1	1	2	1	2	3	
2	1	3	2	3	4	
3	2	5				
4	3	5				



aba				. . .
SID	EID (a)	EID(b)	EID(a)	. . .
1	1	2	3	
2	1	3	4	

PrefixSpan: A Pattern-Growth Approach

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

min_sup = 2

Prefix	Suffix (Projection)
<a>	<(abc)(ac)d(cf)>
<aa>	<(_bc)(ac)d(cf)>
<ab>	<(_c)(ac)d(cf)>

- Prefix and suffix
  - Given <a(abc)(ac)d(cf)>
  - Prefixes: <a>, <aa>, <a(ab)>, <a(abc)>, …
  - Suffix: Prefixes-based projection

- PrefixSpan Mining: Prefix Projections
  - Step 1: Find length-1 sequential patterns
    - <a>, <b>, <c>, <d>, <e>, <f>
  - Step 2: Divide search space and mine each projected DB
    - <a>-projected DB,
    - <b>-projected DB,
    - …
    - <f>-projected DB, …

PrefixSpan (Prefix-projected Sequential pattern mining) Pei, et al. @TKDE'04

PrefixSpan: Mining Prefix-Projected DBs

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

min_sup = 2

Length-1 sequential patterns
<a>, <b>, <c>, <d>, <e>, <f>

prefix <a>

<a>-projected DB
<(abc)(ac)d(cf)>
<(_d)c(bc)(ae)>
<(_b)(df)cb>
<(_f)cbc>

Length-2 sequential patterns
<aa>, <ab>, <(ab)>,
<ac>, <ad>, <af>

prefix <b>

<b>-projected DB

… …

prefix <c>, …, <f>

…

prefix <aa>

<aa>-projected DB

..

prefix <af>

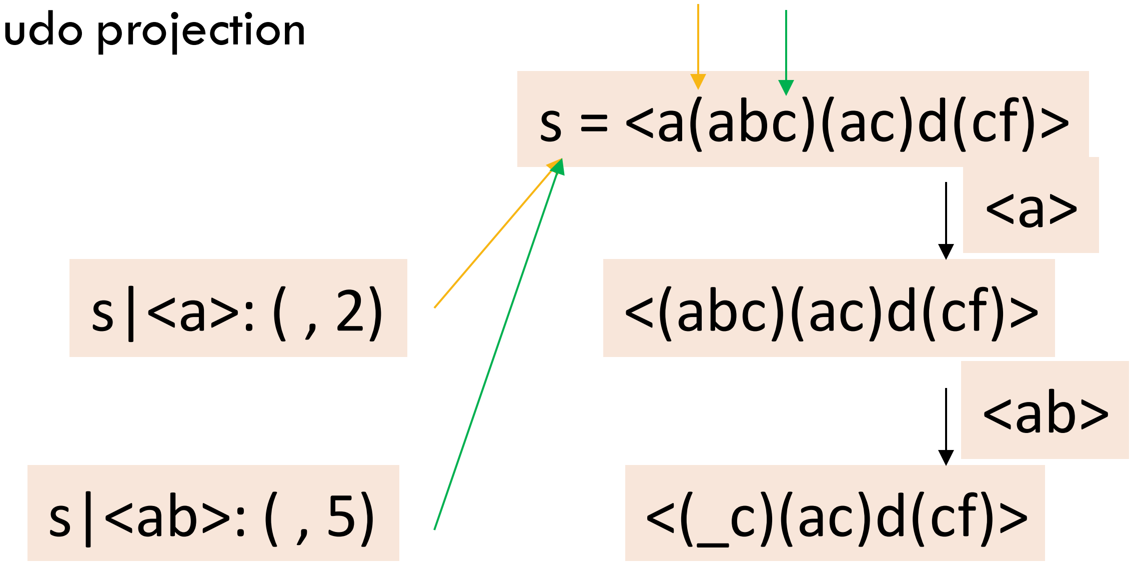
<af>-projected DB

Major strength of PrefixSpan:

- No candidate subseqs. to be generated
- Projected DBs keep shrinking

Consideration:
Pseudo-Projection vs. Physical PrImplementation ojection

- Major cost of PrefixSpan: Constructing projected DBs
  - Suffixes largely repeating in recursive projected DBs
- When DB can be held in main memory, use pseudo projection
  - No physically copying suffixes
  - Pointer to the sequence
  - Offset of the suffix
  - But if it does not fit in memory
    - Physical projection
  - Suggested approach:
    - Integration of physical and pseudo-projection
    - Swapping to pseudo-projection when the data fits in memory


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

<a>

<(abc)(ac)d(cf)>

<ab>

<(_c)(ac)d(cf)>

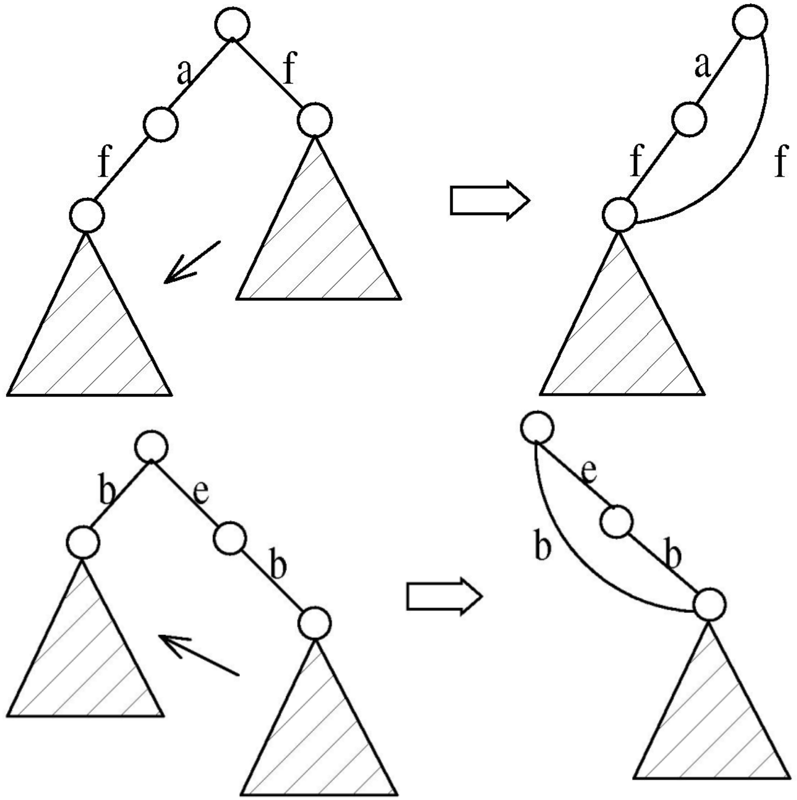
s|<a>: (, 2)

s|<ab>: (, 5)

CloSpan: Mining Closed Sequential Patterns

- A closed sequential pattern *s*: There exists no superpattern *s’* such that $s' \supset s$, and *s’* and *s* have the same support
- Which ones are closed? <abc>: 20, <abcd>:20, <abcde>: 15

- Why directly mine closed sequential patterns?
  - Reduce # of (redundant) patterns
  - Attain the same expressive power
- Property P_1: If $s \supset s_1$, s is closed iff two project DBs have the same size
- Explore *Backward Subpattern* and *Backward Superpattern* pruning to prune redundant search space
- Greatly enhances efficiency (Yan, et al., SDM’03)

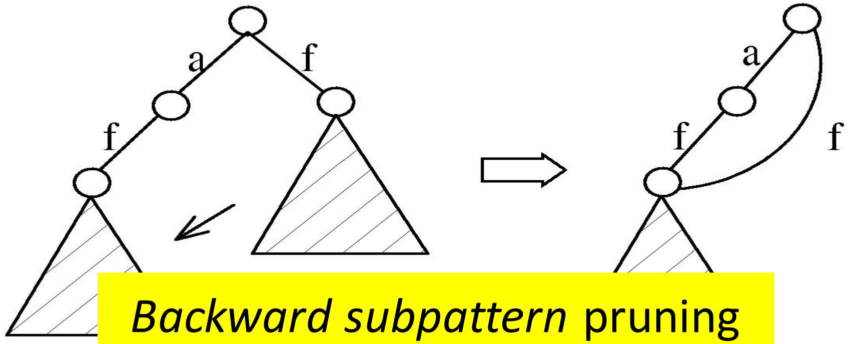


CloSpan: When Two Projected DBs Have the Same Size

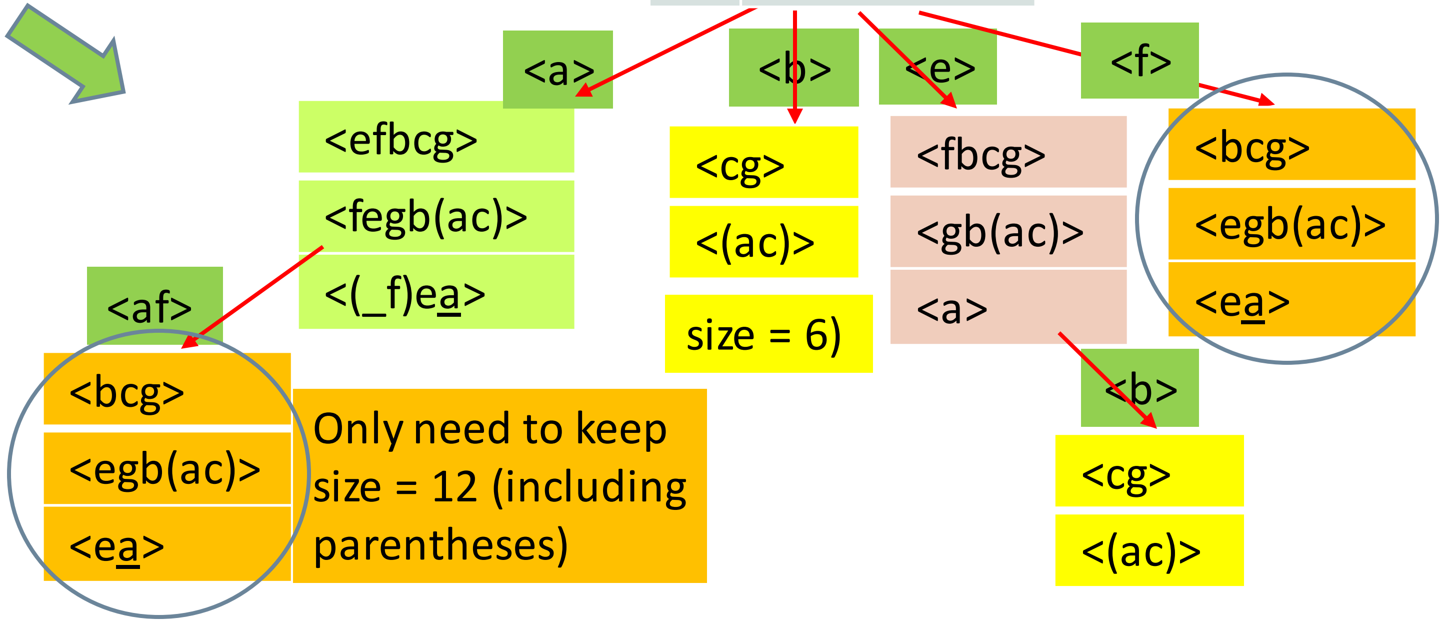
- If $s \supset s_1$, s is closed iff two project DBs have the same size
  - When two projected sequence DBs have the same size?
    - Here is one example:

ID	Sequence
1	<aefbcg>
2	<afegb(ac)>
3	<(af)ea>

min_sup = 2



Backward subpattern pruning



<a>
<efbcg>
<fegb(ac)>
<(_f)ea>

<af>
<bcg>
<egb(ac)>
<ea>

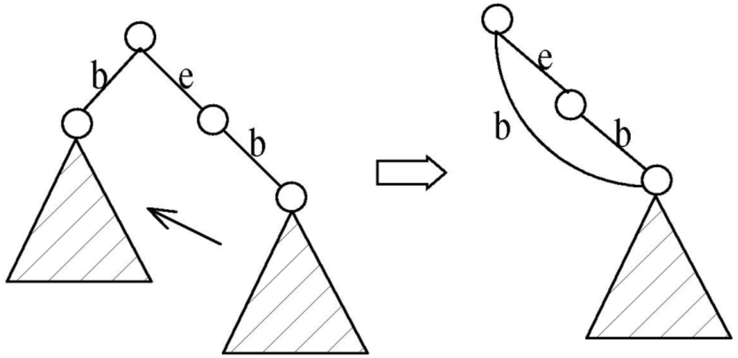
Only need to keep size = 12 (including parentheses)

<b>
<cg>
<(ac)>
size = 6)

<e>
<fbcg>
<gb(ac)>
<a>

<b>
<cg>
<(ac)>

<f>
<bcg>
<egb(ac)>
<ea>



Backward superpattern pruning

Chapter 7 : Advanced Frequent Pattern Mining

- Mining Diverse Patterns
- Sequential Pattern Mining
- Constraint-Based Frequent Pattern Mining
- Graph Pattern Mining
- Pattern Mining Application: Mining Software Copy-and-Paste Bugs
- Summary

Constraint-Based Pattern Mining

- Why Constraint-Based Mining?
- Different Kinds of Constraints: Different Pruning Strategies
- Constrained Mining with Pattern Anti-Monotonicity
- Constrained Mining with Pattern Monotonicity
- Constrained Mining with Data Anti-Monotonicity
- Constrained Mining with Succinct Constraints
- Constrained Mining with Convertible Constraints
- Handling Multiple Constraints
- Constraint-Based Sequential-Pattern Mining

Why Constraint-Based Mining?

- Finding all the patterns in a dataset autonomously?—unrealistic!
  - Too many patterns but not necessarily user-interested!
- Pattern mining in practice: Often a user-guided, interactive process
  - User directs what to be mined using a data mining query language (or a graphical user interface), specifying various kinds of constraints
- What is constraint-based mining?
  - Mine together with user-provided constraints
- Why constraint-based mining?
  - User flexibility: User provides constraints on what to be mined
  - Optimization: System explores such constraints for mining efficiency
    - E.g., Push constraints deeply into the mining process

Various Kinds of User-Specified Constraints in Data Mining

- Knowledge type constraint—Specifying what kinds of knowledge to mine
  - Ex.: Classification, association, clustering, outlier finding, …
- Data constraint—using SQL-like queries
  - Ex.: Find products sold together in NY stores this year
- Dimension/level constraint—similar to projection in relational database
  - Ex.: In relevance to region, price, brand, customer category
- Interestingness constraint—various kinds of thresholds
  - Ex.: Strong rules: min_sup $\geq$ 0.02, min_conf $\geq$ 0.6, min_correlation $\geq$ 0.7
- Rule (or pattern) constraint ⇐ The focus of this study
  - Ex.: Small sales (price < \$10) triggers big sales (sum > \$200)

Pattern Space Pruning with Pattern Anti-Monotonicity

TID	Transaction
10	a, b, c, d, f, h
20	b, c, d, f, g, h
30	b, c, d, f, g
40	a, c, e, f, g

min_sup = 2

Item	Price	Profit
a	100	40
b	40	0
c	150	−20
d	35	−15
e	55	−30
f	45	−10
g	80	20
h	10	5

- A constraint *c* is ***anti-monotone***
  - If an itemset S **violates** constraint *c*, so does any of its superset
  - That is, mining on itemset S can be terminated
- Ex. 1: c_1: $sum(S.price) \leq v$ is anti-monotone
- Ex. 2: c_2: range(S.profit) $\leq$ 15 is anti-monotone
  - Itemset *ab* violates c_2 (range(ab) = 40)
  - So does every superset of *ab*
- Ex. 3. c_3: $sum(S.Price) \geq v$ is not anti-monotone
- Ex. 4. Is c_4: $support(S) \geq \sigma$ anti-monotone?
  - Yes! Apriori pruning is essentially pruning with an anti-monotonic constraint!

Note: item.price > 0
Profit can be negative

Pattern Monotonicity and Its Roles

TID	Transaction
10	a, b, c, d, f, h
20	b, c, d, f, g, h
30	b, c, d, f, g
40	a, c, e, f, g

min_sup = 2

Item	Price	Profit
a	100	40
b	40	0
c	150	−20
d	35	−15
e	55	−30
f	45	−10
g	80	20
h	10	5

- A constraint *c* is *monotone*: If an itemset S **satisfies** the constraint c, so does any of its superset
  - That is, we do not need to check *c* in subsequent mining
- Ex. 1: c_1: $sum(S.Price) \geq v$ is monotone
- Ex. 2: c_2: $min(S.Price) \leq v$ is monotone
- Ex. 3: c_3: range(S.profit) ≥ 15 is monotone
  - Itemset *ab* satisfies c_3
  - So does every superset of *ab*

Note: item.price > 0
Profit can be negative

Data Space Pruning with Data Anti-Monotonicity

TID	Transaction
10	a, b, c, d, f, h
20	b, c, d, f, g, h
30	b, c, d, f, g
40	a, c, e, f, g

min_sup = 2

Item	Price	Profit
a	100	40
b	40	0
c	150	−20
d	35	−15
e	55	−30
f	45	−10
g	80	20
h	10	5

- A constraint c is *data anti-monotone*: In the mining process, if a data entry *t* cannot satisfy a pattern *p* under c, *t* cannot satisfy *p*'s superset either
  - Data space pruning: Data entry *t* can be pruned
- Ex. 1: c_1: $sum(S.Profit) \geq v$ is data anti-monotone
  - Let constraint c_1 be: $sum(S.Profit) \geq 25$
    - T_{30}: {b, c, d, f, g} can be removed since none of their combinations can make an S whose sum of the profit is ≥ 25
- Ex. 2: c_2: $min(S.Price) \leq v$ is data anti-monotone
    - Consider $v = 5$ but every item in a transaction, say T_{50}, has a price higher than 10
- Ex. 3: c_3: $range(S.Profit) > 25$ is data anti-monotone

Note: item.price > 0
Profit can be negative

Expressing Patterns in Compressed Form: Closed Patterns

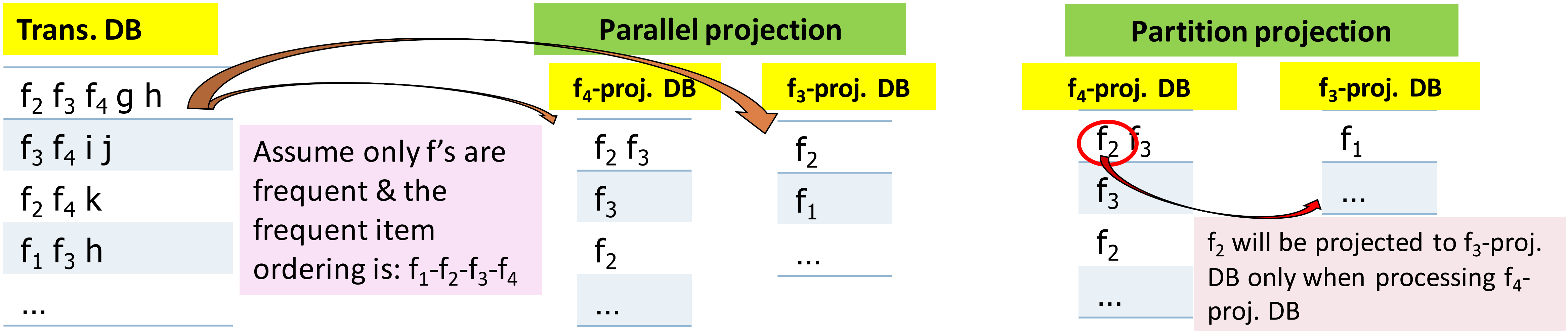
- How to handle such a challenge?
- Solution 1: **Closed patterns:** A pattern (itemset) X is closed if X is *frequent*, and there exists *no super-pattern* Y ⊃ X, *with the same support* as X
  - Let Transaction DB TDB_1: T_1: $\{a_1, \ldots, a_{50}\}$; T_2: $\{a_1, \ldots, a_{100}\}$
  - Suppose *minsup* = 1. How many closed patterns does TDB_1 contain?
    - Two: P_1: "$\{a_1, \ldots, a_{50}\}$: 2"; P_2: "$\{a_1, \ldots, a_{100}\}$: 1"
- Closed pattern is a lossless compression of frequent patterns
  - Reduces the # of patterns but does not lose the support information!
  - You will still be able to say: "$\{a_2, \ldots, a_{40}\}$: 2", "$\{a_5, a_{51}\}$: 1"

Expressing Patterns in Compressed Form: Max-Patterns

- Solution 2: **Max-patterns:** A pattern X is a maximal frequent pattern or max-pattern if X is frequent and there exists no frequent super-pattern Y ⊃ X
- Difference from close-patterns?
  - Do not care the real support of the sub-patterns of a max-pattern
  - Let Transaction DB TDB$_1$: T$_1$: $\{a_1, \ldots, a_{50}\}$; T$_2$: $\{a_1, \ldots, a_{100}\}$
  - Suppose *minsup* = 1. How many max-patterns does TDB$_1$ contain?
    - One: P: "$\{a_1, \ldots, a_{100}\}$: 1"
- Max-pattern is a lossy compression!
  - We only know $\{a_1, \ldots, a_{40}\}$ is frequent
  - But we do not know the real support of $\{a_1, \ldots, a_{40}\}$, …, any more!
  - Thus in many applications, close-patterns are more desirable than max-patterns

Scaling FP-growth by Item-Based Data Projection

- What if FP-tree cannot fit in memory?—Do not construct FP-tree
  - “Project” the database based on frequent single items
  - Construct & mine FP-tree for each projected DB
- Parallel projection vs. partition projection
  - Parallel projection: Project the DB on each frequent item
    - Space costly, all partitions can be processed in parallel
  - Partition projection: Partition the DB in order
    - Passing the unprocessed parts to subsequent partitions



Trans. DB

f_2 f_3 f_4 g h
f_3 f_4 i j
f_2 f_4 k
f_1 f_3 h
…

Assume only f’s are frequent & the frequent item ordering is: f_1-f_2-f_3-f_4

Parallel projection

f_4-proj. DB

f_2 f_3
f_3
f_2
…

f_3-proj. DB

f_2
f_1
…

Partition projection

f_4-proj. DB

f_2 f_3
f_3
f_2
…

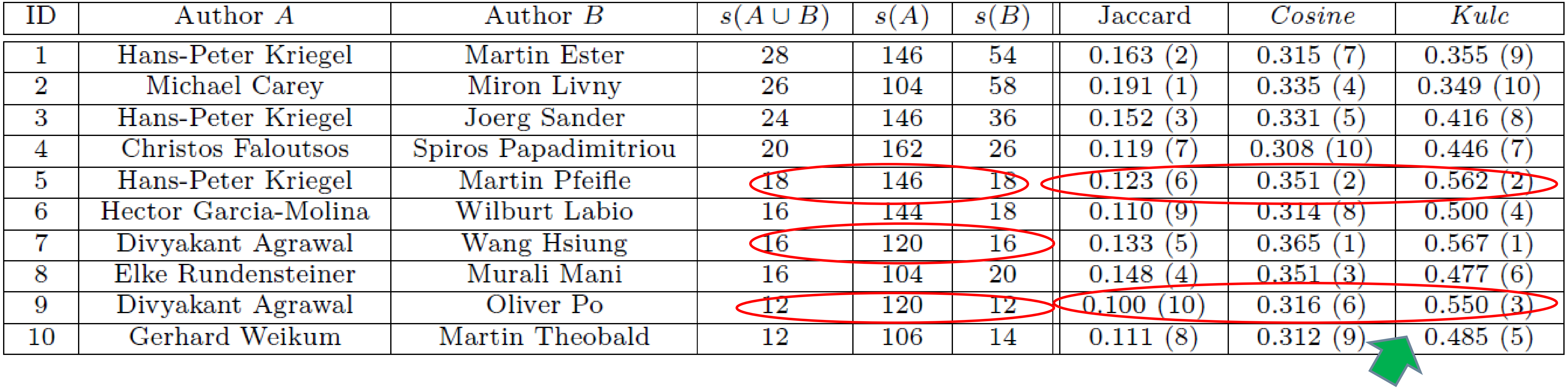
f_3-proj. DB

f_1
…

f_2 will be projected to f_3-proj. DB only when processing f_4-proj. DB

Analysis of DBLP Coauthor Relationships

- DBLP: Computer science research publication bibliographic database
  - > 3.8 million entries on authors, paper, venue, year, and other information



ID	Author A	Author B	$s(A \cup B)$	$s(A)$	$s(B)$	Jaccard	*Cosine*	*Kulc*
1	Hans-Peter Kriegel	Martin Ester	28	146	54	0.163 (2)	0.315 (7)	0.355 (9)
2	Michael Carey	Miron Livny	26	104	58	0.191 (1)	0.335 (4)	0.349 (10)
3	Hans-Peter Kriegel	Joerg Sander	24	146	36	0.152 (3)	0.331 (5)	0.416 (8)
4	Christos Faloutsos	Spiros Papadimitriou	20	162	26	0.119 (7)	0.308 (10)	0.446 (7)
5	Hans-Peter Kriegel	Martin Pfeifle	18	146	18	0.123 (6)	0.351 (2)	0.562 (2)
6	Hector Garcia-Molina	Wilburt Labio	16	144	18	0.110 (9)	0.314 (8)	0.500 (4)
7	Divyakant Agrawal	Wang Hsiung	16	120	16	0.133 (5)	0.365 (1)	0.567 (1)
8	Elke Rundensteiner	Murali Mani	16	104	20	0.148 (4)	0.351 (3)	0.477 (6)
9	Divyakant Agrawal	Oliver Po	12	120	12	0.100 (10)	0.316 (6)	0.550 (3)
10	Gerhard Weikum	Martin Theobald	12	106	14	0.111 (8)	0.312 (9)	0.485 (5)

Advisor-advisee relation: Kulc: high, Jaccard: low, cosine: middle

- Which pairs of authors are strongly related?
  - Use Kulc to find Advisor-advisee, close collaborators

Analysis of DBLP Coauthor Relationships

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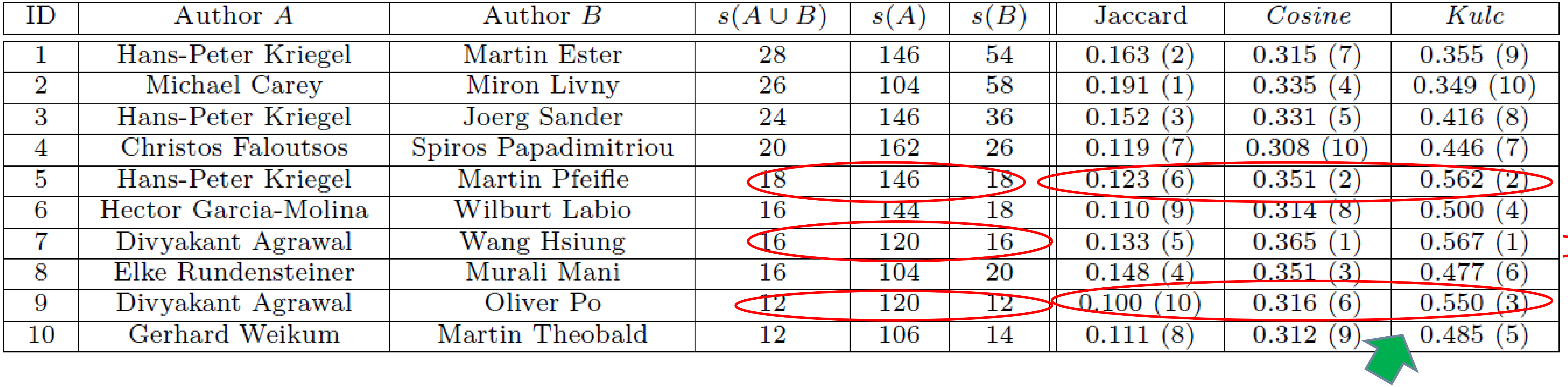

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5	Hans-Peter Kriegel	Martin Pfeifle	18	146	18	0.123 (6)	0.351 (2)	0.562 (2)
6	Hector Garcia-Molina	Wilburt Labio	16	144	18	0.110 (9)	0.314 (8)	0.500 (4)
7	Divyakant Agrawal	Wang Hsiung	16	120	16	0.133 (5)	0.365 (1)	0.567 (1)
8	Elke Rundensteiner	Murali Mani	16	104	20	0.148 (4)	0.351 (3)	0.477 (6)
9	Divyakant Agrawal	Oliver Po	12	120	12	0.100 (10)	0.316 (6)	0.550 (3)
10	Gerhard Weikum	Martin Theobald	12	106	14	0.111 (8)	0.312 (9)	0.485 (5)

Advisor-advisee relation: Kulc: high, Jaccard: low, cosine: middle

- Which pairs of authors are strongly related?
  - Use Kulc to find Advisor-advisee, close collaborators

What Measures to Choose for Effective Pattern Evaluation?

- Null value cases are predominant in many large datasets
  - Neither milk nor coffee is in most of the baskets; neither Mike nor Jim is an author in most of the papers; ……
- *Null-invariance* is an important property
- Lift, χ^2 and cosine are good measures if null transactions are not predominant
  - Otherwise, *Kulczynski* + *Imbalance Ratio* should be used to judge the interestingness of a pattern
- Exercise: Mining research collaborations from research bibliographic data
  - Find a group of frequent collaborators from research bibliographic data (e.g., DBLP)
  - Can you find the likely advisor-advisee relationship and during which years such a relationship happened?
  - Ref.: C. Wang, J. Han, Y. Jia, J. Tang, D. Zhang, Y. Yu, and J. Guo, "Mining Advisor-Advisee Relationships from Research Publication Networks", KDD'10

Mining Compressed Patterns

Pat-ID	Item-Sets	Support
P1	{38,16,18,12}	205227
P2	{38,16,18,12,17}	205211
P3	{39,38,16,18,12,17}	101758
P4	{39,16,18,12,17}	161563
P5	{39,16,18,12}	161576

- Closed patterns
  - P1, P2, P3, P4, P5
  - Emphasizes too much on support
  - There is no compression
- Max-patterns
  - P3: information loss
- Desired output (a good balance):
  - P2, P3, P4

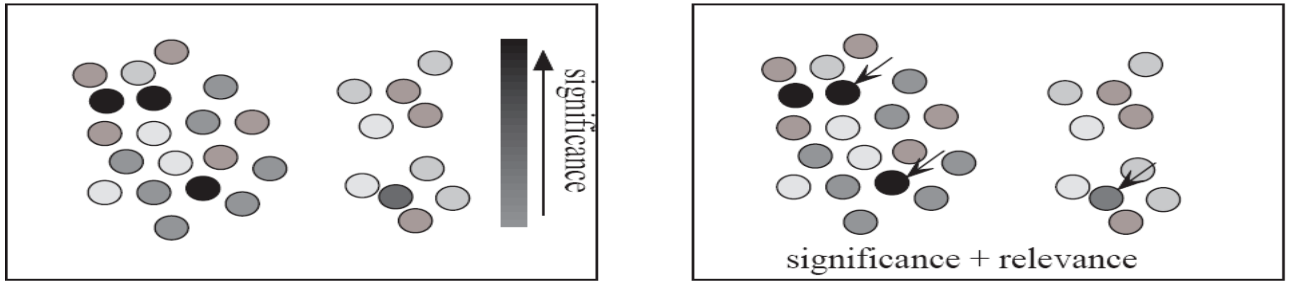
- Why mining compressed patterns?
  - Too many scattered patterns but not so meaningful
- Pattern distance measure

$$Dist(P_1, P_2) = 1 - \frac{|T(P_1) \cap T(P_2)|}{|T(P_1) \cup T(P_2)|}$$

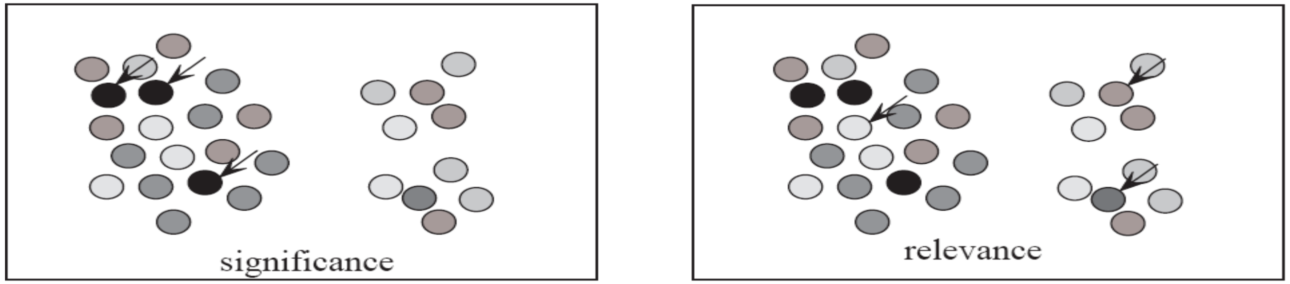
- δ-clustering: For each pattern P, find all patterns which can be expressed by P and whose distance to P is within δ (δ-cover)
- All patterns in the cluster can be represented by P
- Method for efficient, direct mining of compressed frequent patterns (e.g., D. Xin, J. Han, X. Yan, H. Cheng, "On Compressing Frequent Patterns", Knowledge and Data Engineering, 60:5-29, 2007)

Redundancy-Aware Top-k Patterns

- Desired patterns: high significance & low redundancy



(a) a set of patterns (b) redundancy-aware top-k



(c) traditional top-k (d) summarization

- Method: Use MMS (Maximal Marginal Significance) for measuring the combined significance of a pattern set
- Xin et al., Extracting Redundancy-Aware Top-K Patterns, KDD'06

Redundancy Filtering at Mining Multi-Level Associations

- Multi-level association mining may generate many redundant rules
- Redundancy filtering: Some rules may be redundant due to "ancestor" relationships between items
  - milk ⇒ wheat bread [support = 8%, confidence = 70%] (1)
  - 2% milk ⇒ wheat bread [support = 2%, confidence = 72%] (2)
    - Suppose the "2% milk" sold is about "¼" of milk sold
      - Does (2) provide any novel information?
- A rule is *redundant* if its support is close to the "expected" value, according to its "ancestor" rule, and it has a similar confidence as its "ancestor"
  - Rule (1) is an ancestor of rule (2), which one to prune?

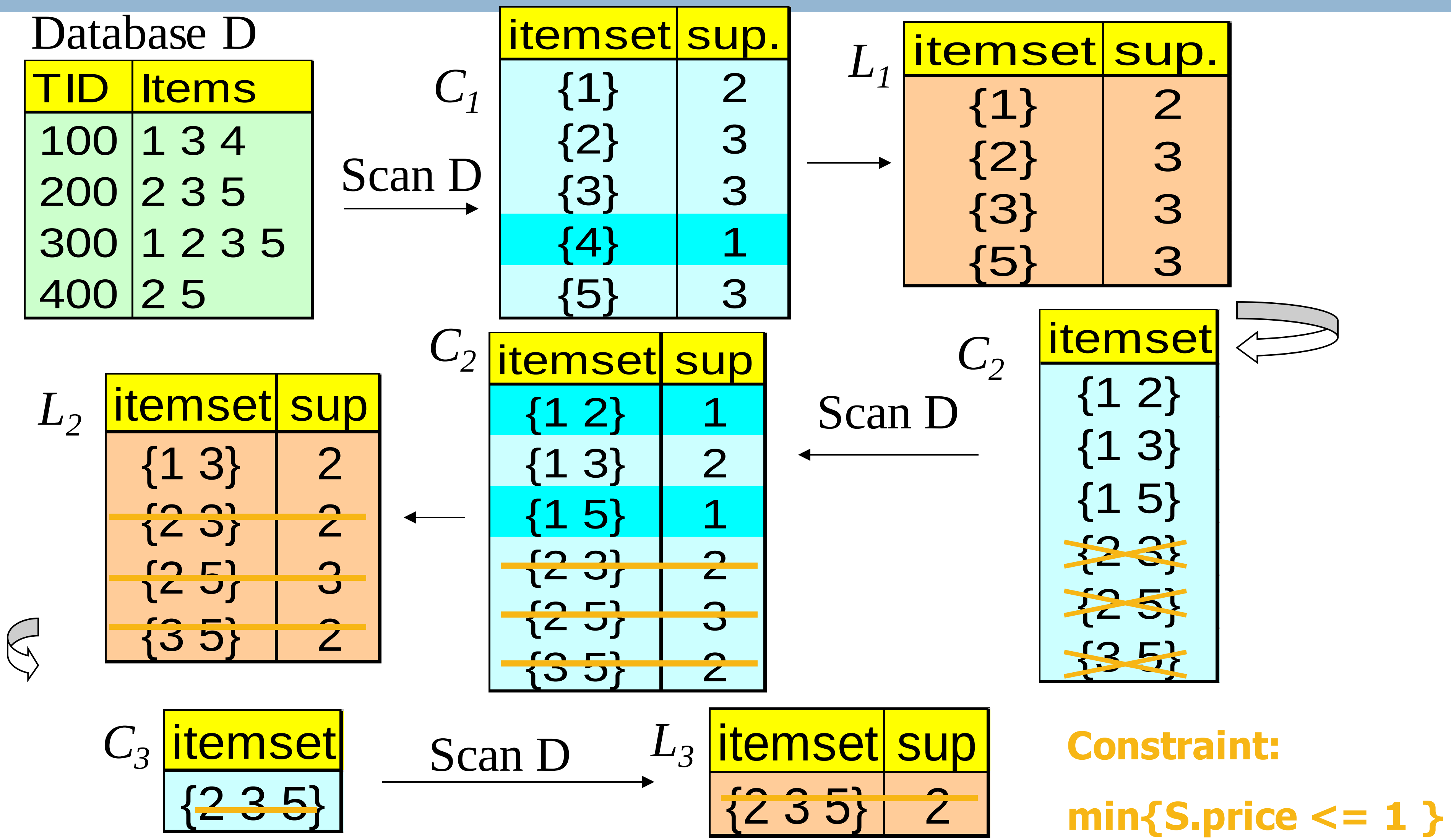
Succinctness

- Succinctness:
  - Given A_1, the set of items satisfying a succinctness constraint C, then any set S satisfying C is based on A_1 , i.e., S contains a subset belonging to A_1
  - Idea: Without looking at the transaction database, whether an itemset S satisfies constraint C can be determined based on the selection of items
  - $min(S.Price) \leq v$ is succinct
  - $sum(S.Price) \geq v$ is not succinct
- Optimization: If C is succinct, C is pre-counting pushable

Which Constraints Are Succinct?

Constraint	Succinct
$v \in S$	yes
$S \supseteq V$	yes
$S \subseteq V$	yes
$\min(S) \le v$	yes
$\min(S) \ge v$	yes
$\max(S) \le v$	yes
$\max(S) \ge v$	yes
$\text{sum}(S) \le v$ ($a \in S, a \ge 0$)	no
$\text{sum}(S) \ge v$ ($a \in S, a \ge 0$)	no
$\text{range}(S) \le v$	no
$\text{range}(S) \ge v$	no
$\text{avg}(S)\ \theta\ v, \theta \in \{=, \le, \ge\}$	no
$\text{support}(S) \ge \xi$	no
$\text{support}(S) \le \xi$	no

Push a Succinct Constraint Deep



Database D

TID	Items
100	1 3 4
200	2 3 5
300	1 2 3 5
400	2 5

Scan D

C_1

itemset	sup.
{1}	2
{2}	3
{3}	3
{4}	1
{5}	3

L_1

itemset	sup.
{1}	2
{2}	3
{3}	3
{5}	3

C_2

itemset
{1 2}
{1 3}
{1 5}
~~{2 3}~~
~~{2 5}~~
~~{3 5}~~

Scan D

C_2

itemset	sup
{1 2}	1
{1 3}	2
{1 5}	1
~~{2 3}~~	~~2~~
~~{2 5}~~	~~3~~
~~{3 5}~~	~~2~~

L_2

itemset	sup
{1 3}	2
~~{2 3}~~	~~2~~
~~{2 5}~~	~~3~~
~~{3 5}~~	~~2~~

C_3

itemset
~~{2 3 5}~~

Scan D

L_3

itemset	sup
~~{2 3 5}~~	~~2~~

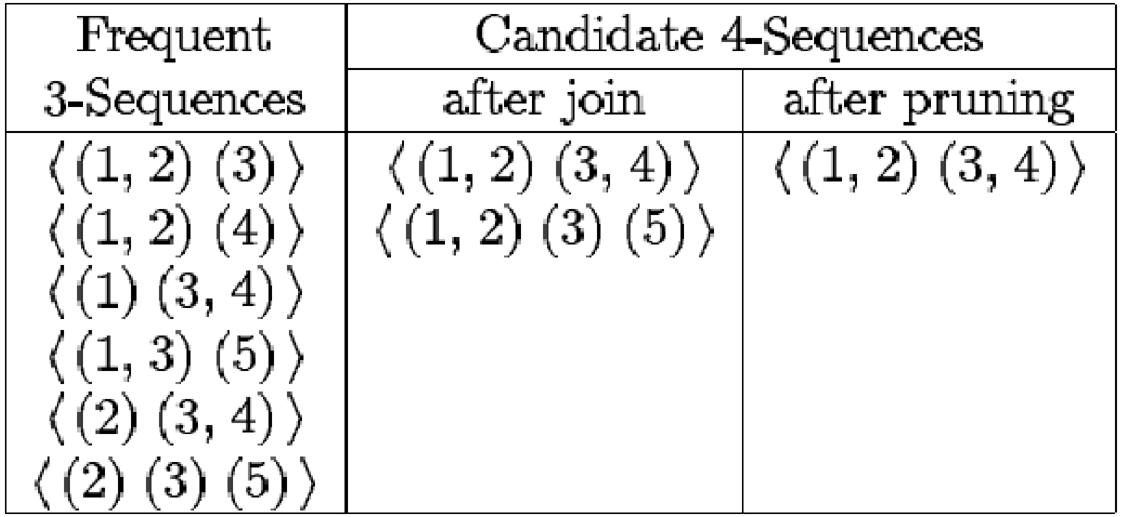
Constraint:

min{S.price <= 1 }

Sequential Pattern Mining

- Sequential Pattern and Sequential Pattern Mining
- GSP: Apriori-Based Sequential Pattern Mining
- SPADE: Sequential Pattern Mining in Vertical Data Format
- PrefixSpan: Sequential Pattern Mining by Pattern-Growth
- CloSpan: Mining Closed Sequential Patterns

GSP: Candidate Generation

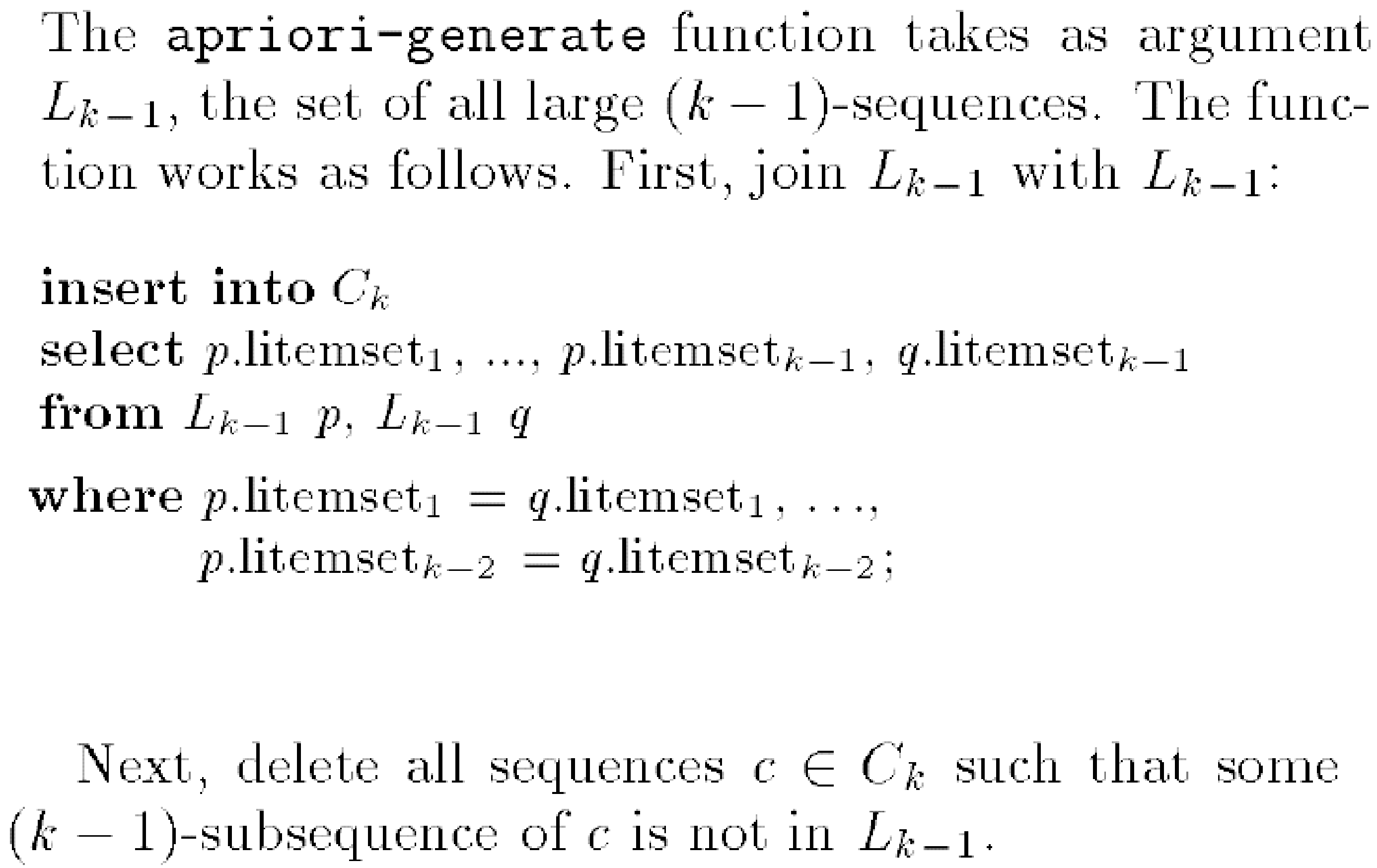


Frequent	Candidate 4-Sequences	
3-Sequences	after join	after pruning
⟨(1, 2) (3)⟩	⟨(1, 2) (3, 4)⟩	⟨(1, 2) (3, 4)⟩
⟨(1, 2) (4)⟩	⟨(1, 2) (3) (5)⟩	
⟨(1) (3, 4)⟩		
⟨(1, 3) (5)⟩		
⟨(2) (3, 4)⟩		
⟨(2) (3) (5)⟩		

Figure 3: Candidate Generation: Example

The sequence **< (1,2) (3) (5) >** is dropped in the pruning phase, since its contiguous subsequence **< (1) (3) (5) >** is not frequent.

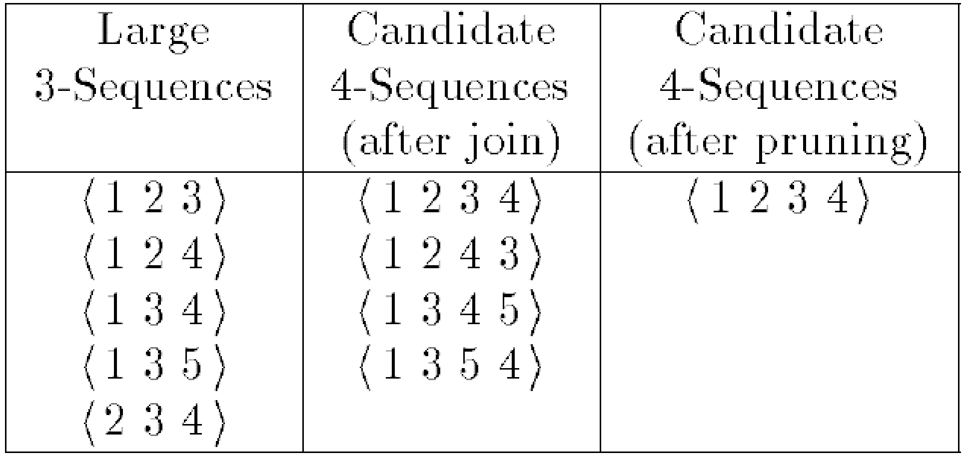
GSP Algorithm: Apriori Candidate Generation



The `apriori-generate` function takes as argument L_{k-1}, the set of all large $(k-1)$-sequences. The function works as follows. First, join L_{k-1} with L_{k-1}:

```
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$_{k-2}$;
```

Next, delete all sequences $c \in C_k$ such that some $(k-1)$-subsequence of c is not in L_{k-1}.



Large 3-Sequences	Candidate 4-Sequences (after join)	Candidate 4-Sequences (after pruning)
$\langle 1\ 2\ 3 \rangle$	$\langle 1\ 2\ 3\ 4 \rangle$	$\langle 1\ 2\ 3\ 4 \rangle$
$\langle 1\ 2\ 4 \rangle$	$\langle 1\ 2\ 4\ 3 \rangle$	
$\langle 1\ 3\ 4 \rangle$	$\langle 1\ 3\ 4\ 5 \rangle$	
$\langle 1\ 3\ 5 \rangle$	$\langle 1\ 3\ 5\ 4 \rangle$	
$\langle 2\ 3\ 4 \rangle$		

Figure 7: Candidate Generation

Mining Sequential Patterns, Agrawal et al., ICDE'95