Data Mining

Chapter 6
Association Analysis: Advance Concepts

Introduction to Data Mining, 2nd Edition by Tan, Steinbach, Karpatne, Kumar

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Data Mining Association Analysis: Advanced Concepts

Extensions of Association Analysis to Continuous and Categorical Attributes and Multi-level Rules

Continuous and Categorical Attributes

How to apply association analysis to non-asymmetric binary variables?

Gender	 Age	Annual	No of hours spent	No of email	Privacy
		Income	online per week	accounts	Concern
Female	 26	90K	20	4	Yes
Male	 51	135K	10	2	No
Male	 29	80K	10	3	Yes
Female	 45	120K	15	3	Yes
Female	 31	95K	20	5	Yes
Male	 25	55K	25	5	Yes
Male	 37	100K	10	1	No
Male	 41	65K	8	2	No
Female	 26	85K	12	1	No

Example of Association Rule:

 $\{Gender=Male, Age \in [21,30)\} \rightarrow \{No \text{ of hours online} \ge 10\}$

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Handling Categorical Attributes

Example: Internet Usage Data

Gender	Level of	State	Computer	Online	Chat	Online	Privacy
	Education		at Home	Auction	Online	Banking	Concerns
Female	Graduate	Illinois	Yes	Yes	Daily	Yes	Yes
Male	College	California	No	No	Never	No	No
Male	Graduate	Michigan	Yes	Yes	Monthly	Yes	Yes
Female	College	Virginia	No	Yes	Never	Yes	Yes
Female	Graduate	California	Yes	No	Never	No	Yes
Male	College	Minnesota	Yes	Yes	Weekly	Yes	Yes
Male	College	Alaska	Yes	Yes	Daily	Yes	No
Male	High School	Oregon	Yes	No	Never	No	No
Female	Graduate	Texas	No	No	Monthly	No	No

{Level of Education=Graduate, Online Banking=Yes}

→ {Privacy Concerns = Yes}

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Handling Categorical Attributes

 Introduce a new "item" for each distinct attributevalue pair

Male	Female	Education	Education	Education	 Privacy	Privacy
		= Graduate	= College	= High School	= Yes	= No
0	1	1	0	0	 1	0
1	0	0	1	0	 0	1
1	0	1	0	0	 1	0
0	1	0	1	0	 1	0
0	1	1	0	0	 1	0
1	0	0	1	0	 1	0
1	0	0	0	0	 0	1
1	0	0	0	1	 0	1
0	1	1	0	0	 0	1

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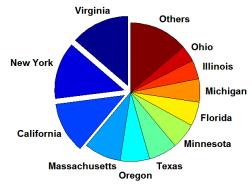
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Handling Categorical Attributes

- Some attributes can have many possible values
 - Many of their attribute values have very low support
 - Potential solution: Aggregate the low-support attribute values



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Handling Categorical Attributes

- Distribution of attribute values can be highly skewed
 - Example: 85% of survey participants own a computer at home
 - ◆ Most records have Computer at home = Yes
 - Computation becomes expensive; many frequent itemsets involving the binary item (Computer at home = Yes)
 - Potential solution:
 - discard the highly frequent items
 - Use alternative measures such as h-confidence
- Computational Complexity
 - Binarizing the data increases the number of items
 - But the width of the "transactions" remain the same as the number of original (non-binarized) attributes
 - Produce more frequent itemsets but maximum size of frequent itemset is limited to the number of original attributes

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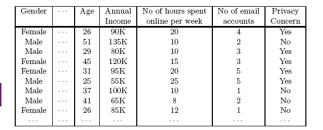
Handling Continuous Attributes

- Different methods:
 - Discretization-based
 - Statistics-based
 - Non-discretization based
 - minApriori
- Different kinds of rules can be produced:
 - {Age∈[21,30), No of hours online∈[10,20)}
 - → {Chat Online =Yes}
 - {Age∈[15,30), Covid-Positive = Yes}
 - → Full recovery

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Discretization-based Methods



Male	Female	 Age	Age	Age	 Privacy	Privacy
		 < 13	\in [13, 21)	$\in [21, 30)$	 = Yes	= No
0	1	 0	0	1	 1	0
1	0	 0	0	0	 0	1
1	0	 0	0	1	 1	0
0	1	 0	0	0	 1	0
0	1	 0	0	0	 1	0
1	0	 0	0	1	 1	0
1	0	 0	0	0	 0	1
1	0	 0	0	0	 0	1
0	1	 0	0	1	 0	1

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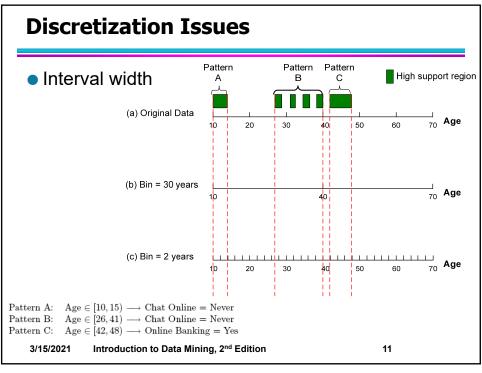
Discretization-based Methods

- Unsupervised:
 - Equal-width binning
 <1 2 3> <4 5 6> <7 8 9>
 - Equal-depth binning <12><34567><89>
 - Cluster-based
- Supervised discretization

	Continuous attribute, v								
	1	2	3	4	5	6	7	8	9
Chat Online = Yes	0	0	20	10	20	0	0	0	0
Chat Online = No	150	100	0	0	0	100	100	150	100
	b	ý ini		bina			bi	n3	

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Discretization Issues

- Interval too wide (e.g., Bin size= 30)
 - May merge several disparate patterns
 - Patterns A and B are merged together
 - May lose some of the interesting patterns
 - Pattern C may not have enough confidence
- Interval too narrow (e.g., Bin size = 2)
 - Pattern A is broken up into two smaller patterns
 - Can recover the pattern by merging adjacent subpatterns
 - Pattern B is broken up into smaller patterns
 - Cannot recover the pattern by merging adjacent subpatterns
 - Some windows may not meet support threshold

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Discretization: all possible intervals

Number of intervals = k Total number of Adjacent intervals = k(k-1)/2



- Execution time
 - If the range is partitioned into k intervals, there are O(k²) new items
 - If an interval [a,b) is frequent, then all intervals that subsume [a,b) must also be frequent
 - ◆ E.g.: if {Age ∈[21,25), Chat Online=Yes} is frequent, then {Age ∈[10,50), Chat Online=Yes} is also frequent
 - Improve efficiency:
 - Use maximum support to avoid intervals that are too wide

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Statistics-based Methods

Example:

{Income > 100K, Online Banking=Yes} \rightarrow Age: μ =34

- Rule consequent consists of a continuous variable, characterized by their statistics
 - mean, median, standard deviation, etc.
- Approach:
 - Withhold the target attribute from the rest of the data
 - Extract frequent itemsets from the rest of the attributes
 - Binarize the continuous attributes (except for the target attribute)
 - For each frequent itemset, compute the corresponding descriptive statistics of the target attribute
 - Frequent itemset becomes a rule by introducing the target variable as rule consequent
 - Apply statistical test to determine interestingness of the rule

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Statistics-based Methods

Gender	 Age	Annual	Annual No of hours spent		Privacy
		Income	online per week	accounts	Concern
Female	 26	90K	20	4	Yes
Male	 51	135K	10	2	No
Male	 29	80K	10	3	Yes
Female	 45	120K	15	3	Yes
Female	 31	95K	20	5	Yes
Male	 25	55K	25	5	Yes
Male	 37	100K	10	1	No
Male	 41	65K	8	2	No
Female	 26	85K	12	1	No



Frequent Itemsets:

{Male, Income > 100K} {Income < 30K, No hours ∈[10,15)} {Income > 100K, Online Banking = Yes}

Association Rules:

{Male, Income > 100K} \rightarrow Age: μ = 30 {Income < 40K, No hours \in [10,15)} \rightarrow Age: μ = 24 {Income > 100K,Online Banking = Yes} \rightarrow Age: μ = 34

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Statistics-based Methods

- How to determine whether an association rule interesting?
 - Compare the statistics for segment of population covered by the rule vs segment of population not covered by the rule:

$$A \Rightarrow B: \mu$$
 versus $\overline{A} \Rightarrow B: \mu'$

- Statistical hypothesis testing:
 - Null hypothesis: H0: μ ' = μ + Δ
 - Alternative hypothesis: H1: $\mu' > \mu + \Delta$
- $Z = \frac{\mu \mu \Delta}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}}$
- ◆ Z has zero mean and variance 1 under null hypothesis

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Statistics-based Methods

• Example:

r: Covid-Postive & Quick_Recovery=Yes \rightarrow Age: μ =23

- Rule is interesting if difference between μ and μ ' is more than 5 years (i.e., Δ = 5)
- For r, suppose n1 = 50, s1 = 3.5
- For r' (complement): n2 = 250, s2 = 6.5

$$Z = \frac{\mu' - \mu - \Delta}{\sqrt{\frac{s_1^2}{n_1} + \frac{s_2^2}{n_2}}} = \frac{30 - 23 - 5}{\sqrt{\frac{3.5^2}{50} + \frac{6.5^2}{250}}} = 3.11$$

- For 1-sided test at 95% confidence level, critical Z-value for rejecting null hypothesis is 1.64.
- Since Z is greater than 1.64, r is an interesting rule

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Min-Apriori

Document-term matrix:

TID	W1	W2	W3	W4	W5
D1	2	2	0	0	1
D2	0	0	1	2	2
D3	2	3	0	0	0
D4	0	0	1	0	1
D5	1	1	1	0	2

Example:

W1 and W2 tends to appear together in the same document

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Min-Apriori

- Data contains only continuous attributes of the same "type"
 - e.g., frequency of words in a document

TID	W1	W2	W3	W4	W5
D1	2	2	0	0	1
D2	0	0	1	2	2
D3	2	3	0	0	0
D4	0	0	1	0	1
D5	1	1	1	0	2

- Potential solution:
 - Convert into 0/1 matrix and then apply existing algorithms
 - lose word frequency information
 - Discretization does not apply as users want association among words based on how frequently they co-occur, not if they occur with similar frequencies

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Min-Apriori

- How to determine the support of a word?
 - If we simply sum up its frequency, support count will be greater than total number of documents!
 - ◆ Normalize the word vectors e.g., using L₁ norms
 - Each word has a support equals to 1.0

TID	W1	W2	W3	W4	W5
D1	2	2	0	0	1
D2	0	0	1	2	2
D3	2	3	0	0	0
D4	0	0	1	0	1
D5	1	1	1	0	2

Normalize

 TID
 W1
 W2
 W3
 W4
 W5

 D1
 0.40
 0.33
 0.00
 0.00
 0.17

 D2
 0.00
 0.00
 0.33
 1.00
 0.33

 D3
 0.40
 0.50
 0.00
 0.00
 0.00

 D4
 0.00
 0.00
 0.33
 0.00
 0.17

 D5
 0.20
 0.17
 0.33
 0.00
 0.33

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Min-Apriori

New definition of support:

$$\sup(C) = \sum_{i \in T} \min_{j \in C} D(i, j)$$

TID	W1	W2	W3	W4	W5
D1	0.40	0.33	0.00 0.33 0.00 0.33 0.33	0.00	0.17
D2	0.00	0.00	0.33	1.00	0.33
D3	0.40	0.50	0.00	0.00	0.00
D4	0.00	0.00	0.33	0.00	0.17
D5	0.20	0.17	0.33	0.00	0.33

Example:

Sup(W1,W2)

$$= .33 + 0 + .4 + 0 + 0.17$$

= 0.9

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Anti-monotone property of Support

			W3		
D1	0.40	0.33	0.00	0.00	0.17
D2	0.00	0.00	0.33	1.00	0.33
D3	0.40	0.50	0.00	0.00	0.00
D4	0.00	0.00	0.33	0.00	0.17
D5	0.20	0.17	0.33	0.00	0.33

Example:

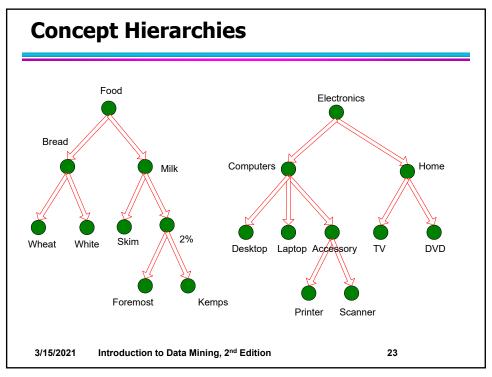
$$Sup(W1) = 0.4 + 0 + 0.4 + 0 + 0.2 = 1$$

$$Sup(W1, W2) = 0.33 + 0 + 0.4 + 0 + 0.17 = 0.9$$

$$Sup(W1, W2, W3) = 0 + 0 + 0 + 0 + 0.17 = 0.17$$

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Multi-level Association Rules

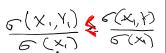
- Why should we incorporate concept hierarchy?
 - Rules at lower levels may not have enough support to appear in any frequent itemsets
 - Rules at lower levels of the hierarchy are overly specific
 - e.g., following rules are indicative of association between milk and bread
 - skim milk \rightarrow white bread,
 - -2% milk \rightarrow wheat bread,
 - skim milk \rightarrow wheat bread, etc.
 - Rules at higher level of hierarchy may be too generic
 - e.g., electronics → food

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Multi-level Association Rules

- How do support and confidence vary as we traverse the concept hierarchy?
 - If $\sigma(X1 \cup Y1) \ge \text{minsup}$, and X is parent of X1, Y is parent of Y1 then $\sigma(X \cup Y1) \ge \text{minsup}$, $\sigma(X1 \cup Y) \ge \text{minsup}$ $\sigma(X \cup Y) \ge \text{minsup}$
 - If conf(X1 ⇒ Y1) ≥ minconf,
 then conf(X1 ⇒ Y) ≥ minconf



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Multi-level Association Rules

- Approach 1:
 - Extend current association rule formulation by augmenting each transaction with higher level items

Original Transaction: {skim milk, wheat bread}

Augmented Transaction:

{skim milk, wheat bread, milk, bread, food}

- Issues:
 - Items that reside at higher levels have much higher support counts
 - if support threshold is low, too many frequent patterns involving items from the higher levels
 - Increased dimensionality of the data

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Multi-level Association Rules

- Approach 2:
 - Generate frequent patterns at highest level first
 - Then, generate frequent patterns at the next highest level, and so on
- Issues:
 - I/O requirements will increase dramatically because we need to perform more passes over the data
 - May miss some potentially interesting cross-level association patterns

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Sequential Patterns

Examples of Sequence

- Sequence of different transactions by a customer at an online store:
 - < {Digital Camera,iPad} {memory card} {headphone,iPad cover} >
- Sequence of initiating events causing the nuclear accident at 3-mile Island:

(http://stellar-one.com/nuclear/staff_reports/summary_SOE_the_initiating_event.htm)

- < {clogged resin} {outlet valve closure} {loss of feedwater} {condenser polisher outlet valve shut} {booster pumps trip} {main waterpump trips} {main turbine trips} {reactor pressure increases}>
- Sequence of books checked out at a library:

<{Fellowship of the Ring} {The Two Towers} {Return of the King}>

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Sequential Pattern Discovery: Examples

- In telecommunications alarm logs,
 - Inverter_Problem:

```
(Excessive_Line_Current) (Rectifier_Alarm) --> (Fire_Alarm)
```

- In point-of-sale transaction sequences,
 - Computer Bookstore:

```
(Intro_To_Visual_C) (C++_Primer) --> (Perl_for_dummies,Tcl_Tk)
```

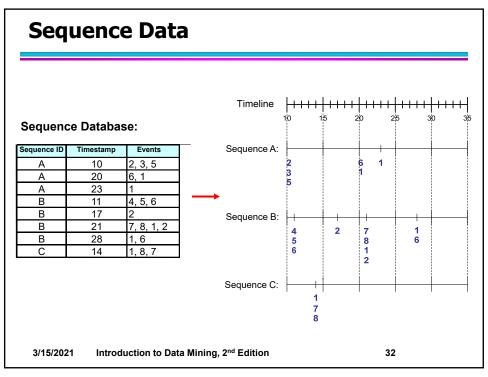
Athletic Apparel Store:

(Shoes) (Racket, Racketball) --> (Sports_Jacket)

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Sequence Data Sequence **Element** Sequence **Event Database** (Transaction) (Item) A set of items bought by Customer Purchase history of a given Books, diary products, customer a customer at time t CDs, etc Web Data Browsing activity of a A collection of files Home page, index particular Web visitor viewed by a Web visitor page, contact info, etc after a single mouse click History of events generated Events triggered by a Event data Types of alarms by a given sensor sensor at time t generated by sensors Genome DNA sequence of a An element of the DNA Bases A,T,G,C sequences particular species sequence Element Event (Transaction) E1 É3 (Item) E2 Sequence 3/15/2021 Introduction to Data Mining, 2nd Edition 31



Sequence Data vs. Market-basket Data

Sequence Database:

Customer	Date	Items bought
Α	10	2, 3, 5
А	20	1,6
А	23	1
В	11	4, 5, 6
В	17	2
В	21	1,2,7,8
В	28	1, 6
С	14	1,7,8

Market- basket Data

Events
2, 3, 5
1,6
1
4,5,6
2
1,2,7,8
1,6
1.7.8

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Sequence Data vs. Market-basket Data

Sequence Database:

Customer	Date	Items bought	
Α	10	2 , 3, 5	
Α	20	1 ,6	
А	23	1	
В	11	4, 5, 6	
В	17	2	
В	21	1,2,7,8	
В	28	1, 6	
С	14	1,7,8	

Market- basket Data

Events
2, 3, 5
1,6
1
4,5,6
2
1,2,7,8
1,6
1,7,8

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Formal Definition of a Sequence

A sequence is an ordered list of elements

$$s = < e_1 e_2 e_3 ... >$$

Each element contains a collection of events (items)

$$e_i = \{i_1, i_2, ..., i_k\}$$

- Length of a sequence, |s|, is given by the number of elements in the sequence
- A k-sequence is a sequence that contains k events (items)
 - <{a,b} {a}> has a length of 2 and it is a 3-sequence

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Formal Definition of a Subsequence

- A sequence t: <a₁ a₂ ... a_n> is contained in another sequence s: <b₁ b₂ ... b_m> (m ≥ n) if there exist integers i₁ < i₂ < ... < i_n such that a₁ ⊆ b_{i1}, a₂ ⊆ b_{i2}, ..., a_n ⊆ b_{in}
- Illustrative Example:

s: t: b₁

 b_2 b_3 a_1 a_2

b₄

t is a subsequence of s if $a_1 \subseteq b_2$, $a_2 \subseteq b_3$, $a_3 \subseteq b_5$.

Data sequence	Subsequence	Contain?
< {2,4} {3,5,6} {8} >	< {2} {8} >	Yes
< {1,2} {3,4} >	< {1} {2} >	No
< {2,4} {2,4} {2,5} >	< {2} {4} >	Yes
<{2,4} {2,5} {4,5}>	< {2} {4} {5} >	No
<{2,4} {2,5} {4,5}>	< {2} {5} {5} >	Yes
<{2,4} {2,5} {4,5}>	< {2, 4, 5} >	No

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Sequential Pattern Mining: Definition

- The support of a subsequence w is defined as the fraction of data sequences that contain w
- A sequential pattern is a frequent subsequence
 (i.e., a subsequence whose support is ≥ minsup)
- Given:
 - a database of sequences
 - a user-specified minimum support threshold, minsup
- Task:
 - Find all subsequences with support ≥ minsup

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Sequential Pattern Mining: Example

Object	Timestamp	Events
Α	1	1,2,4
Α	2	2,3
Α	3	5
В	1	1,2
В	2	2,3,4 1, 2 2,3,4 2,4,5
С	1	1, 2
С	2	2,3,4
С	3	2,4,5
D	1	2
D	2	3, 4
D	3	4, 5
E	1	1, 3
E	2	2, 4, 5

```
Minsup = 50%
```

Examples of Frequent Subsequences:

```
< {1,2} >
                  s=60%
< {2,3} >
                  s=60%
                  s=80%
< {2,4}>
< {3} {5}>
                  s=80%
< {1} {2} >
                  s=80%
                  s=60%
< {2} {2} >
                  s=60%
< {2} {2,3} >
                  s=60%
< {1,2} {2,3} >
                  s=60%
```

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Sequence Data vs. Market-basket Data

Sequence Database:

Customer	Date	Items bought	
Α	10	2 , 3, 5	
А	20	1 ,6	
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В	11	4, 5, 6	
В	17	2	
В	21	1,2,7,8	
В	28	1, 6	
С	14	1,7,8	

{2}
$$\rightarrow$$
 {1}
$$conf({2} \rightarrow {1}) = \frac{\sigma({2} {1})}{\sigma({2})}$$

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Market- basket Data

Events
2, 3, 5
1,6
1
4,5,6
2
1,2,7,8
1,6
1,7,8

(1,8) -> (7)
$$conf(1,8) \to (7)) = \frac{\sigma(1,7,8)}{\sigma(\{1,8\})}$$

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Extracting Sequential Patterns

- Given n events: i_1 , i_2 , i_3 , ..., i_n
- Candidate 1-subsequences:

Candidate 2-subsequences:

$$<\{i_1, i_2\}>, <\{i_1, i_3\}>, ...,$$

 $<\{i_1\} \{i_1\}>, <\{i_1\} \{i_2\}>, ..., <\{i_n\} \{i_n\}>$

Candidate 3-subsequences:

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Extracting Sequential Patterns: Simple example

- Given 2 events: a, b
- Candidate 1-subsequences:



Item-set patterns

Candidate 2-subsequences:

Candidate 3-subsequences:

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Generalized Sequential Pattern (GSP)

- Step 1:
 - Make the first pass over the sequence database D to yield all the 1element frequent sequences
- Step 2:

Repeat until no new frequent sequences are found

- Candidate Generation:
 - Merge pairs of frequent subsequences found in the (k-1)th pass to generate candidate sequences that contain k items
- Candidate Pruning:
 - ◆ Prune candidate k-sequences that contain infrequent (k-1)-subsequences
- Support Counting:
 - Make a new pass over the sequence database D to find the support for these candidate sequences
- Candidate Elimination:
 - Eliminate candidate k-sequences whose actual support is less than minsup

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Candidate Generation

- Base case (k=2):
 - Merging two frequent 1-sequences $\{i_1\}$ and $\{i_2\}$ will produce the following candidate 2-sequences: $\{i_1\}$ $\{i_1\}$, $\{i_1\}$, $\{i_2\}$, $\{i_2\}$ $\{i_2\}$, $\{i_2\}$ and $\{i_1, i_2\}$. (**Note**: $\{i_1\}$ can be merged with itself to produce: $\{i_1\}$ $\{i_1\}$)
- General case (k>2):
 - A frequent (k-1)-sequence w₁ is merged with another frequent (k-1)-sequence w₂ to produce a candidate k-sequence if the subsequence obtained by removing an event from the first element in w₁ is the same as the subsequence obtained by removing an event from the last element in w₂

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Candidate Generation

- Base case (k=2):
 - Merging two frequent 1-sequences $<\{i_1\}>$ and $<\{i_2\}>$ will produce the following candidate 2-sequences: $<\{i_1\}$ $\{i_1\}>$, $<\{i_1\}$ $\{i_2\}>$, $<\{i_2\}$ $\{i_2\}>$, $<\{i_2\}$ $\{i_1\}>$ and $<\{i_1,i_2\}>$. (**Note**: $<\{i_1\}>$ can be merged with itself to produce: $<\{i_1\}$ $\{i_1\}>$)
- General case (k>2):
 - A frequent (k-1)-sequence w₁ is merged with another frequent (k-1)-sequence w₂ to produce a candidate k-sequence if the subsequence obtained by removing an event from the first element in w₁ is the same as the subsequence obtained by removing an event from the last element in w₂
 - \bullet The resulting candidate after merging is given by extending the sequence $w_1\,$ as follows-
 - If the last element of w₂ has only one event, append it to w₁
 - Otherwise add the event from the last element of w₂ (which is absent in the last element of w₁) to the last element of w₁

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Candidate Generation Examples

- Merging w₁=<{1 2 3} {4 6}> and w₂ =<{2 3} {4 6} {5}> produces the candidate sequence < {1 2 3} {4 6} {5}> because the last element of w₂ has only one event
- Merging w_1 =<{1} {2 3} {4}> and w_2 =<{2 3} {4 5}> produces the candidate sequence < {1} {2 3} {4 5}> because the last element in w_2 has more than one event
- Merging w₁=<{1 2 3} > and w₂ =<{2 3 4} > produces the candidate sequence < {1 2 3 4}> because the last element in w₂ has more than one event
- We do not have to merge the sequences $w_1 = <\{1\} \{2 \ 6\} \{4\} >$ and $w_2 = <\{1\} \{2 \ 6\} \{4 \ 5\} >$ to produce the candidate $<\{1\} \{2 \ 6\} \{4 \ 5\} >$ because if the latter is a viable candidate, then it can be obtained by merging w_1 with $<\{2 \ 6\} \{4 \ 5\} >$

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Candidate Generation: Examples (ctd)

- Can <{a},{b},{c}> merge with <{b},{c},{f}> ?
- Can <{a},{b},{c}> merge with <{b,c},{f}>?
- Can <{a},{b},{c}> merge with <{b},{c,f}>?
- Can <{a,b},{c}> merge with <{b},{c,f}> ?
- Can <{a,b,c}> merge with <{b,c,f}>?
- Can <{a}> merge with <{a}>?

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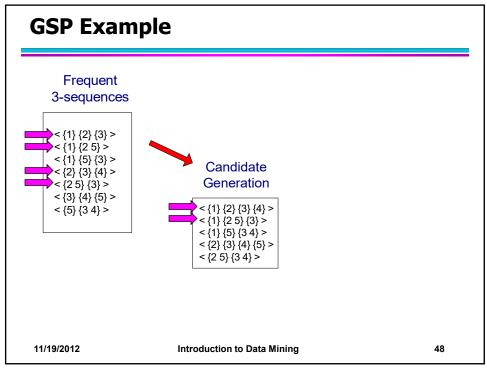
Candidate Generation: Examples (ctd)

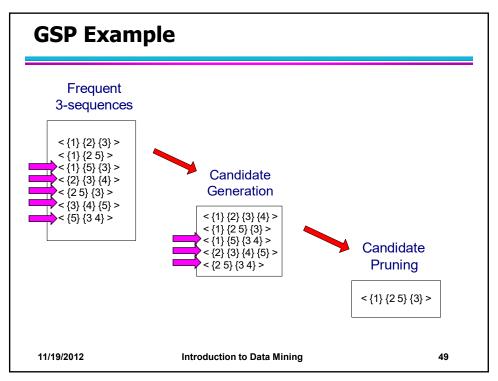
- <{a},{b},{c}> can be merged with <{b},{c},{f}> to produce <{a},{b},{c},{f}>
- <{a},{b},{c}> cannot be merged with <{b,c},{f}>
- <{a},{b},{c}> can be merged with <{b},{c,f}> to produce <{a},{b},{c,f}>
- <{a,b},{c}> can be merged with <{b},{c,f}> to produce <{a,b},{c,f}>
- <{a,b,c}> can be merged with <{b,c,f}> to produce <{a,b,c,f}>
- <{a}{b}{a}> can be merged with <{b}{a}{b}> to produce <{a},{b},{a},{b}>
- <{b}{a}{b}> can be merged with <{a}{b}{a}> to produce <{b},{a},{b},{a}>

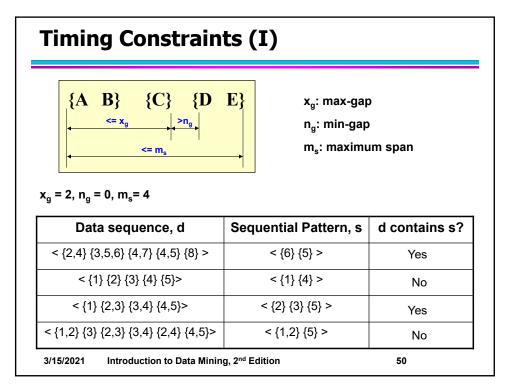
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Mining Sequential Patterns with Timing Constraints

- Approach 1:
 - Mine sequential patterns without timing constraints
 - Postprocess the discovered patterns
- Approach 2:
 - Modify GSP to directly prune candidates that violate timing constraints
 - Question:
 - ◆ Does Apriori principle still hold?

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Apriori Principle for Sequence Data

Object	Timestamp	Events
Α	1	1,2,4
Α	2	2,3
Α	3	5
В	1	1,2
В	2	231
С	1	1, 2
С	2	2,3,4 2,4,5
С	3	2,4,5
D	1	2
D	2	3, 4
D	3	4, 5
Е	1	1, 3
F	2	2.4.5

Suppose:

$$x_g = 1 \text{ (max-gap)}$$

 $n_g = 0 \text{ (min-gap)}$
 $m_s = 5 \text{ (maximum span)}$
 $minsup = 60\%$

Problem exists because of max-gap constraint

No such problem if max-gap is infinite

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Contiguous Subsequences

s is a contiguous subsequence of

$$w = \langle e_1 \rangle \langle e_2 \rangle ... \langle e_k \rangle$$

if any of the following conditions hold:

- 1. s is obtained from w by deleting an item from either e₁ or e_k
- 2. s is obtained from w by deleting an item from any element \mathbf{e}_i that contains at least 2 items
- 3. s is a contiguous subsequence of s' and s' is a contiguous subsequence of w (recursive definition)
- Examples: s = < {1} {2} >
 - is a contiguous subsequence of

is not a contiguous subsequence of < {1} {3} {2}> and < {2} {1} {3} {2}>

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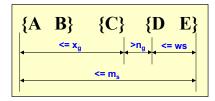
Modified Candidate Pruning Step

- Without maxgap constraint:
 - A candidate k-sequence is pruned if at least one of its (k-1)-subsequences is infrequent
- With maxgap constraint:
 - A candidate k-sequence is pruned if at least one of its contiguous (k-1)-subsequences is infrequent

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Timing Constraints (II)



x_g: max-gap

n_q: min-gap

ws: window size

m_s: maximum span

$$x_g = 2$$
, $n_g = 0$, ws = 1, $m_s = 5$

Data sequence, d	Sequential Pattern, s	d contains s?
< {2,4} {3,5,6} {4,7} {4,5} {8} >	< {3,4,5}>	Yes
< {1} {2} {3} {4} {5}>	< {1,2} {3,4} >	No
< {1,2} {2,3} {3,4} {4,5}>	< {1,2} {3,4} >	Yes

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Modified Support Counting Step

- Given a candidate sequential pattern: <{a, c}>
 - Any data sequences that contain

<... {a} ... {c}...> (where time({c}) – time({a})
$$\leq$$
 ws) <...{c} ... {a} ...> (where time({a}) – time({c}) \leq ws)

$$<...\{c\}...\{a\}...>$$
 (where time($\{a\}$) – time($\{c\}$) \leq ws)

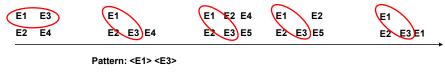
will contribute to the support count of candidate pattern

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Other Formulation

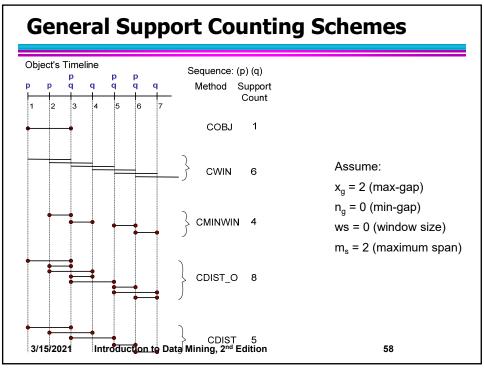
- In some domains, we may have only one very long time series
 - Example:
 - monitoring network traffic events for attacks
 - monitoring telecommunication alarm signals
- Goal is to find frequent sequences of events in the time series
 - This problem is also known as frequent episode mining



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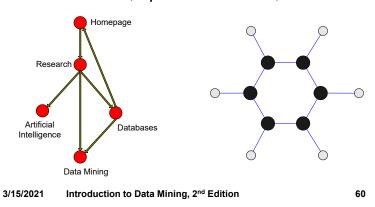
Data Mining Association Analysis: Advanced Concepts

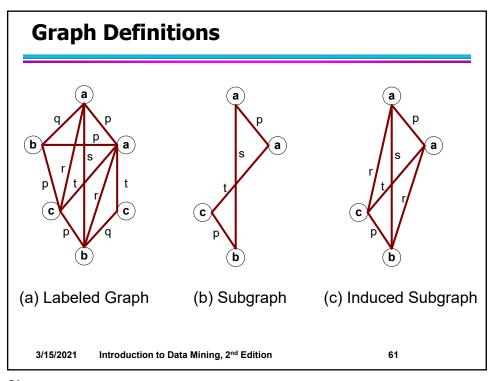
Subgraph Mining

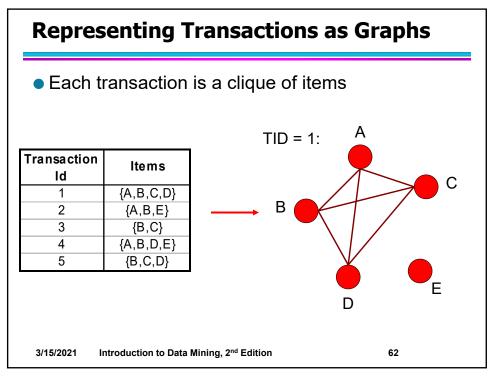
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Frequent Subgraph Mining

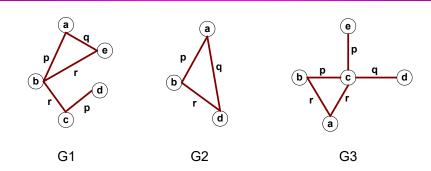
- Extends association analysis to finding frequent subgraphs
- Useful for Web Mining, computational chemistry, bioinformatics, spatial data sets, etc











ſ		(a,b,p)	(a,b,q)	(a,b,r)	(b,c,p)	(b,c,q)	(b,c,r)	 (d,e,r)
Ī	G1	1	0	0	0	0	1	 0
	G2	1	0	0	0	0	0	 0
	G3	0	0	1	1	0	0	 0
	G3							

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Challenges

- Node may contain duplicate labels
- Support and confidence
 - How to define them?
- Additional constraints imposed by pattern structure
 - Support and confidence are not the only constraints
 - Assumption: frequent subgraphs must be connected
- Apriori-like approach:
 - Use frequent k-subgraphs to generate frequent (k+1) subgraphs
 - ♦What is k?

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Challenges...

- Support:
 - number of graphs that contain a particular subgraph
- Apriori principle still holds
- Level-wise (Apriori-like) approach:
 - Vertex growing:
 - k is the number of vertices
 - Edge growing:
 - ♦ k is the number of edges

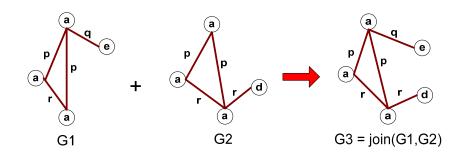
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Vertex Growing

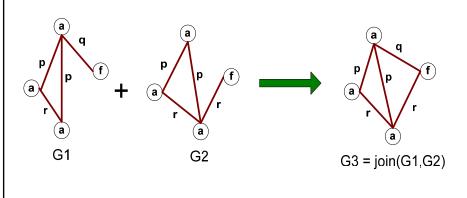


$$M_{G1} = \begin{pmatrix} 0 & p & p & q \\ p & 0 & r & 0 \\ p & r & 0 & 0 \\ q & 0 & 0 & 0 \end{pmatrix} \qquad M_{G2} = \begin{pmatrix} 0 & p & p & 0 \\ p & 0 & r & 0 \\ p & r & 0 & r \\ 0 & 0 & r & 0 \end{pmatrix} \qquad M_{G3} = \begin{pmatrix} 0 & p & p & q & 0 \\ p & 0 & r & 0 & 0 \\ p & r & 0 & 0 & r \\ q & 0 & 0 & 0 & ? \\ 0 & 0 & r & ? & 0 \end{pmatrix}$$

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Edge Growing



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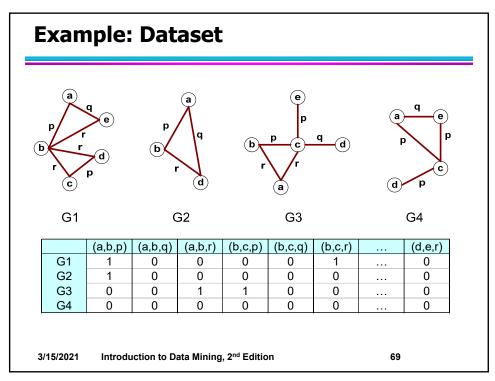
Apriori-like Algorithm

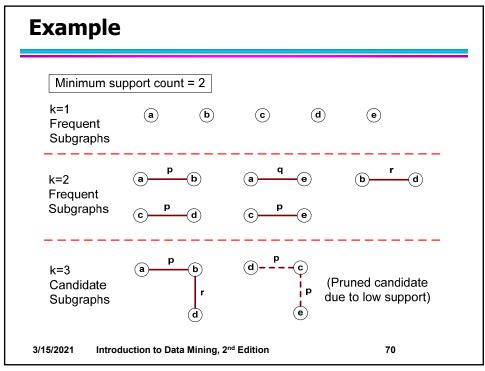
- Find frequent 1-subgraphs
- Repeat
 - Candidate generation
 - ◆ Use frequent (*k-1*)-subgraphs to generate candidate *k*-subgraph
 - Candidate pruning
 - ◆ Prune candidate subgraphs that contain infrequent (k-1)-subgraphs
 - Support counting
 - Count the support of each remaining candidate
 - Eliminate candidate k-subgraphs that are infrequent

In practice, it is not as easy. There are many other issues

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Candidate Generation

- In Apriori:
 - Merging two frequent k-itemsets will produce a candidate (k+1)-itemset
- In frequent subgraph mining (vertex/edge growing)
 - Merging two frequent k-subgraphs may produce more than one candidate (k+1)-subgraph

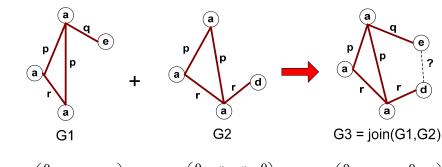
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Multiplicity of Candidates (Vertex Growing)



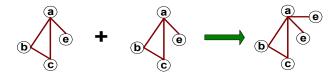
$$M_{a1} = \begin{pmatrix} 0 & p & p & q \\ p & 0 & r & 0 \\ p & r & 0 & 0 \\ q & 0 & 0 & 0 \end{pmatrix} \qquad M_{a2} = \begin{pmatrix} 0 & p & p & 0 \\ p & 0 & r & 0 \\ p & r & 0 & r \\ 0 & 0 & r & 0 \end{pmatrix} \qquad M_{a3} = \begin{pmatrix} 0 & p & p & 0 & q \\ p & 0 & r & 0 & 0 \\ p & r & 0 & r & 0 \\ 0 & 0 & r & 0 & ? \\ q & 0 & 0 & ? & 0 \end{pmatrix}$$

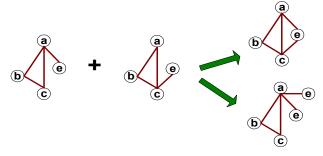
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Multiplicity of Candidates (Edge growing)

Case 1: identical vertex labels





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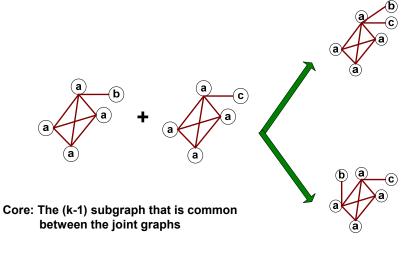
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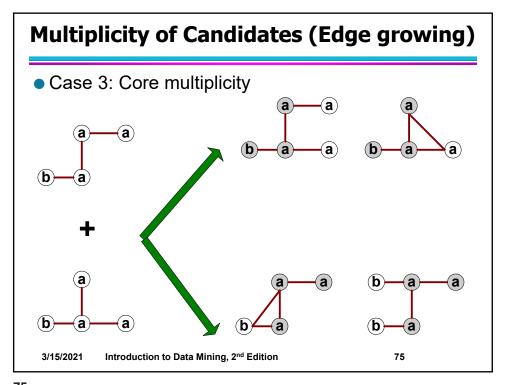
Multiplicity of Candidates (Edge growing)

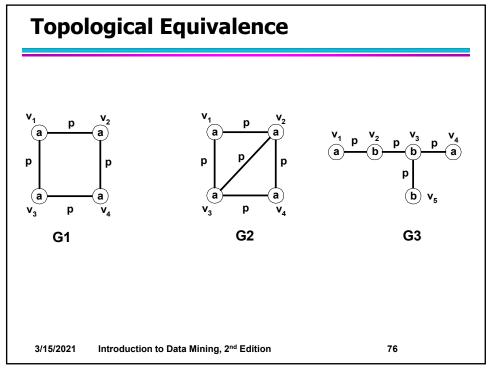
Case 2: Core contains identical labels



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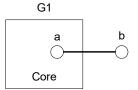
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Candidate Generation by Edge Growing

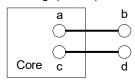
• Given:



Core d

Case 1: a ≠ c and b ≠ d

G3 = Merge(G1,G2)



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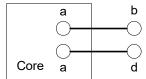
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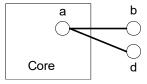
Candidate Generation by Edge Growing

• Case 2: a = c and b ≠ d

G3 = Merge(G1,G2)



G3 = Merge(G1,G2)



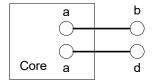
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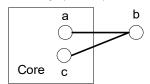
Candidate Generation by Edge Growing

Case 3: a ≠ c and b = d

G3 = Merge(G1,G2)



G3 = Merge(G1,G2)



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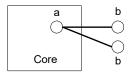
Candidate Generation by Edge Growing

• Case 4: a = c and b = d

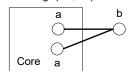
G3 = Merge(G1,G2)



G3 = Merge(G1,G2)



G3 = Merge(G1,G2)

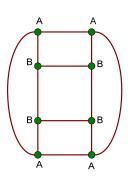


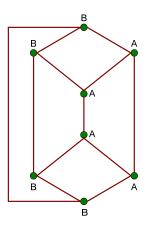
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Graph Isomorphism

 A graph is isomorphic if it is topologically equivalent to another graph





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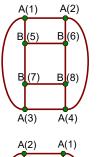
Graph Isomorphism

- Test for graph isomorphism is needed:
 - During candidate generation step, to determine whether a candidate has been generated
 - During candidate pruning step, to check whether its (k-1)-subgraphs are frequent
 - During candidate counting, to check whether a candidate is contained within another graph

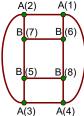
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	A(1)	A(2)	A(3)	A(4)	B(5)	B(6)	B(7)	B(8)
A(1)	1	1	1	0	1	0	0	0
A(2)	1	1	0	1	0	1	0	0
A(3)	1	0	1	1	0	0	1	0
A(4)	0	1	1	1	0	0	0	1
B(5)	1	0	0	0	1	1	1	0
B(6)	0	1	0	0	1	1	0	1
B(7)	0	0	1	0	1	0	1	1
B(8)	0	0	0	1	0	1	1	1



	A(1)	A(2)	A(3)	A(4)	B(5)	B(6)	B(7)	B(8)
A(1)	1	1	0	1	0	1	0	0
A(2)	1	1	1	0	0	0	1	0
A(3)	0	1	1	1	1	0	0	0
A(4)	1	0	1	1	0	0	0	1
B(5)	0	0	1	0	1	0	1	1
B(6)	1	0	0	0	0	1	1	1
B(7)	0	1	0	0	1	1	1	0
B(8)	0	0	0	1	1	1	0	1

· The same graph can be represented in many ways

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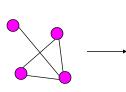
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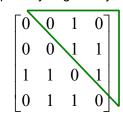
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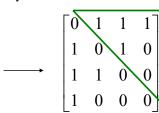
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Graph Isomorphism

- Use canonical labeling to handle isomorphism
 - Map each graph into an ordered string representation (known as its code) such that two isomorphic graphs will be mapped to the same canonical encoding
 - Example:
 - Lexicographically largest adjacency matrix







String: 011011

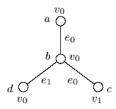
Canonical: 111100

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Example of Canonical Labeling (Kuramochi & Karypis, ICDM 2001)

• Graph:



Adjacency matrix representation:

id	a	b	c	d
label	v_0	v_0	v_1	v_0
\overline{a}	0	e_0	0	0
b	e_0	0	e_0	e_1
c	0	e_0	0	0
d	0	e_1	0	0

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Example of Canonical Labeling (Kuramochi & Karypis, ICDM 2001)

• Order based on vertex degree:

id	a	c	d	b
label	v_0	v_1	v_0	v_0
partition		0		1
a	0	0	0	e_0
c	0	0	0	e_0
d	0	0	0	e_1
b	e_0	e_0	e_1	0

Order based on vertex labels:

id	d	a	c	b
label	v_0	v_0	v_1	v_0
partition	0		1	2
d	0	0	0	e_1
a	0	0	0	e_0
c	0	0	0	e_0
b	e_1	e_0	e_0	0

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Example of Canonical Labeling (Kuramochi & Karypis, ICDM 2001)

• Find canonical label:

id	d	a	c	b
label	v_0	v_0	v_1	v_0
partition	0		1	2
d	0	0	0	e_1
a	0	0	0	e_0
c	0	0	0	e_0
b	e_0	e_1	e_0	0

id	a	d	c	b
label	v_0	v_0	v_1	v_0
partition	0		1	2
a	0	0	0	e_0
d	0	0	0	e_1
c	0	0	0	e_0
b	e_0	e_1	e_0	0

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0 0 0 e₁ e₀ e₀ > 0 0 0 e₀ e₁ e₀

(Canonical Label)

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