

2009년 연구 결과

- ▶ 두 편의 데이터 베이스 분야의 Top Conference 논문 게재 및 게재 승인
 - Wook-Shin Han and Jinsoo Lee, “*Dependency-Aware Reordering for Parallelizing Query Optimization in Multi-Core CPUs,*” In SIGMOD 2009.
 - Wook-Shin Han, Wooseong Kwak, and Hwanjo Yu, “*On Supporting Effective Web Extraction,*” In ICDE 2010.



The screenshot shows a web browser window with a search result for "ATP". The main content is a table with columns: Gene Symbol, Gene Name, and Matching Alias. The table lists three gene entities: ABCA1, ABCA2, and ABCA3. A red box highlights a RAQuery window with the following text:

```
RAQuery
For e1 in Match(text="Gene Symbol") and
all in Match(e1)
where F1(e1, e1) is STARTS or DURING or FINISHES or EQUAL,
return e1.text()
Filter=Match XPath1
//*/A
Reference elements
Text
Gene Symbol
Position
(160, 195)
```

Graph Indexing: A Frequent Structure-based Approach

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January 2010

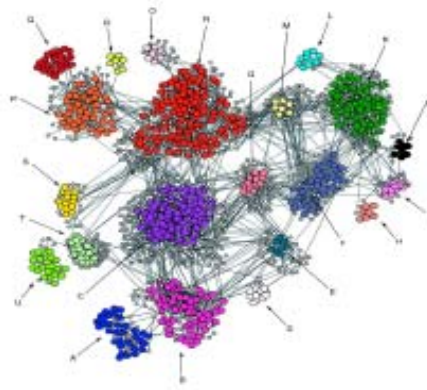
Xifeng Yan, Philip S. Yu, and Jiawei Han, "Graph Indexing: A Frequent Structure-based Approach," In SIGMOD 2004

Why Graph Searching?

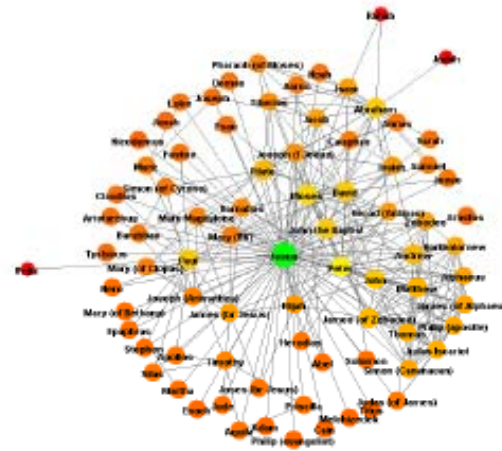
- ▶ Graphs are ubiquitous
 - Chemical compounds (Cheminformatics)
 - Protein structures, biological pathways/networks (Bioinformatics)
 - Program control flow, traffic flow, and work flow analysis
 - XML databases, Web, and social network analysis
- ▶ Graph is a general model
 - Trees, lattices, sequences, and items are degenerated graphs
- ▶ Complexity of algorithms: many problems are of high complexity

Graphs are Everywhere

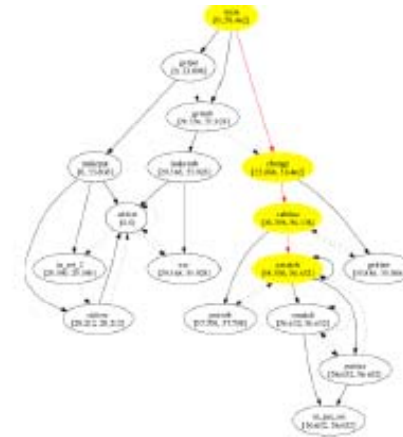
Magwene et al. *Genome Biology* 2004 5: R100



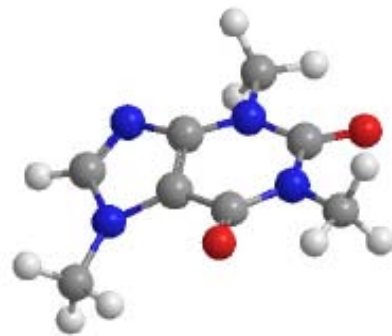
Co-expression Network



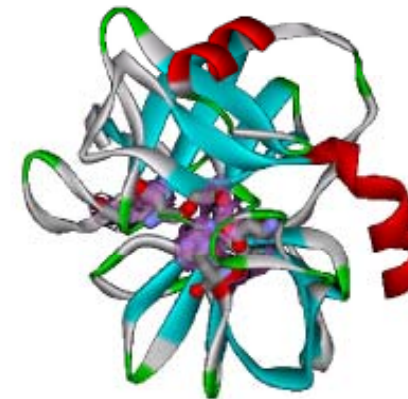
Social Network



Program Flow



Chemical Compound

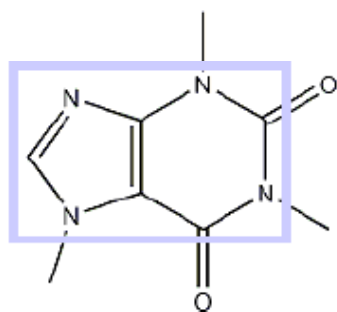


Protein Structure

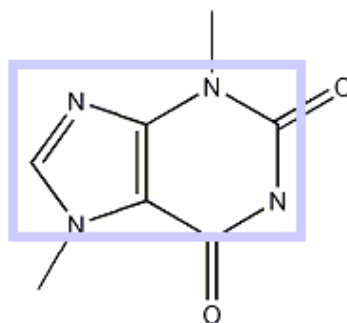
(c) Copyright by Han, Yan, Yu 2006

Example 1: Frequent Subgraphs

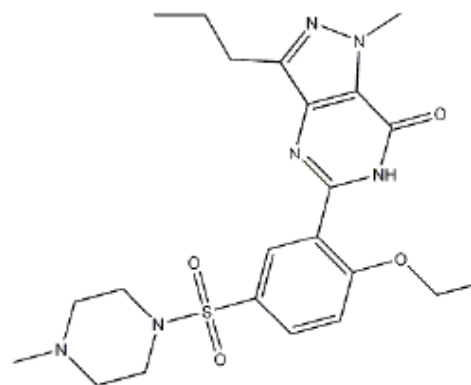
CHEMICAL COMPOUNDS



(a) caffeine



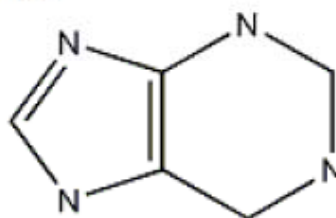
(b) diurobromine



(c) viagra

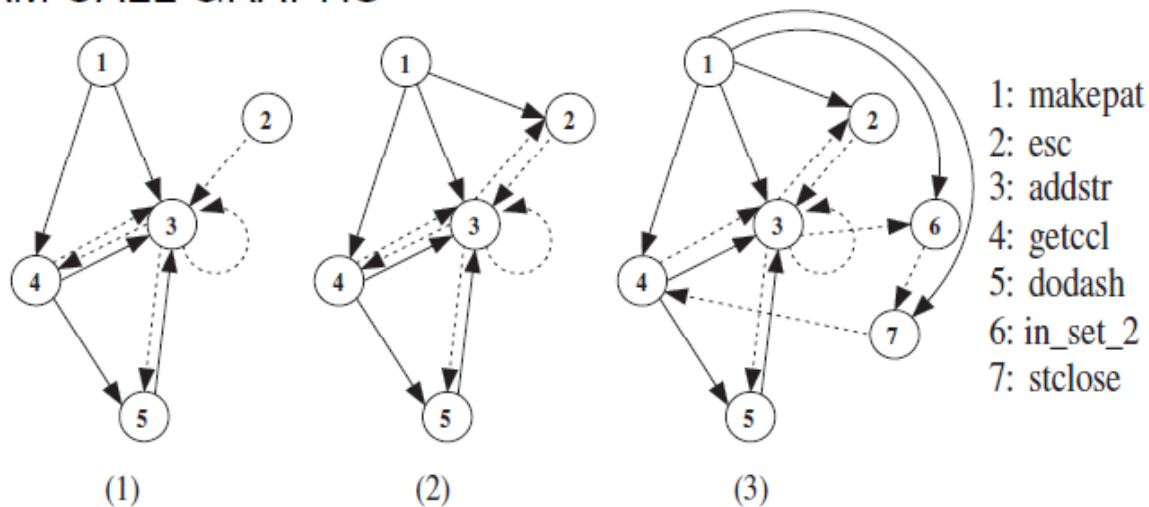
...

FREQUENT SUBGRAPH

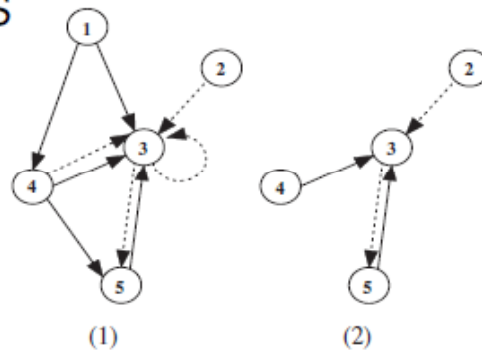


Example 2: Frequent Subgraphs

PROGRAM CALL GRAPHS

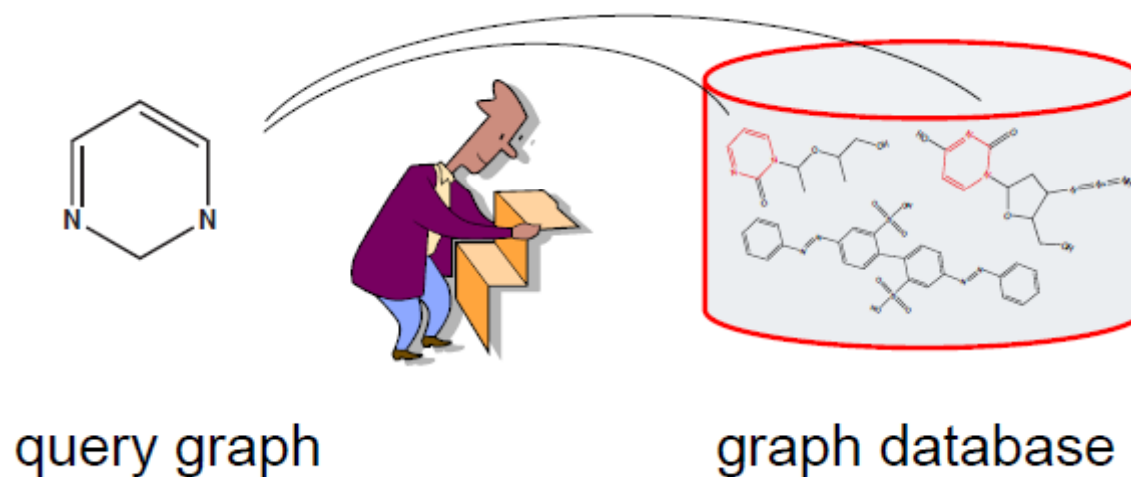


FREQUENT SUBGRAPHS (MIN SUPPORT IS 2)



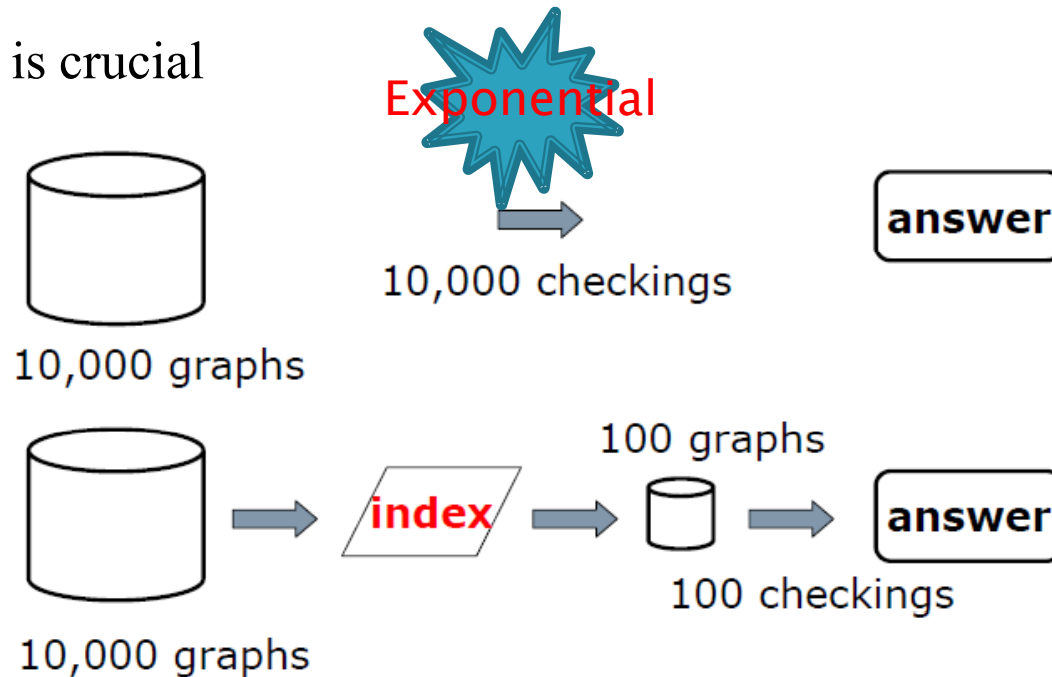
Graph Searching

- ▶ Find all of the graphs in a database that contain the query graph



Indexing Graphs

- ▶ Indexing is crucial



- ▶ Many graph indexing techniques are introduced.
 - GraphGrep, *gIndex*, Closure-Tree, Tree+Delta, GCoding, FG-Index, TreePI, SWIFT-Index ...

Problem Definition

- ▶ Find all of the graphs in a database that contain the query graph
- ▶ Given a graph database $D = \{g_1, g_2, \dots, g_n\}$ and a query graph q , finds the query answer set $D_q = \{g_i | q \subseteq g_i, g_i \in D\}$
- ▶ (Example) For the query q shown in Figure 2, the query answer set, D_q , has only one element: graph (c) in Figure 1.

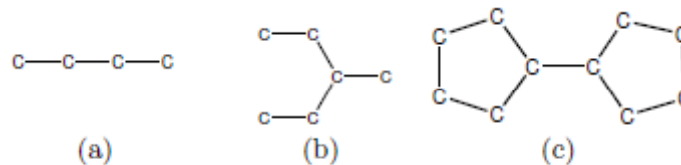


Figure 1: A Sample Database

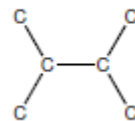


Figure 2: A Sample Query

Overview of the Framework

- ▶ Index construction (preprocessing step)
 - Enumerating all sub-graphs in a database D .
 - *Selecting graph feature set F* from the results of the first step.
 - The gIndex selects graph features which are frequent and discriminative
 - *Indexing graph feature set F* to find $D_f = \{g_i | f \subseteq g_i, g_i \in D\}$ efficiently for given $f \in F$.
 - Indexing selected graph features as a prefix tree
- ▶ Query processing
 - Filter: enumerates all the features in a query graph q , and *finds candidate query answer set* $C_q = \bigcap_f D_f (f \subseteq q \wedge f \in F)$ using the index.
 - Verify: verify graph g in C_q whether q is really a sub-graph of g (sub-graph isomorphic test).

Frequent Fragment

- ▶ $Support(g)$: the number of graphs in D where g is a sub-graph ($=|D_g|$).
- ▶ Frequent graph (Fragment): if $support(g) \geq minSup$, graph g is frequent.
 - (Example) graphs (a) and (b) in Figure 3 are frequent, if $minSup = 2$.

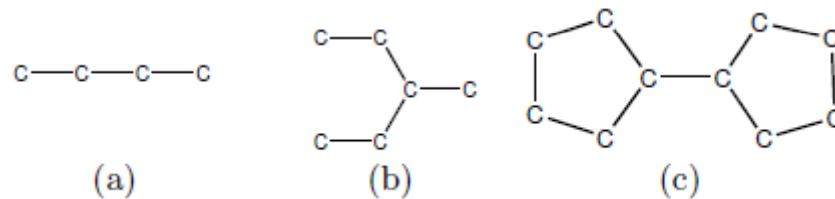


Figure 1: A Sample Database

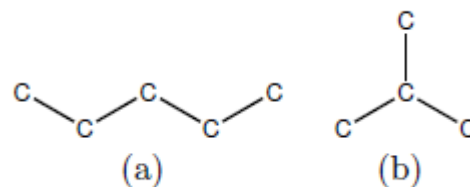


Figure 3: Frequent Fragments

Discriminativity

- ▶ $f \subseteq f'$ and $D_f = D_{f'}$ (and $support(f) = support(f')$)
 - f' does not provide more information than f if both are selected as indexing features.
 - f is more *discriminative* than f' .
 - f' should be removed from the feature set.

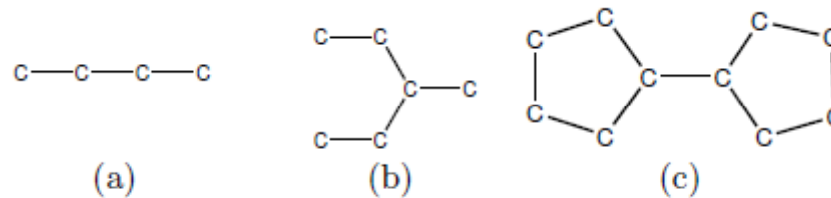
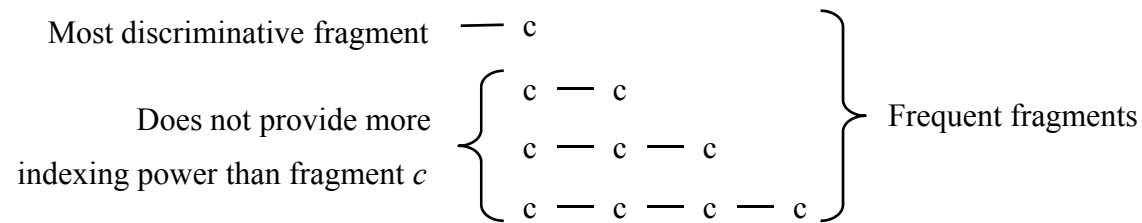


Figure 1: A Sample Database

Discriminative Ratio

- ▶ The measurement of the discriminativeness of a fragment x .
- ▶ Calculated by the following formula:

A set of graphs which contain the sub-graphs of x in the feature set

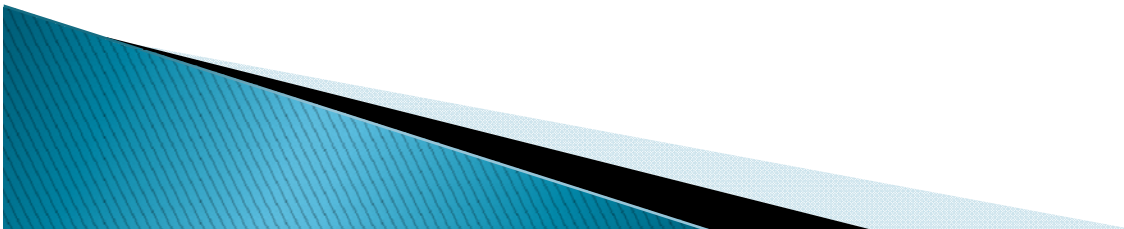
$$\gamma = \frac{\left| \bigcap_i D_{f_{\varphi_i}} \right|}{\left| D_x \right|}, f_{\varphi_i} \subseteq x, f_{\varphi_i} \in F, 1 \leq i \leq n$$

A set of graphs containing graph x

- ▶ Properties:
 - $\gamma \geq 1$.
 - when $\gamma = 1$, fragment x is completely redundant.
 - when $\gamma \gg 1$, fragment x is more discriminative than the combination of fragments f_{φ_i} .
- ▶ **Select frequent fragments whose γ is no less than pre-defined minimum discriminative ratio $\gamma_{min}(=2.0)$.**

Index Construction

- ▶ **Translates fragments** into sequences and holds them in a **prefix tree**.
- ▶ Each fragment is associated with (graph) id list (ids of graphs containing this fragment).
- ▶ Translating fragments: use the canonical DFS coding in *gSpan* [Yan02].
- ▶ Prefix tree: gIndex Tree proposed in this paper.



Algorithm – Search

Algorithm 2 Search

Input: Graph database D , Feature set F , Query q ,
and Maximum fragment size $maxL$.

Output: Candidate answer set C_q .

```
1: let  $C_q = D$ ;  
2: for each fragment  $x \subseteq q$  and  $len(x) \leq maxL$  do  
3:   if  $x \in F$  then  
4:      $C_q = C_q \cap D_x$ ;  
5: return  $C_q$ ;
```

- ▶ Input: graph database D , feature set F , query q , and maximum fragment size $maxL$.
- ▶ Output: candidate answer set C_q .

- ▶ Algorithm
 1. Enumerates all fragments up to a maximum size.
 2. Find graph id list using the gIndex.
 3. Intersects the id lists associated with these fragments.

- ▶ Optimization
 - Apriori pruning
 - Maximum discriminative fragments
 - Inner support

References

- ▶ [Sha02] D. Shasha, J. T-L Wnag, and R. Giugno. Algorithmics and applications of tree and graph searching, In PODS 2002.
- ▶ [Yan02] X. Yan and J. Han, gSpan: Graph-based substructure pattern mining, In ICDM 2002.