Mining Frequent Subgraphs from Linear Graphs

Yasuo Tabei

Computational Biology Research Center, AIST

Joint work with
Daisuke Okanohara (Univ. of Tokyo),
Shuichi Hirose (AIST),
Koji Tsuda (AIST)

Goal of this talk

- What is a linear graph?
- A property of linear graphs.
- Subgraph mining algorithm from linear graphs.

Outline

- Motivation
  - The needs for frequent subgraph mining algorithm
  - What is a linear graph?
- Method
  - Subgraph enumeration algorithm from a linear graph
  - Extension to frequent subgraph mining algorithm
- Experiments and Results
  - Motifs extraction from protein 3D-structures in molecular biology
  - Phrase extraction from predicate-argument structures in NLP
- Conclusion

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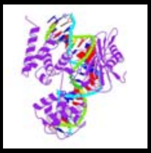
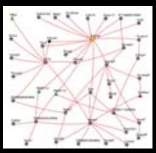
Data Represented as Graphs

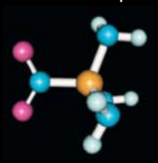
Protein 3D-Structure



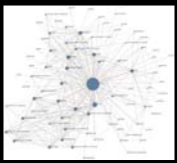
Gene co-expression Network



Chemical Compound



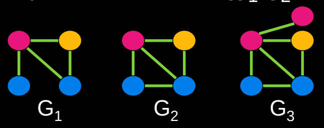
Social Network



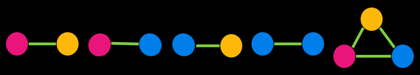
Frequent Subgraph Mining

- Enumerate all frequent subgraphs in a graph database

Input: graph database $G=\{g_1,g_2,\ldots,g_N\}$

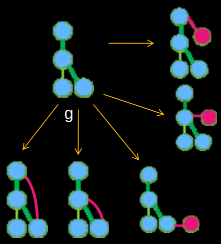


Output: frequent subgraphs appearing in at least m graphs



gSpan algorithm (Yan et al., 2002)

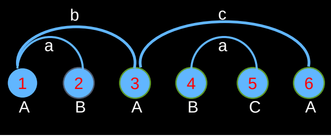
- Rightmost pattern extension
- Duplication can happen
- Minimum DFS code checking
  - Time exponential to pattern size



Linear Graph (Davydov et al., 2004)

- Labeled graph whose vertices are totally ordered
- Linear graph $g=(V,E,L^V,L^E)$
  - $V \subset N$: ordered vertex set
  - $E \subseteq V \times V$: edge set
  - $L^V: V \to \Sigma^V$: vertex labeling
  - $L^E: E \to \Sigma^E$: edge labeling

Ex) RNA, protein, alternative splicing forms, PAS



Linear Graph (Davydov et al., 2004)

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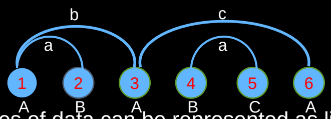


- Many types of data can be represented as linear graphs
  - Protein contact maps
  - Alternative splicing forms
  - RNA secondary structures
  - Predicate-argument structure

Linear Subgraph Relation

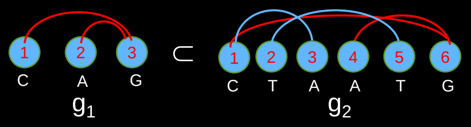
- g_1 is a linear subgraph of g_2

$\Leftrightarrow$ i)The ordinary subgraph condition

- the vertex labels are matched
- all edges of g_1 also exit in g_2 with the correct labels

ii) The order of vertices are conserved

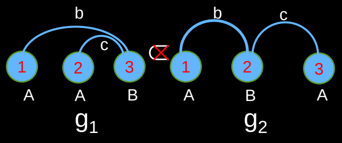
Ex)



Example of Not Linear Subgraph

- g_1 is not a linear subgraph of g_2
  - vertex labels are matched
  - all edges of g_1 also exit in g_2 with the correct labels
  - the order of vertices is not conserved

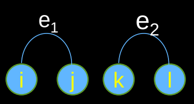
Ex)

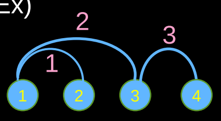


Total order among edges in a linear graph

- Compare the left nodes first. If they are identical, look at the right nodes
- $\forall e_1=(i,j), e_2=(k,l) \in E_g$, $e_1 <_e e_2$ if and only if (i)i<k or (ii)i=k, j < l

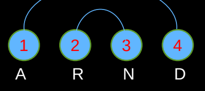
Ex)

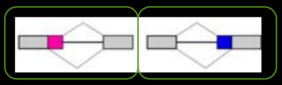




Disconnected Patterns

- Linear Graph: Sequence + Graph
- In sequence mining, gapped patterns are considered
- Need to mine disconnected patterns as well
- Data represented as disconnected patterns
  - Protein contact maps
  - RNA secondary structure
  - Alternative splicing





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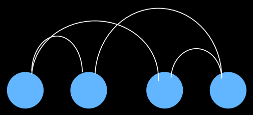
Overview of LGM: Linear Graph Miner

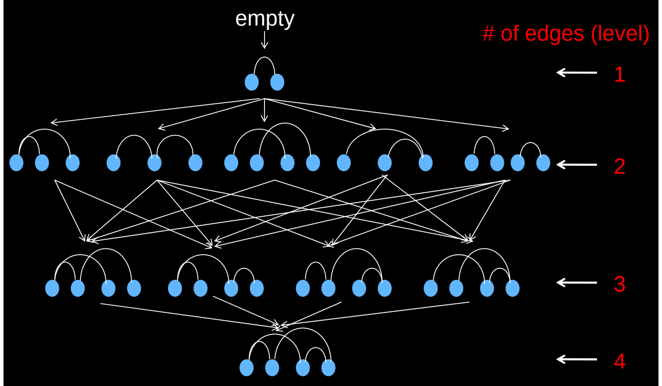
- Mining method of frequent linear subgraphs from a set of linear graphs
  - $|\{i=1,\ldots,|G|: g \subseteq g_i\}| \geq \sigma$ σ : minimum support threshold
- Mining both connected subgraphs and disconnected subgraphs with a unified framework
- For the efficient enumeration, we use reverse search techniques (Avis and Fukuda 1996).
- The computational time is polynomial delay.

Enumeration of All Linear Subgraphs of a Linear Graph

- Before considering a mining algorithm, we have to solve the problem of subgraph enumeration first
- How to enumerate all subgraphs of the following linear graph without duplication?

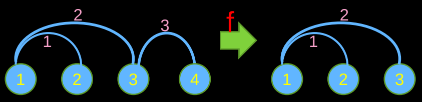


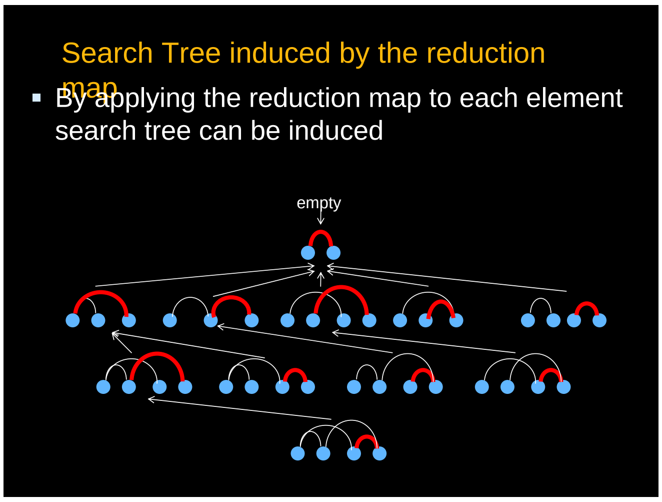
Search Lattice of All Subgraphs



Reverse Search (Avis and Fukuda, 1993)

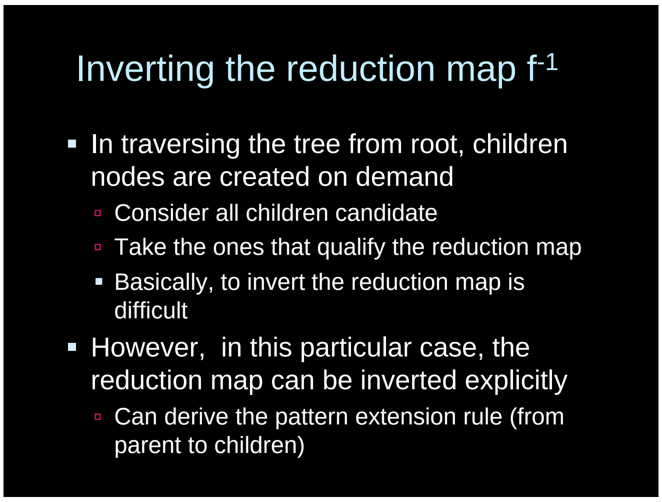
- All subgraphs can be enumerated by traversing the search lattice
  - To prevent duplication is difficult
- Need to define a search tree in the search lattice
- Reduction map f
  - Mapping from a child to its parent
  - Remove the largest edge





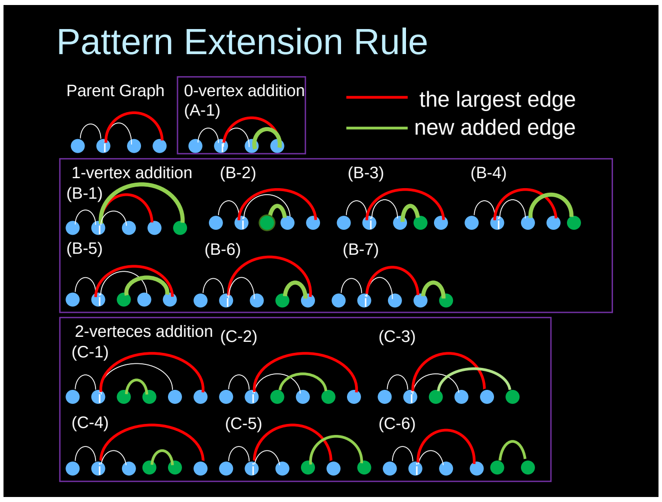
Search Tree induced by the reduction map

- By applying the reduction map to each element search tree can be induced

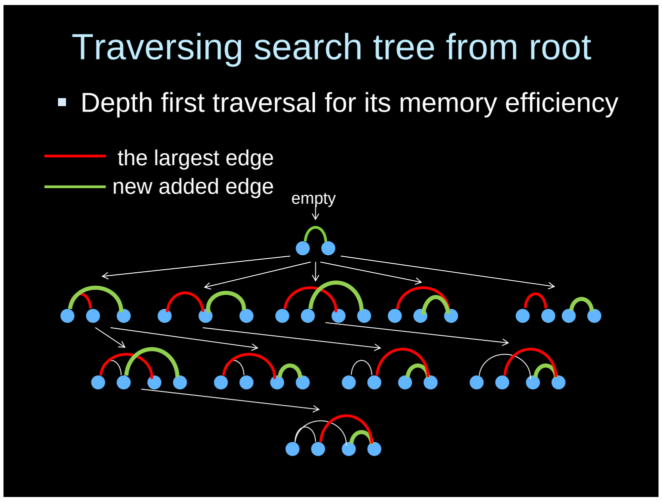


Inverting the reduction map f^{-1}

- In traversing the tree from root, children nodes are created on demand
  - Consider all children candidate
  - Take the ones that qualify the reduction map
  - Basically, to invert the reduction map is difficult
- However, in this particular case, the reduction map can be inverted explicitly
  - Can derive the pattern extension rule (from parent to children)

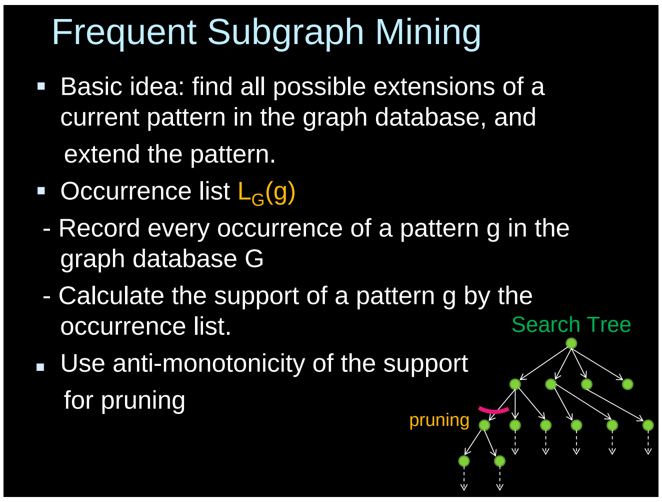


Pattern Extension Rule



Traversing search tree from root

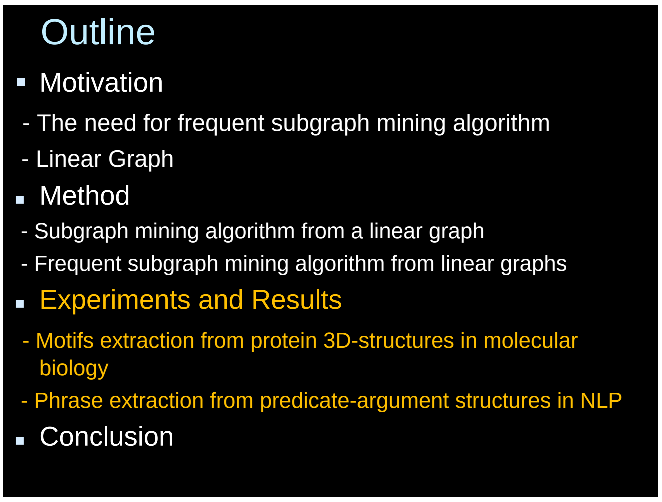
- Depth first traversal for its memory efficiency



Frequent Subgraph Mining

- Basic idea: find all possible extensions of a current pattern in the graph database, and extend the pattern.
- Occurrence list $L_G(g)$
  - Record every occurrence of a pattern g in the graph database G
  - Calculate the support of a pattern g by the occurrence list.
- Use anti-monotonicity of the support for pruning

Search Tree
pruning



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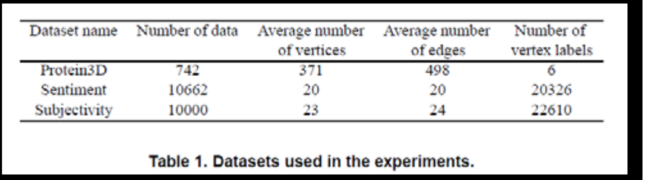
Experiments

- Motif extraction from protein 3D structures
  - Contact Maps
- Phrase discovery from movie evaluation texts
  - Predicate-Argument Structure



Dataset name	Number of data	Average number of vertices	Average number of edges	Number of vertex labels
Protein3D	742	371	498	6
Sentiment	10662	20	20	20326
Subjectivity	10000	23	24	22610

Table 1. Datasets used in the experiments.

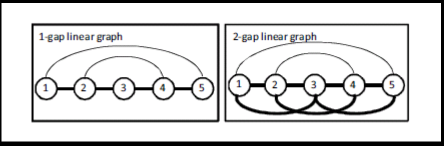
Motif extraction from protein 3D structures

- Pairs of homologous proteins in thermophilic organism and methophilic organism
- Construct a linear graph from a protein
  - Represent each amino acid as a vertex
  - Assign vertex labels from {1,…,6} according to its property (Mirny, 1999).
  - Draw an edge between the pair of amino acid residues whose distance is within 5 Å
  - No edge labels.
- Rank the patterns by statistical significance (p-values)
  - Association to thermophilic/methophilic label
  - Fisher exact test

Applying gSpan

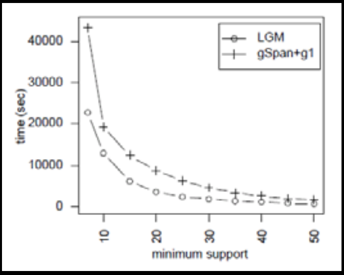
- Want to compare the execution time of our algorithm with that of gSpan
- gSpan is not directly applicable
  - Contact maps are not always connected

- Made 1-gap and 2-gap linear graphs



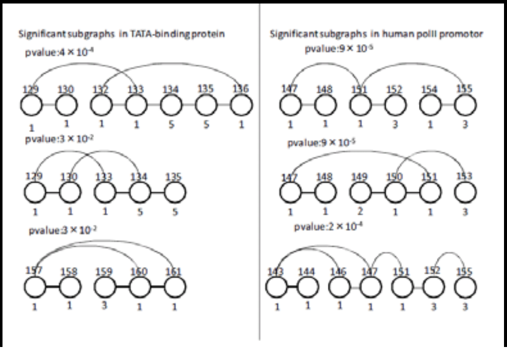
Runtime comparison

- LGM is faster than gSpan
- Execution time of LGM is reasonable.

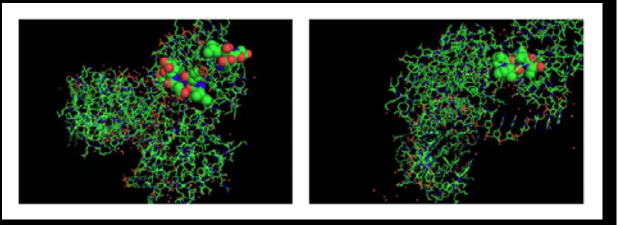


- gSpan does not work on the 2-gap linear graph dataset even if the minimum support threshold is 50.

- Minimum support = 10
- 103 patterns whose p-value < 0.001
- Thermophilic (TATA), Mesophilic (pol II)


Significant subgraphs in TATA-binding protein
pvalue:4 × 10⁻⁴
pvalue:3 × 10⁻²
pvalue:3 × 10⁻²
Significant subgraphs in human polII promotor
pvalue:9 × 10⁻⁵
pvalue:9 × 10⁻⁵
pvalue:2 × 10⁻⁴

Mapping motifs in 3D structure

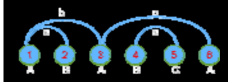


Phrase extraction from predicate-argument structures

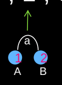
- Internet movie review dataset (Pang et al., 2004)
- Sentiment dataset
  - 5331 positive and 5331 negative opinions
- Subjectivity dataset
  - 5000 subjective and 5000 objective sentences
- PAS by ENJU syntactic parser (Miyao et al., 2008)
- Extract characteristic phrases (subgraph patterns)

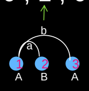
Select salient patterns by linear SVM

- Binary features from patterns
- Each pattern corresponds to an SVM's weight
  - interpretable
- Take the patterns with major weights



(0 , … , 0 , 1 , 0 , … , 0 , 1 , 0 , …)



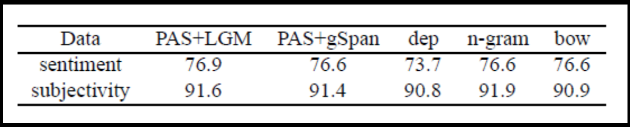


Methods in comparison

- PAS+gSpan
  - Predicate argument structure + gSpan
  - No edges added
- Dep+FREQT
  - Dependency tree (KSDep) + FREQT (Tree Miner)
- N-gram
  - Modified PrefixSpan (Sequence Miner)

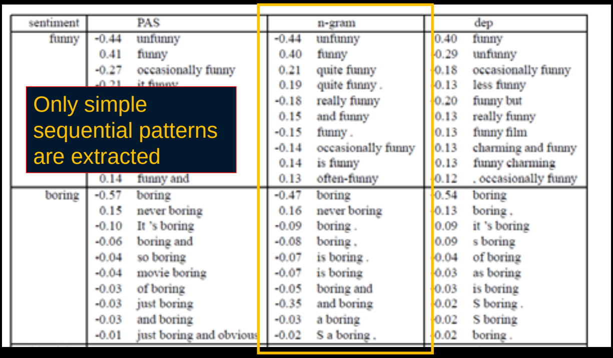
Classification Accuracy

- The accuracy of LGM is better than that of gSpan
- PAS representation is comparable to the other representations.



Data	PAS+LGM	PAS+gSpan	dep	n-gram	bow
sentiment	76.9	76.6	73.7	76.6	76.6
subjectivity	91.6	91.4	90.8	91.9	90.9

Phrase structure extraction from predicate-argument structures

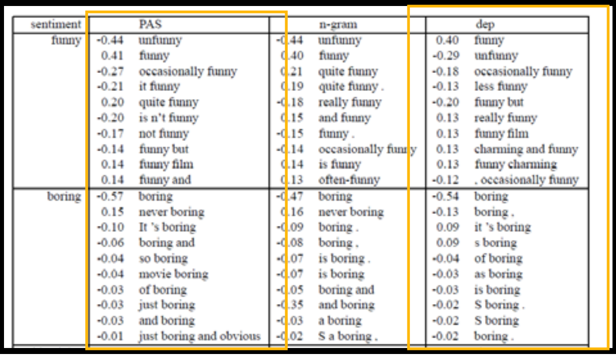


Only simple sequential patterns are extracted

sentiment	PAS		n-gram		dep	
funny	-0.44	unfunny	-0.44	unfunny	0.40	funny
	0.41	funny	0.40	funny	-0.29	unfunny
	-0.27	occasionally funny	0.21	quite funny	-0.18	occasionally funny
	-0.21	it funny	0.19	quite funny .	-0.13	less funny
			-0.18	really funny	-0.20	funny but
			0.15	and funny	0.13	really funny
			-0.15	funny .	0.13	funny film
			-0.14	occasionally funny	0.13	charming and funny
			0.14	is funny	0.13	funny charming
	0.14	funny and	0.13	often-funny	-0.12	. occasionally funny
boring	-0.57	boring	-0.47	boring	-0.54	boring
	0.15	never boring	0.16	never boring	-0.13	boring .
	-0.10	It 's boring	-0.09	boring .	0.09	it 's boring
	-0.06	boring and	-0.08	boring .	0.09	s boring
	-0.04	so boring	-0.07	is boring .	-0.04	of boring
	-0.04	movie boring	-0.07	is boring	-0.03	as boring
	-0.03	of boring	-0.05	boring and	-0.03	is boring
	-0.03	just boring	-0.35	and boring	-0.02	S boring .
	-0.03	and boring	-0.03	a boring	-0.02	S boring
	-0.01	just boring and obvious	-0.02	S a boring .	-0.02	boring .

Phrase structure extraction from predicate-argument structures

Phrase structures were extracted.



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	-0.04	movie boring	-0.07	is boring	-0.03	as boring
	-0.03	of boring	-0.05	boring and	-0.03	is boring
	-0.03	just boring	-0.35	and boring	-0.02	S boring .
	-0.03	and boring	-0.03	a boring	-0.02	S boring
	-0.01	just boring and obvious	-0.02	S a boring .	-0.02	boring .

Conclusions

- Efficient subgraph mining algorithm from linear graphs
- Search tree is defined by reverse search principle
- Patterns include disconnected subgraphs
- Computational time is polynomial-delay
- Interesting patterns from proteins and sentences

Another topics

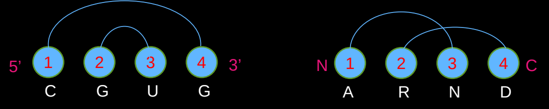
- Alignment algorithms for RNA sequences
  - Ph.D. study
- All pairs similarity search method
  - nearest neighbor graphs

Q & A

Data represented as linear graphs

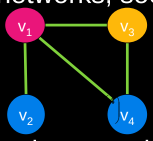
- DNA, RNA, protein-3D structure, predicate argument structure
  - reference point: 5-strand(DNA, RNA), N-terminal (protein)

Ex) RNA Protein (edge: 5Å)

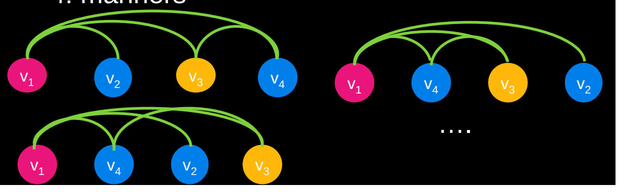


Data NOT represented as linear graphs

- Chemical compounds, Gene co-expression networks, social networks etc

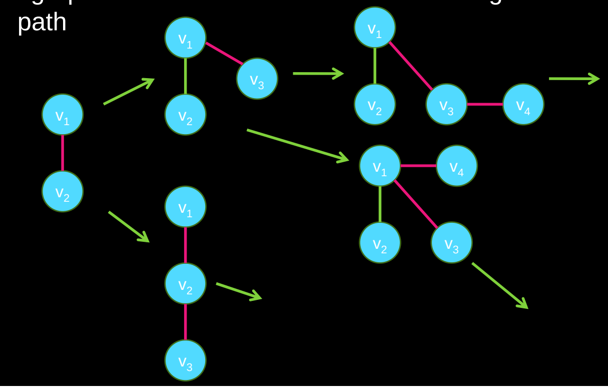


- Can NOT assign an unique vertex order
  - 4! manners



Right most pattern extension

- —— right most path
- A graph is extended from a vertex on the right most path



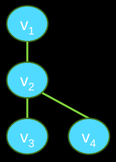
What is a code for an edge

- A code assigned for an edge in a graph

- a set of label ids, vertex labels, edge ids

Ex)

(vertex id1, vertex id2, vertex id1 label, vertex id2 label, edge label)



What is the Minimum DFS Code?

DFS Code: a sequence of codes by depth-first traversal

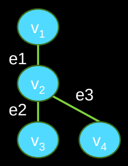
Ex)

- Start from v1

(v1,v2,l_v1,l_v2,l_e1)
(v2,v3,l_v1,l_v3,l_e2)
(v2,v4,l_v1,l_v3,l_e3)

-Start from v2

(v2,v1,l_v1,l_v2,l_e1)
(v2,v3,l_v2,l_v3,l_e2)
(v2,v4,l_v2,l_v4,l_e3)



- A graph is assinged several DFS Codes according to the starting vertex of DFS
- Define Total order among DFS codes
- Chose minimum DFS Code as a canonical code

Motif extraction

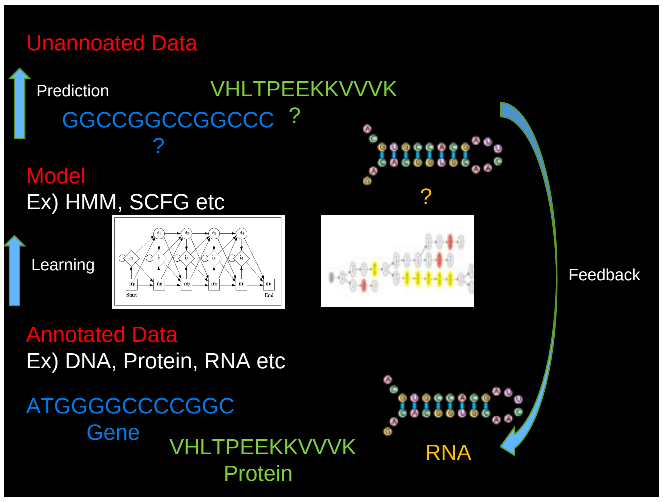
- To extract protein-3D motifs, we use the Fisher's exact test.

	thermophilic	mesophilic	Total
With T	n_{TP}	n_{FP}	n_{T}
Without T	n_{FN}	n_{TN}	$n_{T'}$
Total	n_P	n_N	n

$$\Pr = \frac{\binom{n_T}{n_{NT}}\binom{n_{T'}}{n_{FN}}}{\binom{n}{n_P}} = \frac{n_T!n_{T'}!n_P!n_N!}{n!n_{TP}!n_{FP}!n_{FN}!n_{TN}!}$$

Table1: 2×2 contingency table

- The P-value can be computed by the sum of all probabilities of tables that are more extreme than this table.
- Ranked the frequent subgraphs according to the P-values.
- Focused on a pair of proteins, TATA-binding protein and human polII promotor protein



- Algorithms for prediction and learning are based on Dynamic Programming (DP).
- Ordering in linear graphs is useful for designing DP algorithms