Comparative Analysis of Molecular Interaction Networks

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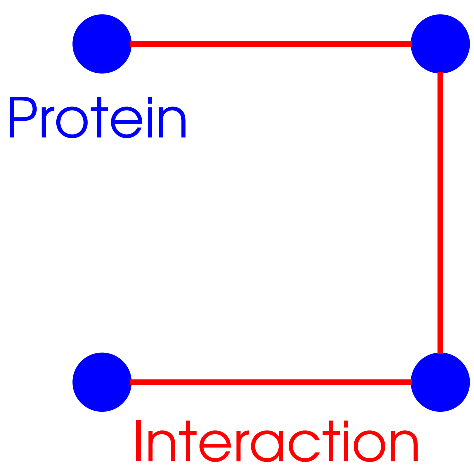
Outline

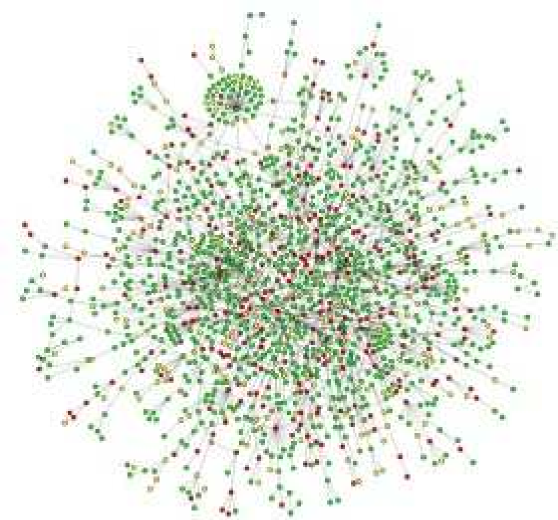
- Molecular Interaction Networks
  - Modeling, evolution, problems, practical implications
- Algorithms for Analyzing Molecular Interaction Networks
  - Mining biological networks for frequent molecular interaction patterns
  - Pairwise Alignment of protein-protein interaction networks
  - Probabilistic models/analyses for assessing statistical significance
- Related Work
  - Inferring function from domain co-evolution
  - Clustering regulatory profiles
- Ongoing Work & Conclusion

Protein-Protein Interaction (PPI) Networks

- Interacting proteins can be identified via high-throughput screening
  - Two-hybrid
  - Mass spectrometry
  - Tandem affinity purification (TAP)



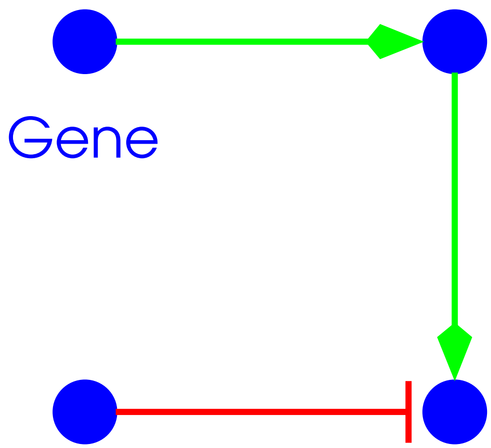
Undirected Graph Model



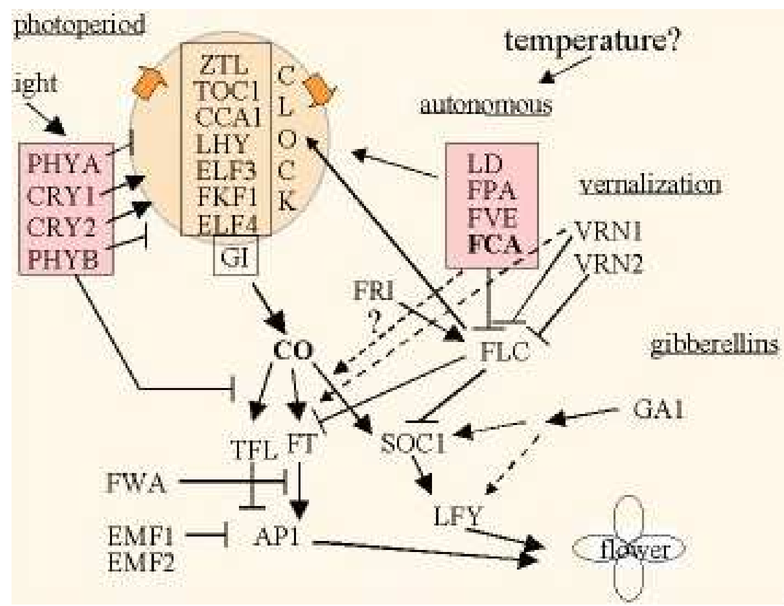
S. Cerevisiae PPI network
(Jeong et al., *Nature*, 2001)

Gene Regulatory Networks

- Expression of genes is dynamically orchestrated through genes controlling each other's transcription
  - Computationally induced from gene expression data and/or sequence level analysis



Boolean Network Model

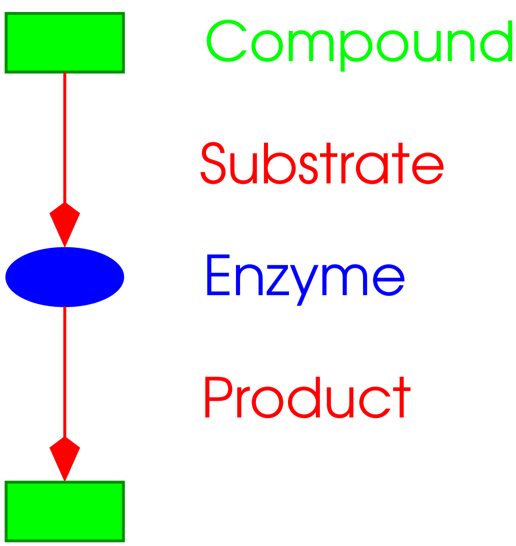


Genetic network that controls flowering time in *A. Thaliania*

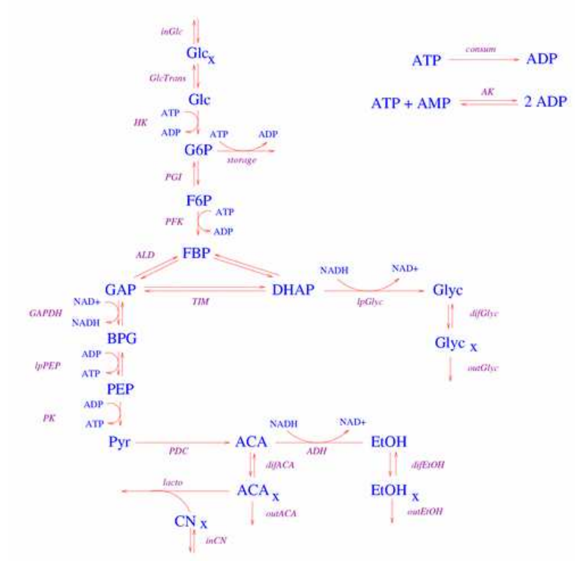
(Blazquez et al, *EMBO Reports*, 2001)

Metabolic Pathways

- Chains of reactions that perform a particular metabolic function
  - Reactions are linked to each other through substrate-product relationships
  - Experimentally derived & computationally extended



Directed Hypergraph Model



Glycolysis pathway in *S. Cerevisiae*

(Hynne et al., *Biophys. Chem.*, 2001)

Evolution of Molecular Interactions

- "Evolution thinks modular" (Vespignani, *Nature Gen.*, 2003)

- Cooperative tasks require all participating units
  - Selective pressure on preserving interactions & interacting proteins
  - Interacting proteins follow similar evolutionary trajectories (Pellegrini et al., *PNAS*, 1999)

- Orthologs of interacting proteins are likely to interact (Wagner, *Mol. Bio. Evol.*, 2001)
  - Conservation of interactions may provide clues relating to conservation of function

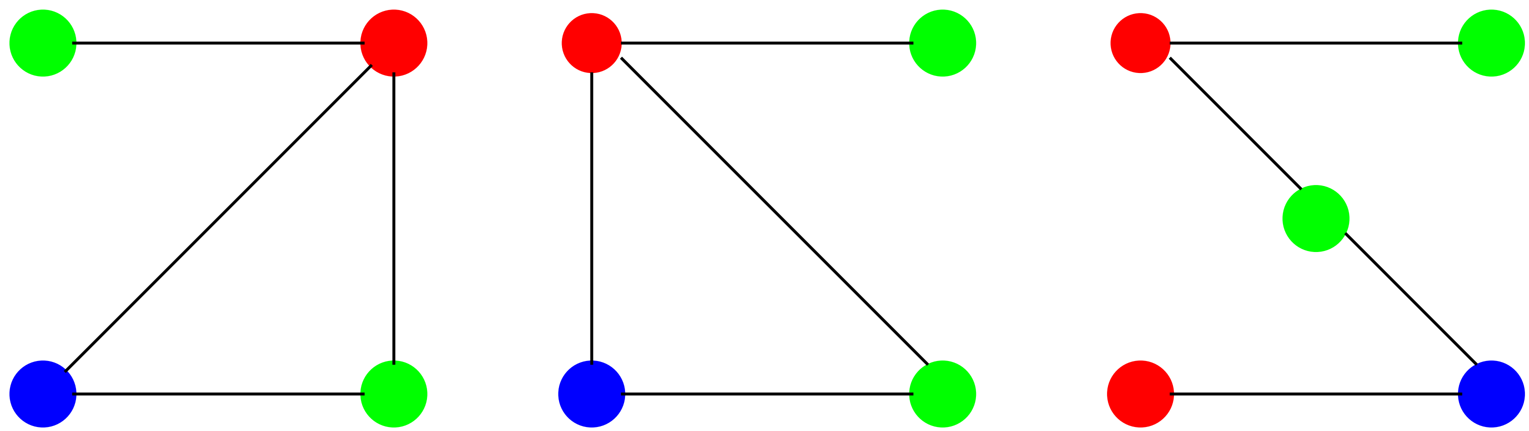
- Modular conservation and aligment hold the key to critical structural, functional, and evolutionary concepts in systems biology

Conserved Interaction Patterns

- Given a collection of interaction networks (belonging to different species), find sub-networks that are common to an interesting subset of these networks (Koyutürk, Grama, & Szpankowski, *ISMB*, 2004)
  - A sub-network is a group of interactions that are tied to each other (connected)
  - Frequency: The number of networks that contain a sub-network, is a coarse measure of statistical significance
  - Computational problem is known as graph mining

- Computational challenges
  - How to relate molecules (proteins) in different organisms?
  - Requires solution of the intractable subgraph isomorphism problem
  - Must be scalable to potentially large number of networks
  - Networks are large (in the range of $10K$ edges)

Graph Mining



Network database

Interaction patterns that are common to all networks

Relating Proteins in Different Species

- Ortholog Databases
  - PPI networks: COG, Homologene, Pfam, ADDA
  - Metabolic pathways: Enzyme nomenclature
  - Reliable, but conservative
  - Domain families rely on domain information, but the underlying domains for most interactions are unknown $\Rightarrow$ Multiple node labels
- Sequence Clustering
  - Cluster protein sequences and label proteins according to this clustering
  - Flexible, but expensive and noisy
- Labels may span a large range of functional relationships, from protein families to ortholog groups
  - Without loss of generality, we call identically labeled proteins as orthologs

Problem Setting

- Given a set of proteins V, a set of interactions E, and a many-to-many mapping from V to a set of ortholog groups $\mathcal{L} = \{l_1, l_2, ..., l_n\}$, the corresponding interaction network is a labeled graph $G = (V, E, \mathcal{L})$.
  - $v \in V(G)$ is associated with a set of ortholog groups $L(v) \subseteq \mathcal{L}$.
  - $uv \in E(G)$ represents an interaction between u and v.

- S is a sub-network of G, *i.e.*, $S \sqsubseteq G$ if there is an injective mapping $\phi : V(S) \rightarrow V(G)$ such that for all $v \in V(S)$, $L(v) \subseteq L(\phi(v))$ and for all $uv \in E(S)$, $\phi(u)\phi(v) \in E(G)$.

Computational Problem

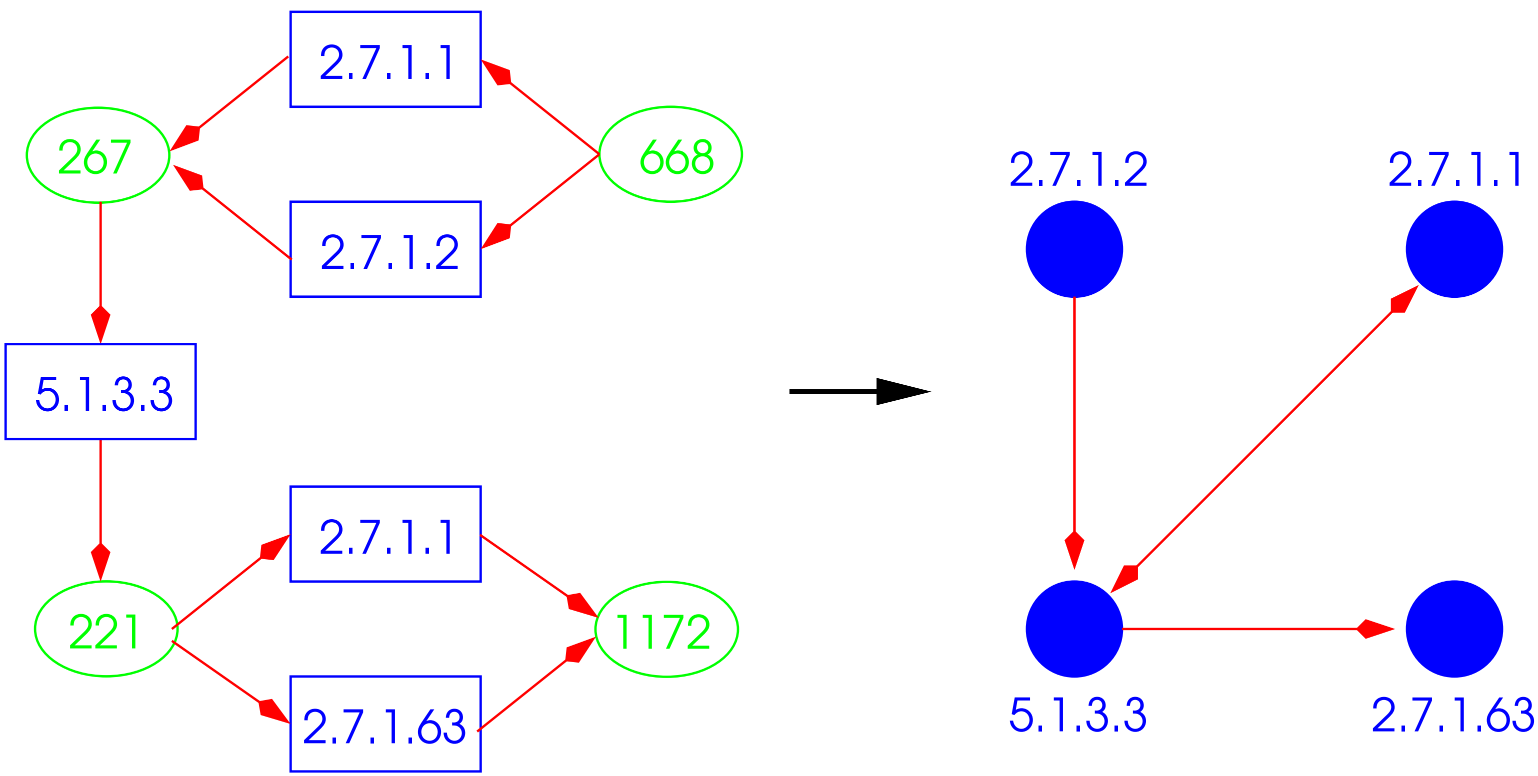
- Conserved sub-network discovery
  - Instance: A set of interaction networks $\mathcal{G} = \{G_1 = (V_1, E_1, \mathcal{L}), G_2 = (V_2, E_2, \mathcal{L}), ..., G_m = (V_m, E_m, \mathcal{L})\}$, each belonging to a different organism, and a frequency threshold σ^*.
  - Problem: Let $H(S) = \{G_i : S \sqsubseteq G_i\}$ be the occurrence set of graph S. Find all connected subgraphs S such that $|H(S)| \geq \sigma^*$, *i.e.*, S is a frequent subgraph in $\mathcal{G}$ and for all $S' \sqsupset S$, $H(S) \neq H(S')$, *i.e.*, S is maximal.

Algorithmic Insight: Ortholog Contraction

- Contract orthologous nodes into a single node
- No subgraph isomorphism
  - Graphs are uniquely identified by their edge sets
- Key observation: Frequent sub-networks are preserved $\Rightarrow$ No information loss
  - Sub-networks that are frequent in general graphs are also frequent in their ortholog-contracted representation
  - Ortholog contraction is a powerful pruning heuristic
- Discovered frequent sub-networks are still biologically interpretable!
  - Interaction between proteins becomes interaction between ortholog groups

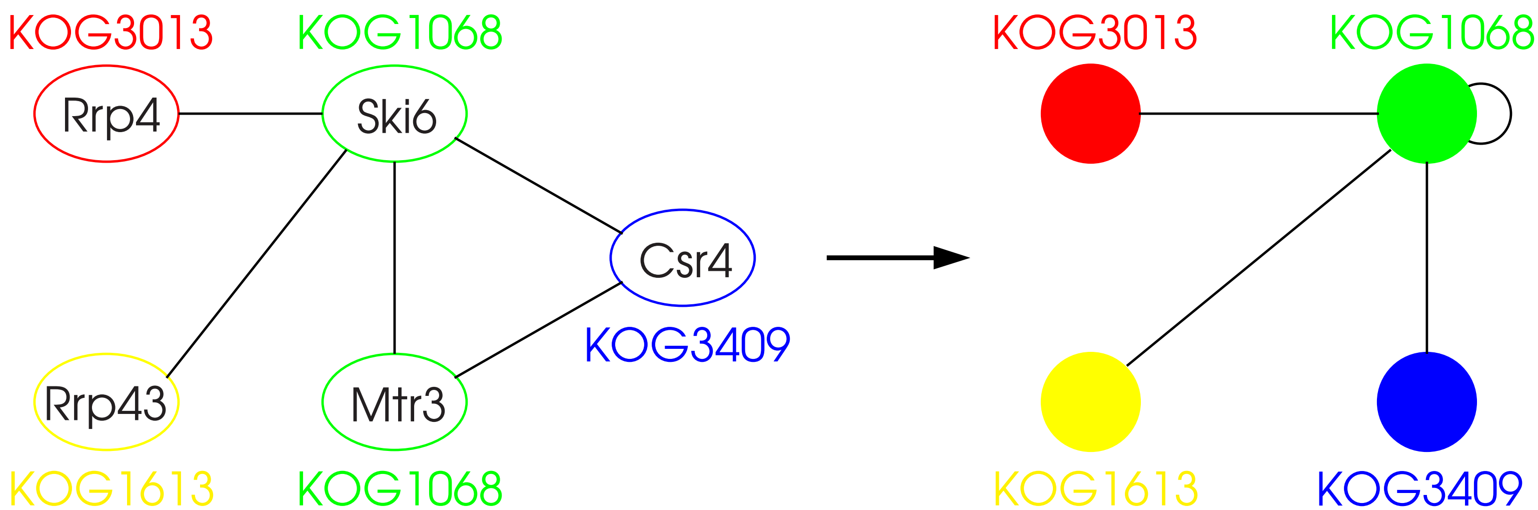
Ortholog Contraction in Metabolic Pathways

- Directed hypergraph → uniquely-labeled directed graph
  - Nodes represent enzymes
  - Global labeling by enzyme nomenclature (EC numbers)
  - A directed edge from one enzyme to the other implies that the second consumes a product of the first



Ortholog Contraction in PPI Networks

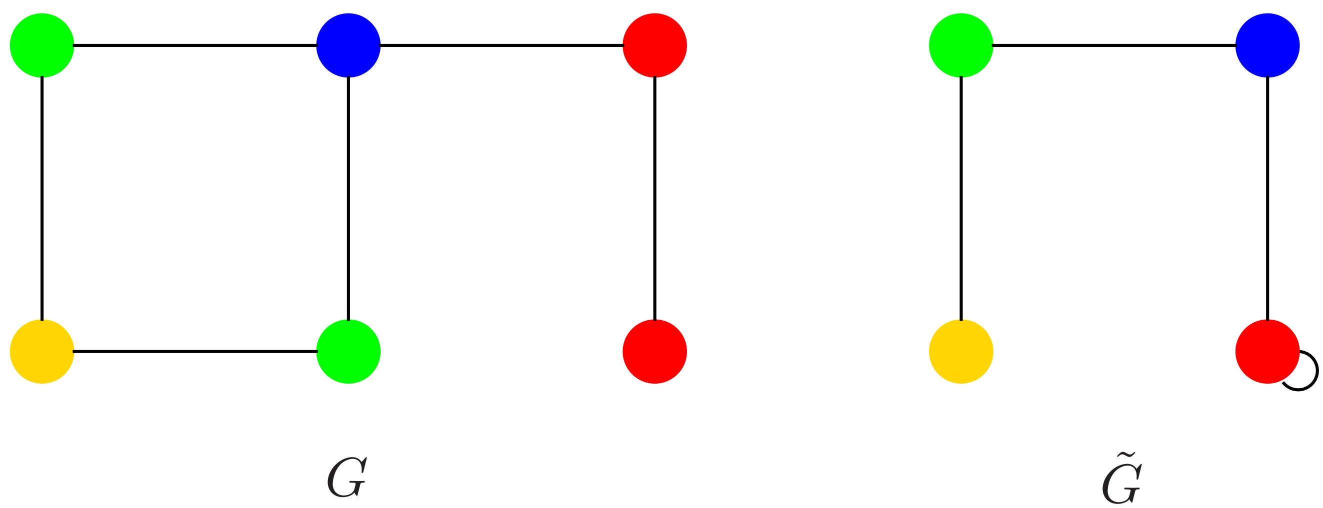
- Interaction between proteins → Interaction between ortholog groups or protein families



Preservation of Sub-networks

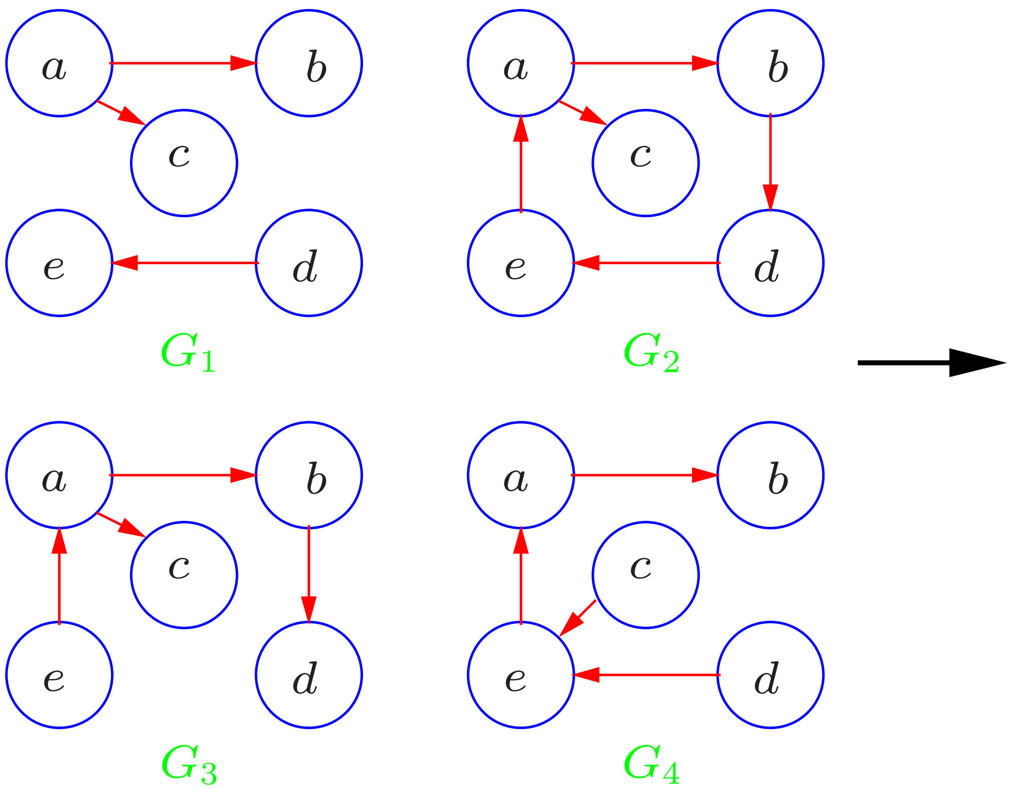
Theorem: Let $\tilde{G}$ be the ortholog-contracted graph obtained by contracting the orthologous nodes of network G. Then, if S is a subgraph of G, $\tilde{S}$ is a subgraph of $\tilde{G}$.

Corollary: The ortholog-contracted representation of any frequent sub-network is also frequent in the set of ortholog-contracted graphs.



Simplifying the Graph Mining Problem

- Observation: An ortholog-contracted graph is uniquely determined by the set of its edges.
  - Conserved Sub-network Discovery Problem $\rightarrow$ Frequent Edge set Discovery Problem



$F_1 = \{ab, ac, de\}$

$F_2 = \{ab, ac, bc, de, ea\}$

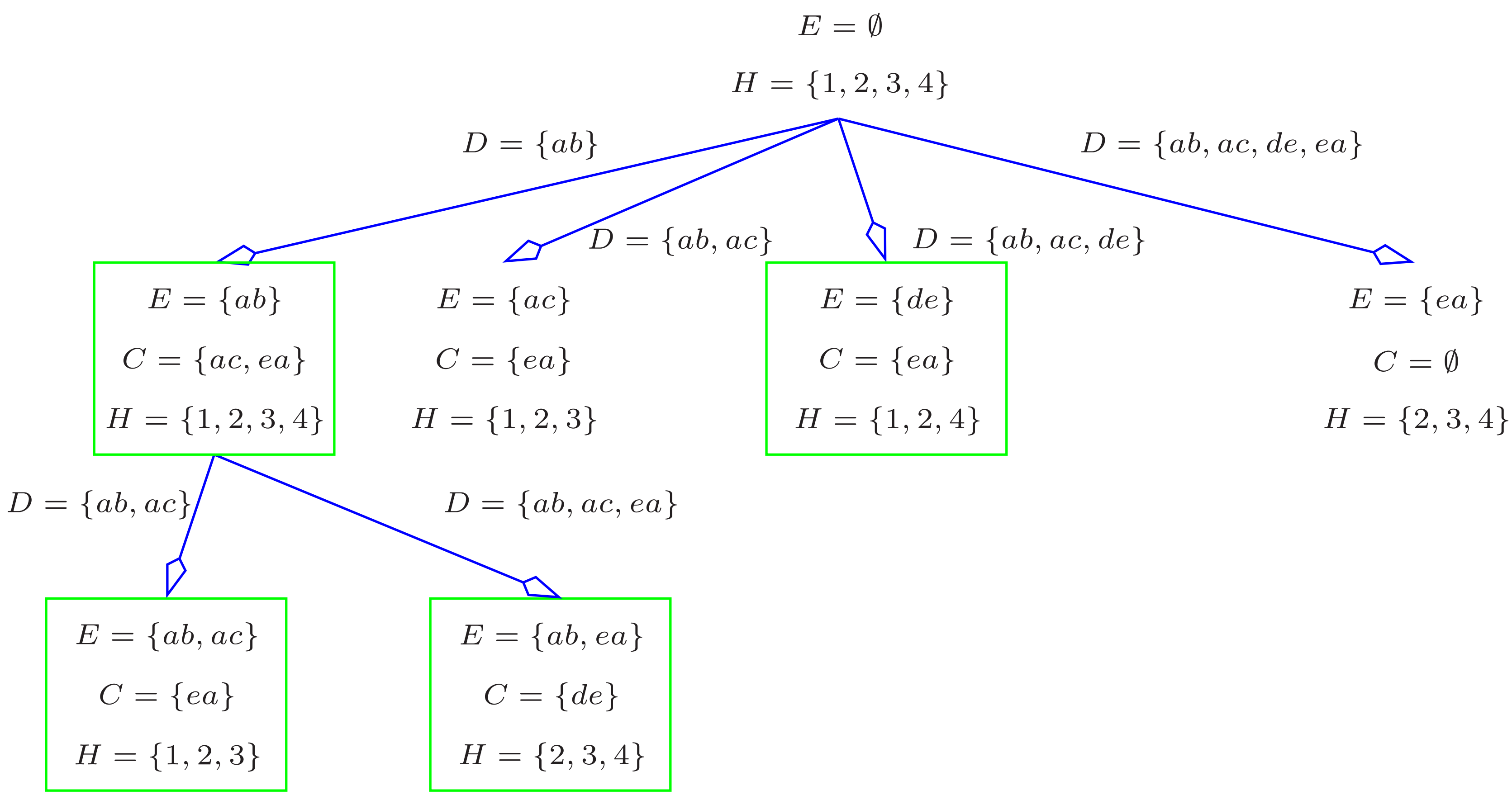
$F_3 = \{ab, ac, bc, ea\}$

$F_4 = \{ab, ce, de, ea\}$

Extending Frequent Itemset Mining to Graph Mining

- Given a set of transactions, find sets of items that are frequent in these transactions
  - Extensively studied in data mining literature
- Algorithms exploit downward closure property
  - An edge set is frequent only if all of its subsets are frequent
  - Generate edge sets (sub-networks) from small to large, pruning supersets of infrequent sets
- No redundancy
- No subgraph enumeration

MULE: Mining Ortholog-Contracted Networks

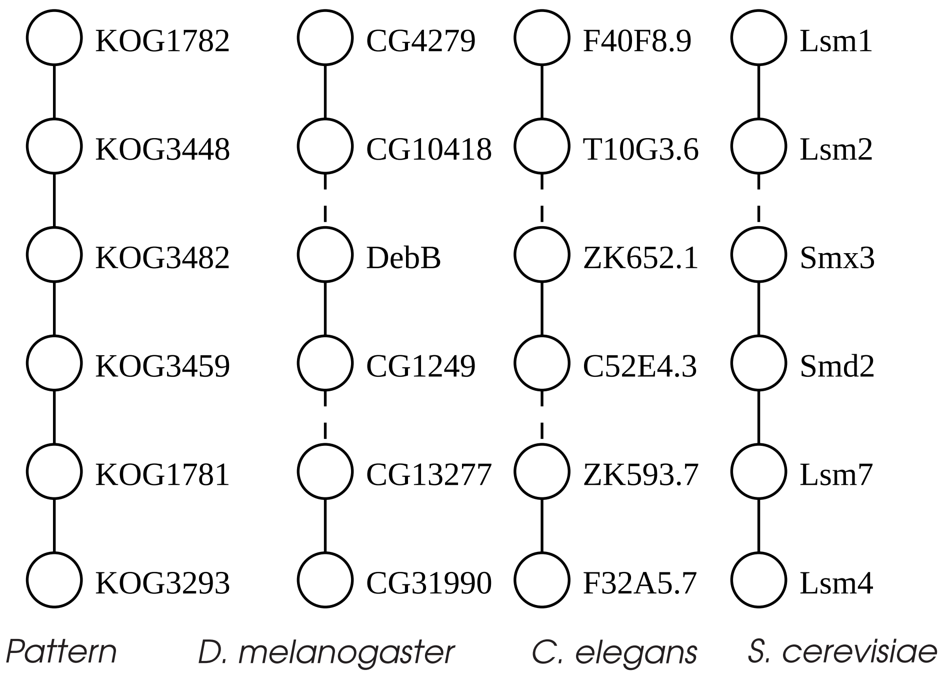


Sample run of MULE for identifying maximal sub-networks that are common to at least 3 organisms

Results: Mining PPI Networks

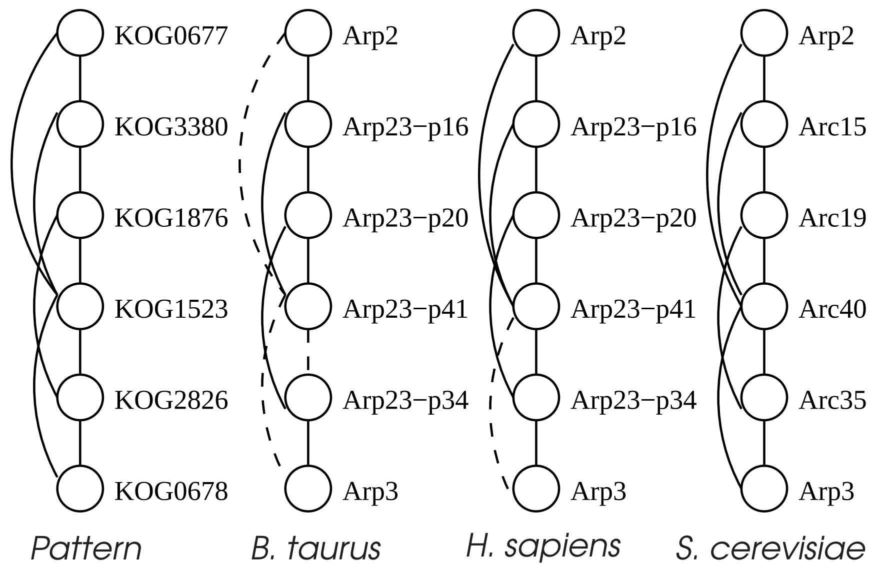
- PPI networks for 9 eukaryotic organisms derived from BIND and DIP
  - *A. thaliania, O. sativa, S. cerevisiae, C. elegans, D. melanogaster, H. sapiens, B. taurus, M. musculus, R. norvegicus*
  - # of proteins ranges from 288 (*Arabidopsis*) to 8577 (*fruit fly*)
  - # of interactions ranges from 340 (*rice*) to 28829 (*fruit fly*)
- Ortholog contraction
  - Group proteins according to existing COG ortholog clusters
  - Merge Homologene groups into COG clusters
  - Cluster remaining proteins via BLASTCLUST
  - Ortholog-contracted *fruit fly* network contains 11088 interactions between 2849 ortholog groups
- MULE is available at `http://www.cs.purdue.edu/homes/koyuturk/mule/`

Frequent Protein Interaction Patterns



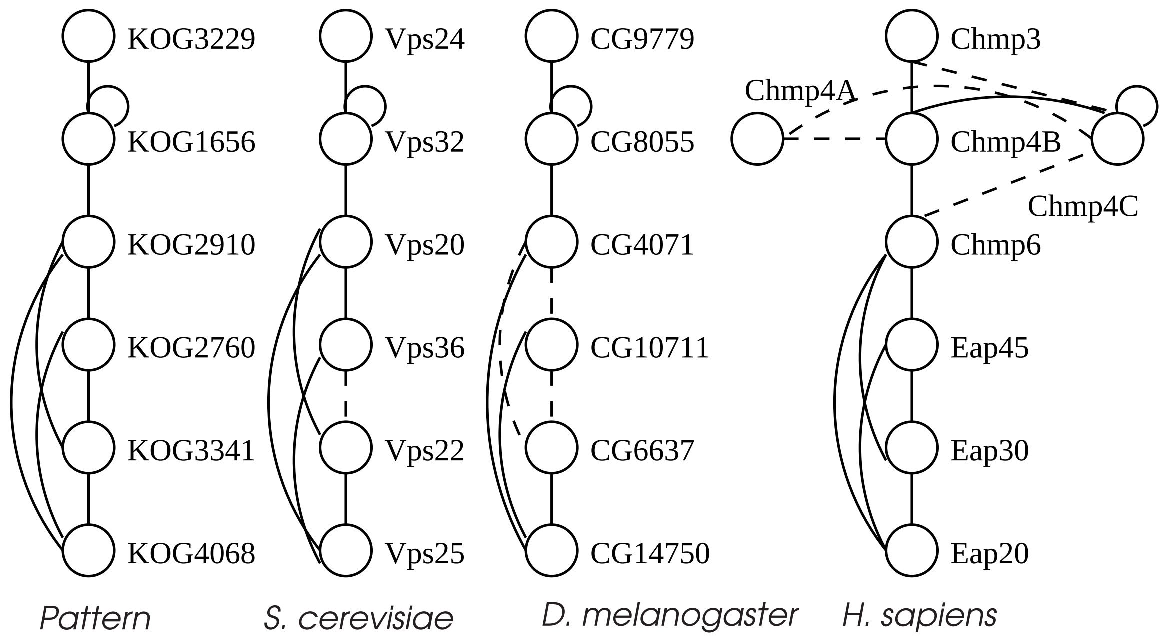
Small nuclear ribonucleoprotein complex ($p < 2e - 43$)

Frequent Protein Interaction Patterns



Actin-related protein Arp2/3 complex ($p < 9e - 11$)

Frequent Protein Interaction Patterns



Endosomal sorting ($p < 1e - 78$)

Runtime Characteristics

Comparison with isomorphism-based algorithms

FSG (Kuramochi & Karypis, *IEEE TKDE*, 2004), gSpan (Yan & Han, *KDD*, 2003)

Dataset	Minimum Support (%)	FSG Runtime (secs.)	FSG Largest pattern	FSG Number of patterns	MULE Runtime (secs.)	MULE Largest pattern	MULE Number of patterns
Glutamate	20	0.2	9	12	0.01	9	12
	16	0.7	10	14	0.01	10	14
	12	5.1	13	39	0.10	13	39
	10	22.7	16	34	0.29	15	34
	8	138.9	16	56	0.99	15	56
Alanine	24	0.1	8	11	0.01	8	11
	20	1.5	11	15	0.02	11	15
	16	4.0	12	21	0.06	12	21
	12	112.7	17	25	1.06	16	25
	10	215.1	17	34	1.72	16	34

Extraction of contracted patterns

Glutamate metabolism, $\sigma = 8\%$ Size of contracted pattern	Extraction time (secs.) FSG	Extraction time (secs.) gSpan	Size of extracted pattern	Alanine metabolism, $\sigma = 10\%$ Size of contracted pattern	Extraction time (secs.) FSG	Extraction time (secs.) gSpan	Size of extracted pattern
15	10.8	1.12	16	16	54.1	10.13	17
14	12.8	2.42	16	16	24.1	3.92	16
13	1.7	0.31	13	12	0.9	0.27	12
12	0.9	0.30	12	11	0.4	0.13	11
11	0.5	0.08	11	8	0.1	0.01	8

Glutamate metabolism:
Total number of patterns: 56
Total runtime of FSG alone: 138.9 secs.
Total runtime of MULE+FSG: 0.99+100.5 secs.
Total runtime of MULE+gSpan: 0.99+16.8 secs.

Alanine metabolism:
Total number of patterns: 34
Total runtime of FSG alone :215.1 secs.
Total runtime of MULE+FSG: 1.72+160.6 secs.
Total runtime of MULE+gSpan: 1.72+31.0 secs.

Discussion

- Ortholog contraction is fast & scalable
  - Graph cartesian product based methods (Sharan et al., *PNAS*, 2004), (Koyutürk et al., *RECOMB*, 2005) create m^n product nodes for an ortholog group that has m proteins in each of n organisms
  - Ortholog contraction represents the same group with only n contracted nodes
  - Isomorphism-based graph mining algorithms do not scale to large networks

- Ortholog contraction implicitly accounts for noise by eliminating false positives through thresholding frequency and false negatives through contraction

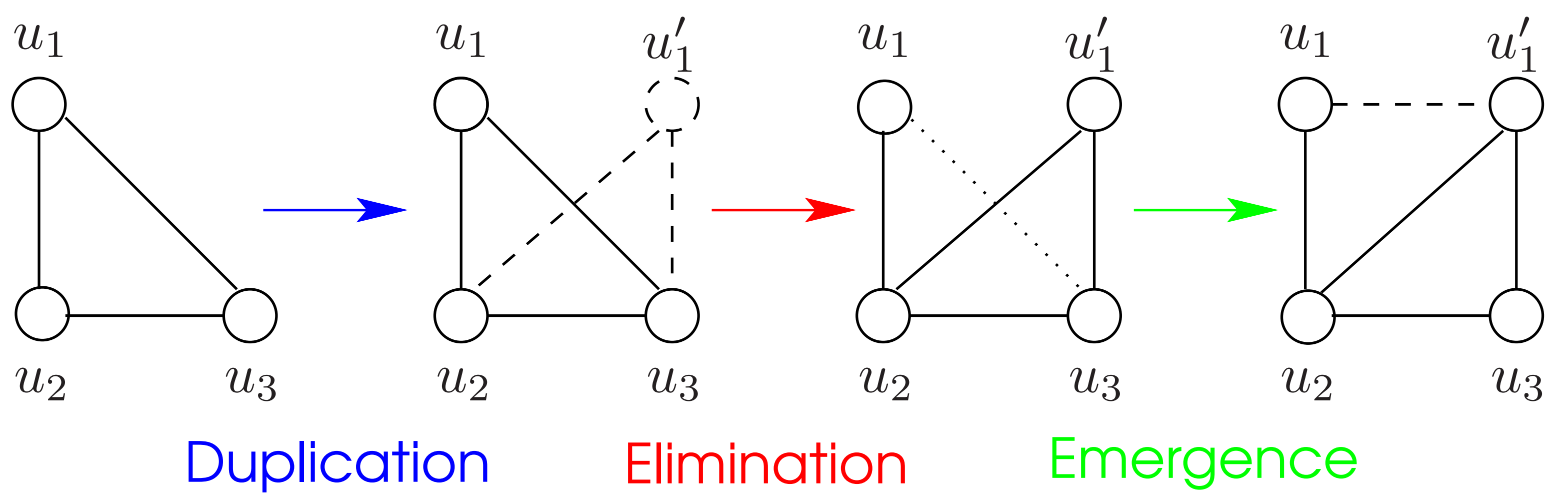
- Frequency-based approach is not easily extendible to weighted graphs (Zhou et al., *ISMB*, 2005)

Alignment of PPI Networks

- Given two PPI networks that belong to two different organisms, identify sub-networks that are similar to each other
  - Biological meaning
  - Mathematical modeling
- Existing algorithms
  - PathBLAST aligns pathways (linear chains) to simplify the problem while maintaining biological meaning (Kelley et al., *PNAS*, 2004)
  - NetworkBLAST compares conserved complex model with null model to identify significantly conserved subnets (Sharan et al., *J. Comp. Biol.*, 2005)
- Our approach (Koyutürk et al., *RECOMB*, 2005) (Koyutürk et al., *J. Comp. Biol.*, 2006)
  - Guided by models of evolution
  - Scores evolutionary events
  - Identifies sets of proteins that induce high-scoring sub-network pairs

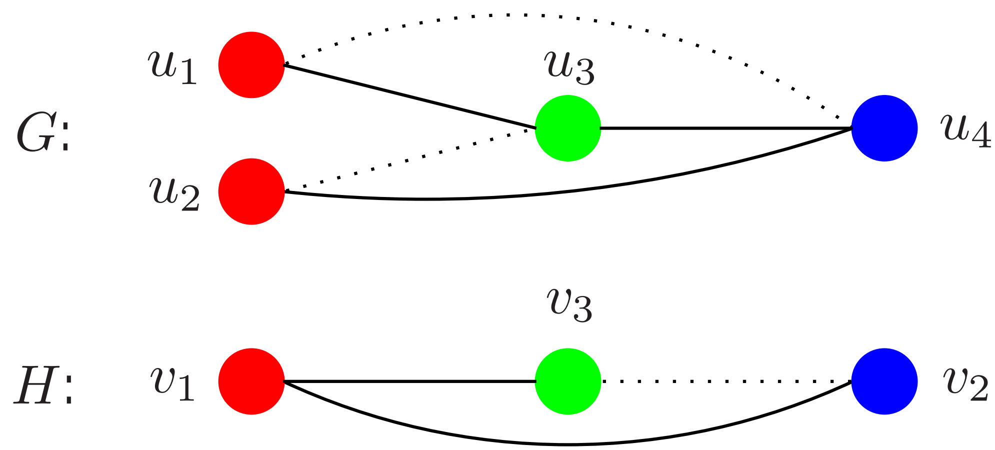
Evolution of PPI Networks

- Duplication/divergence models for the evolution of protein interaction networks
  - Interactions of duplicated proteins are also duplicated
  - Duplicated proteins rapidly lose interactions through mutations
- Allows defining and scoring evolutionary events as graph-theoretical concepts



Match, Mismatch, and Duplication

- Evolutionary events as graph-theoretic concepts
  - A match $\in \mathcal{M}$ corresponds to two pairs of homolog proteins from each organism such that both pairs interact in both PPIs. A match is associated with score μ.
  - A mismatch $\in \mathcal{N}$ corresponds to two pairs of homolog proteins from each organism such that only one pair is interacting. A mismatch is associated with penalty ν.
  - A duplication $\in D$ corresponds to a pair of homolog proteins that are in the same organism. A duplication is associated with score δ.



Scoring Matches, Mismatches and Duplications

- Quantizing similarity between two proteins
  - Confidence in two proteins being orthologous
  - BLAST E-value: $S(u,v) = log_{10}\frac{p(u,v)}{p_{random}}$
  - Ortholog clustering: $S(u,v) = c(u)c(v)$
- Match score
  - $\mu(uu', vv') = \bar{\mu}\min\{S(u,v), S(u',v')\}$
- Mismatch penalty
  - $\nu(uu', vv') = \bar{\nu}\min\{S(u,v), S(u',v')$
- Duplication score
  - $\delta(u,u') = \bar{\delta}(\hat{\delta} - S(u,u'))$
  - $\hat{\delta}$ specifies threshold for sequence similarity to be considered functionally conserved

Pairwise Alignment of PPIs as an Optimization Problem

- Alignment score:
  $\sigma(\mathcal{A}(P)) = \sum_{M \in \mathcal{M}} \mu(M) - \sum_{N \in \mathcal{N}} \nu(N) + \sum_{D \in \mathcal{D}} \delta(D)$
  - Matches are rewarded for conservation of interactions
  - Duplications are rewarded/penalized for functional conservation/differentiation after split
  - Mismatches are penalized for functional divergence (what about experimental error?)

- Scores are functions of similarity between associated proteins

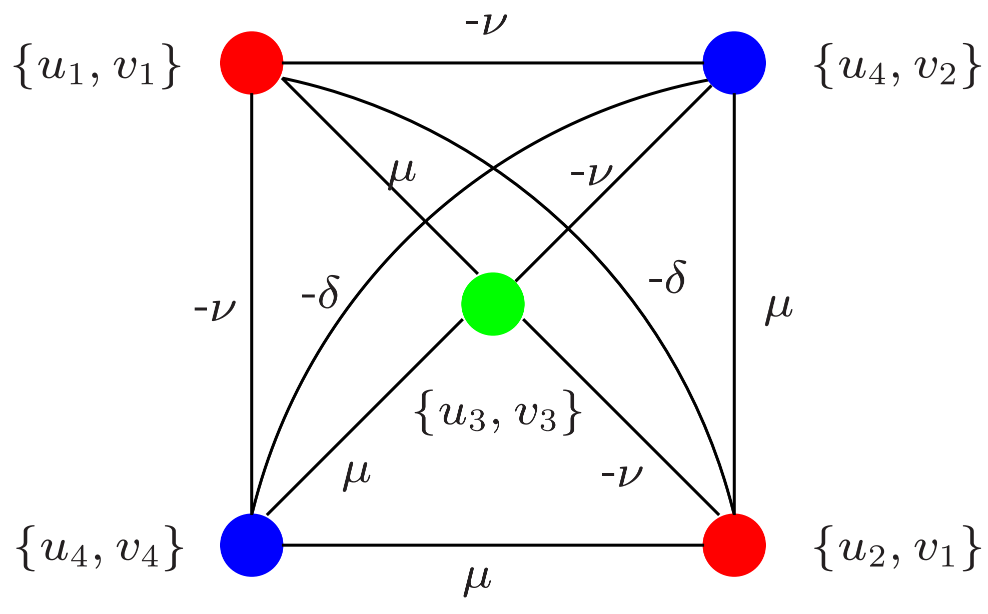
- Problem: Find all protein subset pairs with significant alignment score
  - High scoring protein subsets are likely to correspond to conserved modules

- A graph equivalent to BLAST

Weighted Alignment Graph

- $\mathbf{G}(\mathbf{V},\mathbf{E})$: $\mathbf{V}$ consists of all pairs of homolog proteins $\mathbf{v} = \{u \in U, v \in V\}$

- An edge $\mathbf{vv}' = \{uv\}\{u'v'\}$ in $\mathbf{E}$ is a
  - match edge if $uu' \in E$ and $vv' \in V$, with weight $w(\mathbf{vv}') = \mu(uv, u'v')$
  - mismatch edge if $uu' \in E$ and $vv' \notin V$ or vice versa, with weight $w(\mathbf{vv}') = -\nu(uv, u'v')$
  - duplication edge if $S(u, u') > 0$ or $S(v, v') > 0$, with weight $w(\mathbf{vv}') = \delta(u, u')$ or $w(\mathbf{vv}') = \delta(v, v')$



Maximum Weight Induced Subgraph Problem

- Definition: (MAWISH)
  - Given graph $\mathcal{G}(\mathcal{V}, \mathcal{E})$ and a constant ϵ, find $\tilde{\mathcal{V}} \in \mathcal{V}$ such that $\sum_{\mathbf{v},\mathbf{u} \in \tilde{\mathcal{V}}} w(\mathbf{vu}) \geq \epsilon$.
  - NP-complete by reduction from Maximum-Clique

- Theorem: (MAWISH $\equiv$ Pairwise alignment)
  - If $\tilde{\mathcal{V}}$ is a solution for the MAWISH problem on $\mathcal{G}(\mathcal{V}, \mathcal{E})$, then $P = \{\tilde{U}, \tilde{V}\}$ induces an alignment $\mathcal{A}(P)$ with $\sigma(\mathcal{A}) \geq \epsilon$, where $\tilde{\mathcal{V}} = \tilde{U} \times \tilde{V}$.

- Solution: Local graph partitioning
  - Greedy graph growing + iterative refinement
  - Linear-time heuristic

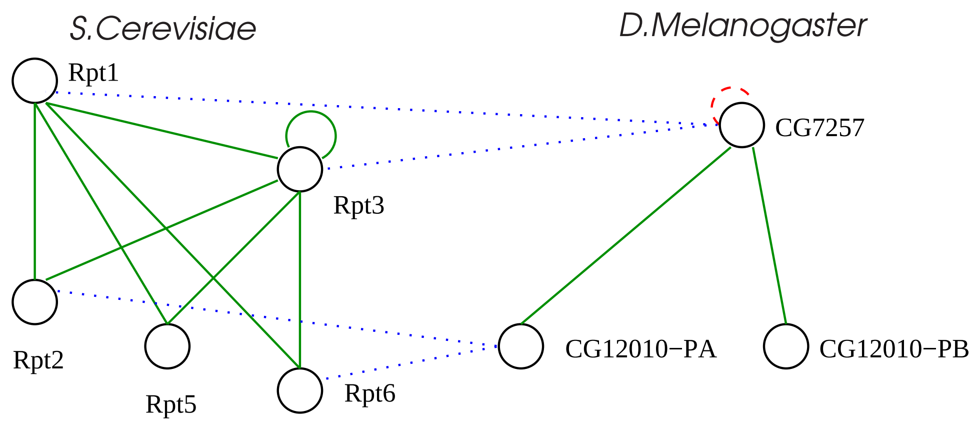
- Source code available at http://www.cs.purdue.edu/homes/koyuturk/mawish/

Alignment of Yeast and Fruit Fly PPI Networks

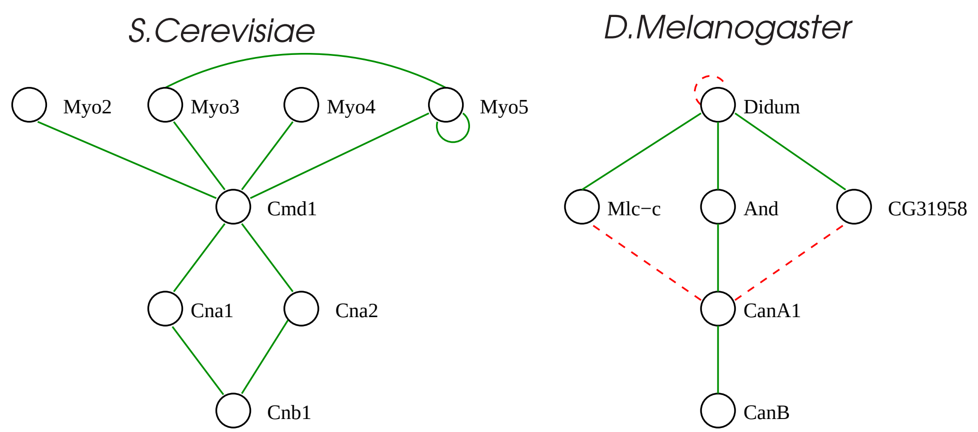
Rank	Score	z-score	# Proteins	# Matches	# Mismatches	# Dups.
1	15.97	6.6	18 (16, 5)	28	6	(4, 0)
	protein amino acid phosphorylation (69%)					
	JAK-STAT cascade (40%)					
2	13.93	3.7	13 (8, 7)	25	7	(3, 1)
	endocytosis (50%) / calcium-mediated signaling (50%)					
5	8.22	13.5	9 (5, 3)	19	11	(1, 0)
	invasive growth (sensu Saccharomyces) (100%)					
	oxygen and reactive oxygen species metabolism (33%)					
6	8.05	7.6	8 (5, 3)	12	2	(0, 1)
	ubiquitin-dependent protein catabolism (100%)					
	mitosis (67%)					
21	4.36	6.2	9 (5, 4)	18	13	(0, 5)
	cytokinesis (100%, 50%)					
30	3.76	39.6	6 (3, 5)	5	1	(0, 6)
	DNA replication initiation (100%, 80%)					

Subnets Conserved in Yeast and Fruit Fly

Proteosome regulatory particle subnet



Calcium-dependent stress-activated signaling pathway



Discussion

- Comparison to other approaches: NetworkBlast (Sharan et al., *PNAS*, 2005), NUKE (Novak et al., *Genome Informatics*, 2005)
  - Much faster than NetworkBLAST, but provides less coverage
  - Comparable to NUKE depending on speed vs coverage trade-off
- Scores evolutionary events
  - Flexible, allows incorporation of different evolutionary models, experimental bases, target structures
  - Somewhat ad-hoc, what is a good weighting of scores?

Analytical Assessment of Statistical Significance

- What is the significance of a dense component in a network?
- What is the significance of a conserved component in multiple networks?
- Existing techniques
  - Mostly computational (*e.g.*, Monte-Carlo simulations)
  - Compute probability that the pattern exists rather than a pattern with the property (*e.g.*, size, density) exists
  - Overestimation of significance

Random Graph Models

- PPI networks generally exhibit power-law property (or exponential, geometric, etc.)
- Analysis simplified through independence assumption (Itzkovitz et al., *Physical Review*, 2003)
- Independence assumption may cause problems for networks with arbitrary degree distribution
- $P(uv \in E) = d_u d_v / |E|$, where d_u is expected degree of u, but generally $d_{\max}^2 > |E|$ for PPI networks
- Analytical techniques based on simplified models (Koyutürk, Grama, Szpankowski, *RECOMB*, 2006)
  - Rigorous analysis on $G(n, p)$ model
  - Extension to piecewise $G(n, p)$ to capture network characteristics more accurately

Significance of Dense Subgraphs

- A subnet of r proteins is said to be ρ-dense if $F(r) \geq \rho r^2$, where $F(r)$ is the number of interactions between these r proteins
- What is the expected size of the largest ρ-dense subgraph in a random graph?
  - Any ρ-dense subgraph with larger size is statistically significant!
- $G(n, p)$ model
  - n proteins, each interaction occurs with probability p
  - Simple enough to facilitate rigorous analysis
  - If we let $p = d_{\max}/n$, largest ρ-dense subgraph in $G(n, p)$ stochastically dominates that in a graph with arbitrary degree distribution
- Piecewise $G(n, p)$ model
  - Few proteins with many interacting partners, many proteins with few interacting partners
  - Captures the basic characteristics of PPI networks
  - Analysis of $G(n, p)$ model immediately generalize to this model

Largest Dense Subgraph

- Theorem: If G is a random graph with n nodes, where every edge exists with probability p, then

$$\lim_{n\to\infty} \frac{R_\rho}{\log n} = \frac{1}{\kappa(p,\rho)} \qquad (pr.), \tag{1}$$

where

$$\kappa(p,\rho) = \rho \log \frac{\rho}{p} + (1-\rho) \log \frac{1-\rho}{1-p}. \tag{2}$$

More precisely,

$$P(R_\rho \geq r_0) \leq O\left(\frac{\log n}{n^{1/\kappa(p,\rho)}}\right), \tag{3}$$

where

$$r_0 = \frac{\log n - \log\log n + \log \kappa(p,\rho)}{\kappa(p,\rho)} \tag{4}$$

for large n.

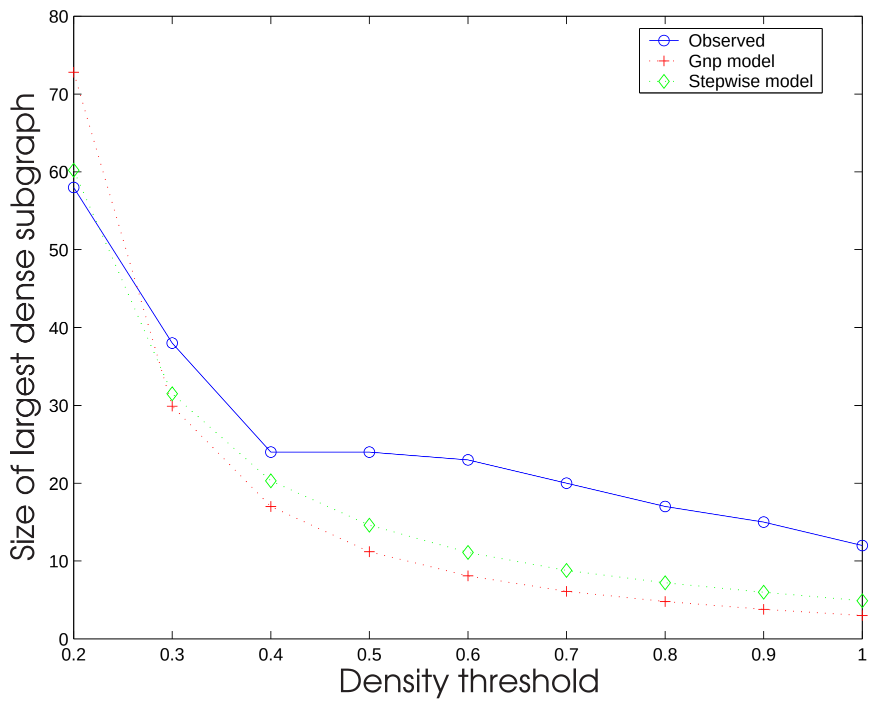
Generalizing Results to Complex Models

- Piecewise $G(n, p)$ model
  - The size of largest dense subgraph is still proportional to $\log n/\kappa$ with a constant factor depending on number of hubs
- More general models
  - Increasing the number of pieces, we approach models with characteristic degree distributions
  - Analysis of power-law graphs in progress
- Multiple networks: Conservation
  - Superpose graphs based on sequence homology

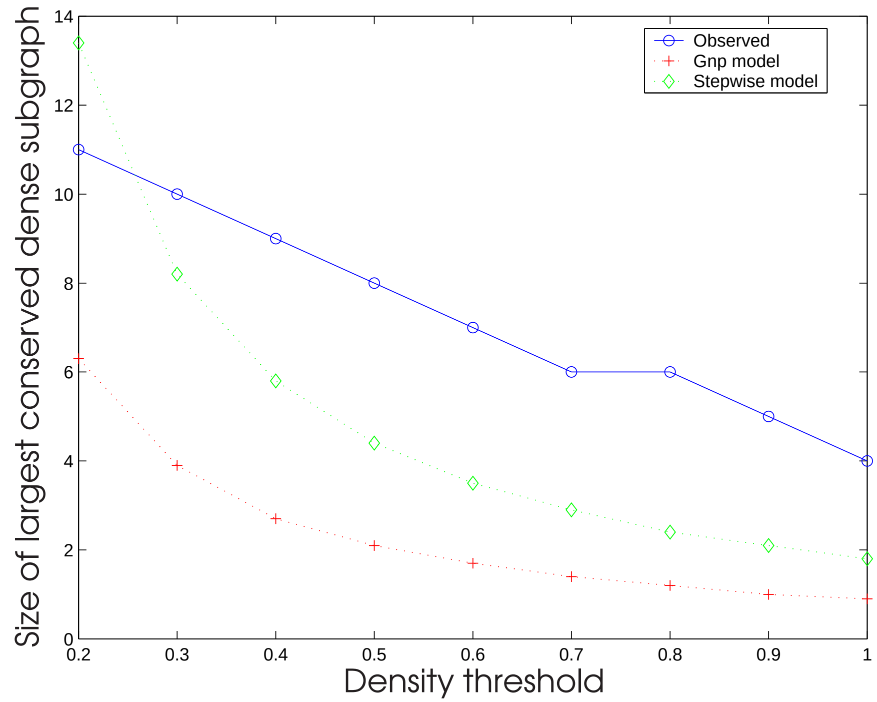
Algorithms Based on Statistical Significance

- Identification of topological modules
- Use statistical significance as a stopping criterion for graph clustering heuristics
- HCS Algorithm (Hartuv & Shamir, *Inf. Proc. Let.*, 2000)
  - Find a minimum-cut bipartitioning of the network
  - If any of the parts is dense enough, record it as a dense cluster of proteins
  - Else, further partition them recursively
- Use statistical significance to determine whether a subgraph is sufficiently dense
  - For given number of proteins and interactions between them, we can determine whether those proteins induce a significantly dense subnet

Largest Dense Subgraph for Varying Density



Yeast PPI network



Yeast & *Fruit Fly* PPI networks

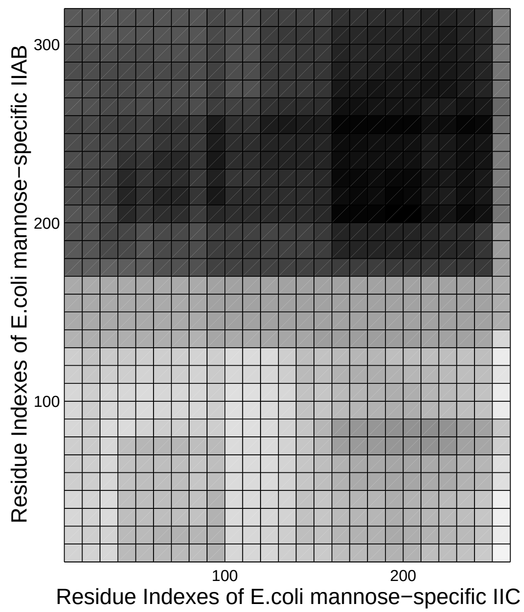
Phylogenetic Analysis for Predicting Interactions

- Functionally related proteins are likely to have co-evolved
  - Construct phylogenetic profile for each genome: Vector of E-values signifying existence of an orthologous protein in each organism
  - Identify pairwise functional associations based on mutual information between phylogenetic profiles (Pellegrini et al., *PNAS*, 1999)
  - Mutual information: $I(X,Y) = H(X) - H(X|Y) = \sum_x \sum_y p(x,y) \log(p(x,y)/p(x)p(y))$
  - Shown to identify functionally associated protein pairs at a coarser level than high-throughput methods

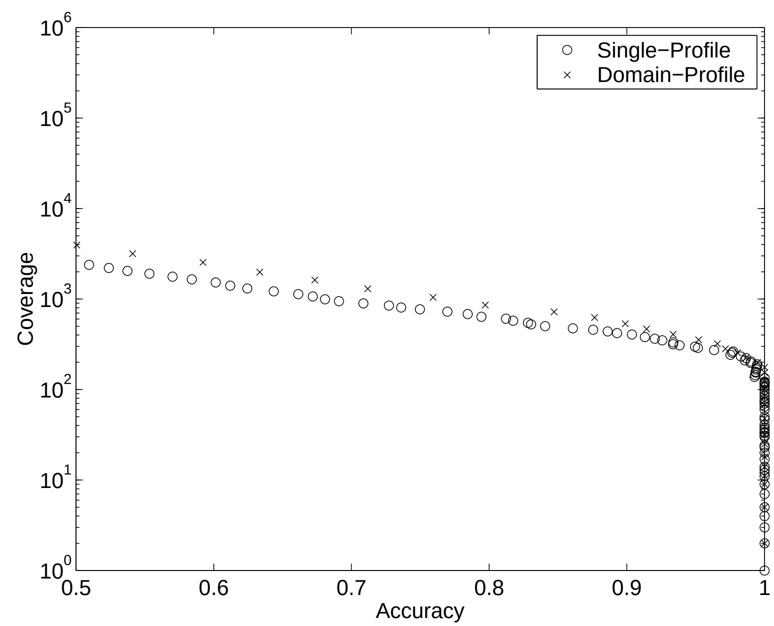
- However, domains, not proteins, co-evolve
  - How can we incorporate domain information to enhance performance of phylogeny-based interaction prediction?

Inferring Function from Domain Co-evolution

- Residue-level phylogenetic analysis (Kim, Koyutürk, Topkara, Grama, & Subramaniam, *Bioinformatics*, 2006)
  - No a-priori knowledge about domains
  - Construct residue phylogenetic profiles from local alignment results
  - Construct mutual information matrix
  - High-information contiguous submatrices that are sufficiently large correspond to putative co-evolved domains



Mutual Information Matrix

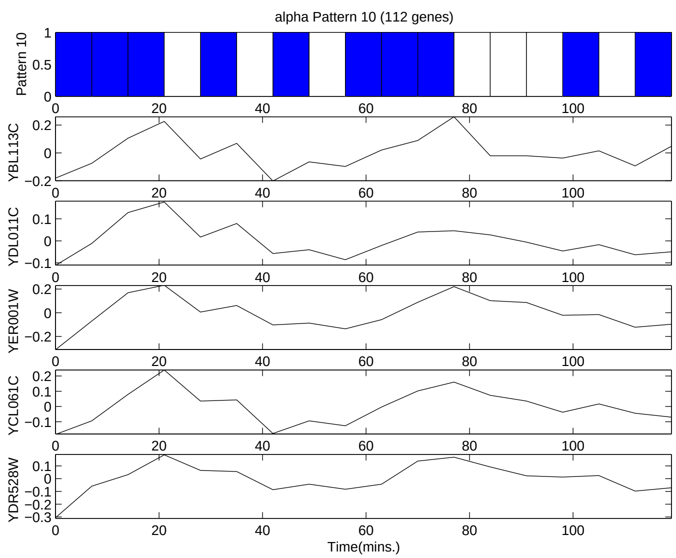


Single vs. Domain Profile

Other Work on Pattern Identification

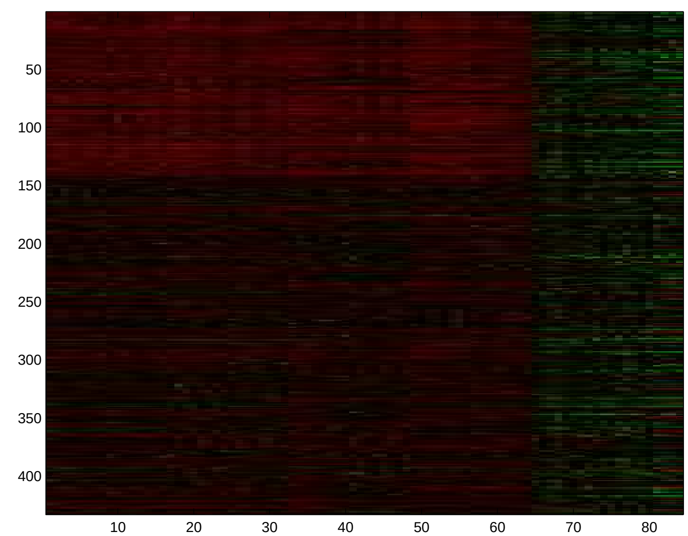
- PROXIMUS: Non-orthogonal decomposition of binary matrices (Koyutürk, Grama, Ramakrishnan, *IEEE TKDE*, 2005)
  - Find a compact set of vectors that represent the entire matrix
  - Recursive decomposition through rank-one approximations
  - Fast (linear-time) iterative heuristics for computing approximations
  - Source code available at `http://www.cs.purdue.edu/homes/koyuturk/proximus/`

Patterns of regulation



"Algorithms for bounded-error correlation of high dimensional data in microarray experiments" (Koyutürk, Grama, Szpankowski: *CSB'03*.)

Biclustering

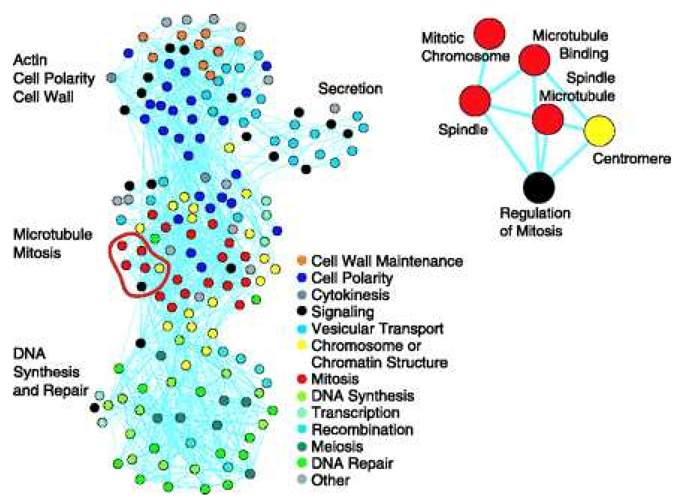


"Biclustering gene-feature matrices for statistically significant dense patterns" (Koyutürk, Grama, Szpankowski: *CSB'04*.)

Identifying "Canonical" Regulatory Pathways

- Can we derive rules in terms of GO terms, *e.g.*, $P_i \rightarrow P_j \dashv P_k$?
  - Statistical challenge: Such patterns have to be significantly abundant
  - Computational challenge: When statistical significance is the basis (as opposed to frequency), monotonicity properties (*e.g.*, downward closure) no longer hold!
  - Our approach: conditional significance, *i.e.*, evaluate significance of a pattern based on the background constructed by its substructures

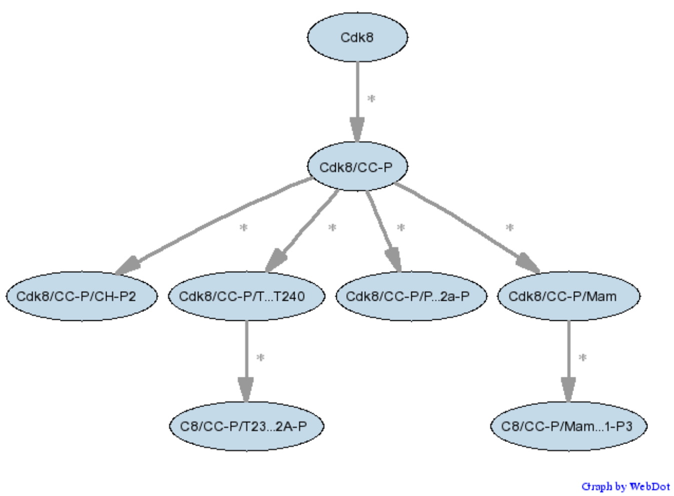
- Final goal: Database of (computationally derived) canonical modules and pathways



A network of GO terms (Tong et al., *Science*, 2004)

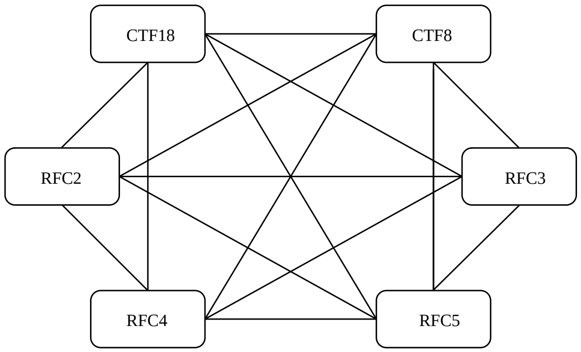
Cell as a State Machine

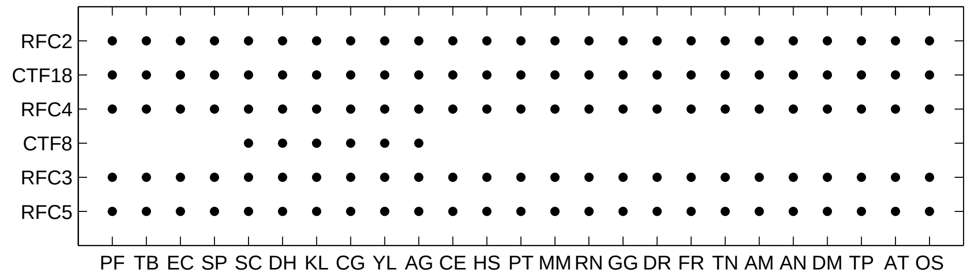
- Signaling pathways can be modeled as a series of transitions between states of protein or peptide molecules, non-protein molecules, (non-)protein complexes, and modules
  - Signaling Gateway provides a database of network states for proteins, a mirror is available to our group via our collaboration with S. Subramaniam
- Constructing signaling pathways from state information for individual molecules
  - Smallest common supergraph problem
  - Identification of specified pathways



State diagram for Cdk8 protein (from Molecule Pages)

Modular Phylogenetics

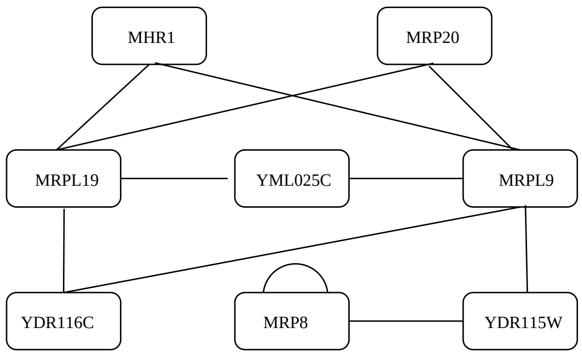


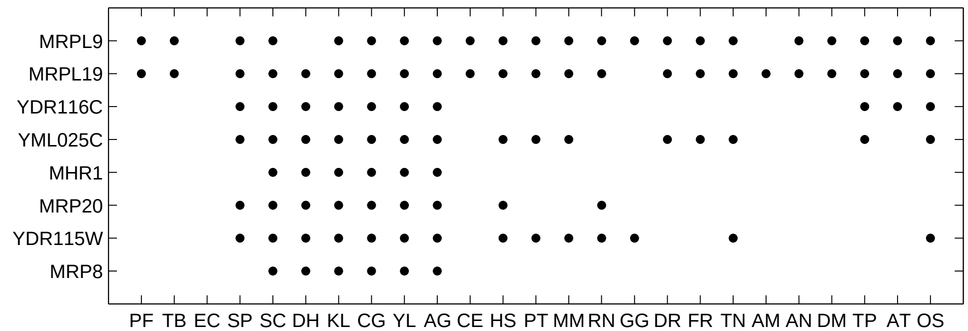


Replication Factor C complex identified on yeast PPI network by MCODE (Bader & Hogue, *BMC Bioinformatics*, 2003) algorithm and the phylogenetic profiles of its proteins on 25 eukaryotic genomes

Conserved in all eukaryotic species!

Modular Phylogenetics





A component of mitochondrial ribosome identified on yeast PPI network by MCODE algorithm and the phylogenetic profiles of its proteins on 25 eukaryotic genomes

Conserved in only yeast species!

- Models and algorithms for quantifying, analyzing, and evaluating modular conservation and divergence across species

Conclusion

- A lot to learn from comparative network analysis
- We have fast algorithms
- We need
  - Enhanced & more detailed network models
  - High quality & comprehensive data
  - Detailed statistical models

Thanks...

- For their guidance, support & friendship
  - Ananth Grama
  - Wojciech Szpankowski
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