Understanding Protein Function on a Genome-scale through the Analysis of Molecular Networks

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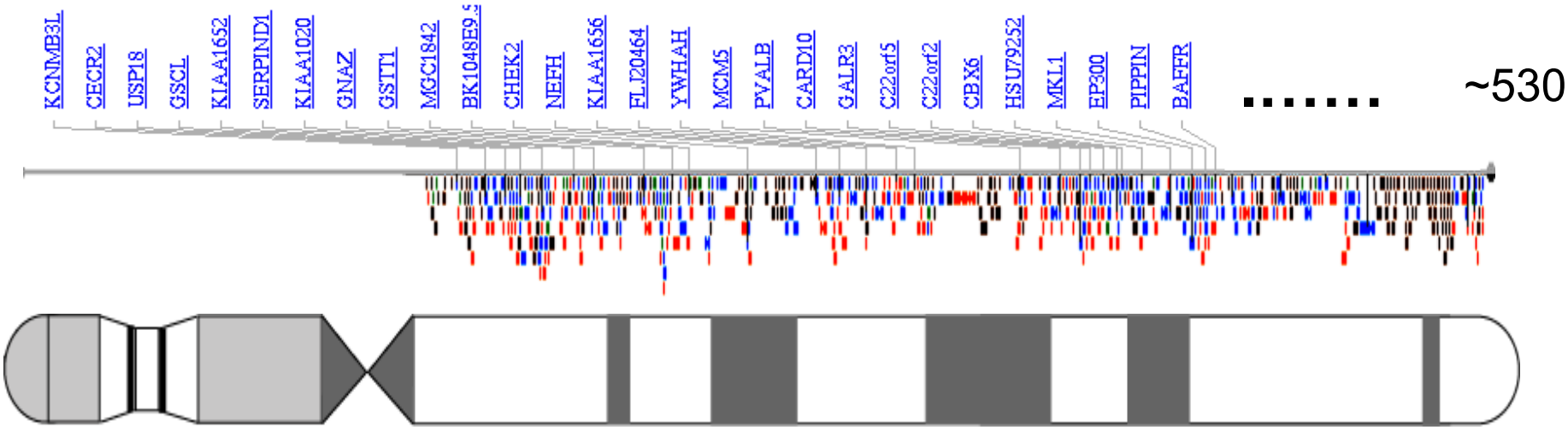
Slides at

Lectures.GersteinLab.org

(See Last Slide for References & More Info.)

The problem: Grappling with Function on a Genome Scale?



- 250 of ~530
  originally characterized on chr. 22
  [Dunham et al. Nature (1999)]

- >25K Proteins in Entire Human Genome
  (with alt. splicing)

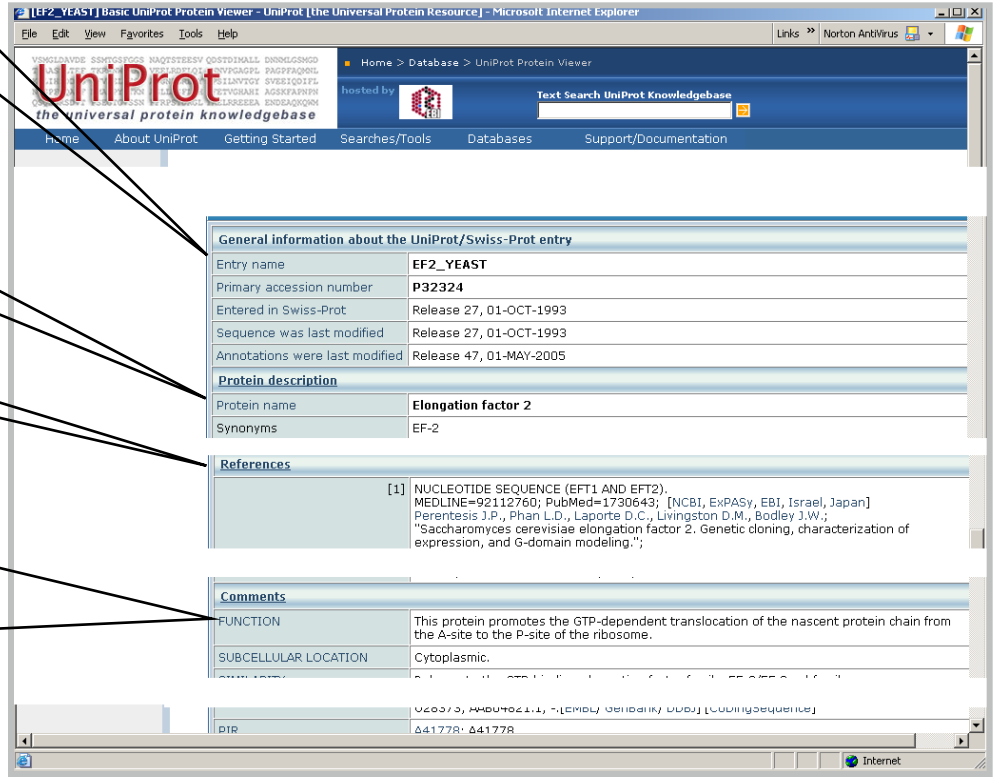
Traditional single molecule way to integrate evidence & describe function

EF2_YEAST

Descriptive Name:
Elongation Factor 2

Lots of references
to papers

Summary sentence describing function:
This protein promotes the GTP-dependent translocation of the nascent protein chain from the A-site to the P-site of the ribosome.



Some obvious issues in scaling single molecule definition to a genomic scale

- Fundamental complexities
  - ◊ Often >2 proteins/function
  - ◊ Multi-functionality:
    2 functions/protein
  - ◊ Role Conflation:
    molecular, cellular, phenotypic

Some obvious issues in scaling single molecule definition to a genomic scale

- Fundamental complexities
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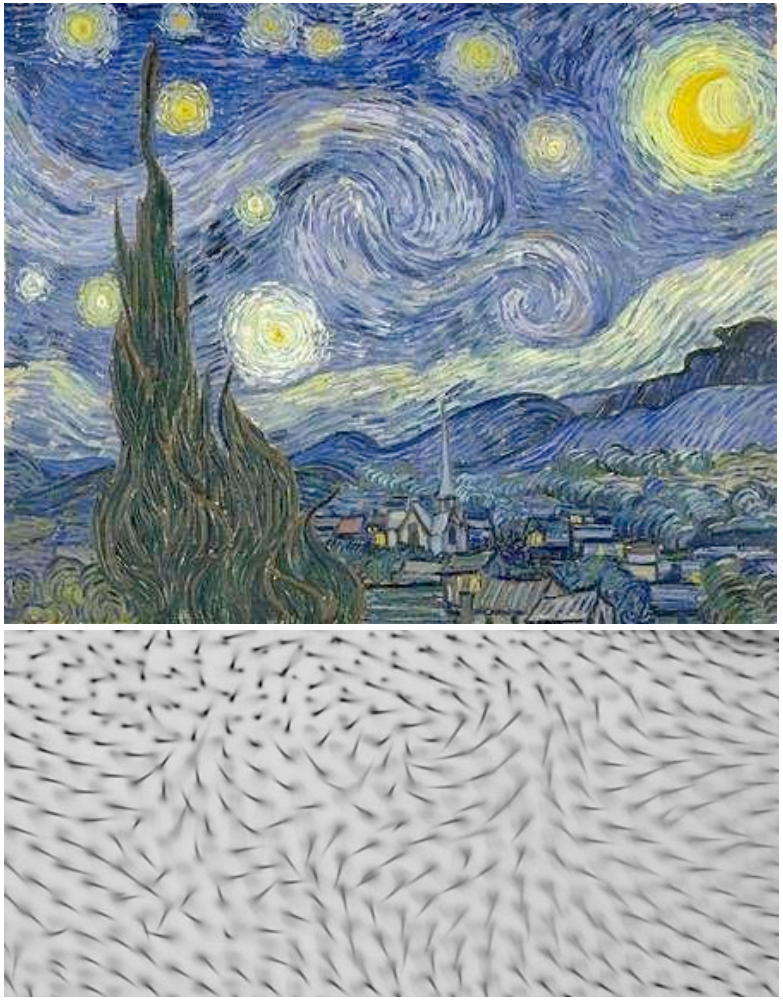
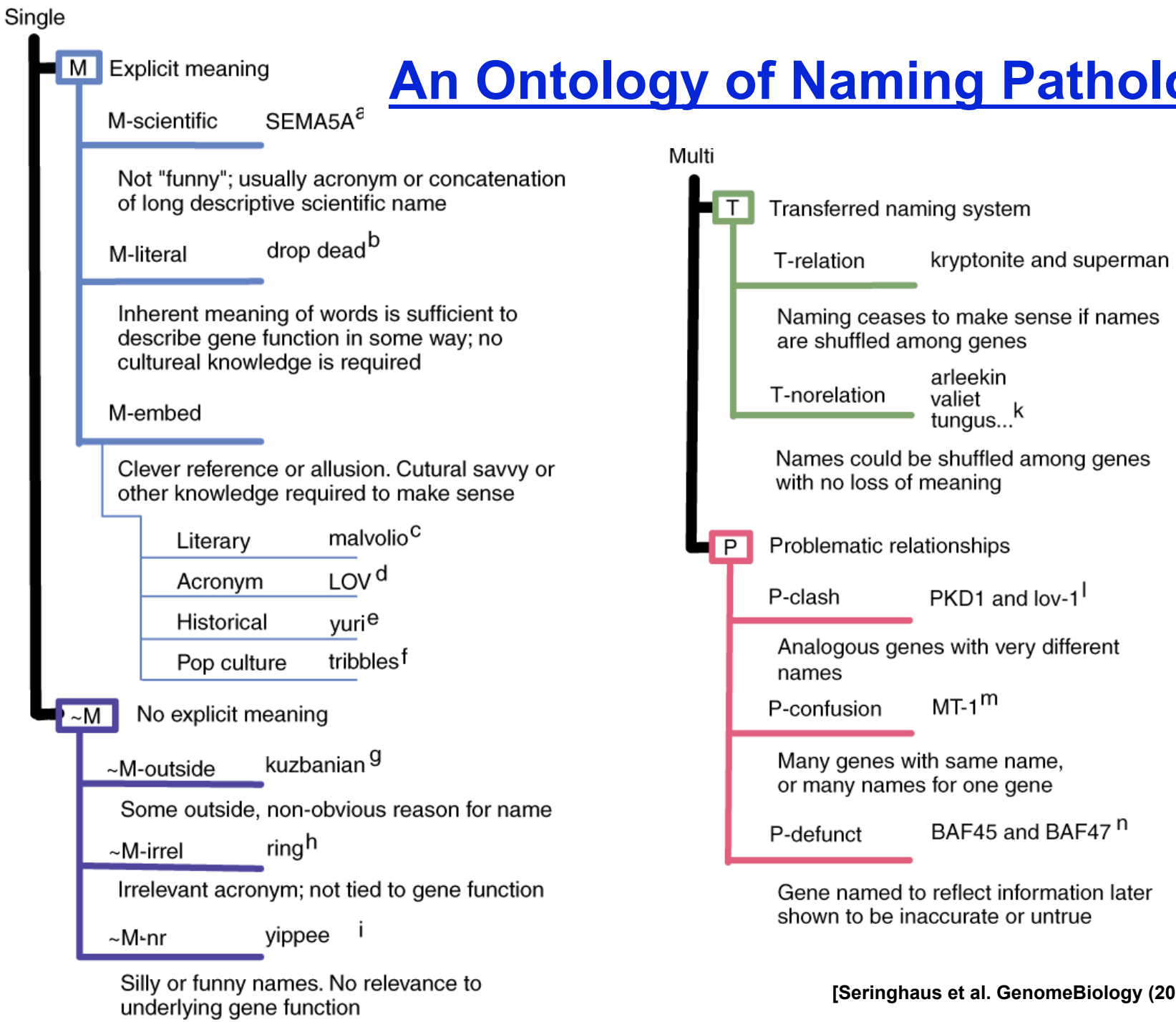
    2 functions/protein
  - ◊ Role Conflation:
    molecular, cellular, phenotypic
- Fun terms… but do they scale?....
  - ◊ **Starry night** (P Adler, '94)



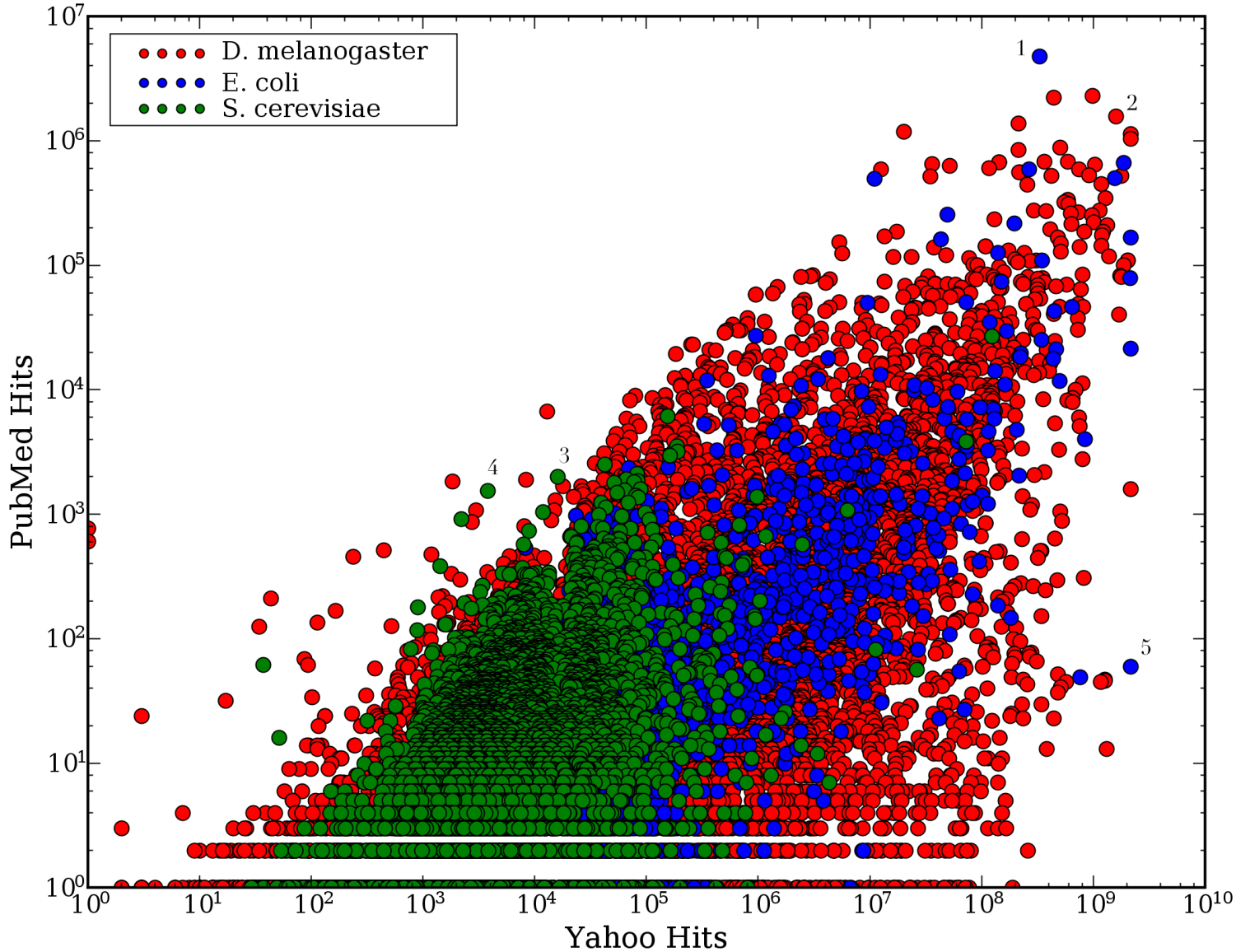
[Seringhaus et al. GenomeBiology (2008)]

An Ontology of Naming Pathologies



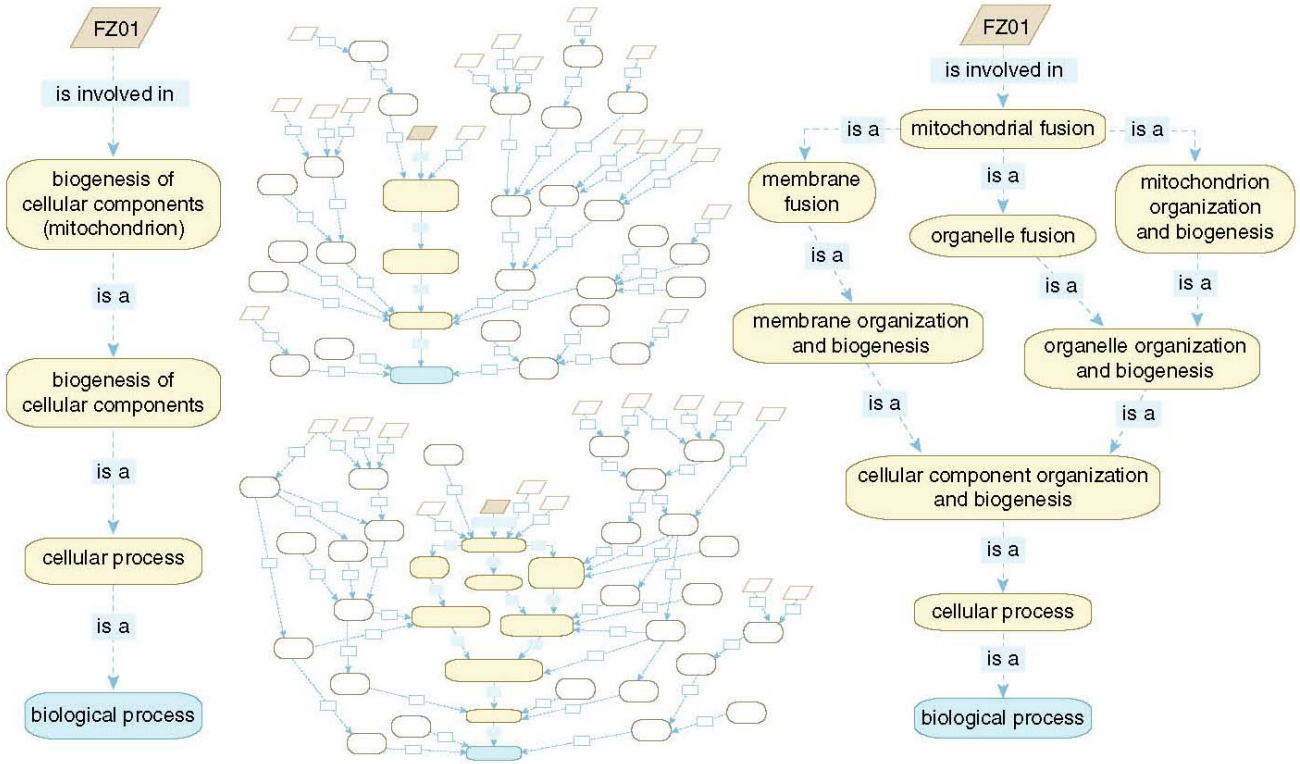
[Seringhaus et al. GenomeBiology (2008)]

Gene Name Skew



[Seringhaus et al. GenomeBiology (2008)]

Hierarchies & DAGs of controlled-vocab terms but still have issues...



MIPS (Mewes et al.) **GO (Ashburner et al.)**

[Seringhaus & Gerstein, Am. Sci. '08]

Towards Developing Standardized Descriptions of Function

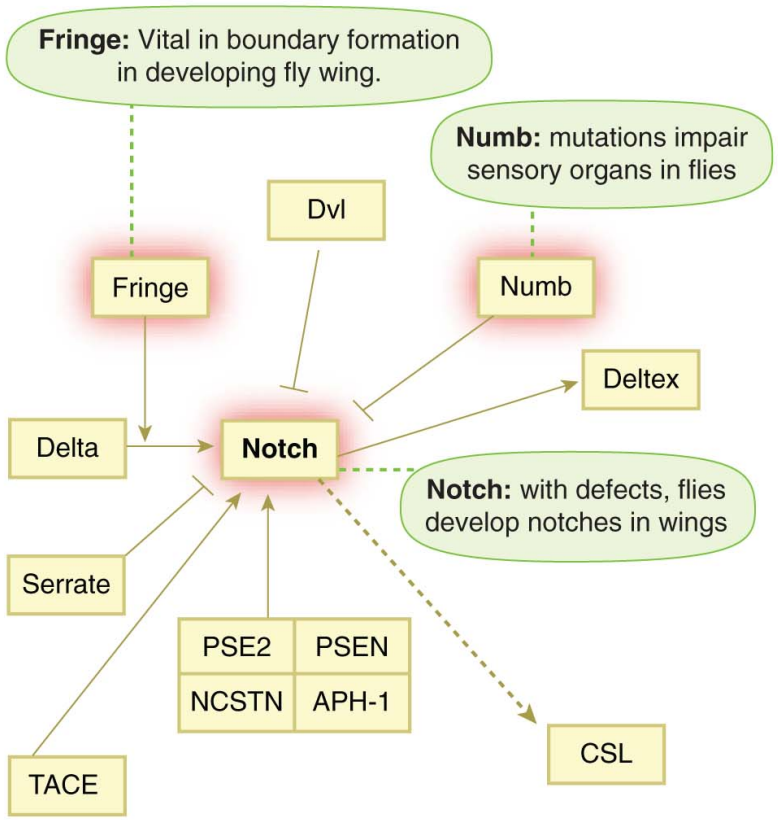
- Subjecting each gene to standardized expt. and cataloging effect
  - ◊ KOs of each gene in a variety of std. conditions => phenotypes
  - ◊ Std. binding expts for each gene (e.g. prot. chip)

- Function as a vector

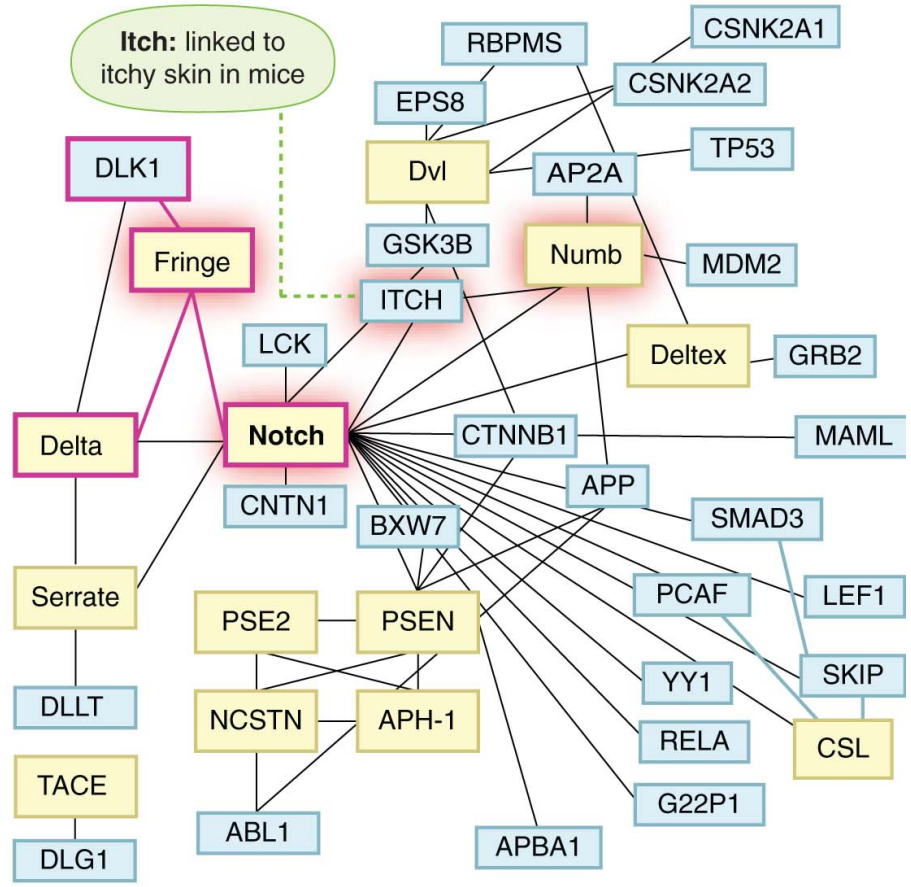
	nucleic acids		small molecules					proteins			
	DNA	RNA	ATP	Metal	CoA	NAD	.....	G protein	CDC28	Calmodulin	.....
protein 1	1.0	0	0	0	0	0	.....	0	0	0	.....
protein 2	0	0.9	0	0	0	0	.....	0	0	0	.....
protein 3	1.0	0	1.0	0	0	0	.....	0	0	0	.....
protein 4	0	0	0	0	0.8	0	.....	0	0	1.0	.....
protein 5	1.0	0	0	0	0	0	.....	0	0.9	0	.....
protein 6	0.9	0					.....				.....
protein 7	0	0.8					.....				.....
.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....	.....

Interaction Vectors [Lan et al, IEEE 90:1848]

Networks (Old & New)



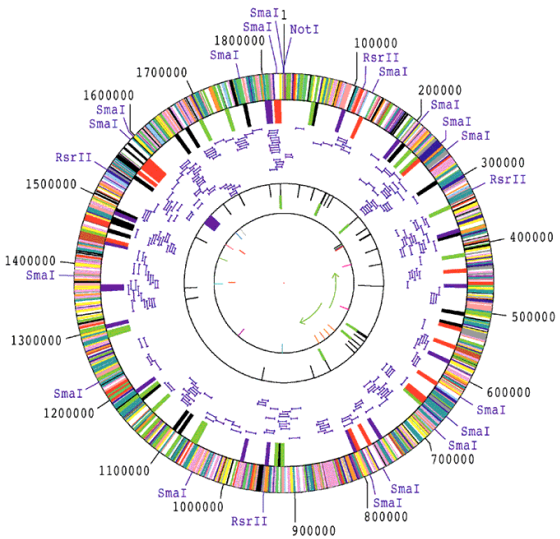
Classical KEGG pathway



Same Genes in High-throughput Network

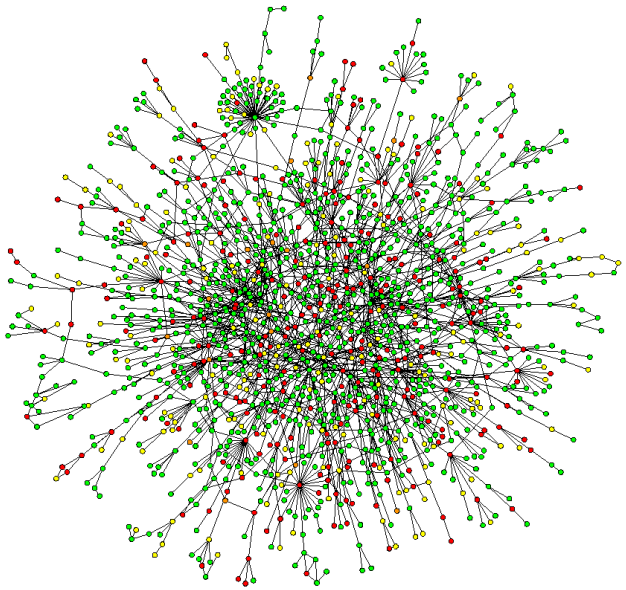
[Seringhaus & Gerstein, Am. Sci. '08]

Networks occupy a midway point in terms of level of understanding



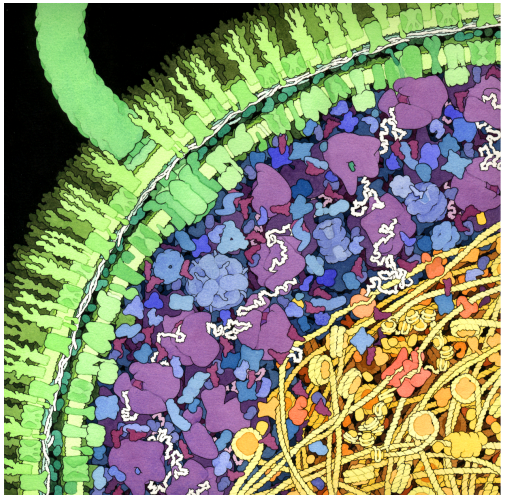
1D: Complete Genetic Partslist

[Fleischmann et al., Science, 269 :496]



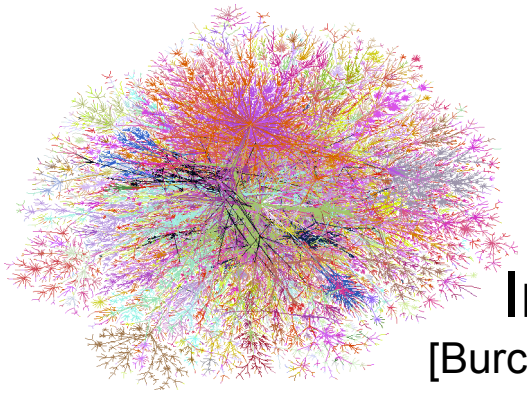
~2D: Bio-molecular Network Wiring Diagram

[Jeong et al. Nature, 41:411]

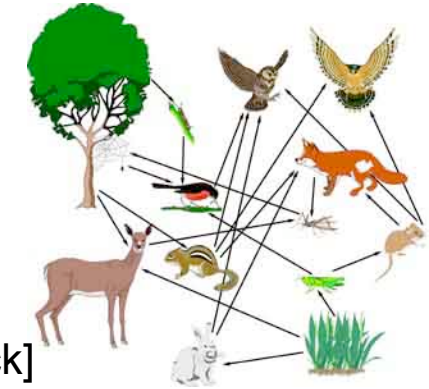


3D: Detailed structural understanding of cellular machinery

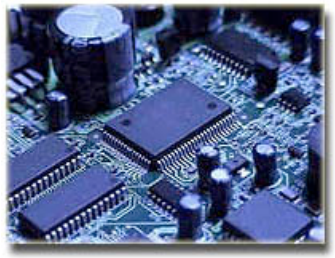
Networks as a universal language



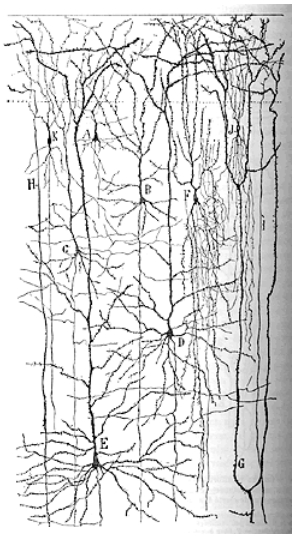
Internet
[Burch & Cheswick]



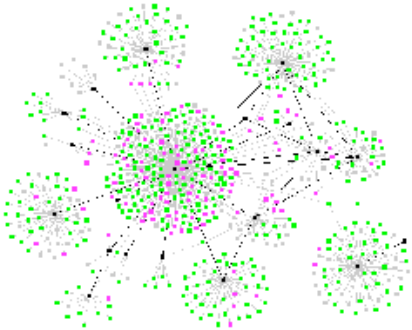
Food Web



Electronic Circuit

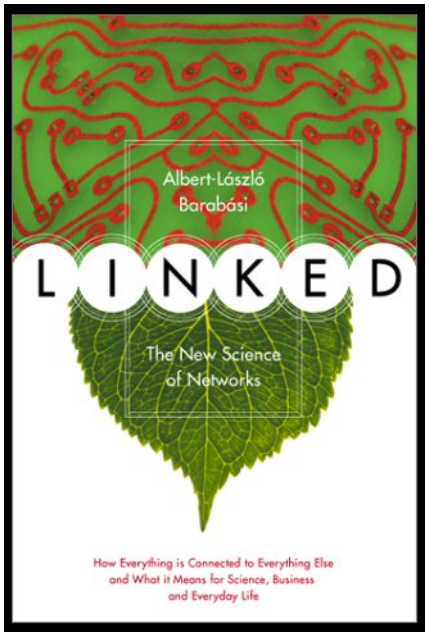


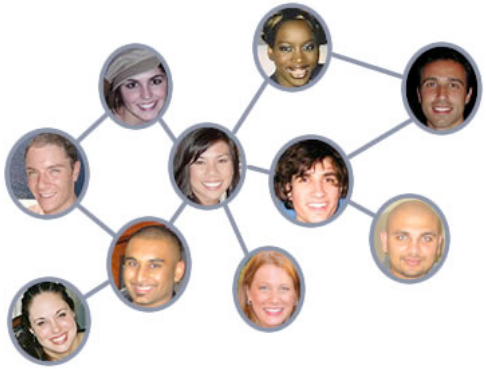
Neural Network
[Cajal]



Disease Spread
[Krebs]

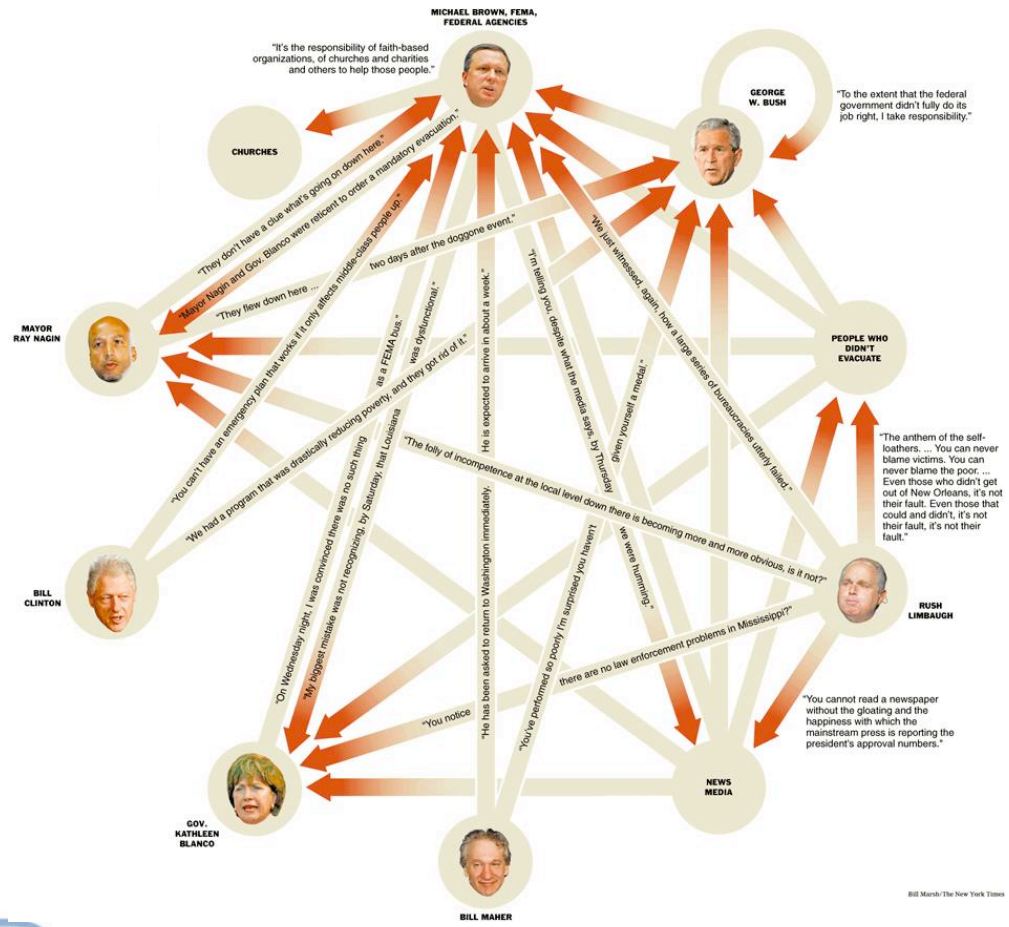
Protein Interactions
[Barabasi]



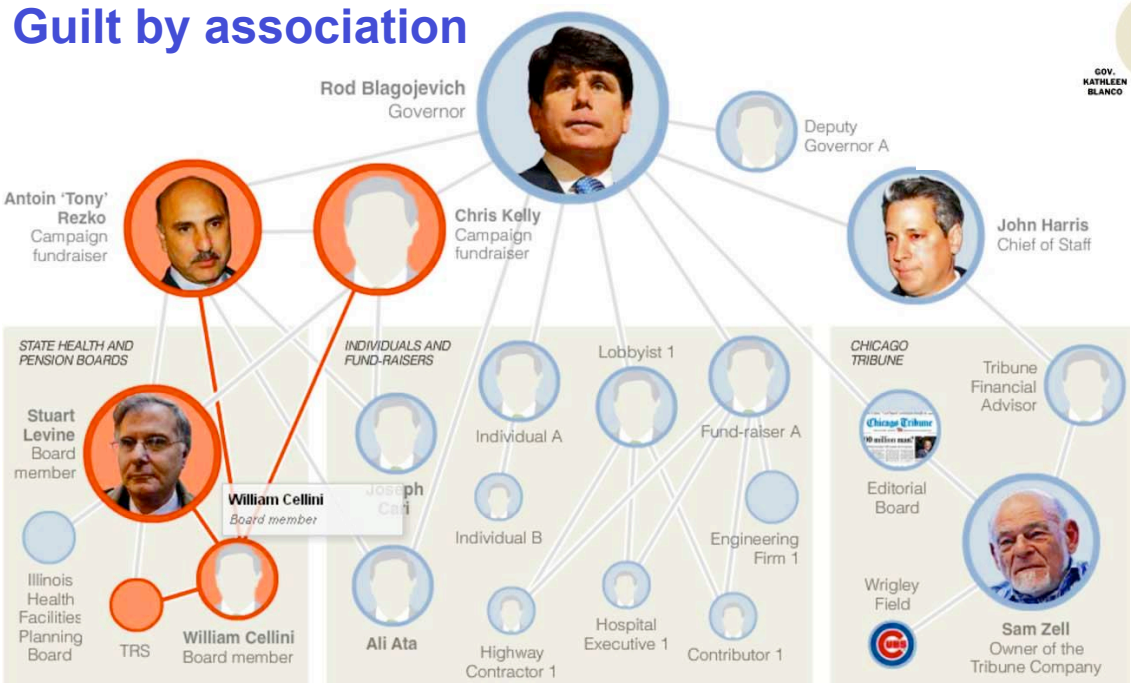


Social Network

Using the position in networks to describe function



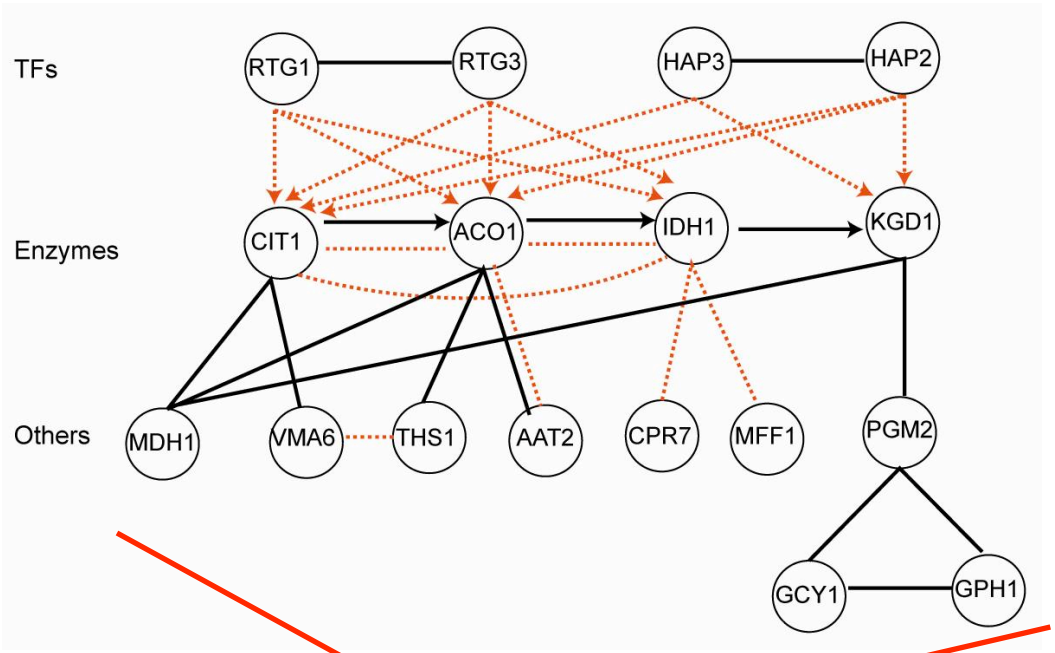
Guilt by association

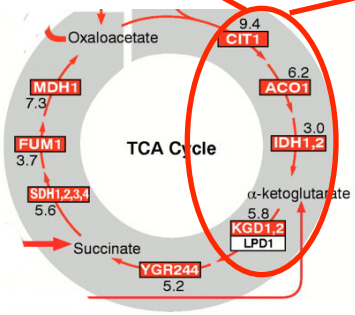


Finding the causal regulator (the "Blame Game")

[NY Times, 2-Oct-05, 9-Dec-08]

Combining networks forms an ideal way of integrating diverse information





Part of the TCA cycle

Metabolic pathway

Transcriptional regulatory network

Physical protein-protein Interaction

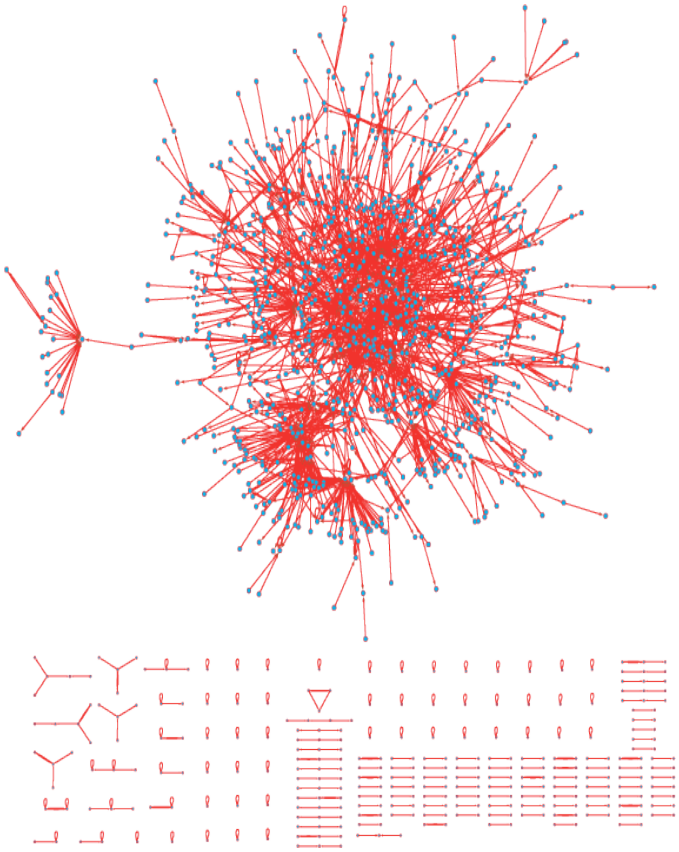
Co-expression Relationship

Genetic interaction (synthetic lethal)
Signaling pathways

Outline: Molecular Networks

- Why Networks?
- Predicting Networks (yeast)
  - ◊ Propagating known information
- Network Structure: Key Positions (yeast)
  - ◊ Hubs & Bottlenecks
- Dynamics & Variation of Networks
  - ◊ Across cellular states (yeast)
  - ◊ Across environments (in prokaryotes)
- Protein Networks & Human Variation

Example: yeast PPI network



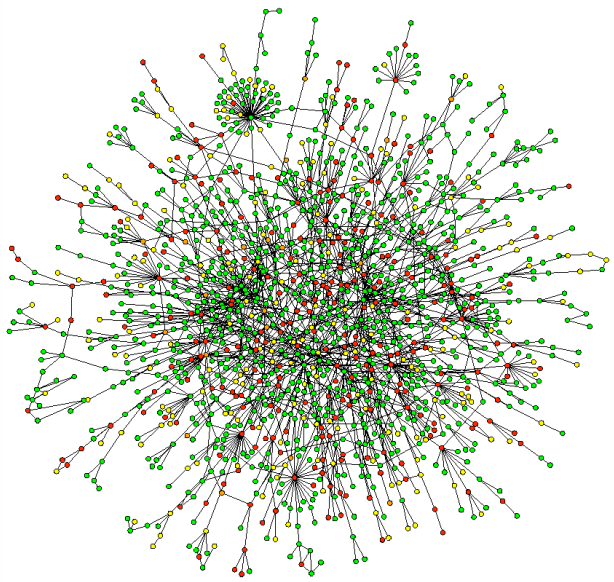
Actual size:

- ~6,000 nodes
  → Computational cost: ~18M pairs
- Estimated ~15,000 edges
  → Sparseness: 0.08% of all pairs (Yu et al., 2008)

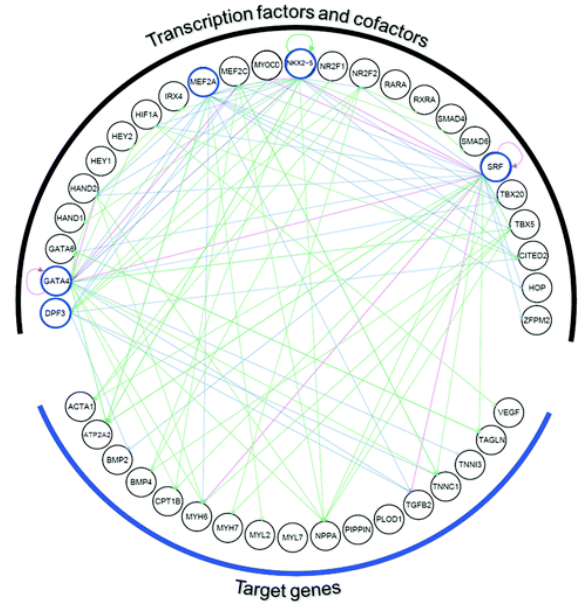
Known interactions:

- Small-scale experiments: accurate but few
  → Overfitting: ~5,000 in BioGRID, involving ~2,300 proteins
- Large-scale experiments: abundant but noisy
  → Noise: false +ve/-ve for yeast two-hybrid data up to 45% and 90% (Huang et al., 2007)

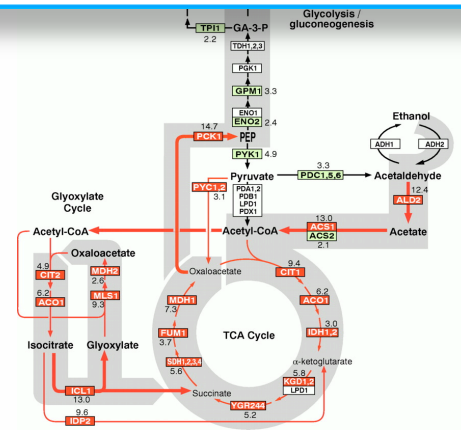
Types of Networks



Interaction networks



Regulatory networks



Metabolic networks

Nodes: proteins or genes
Edges: interactions

[Horak, et al, Genes & Development, 16:3017-3033]

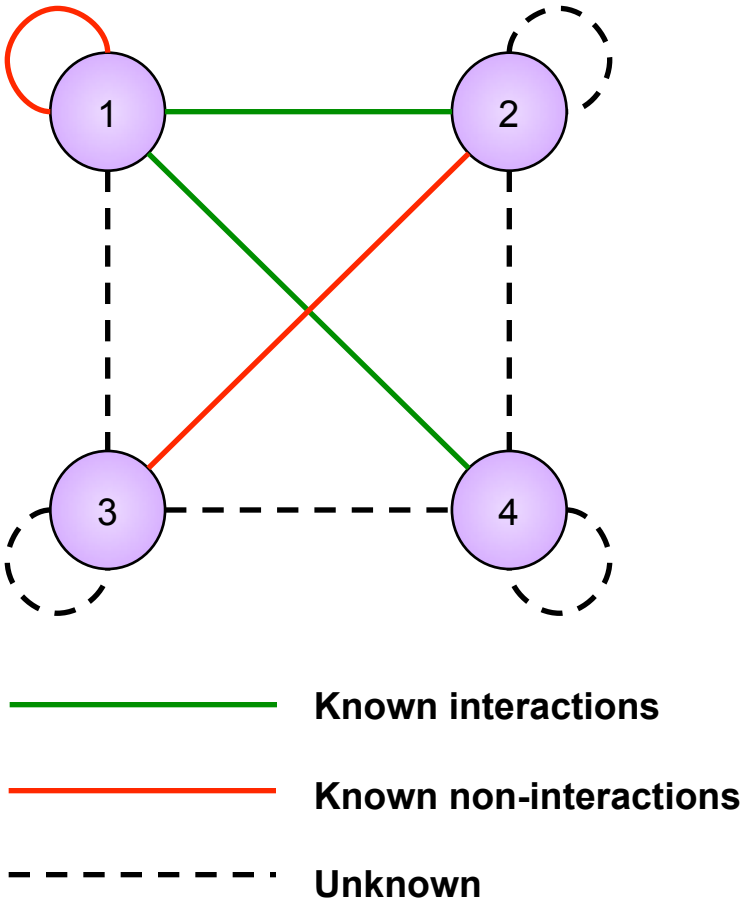
[DeRisi, Iyer, and Brown, Science, 278:680-686]

[Jeong et al, Nature, 41:411]

Predicting Networks

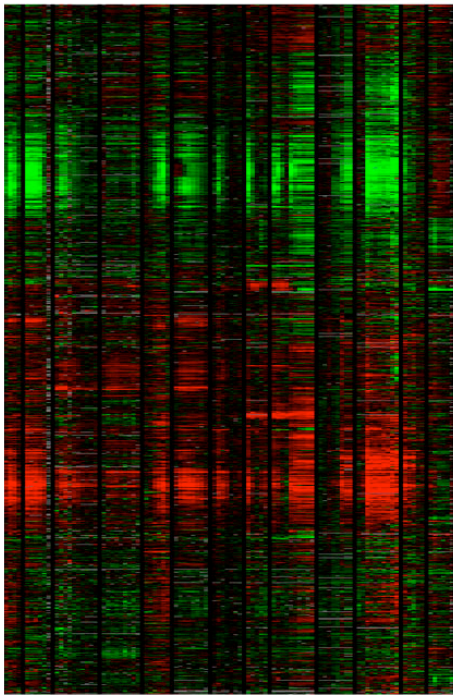
How do we construct large molecular networks?
From extrapolating correlations between functional genomics data with fairly small sets of known interactions, making best use of the known training data.

Network prediction: known information



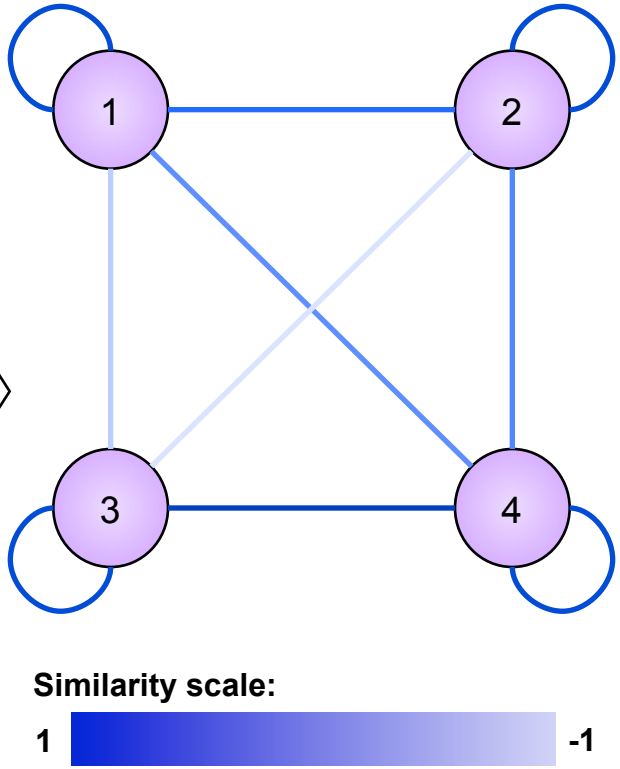
Network prediction: features

- Example 1: gene expression



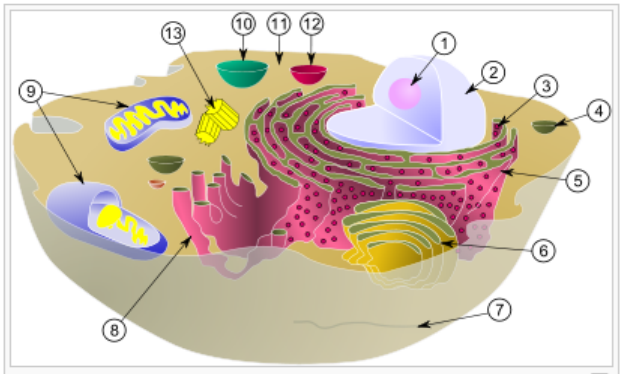
Gasch et al., 2000

$x_1 = (0.2, 2.4, 1.5, \ldots)$
$x_2 = (0.8, 2.2, 1.5, \ldots)$
$x_3 = (4.3, 0.1, 7.5, \ldots)$
…
$\mathrm{sim}(x_1, x_2) = 0.62$
$\mathrm{sim}(x_1, x_3) = -0.58$
…



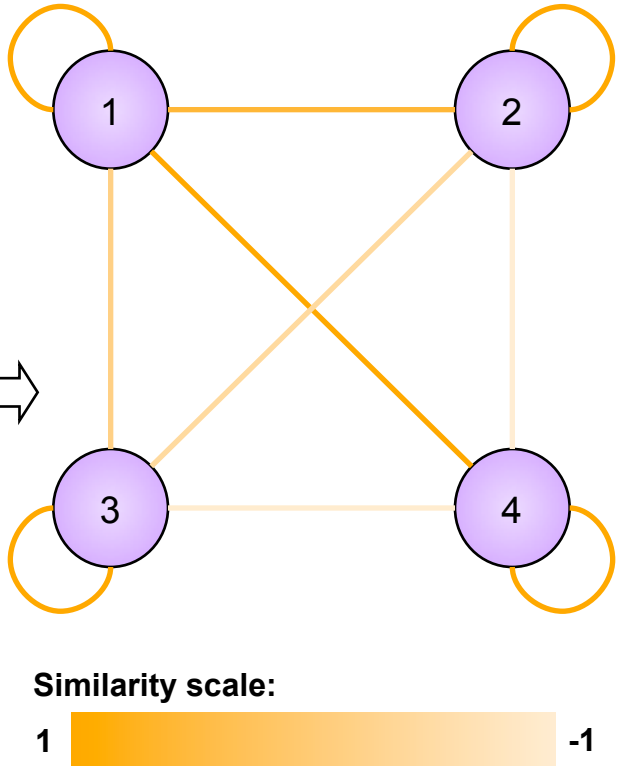
Network prediction: features

- Example 2: sub-cellular localization

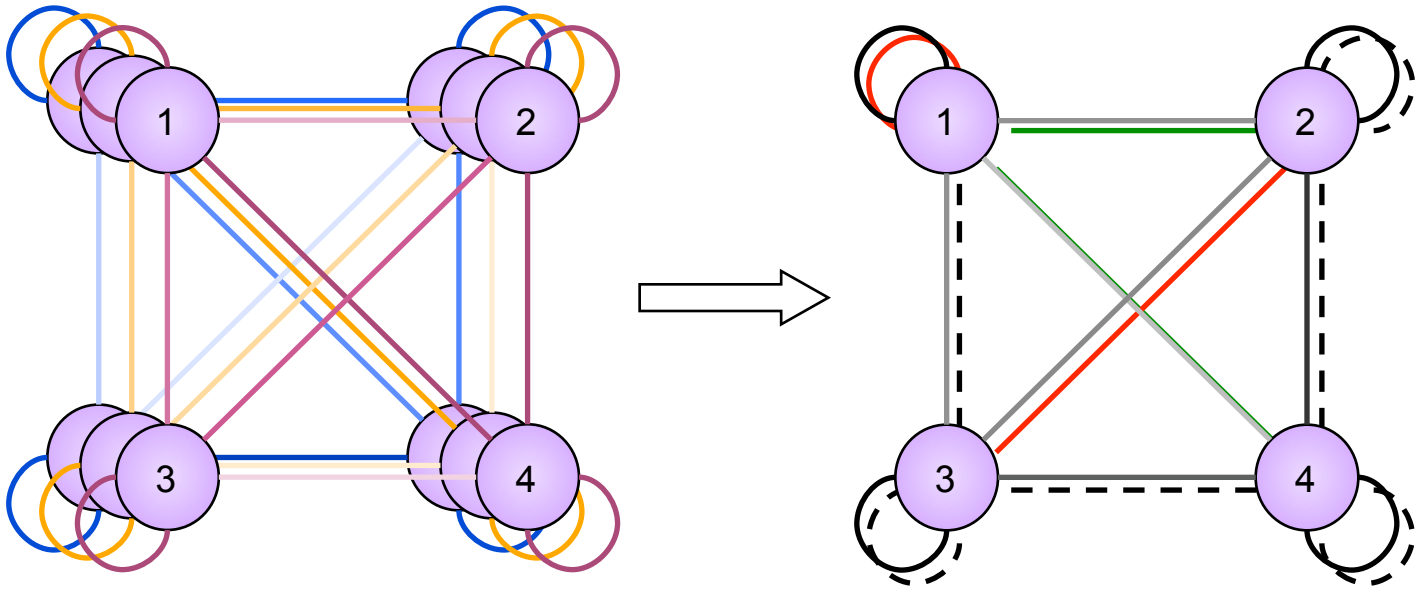


http://www.scq.ubc.ca/wp-content/yeasttwohybridtranscript.gif

$x_1 = (1, 1, 0, 0, \ldots)$
$x_2 = (1, 1, 1, 0, \ldots)$
$x_3 = (1, 0, 1, 0, \ldots)$
…
$\mathrm{sim}(x_1, x_2) = 0.81$
$\mathrm{sim}(x_1, x_3) = 0.12$
…



Network prediction: data integration



Learning methods

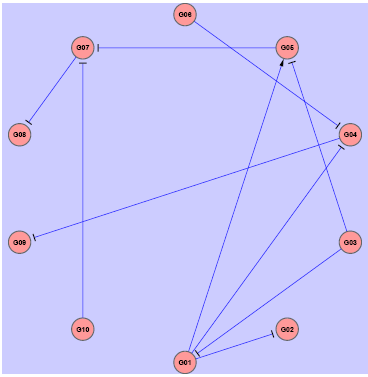
An endless list:

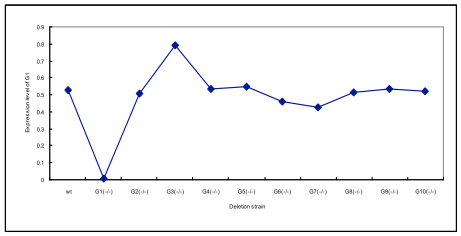
- Docking (e.g. Schoichet and Kuntz 1991)
- Evolutionary (e.g. Ramani and Marcotte, 2003)
- Topological (e.g. Yu et al., 2006)
- Bayesian (e.g. Jansen et al., 2003)
- **Kernel methods**
  - ◊ Global modeling:
    - em (Tsuda et al., 2003)
    - kCCA (Yamanishi et al., 2004)
    - kML (Vert and Yamanishi, 2005)
    - Pairwise kernel (Pkernel) (Ben-Hur and Noble, 2005)
  - ◊ Local modeling:
    - Local modeling (Bleakley et al., 2007)

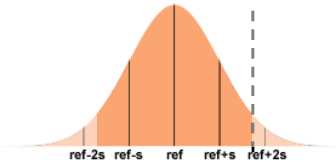
Let's compare in a public challenge!
(DREAM: Dialogue for Reverse Engineering Assessment and Methods)

DREAM3: *in silico* regulatory network reconstruction

Actual network | **Expression data** | **Modeling** | **Predictions**

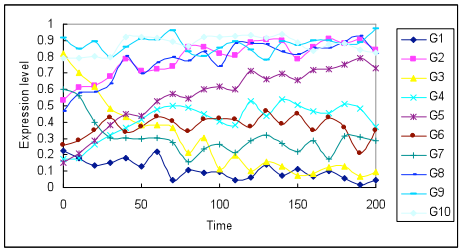






Prob(signal|point)
= 2Φ((point – ref) / s) – 1

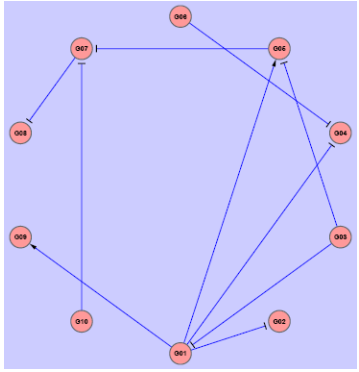
Deletion strains | **Noise models**



$$\frac{dy_j}{dt} = a_{j0} - a_{jj}y_j + \sum_{k \in S} a_{jk} y_k$$

$$\frac{dy_j}{dt} = \frac{b_{j1}}{1 + \exp\left(a_{j0} + \sum_{k \in S} a_{jk} y_k\right)} - b_{j2} y_j$$

$$\frac{dy_j}{dt} = a_{j0} \prod_{k_1 \in S_1} \left(\frac{b_{jk_1}}{y_{k_1}^{c_{jk_1}} + b_{jk_1}} \right) \prod_{k_2 \in S_2} \left(\frac{y_{k_2}^{c_{jk_2}}}{y_{k_2}^{c_{jk_2}} + b_{jk_2}} \right) - a_{j1} y_j$$



Time series after initial perturbation | **Expression rate models**

[Yip et al., DREAM3]

Accuracy (AUC)	E. Coli 1	E. Coli 2	Yeast 1	Yeast 2	Yeast 3
Size-10	0.928	0.912	0.949	0.747	0.714
Size-50	0.930	0.924	0.917	0.792	0.805
Size-100	0.948	0.960	0.915	0.856	0.783

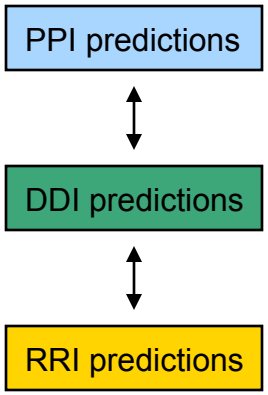
Our work: efficiently propagating known information

Training set expansion

- Motivation: lack of training examples
- Expand training sets horizontally

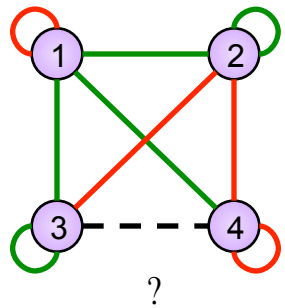
Multi-level learning

- Motivation: hierarchical nature of interaction
- Expand training sets vertically



DREAM3 *in silico* regulatory network reconstruction challenge

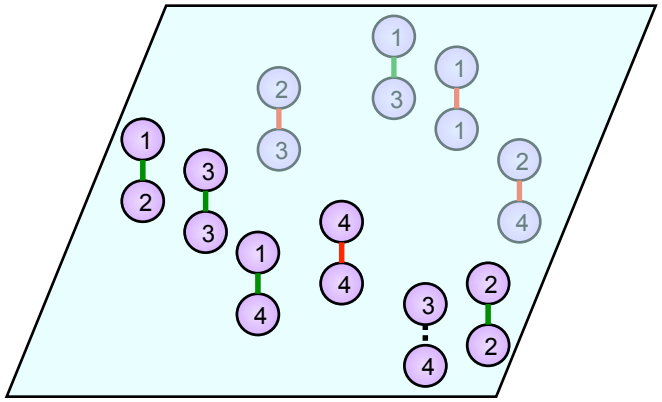
Global vs. local modeling



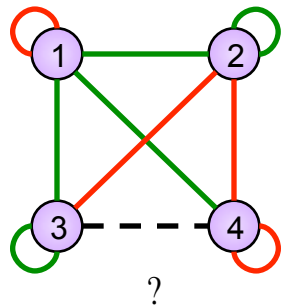
Global modeling: build one model for the whole network

Example - Pairwise kernel: consider object pairs instead of individual objects

Problem: $O(n^2)$ instances, $O(n^4)$ kernel elements

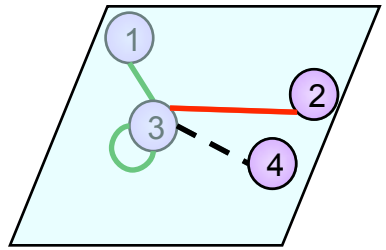


Global vs. local modeling



Local modeling: build one model for each node

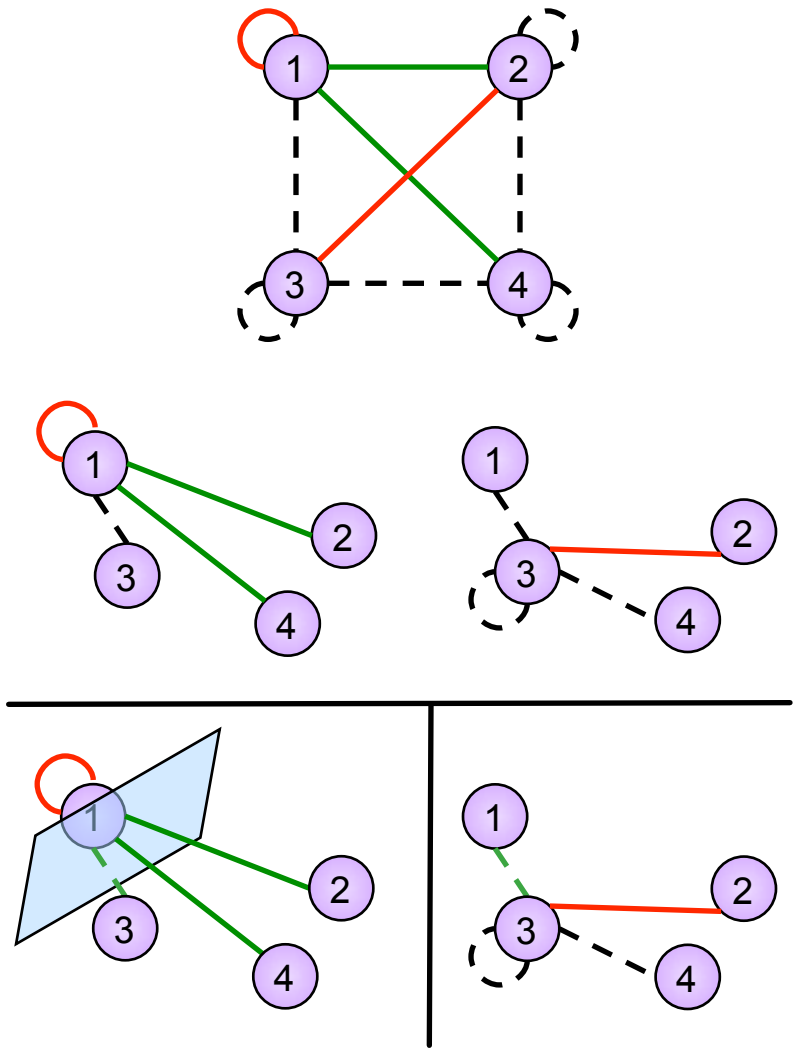
Model for node 3:



Problem: insufficient and unevenly distributed training data (what if node 3 has no known interactions at all?)

Prediction propagation

- Goal: keep the flexibility of local modeling, but tackle the data sparsity problem
- Motivation: some objects have more examples than others
- Our approach:
  - ◊ Learn models for objects with more examples first
  - ◊ Propagate the most confident predictions as auxiliary examples of other objects



[Yip and Gerstein, Bioinformatics ('09)]

Prediction accuracy (AUC)

	phy	loc	exp-gasch	exp-spellman	y2h-ito	y2h-uetz	tap-gavin	tap-krogan	int
Mode 1									
direct	58.04	66.55	64.61	57.41	51.52	52.13	59.37	61.62	70.91
kCCA	65.80	63.86	68.98	65.10	50.89	50.48	57.56	51.85	80.98
kML	63.87	68.10	69.67	68.99	52.76	53.85	60.86	57.69	73.47
em	71.22	75.14	67.53	64.96	55.90	53.13	63.74	68.20	81.65
local	71.67	71.41	72.66	70.63	67.27	67.27	64.60	67.48	75.65
local+pp	73.89	75.25	77.43	75.35	71.60	71.51	74.62	71.39	83.63
local+ki	71.68	71.42	75.89	70.96	69.40	69.05	70.53	72.03	81.74
local+pp+ki	72.40	75.19	77.41	73.81	70.44	70.57	73.59	72.64	83.59

Observations:

- Highest accuracy by training set expansion
- Over fitting of local modeling without training set expansion
- Prediction propagation theoretically related to co -training (Blum and Mitchell, 1998)
  - ◊ Semi-supervised (Similarity with PSI-BLAST)

[Yip and Gerstein, Bioinformatics ('09)]

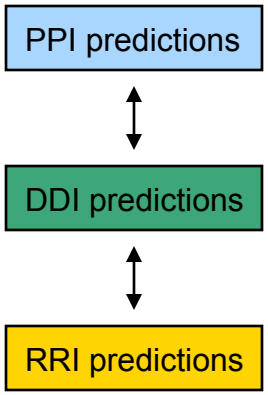
From horizontal to vertical

Training set expansion

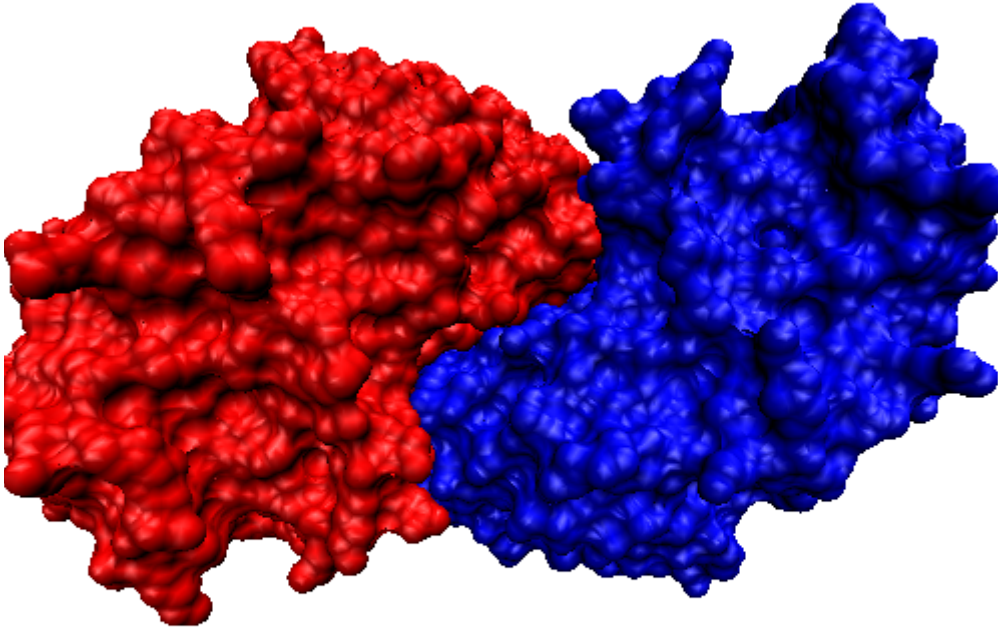
- Motivation: lack of training examples
- Expand training sets horizontally

Multi-level learning

- Motivation: hierarchical nature of interaction
- Expand training sets vertically



Protein interaction

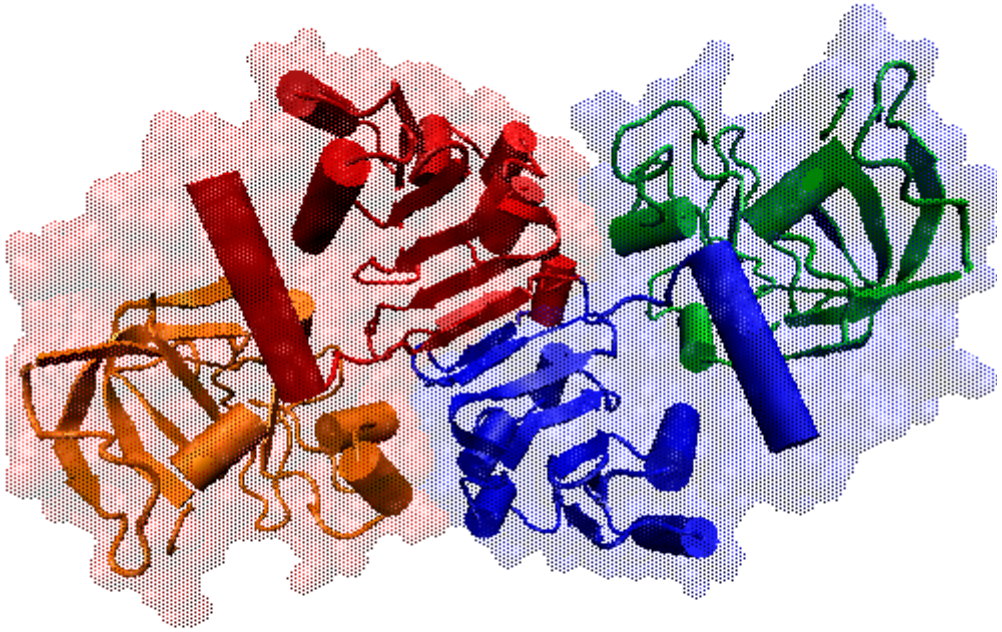


Yeast NADP-dependent alcohol dehydrogenase 6 (PDB: 1piw)

Protein-level features for interaction prediction: functional genomic information

[Yip and Gerstein, in revision]

Domain interaction

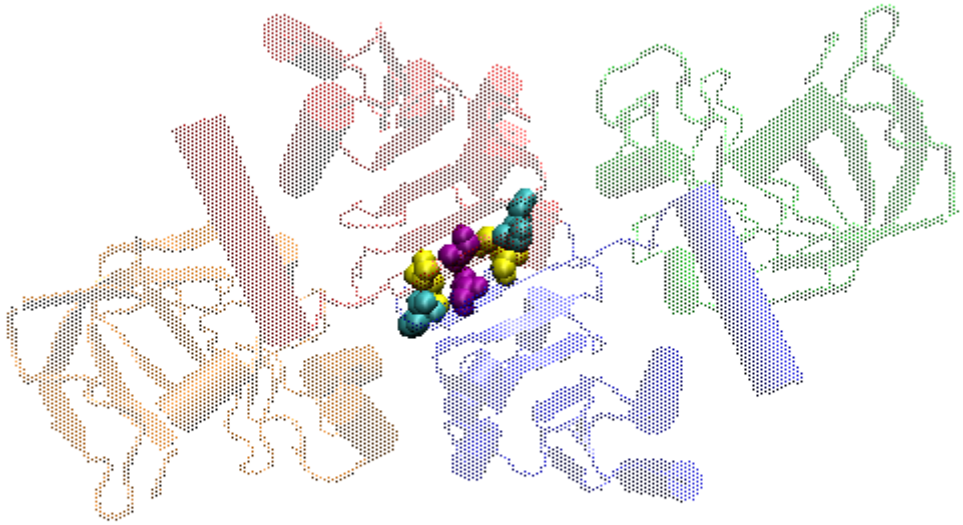


Pfam domains: PF00107 (inner) and PF08240 (outer)

Domain-level features for interaction prediction: evolutionary information

[Yip and Gerstein, in revision]

Residue interaction

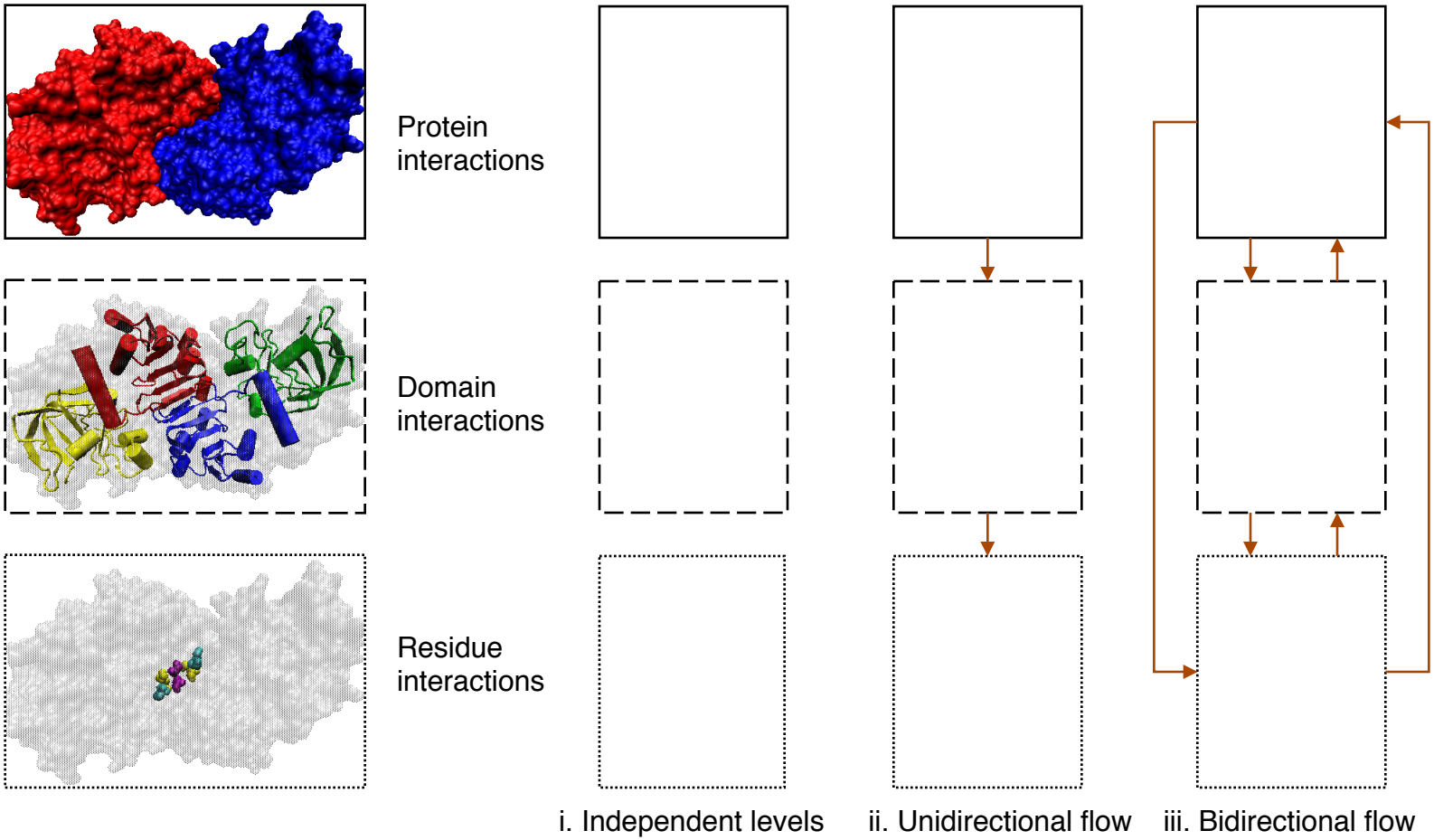


Interacting residues: 283 (yellow) with 287 (cyan), and 285 (purple) with 285

Residue-level features for interaction prediction: physical-chemical information

[Yip and Gerstein, in revision]

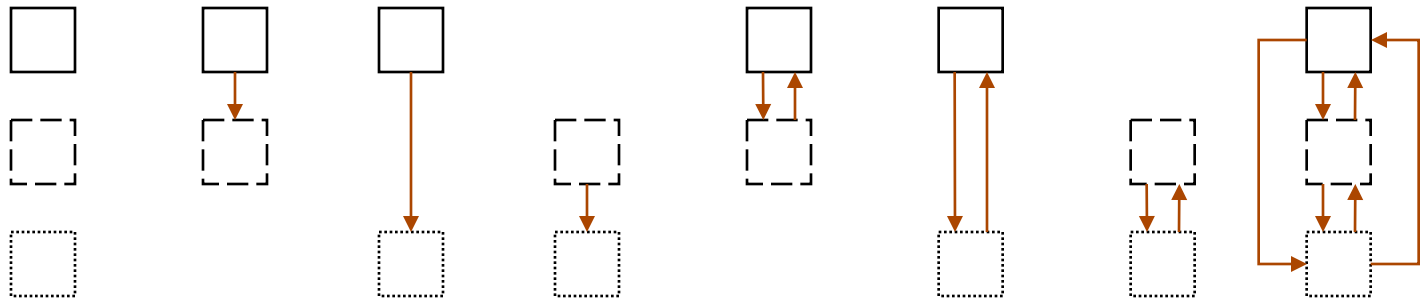
Combining the three problems



[Yip and Gerstein, in revision]

Empirical results (AUCs)

	Ind. levels	Unidirectional flow			Bidirectional flow			
Level		PD	PR	DR	PD	PR	DR	PDR
Proteins	71.68				72.23	72.50		**72.82**
Domains	53.18	61.51			**71.71**		68.94	71.20
Residues	57.36		54.89	53.81		72.26	63.16	**77.86**



- Highest accuracy by bidirectional flow
- Additive effect: 2 vs. 3 levels

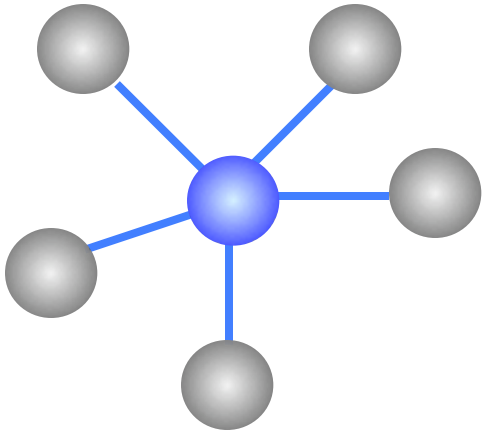
[Yip and Gerstein, in revision]

Finding Central Points in Networks

Where are key points networks ? How do we locate them ?

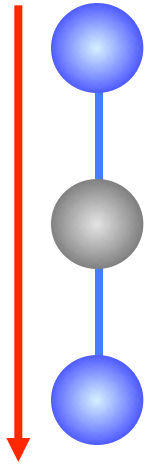
Global topological measures

Indicate the gross topological structure of the network



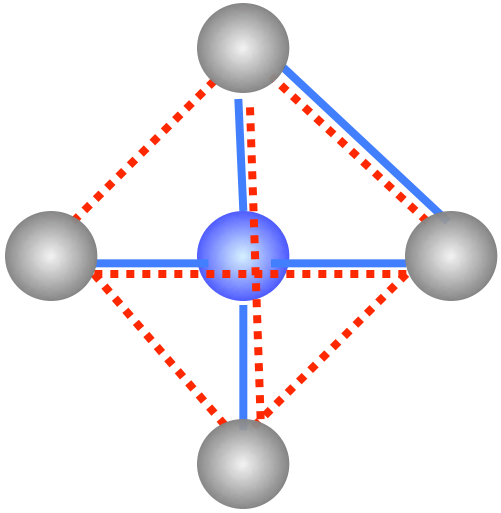
Degree (K)

5



Path length (L)

2



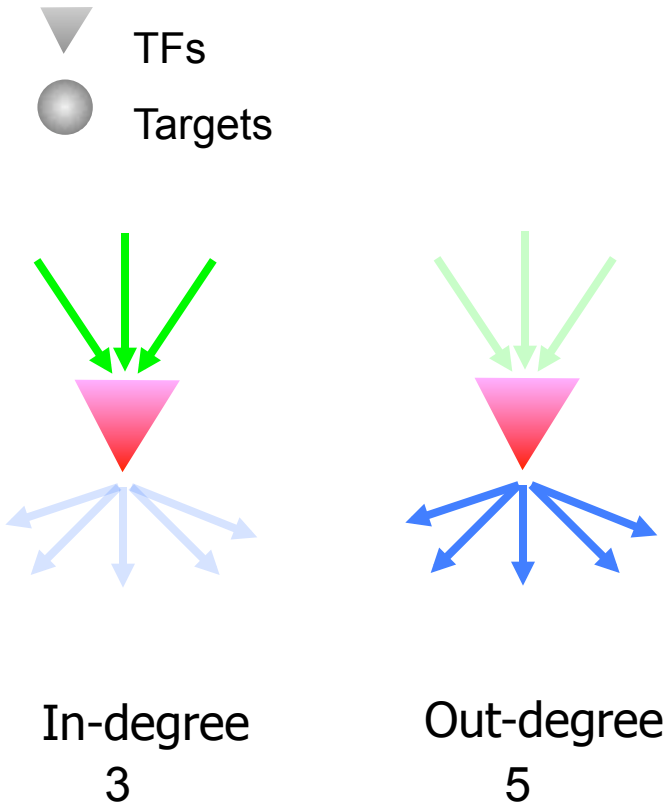
Clustering coefficient (C)

1/6

Interaction and expression networks are ***undirected***

[Barabasi]

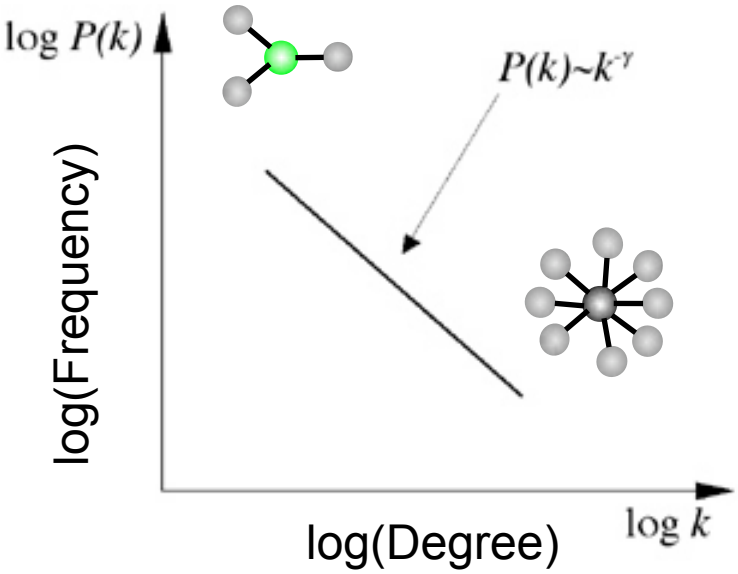
Global topological measures for directed networks

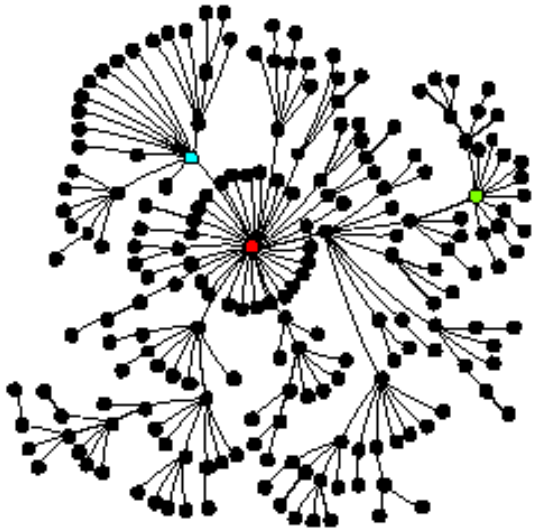


Regulatory and metabolic networks are ***directed***

Scale-free networks

Power-law distribution





Hubs dictate the structure of the network

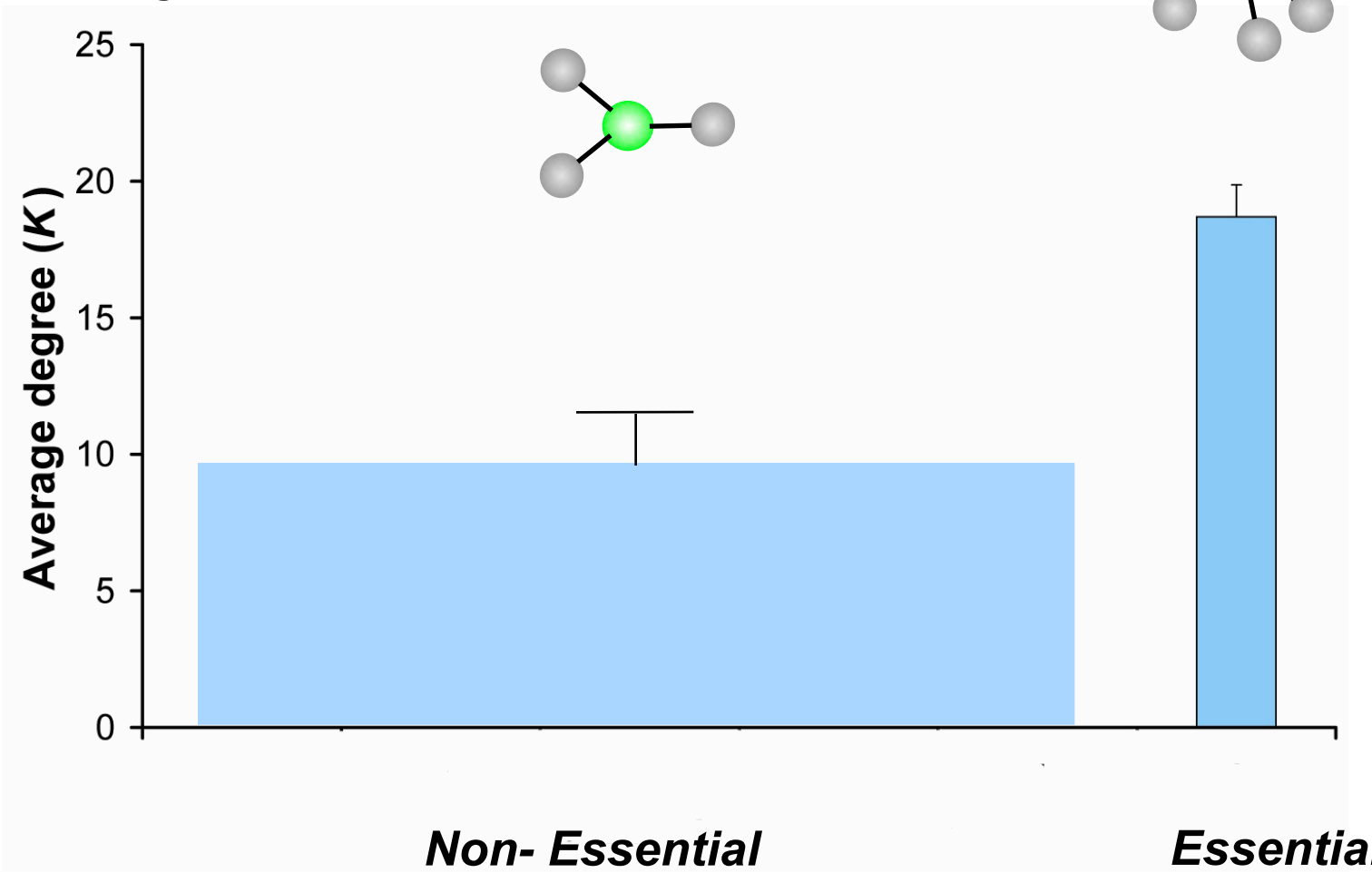
[Barabasi]

Hubs tend to be Essential

Integrate gene essentiality data with protein interaction network. Perhaps hubs represent vulnerable points?

[Lauffenburger, Barabasi]

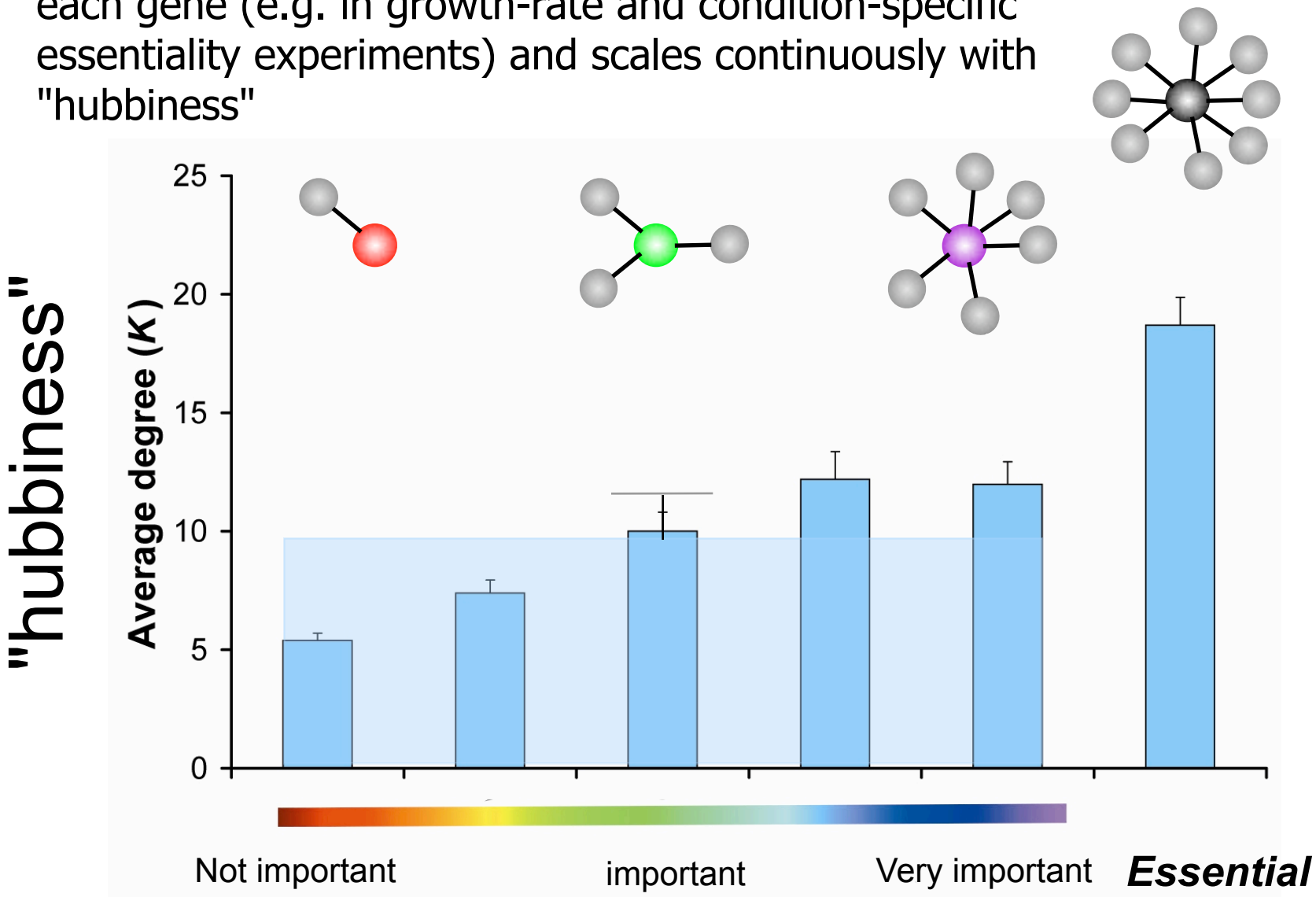
"hubbiness"



[Yu et al., 2003, TIG]

Relationships extends to "Marginal Essentiality"

Marginal essentiality measures relative importance of each gene (e.g. in growth-rate and condition-specific essentiality experiments) and scales continuously with "hubbiness"



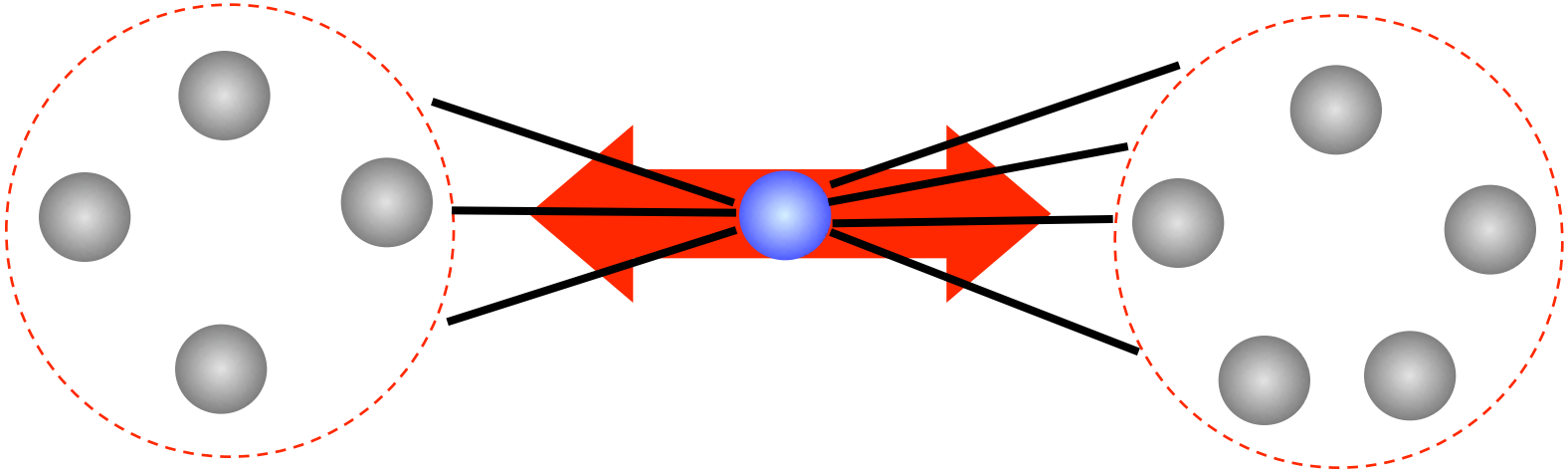
[Yu et al., 2003, TIG]

Another measure of Centrality: Betweenness centrality

Betweenness of a node is the number of shortest paths of pairs of vertices that run through it -- a measure of information flow.

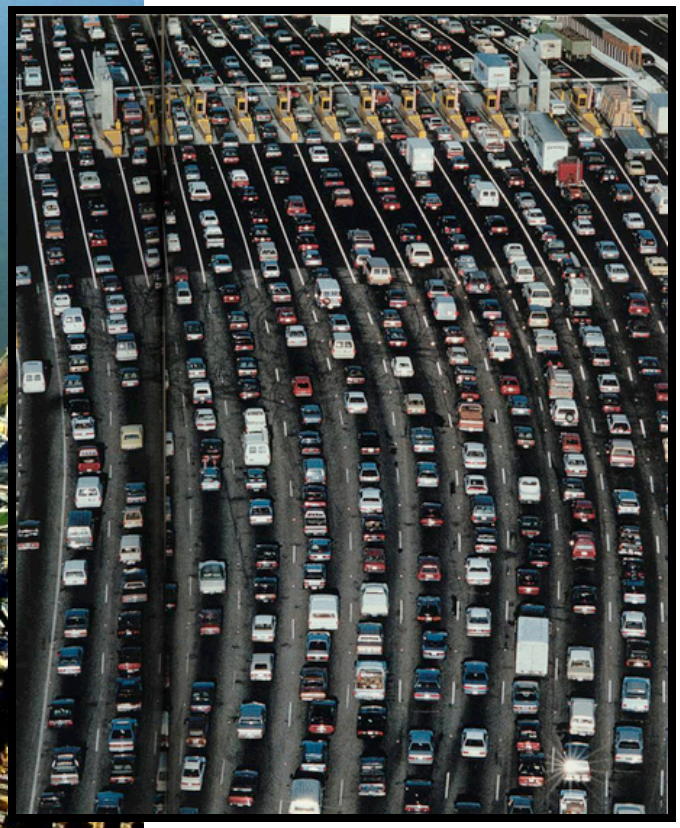
Freeman LC (1977) Set of measures of centrality based on betweenness. Sociometry 40: 35–41.

Girvan & Newman (2002) PNAS 99: 7821.

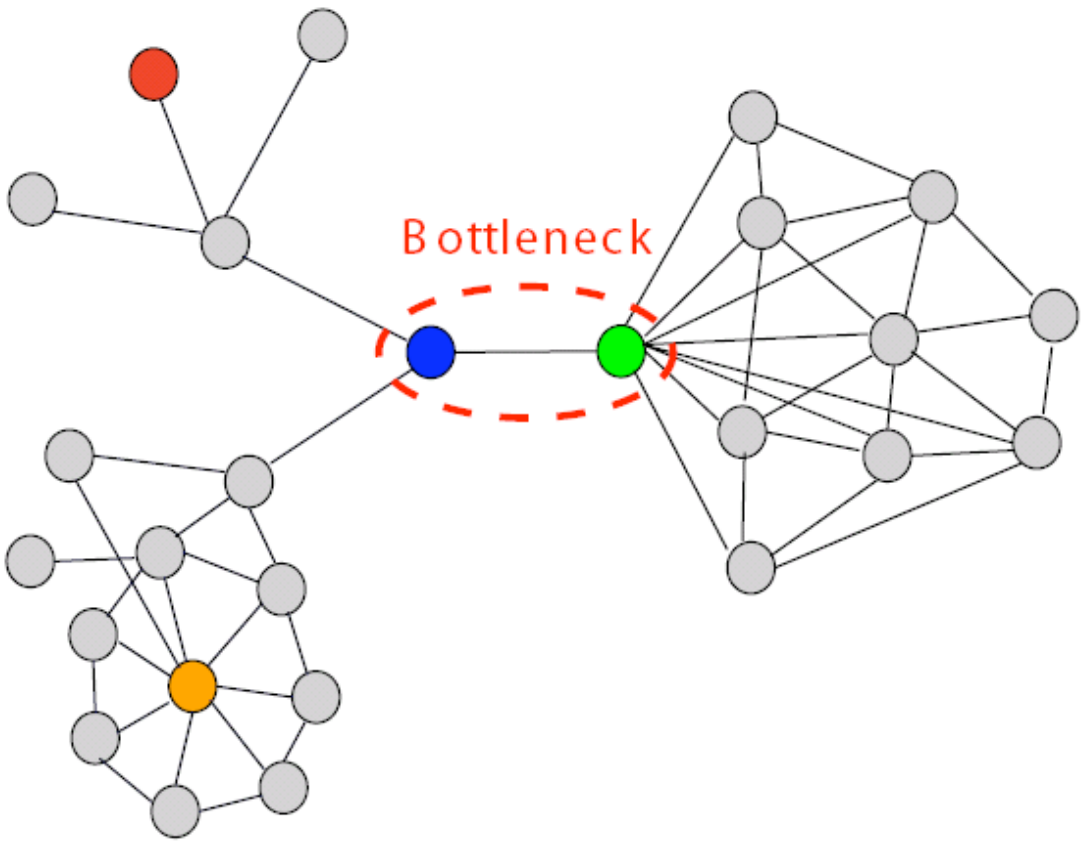


Betweenness centrality -- Bottlenecks

Proteins with high betweenness are defined as *Bottlenecks* (top 20%), in analogy to the traffic system



Bottlenecks & Hubs



Hub-bottleneck **node**

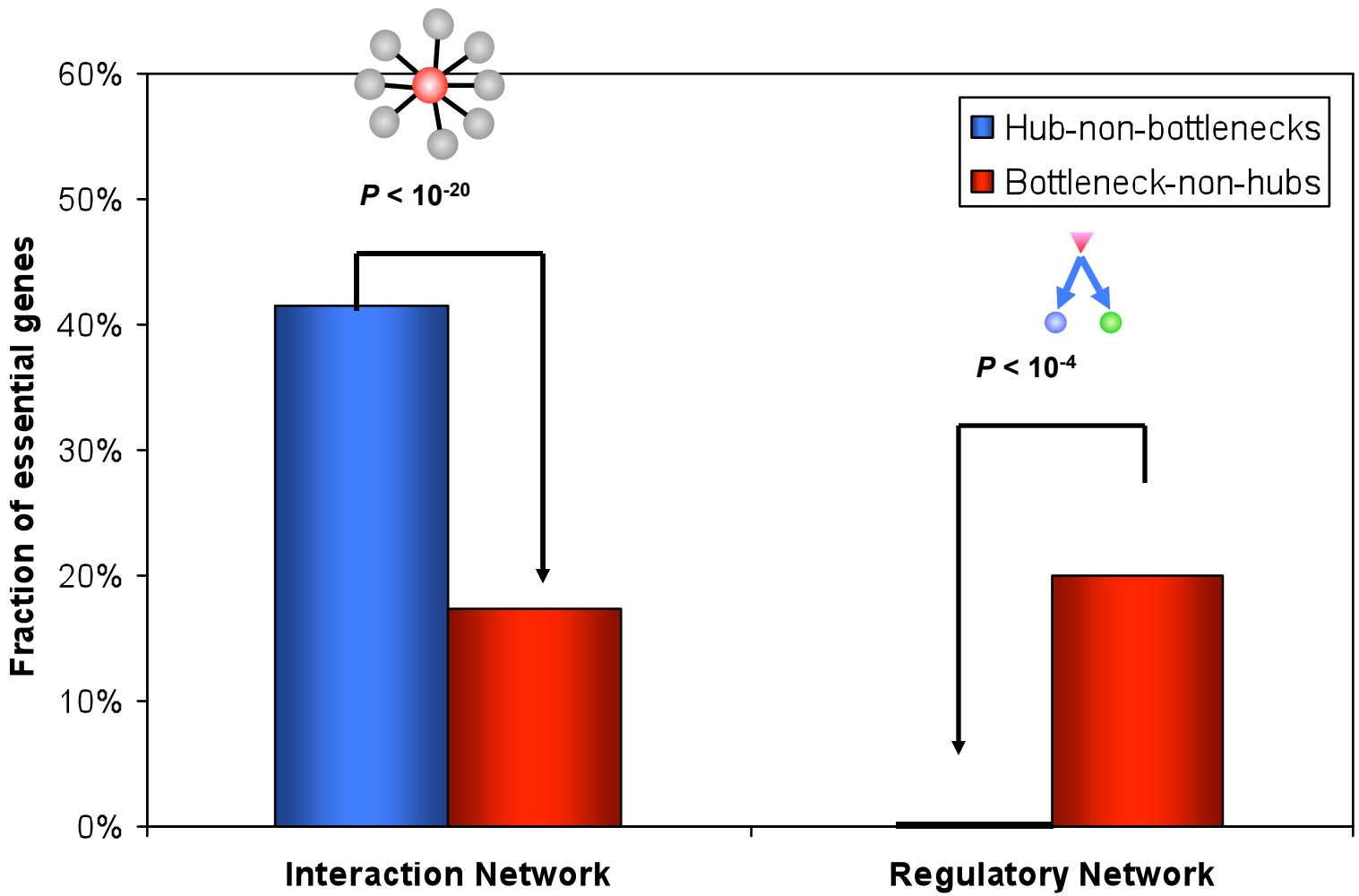
Non-hub-bottleneck **node**

Hub-non-bottleneck **node**

Non-hub-non-bottleneck **node**

[Yu et al., PLOS CB (2007)]

Bottlenecks are what matters in regulatory networks

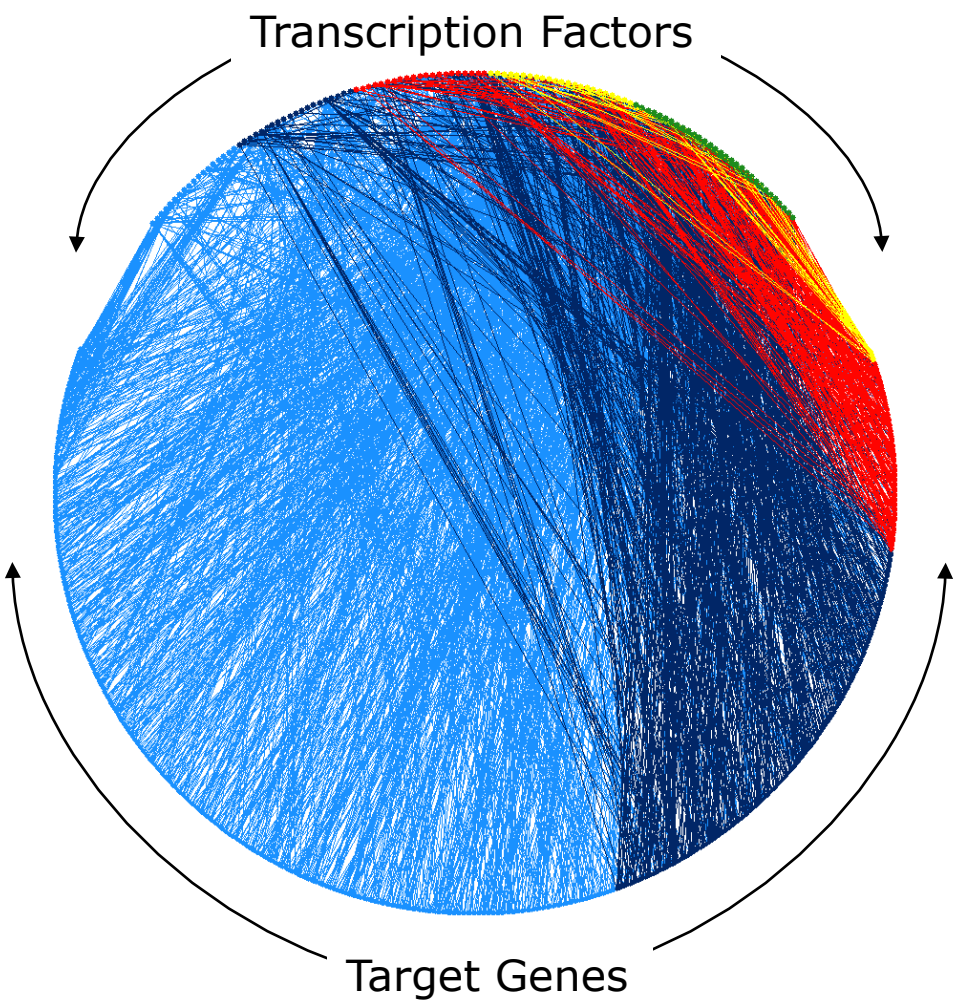


[Yu *et al.*, *PLoS Comput Biol* (2007)]

Network Dynamics #1: Cellular States

How do networks change across different cellular states?
How can this be used to assign function to a protein?

Dynamic Yeast TF network



- Analyzed network as a static entity
- But network is *dynamic*
  - ◊ Different sections of the network are active under different cellular conditions
- Integrate gene expression data

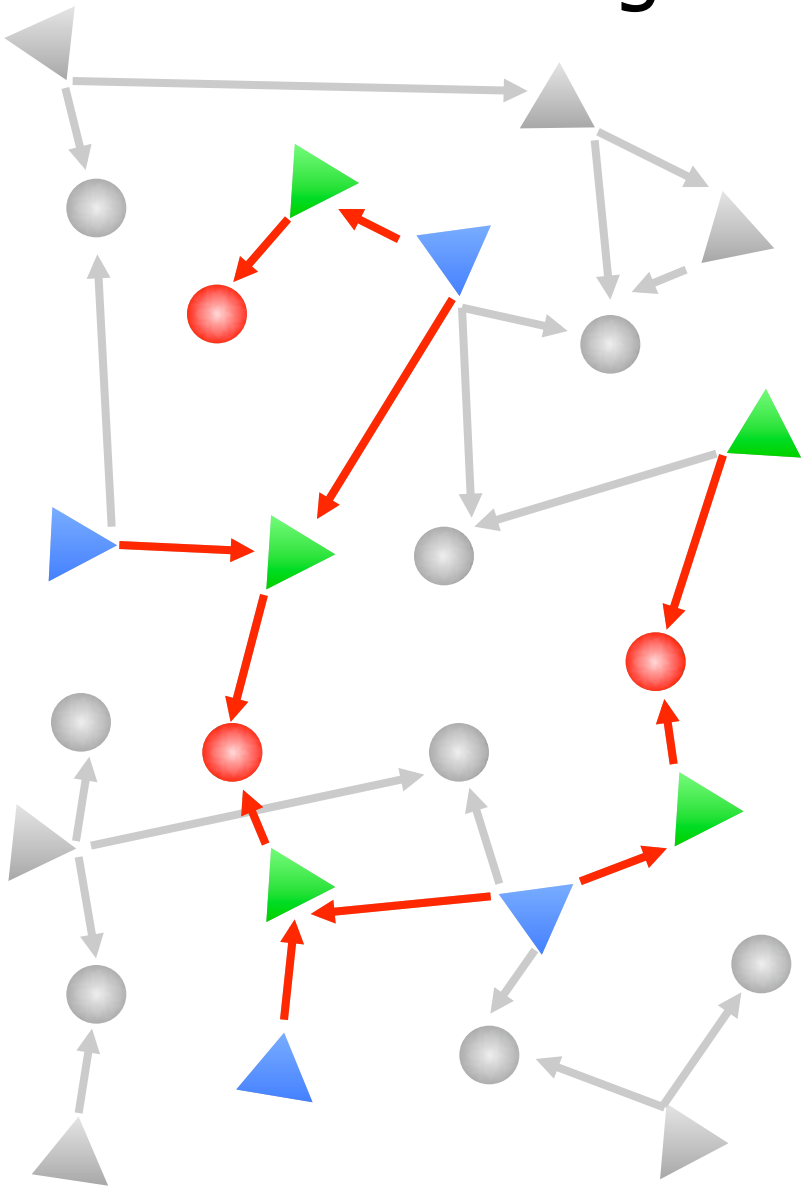
Luscombe et al. Nature 431: 308

Gene expression data for five cellular conditions in yeast

	Cellular condition
Multi-stage	Cell cycle
	Sporulation
Binary	Diauxic shift
	DNA damage
	Stress response

[Brown, Botstein, Davis….]

Backtracking to find active sub-network

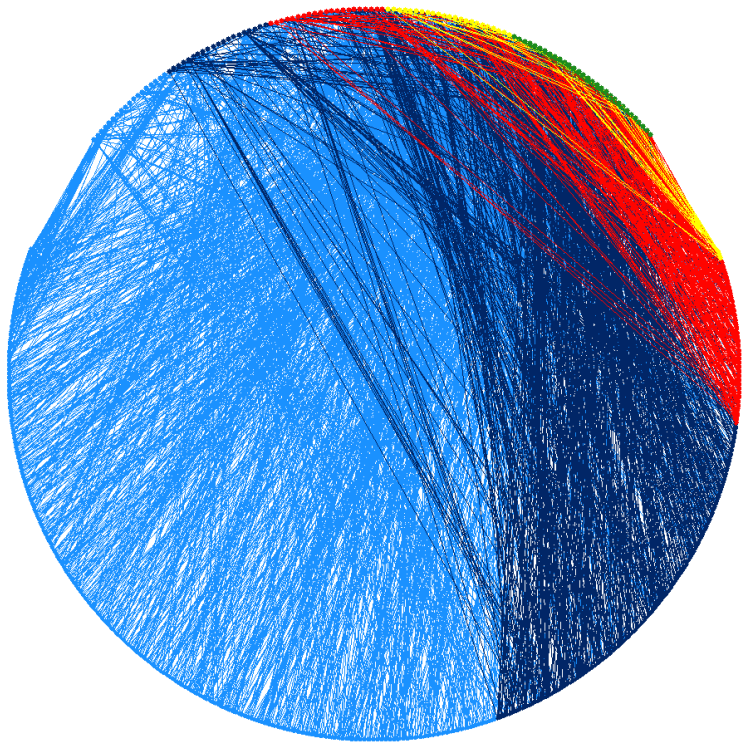


- Define differentially expressed genes
- Identify TFs that regulate these genes
- Identify further TFs that regulate these TFs

Active regulatory sub-network

Network usage under different conditions

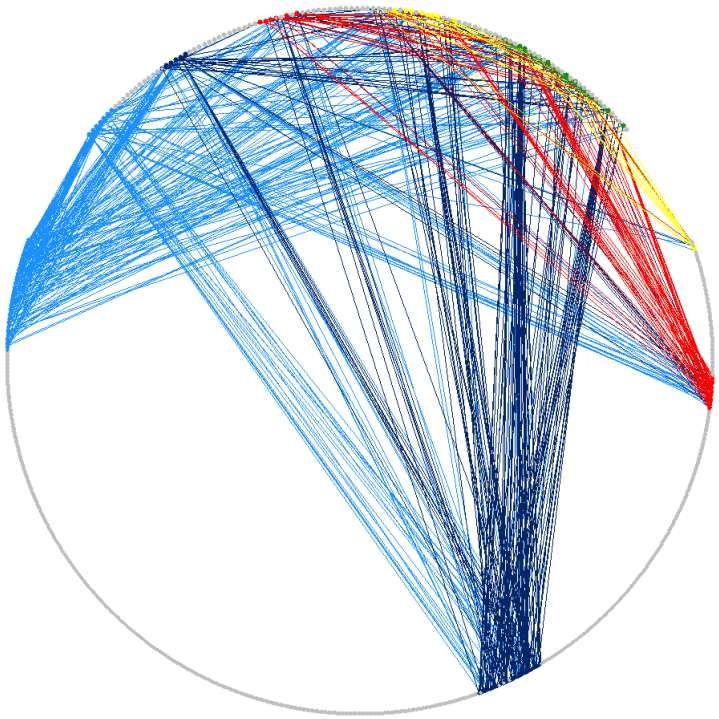
static



Luscombe et al. Nature 431: 308

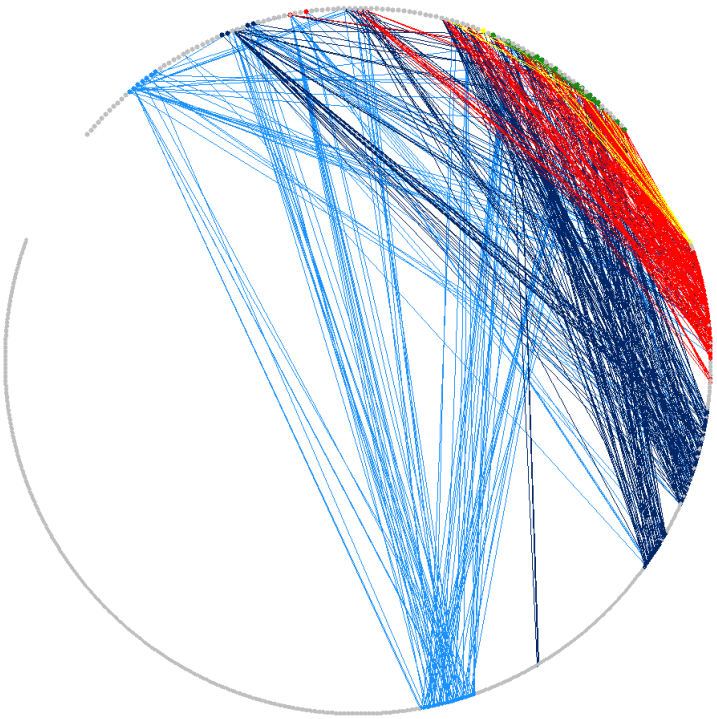
Network usage under different conditions

cell cycle



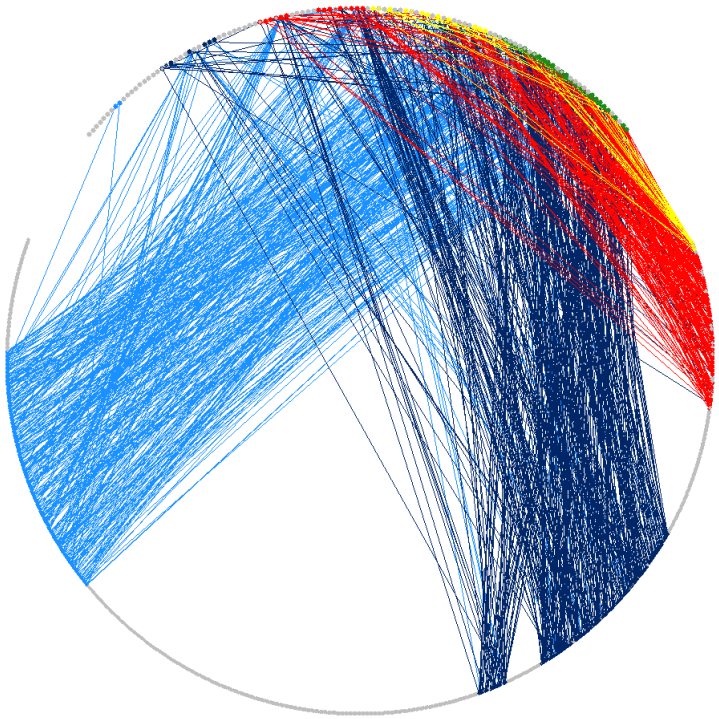
Network usage under different conditions

sporulation



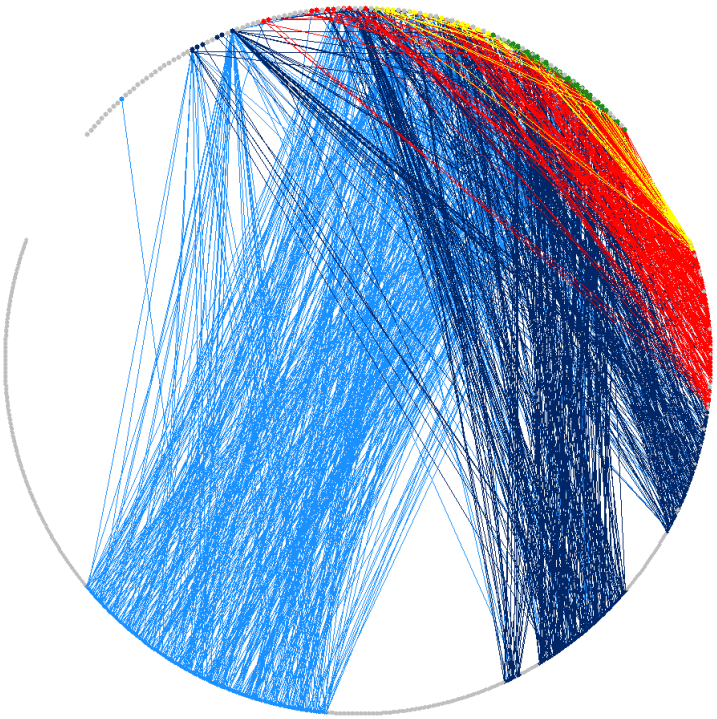
Network usage under different conditions

diauxic shift



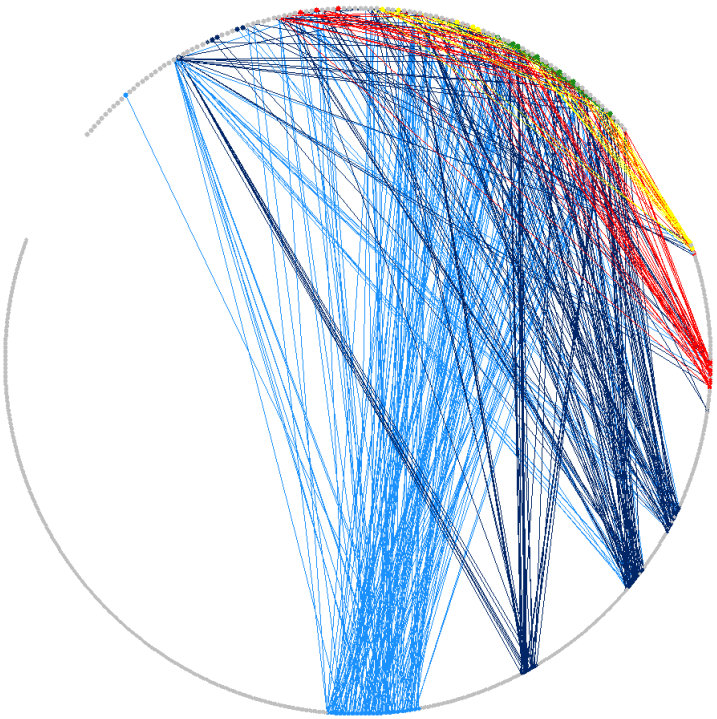
Network usage under different conditions

DNA damage

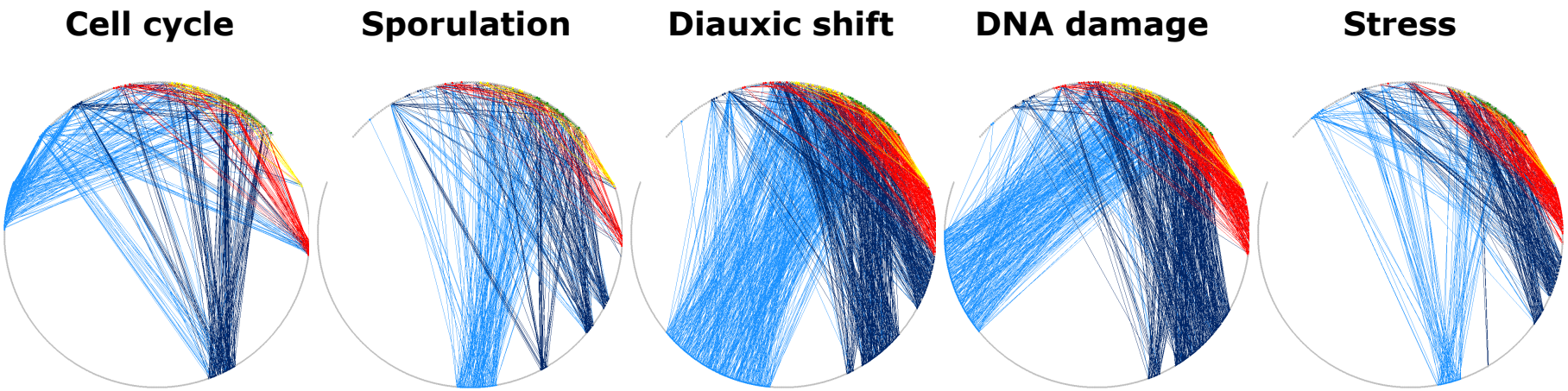


Network usage under different conditions

stress response



Network usage under different conditions



SANDY:

1. Standard graph-theoretic statistics:

- Global topological measures
- Local network motifs

2. Newly derived follow-on statistics:

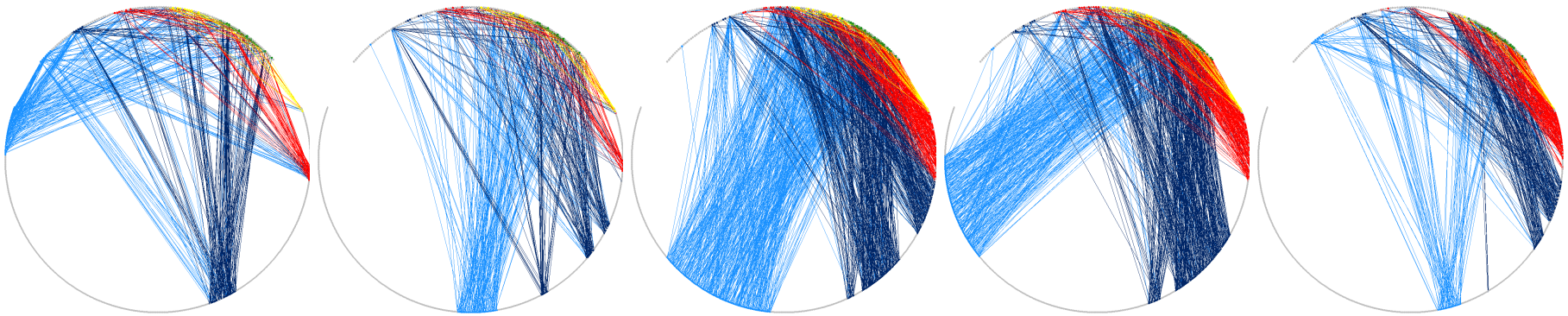
- Hub usage
- Interaction rewiring

3. Statistical validation of results

Luscombe et al. Nature 431: 308

Network usage under different conditions

Cell cycle **Sporulation** **Diauxic shift** **DNA damage** **Stress**



SANDY:

1. Standard graph-theoretic statistics:

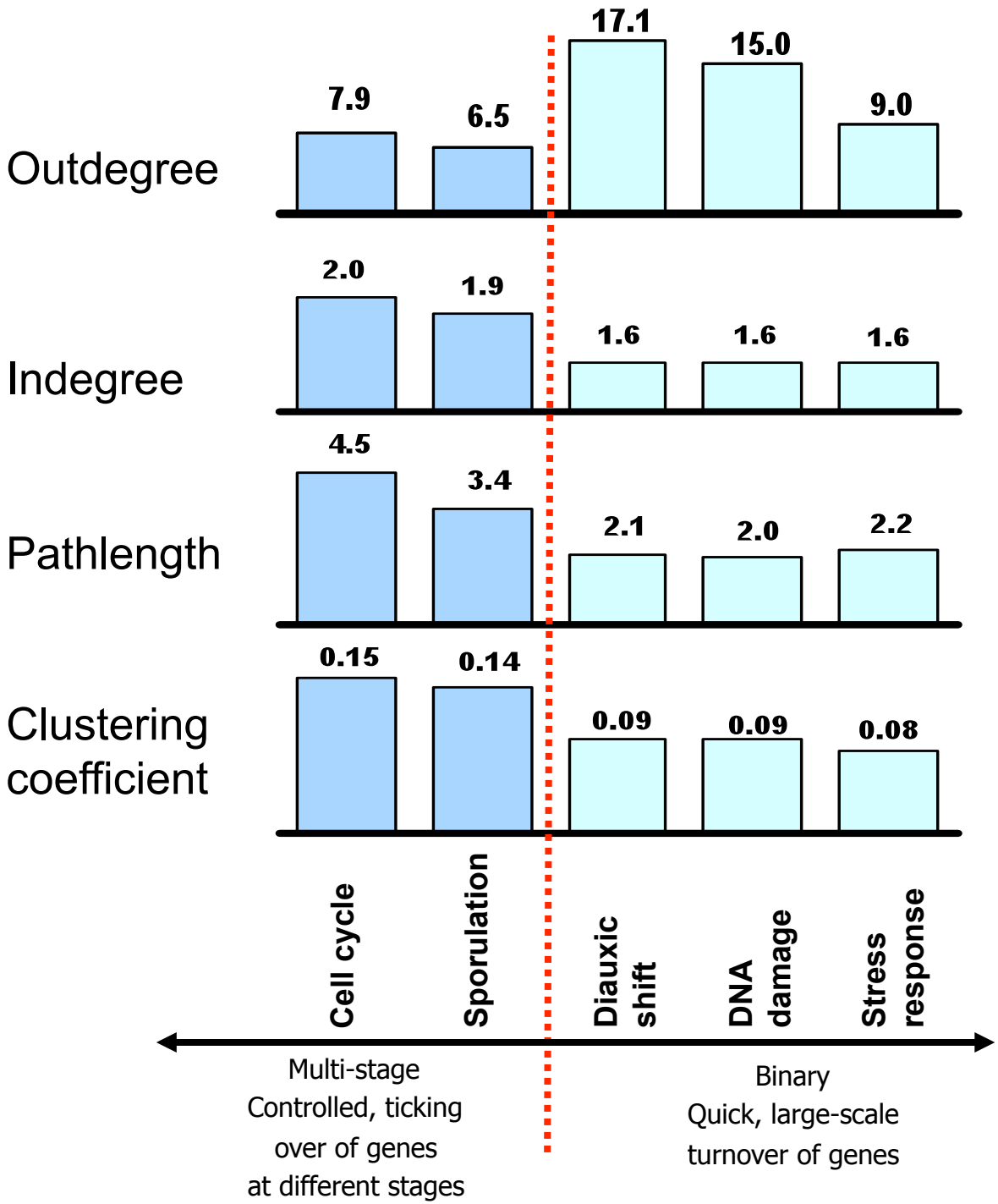
- Global topological measures
- Local network motifs

2. Newly derived follow-on statistics:

- Hub usage
- Interaction rewiring

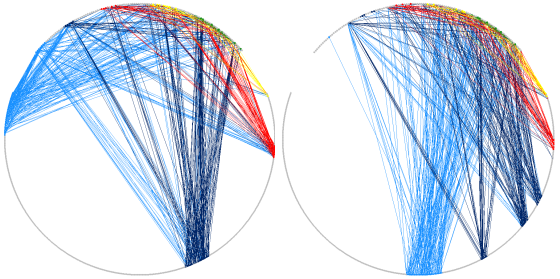
3. Statistical validation of results

Analysis of condition-specific subnetworks in terms of global topological statistics

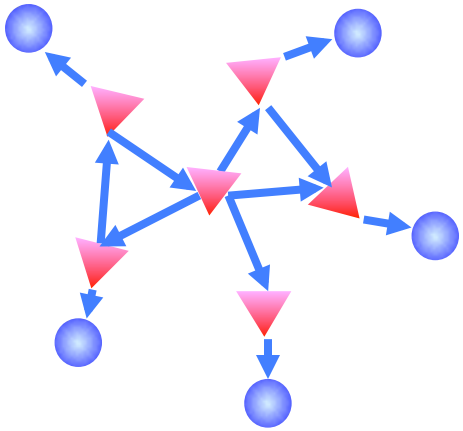


Luscombe et al. Nature 431: 308

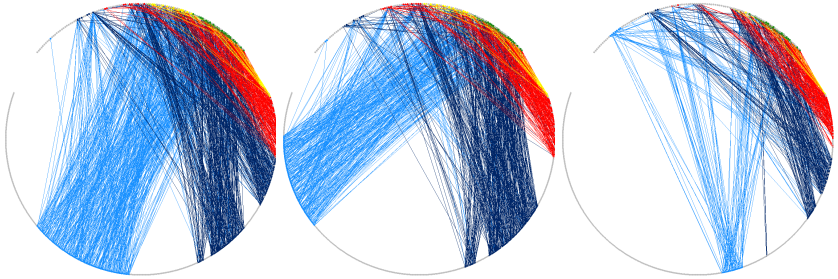
Cell cycle **Sporulation**



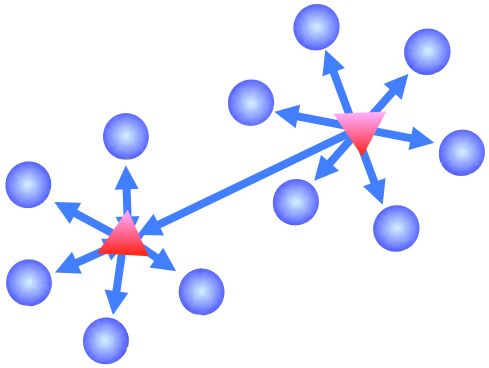
multi-stage conditions



Diauxic shift **DNA damage** **Stress**



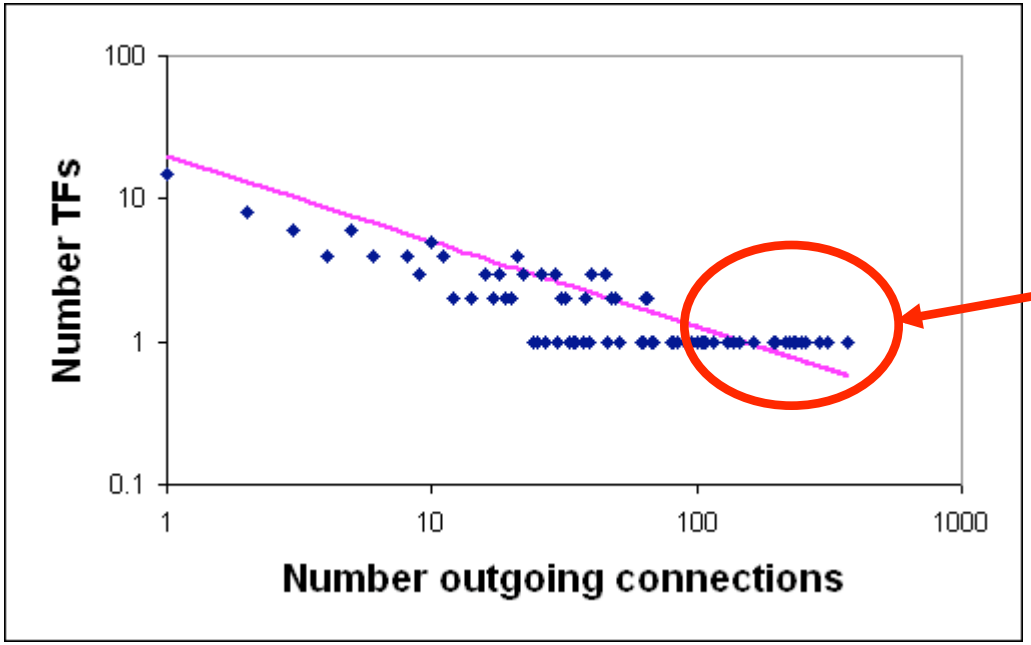
binary conditions

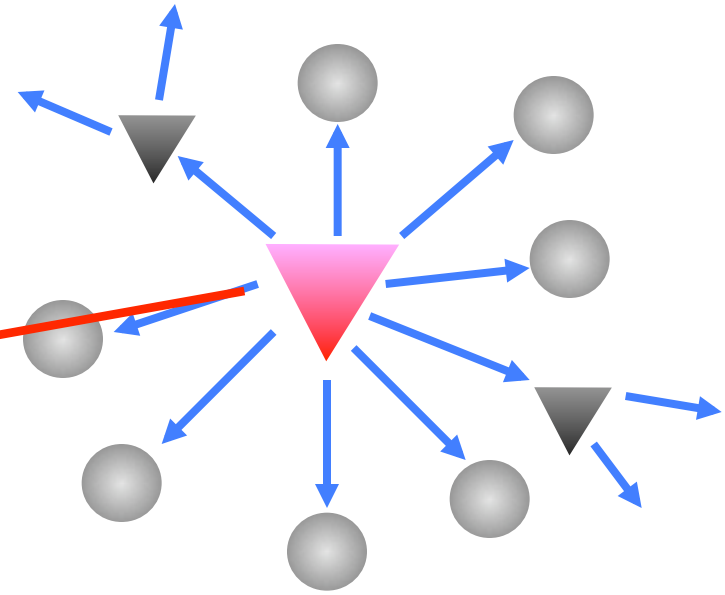


Summary

less pronounced	Hubs	more pronounced
longer	Path Lengths	shorter
more	TF inter-regulation	less
complex loops (FFLs)	Motifs	simpler (SIMs)

Transient Hubs

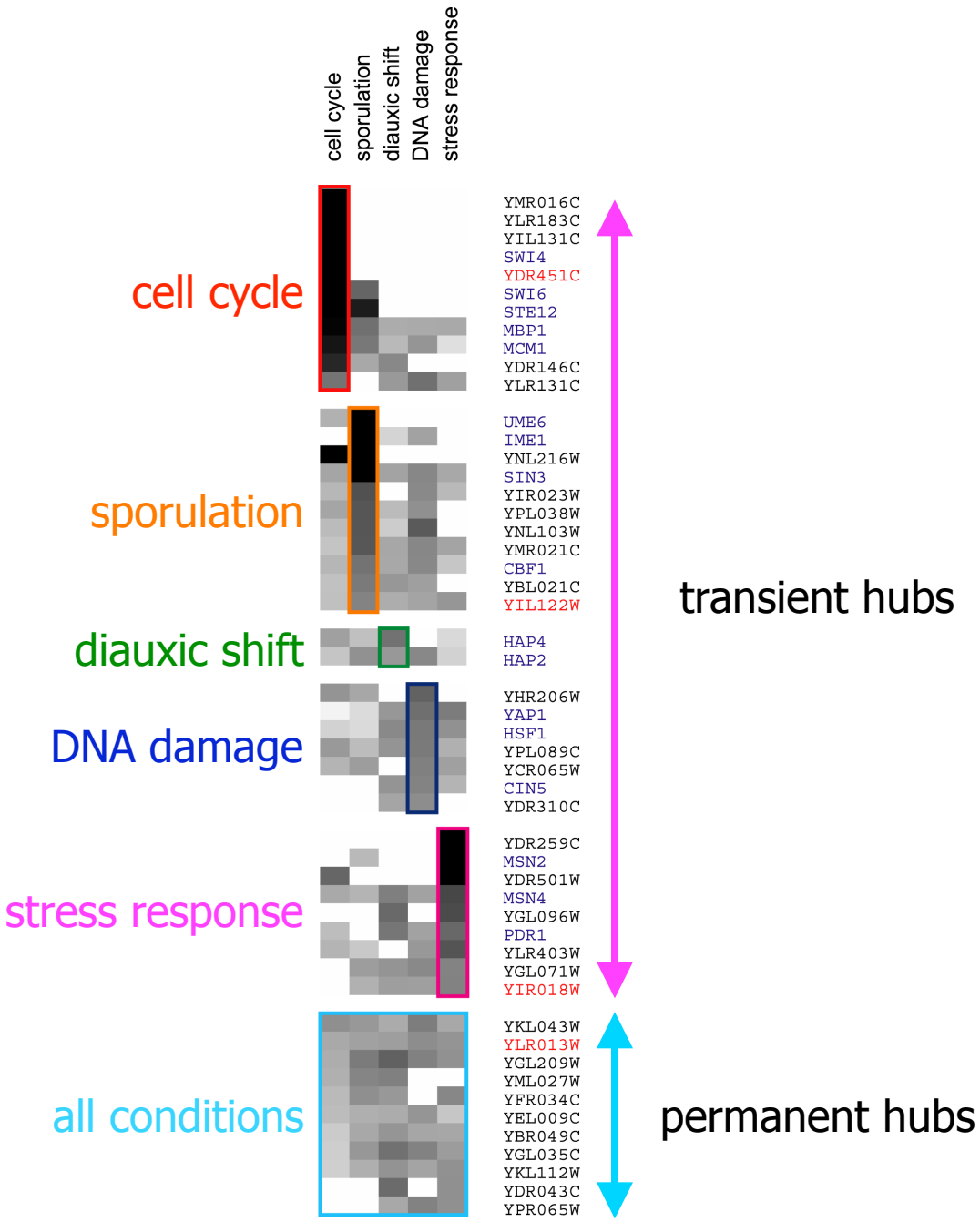




Regulatory hubs

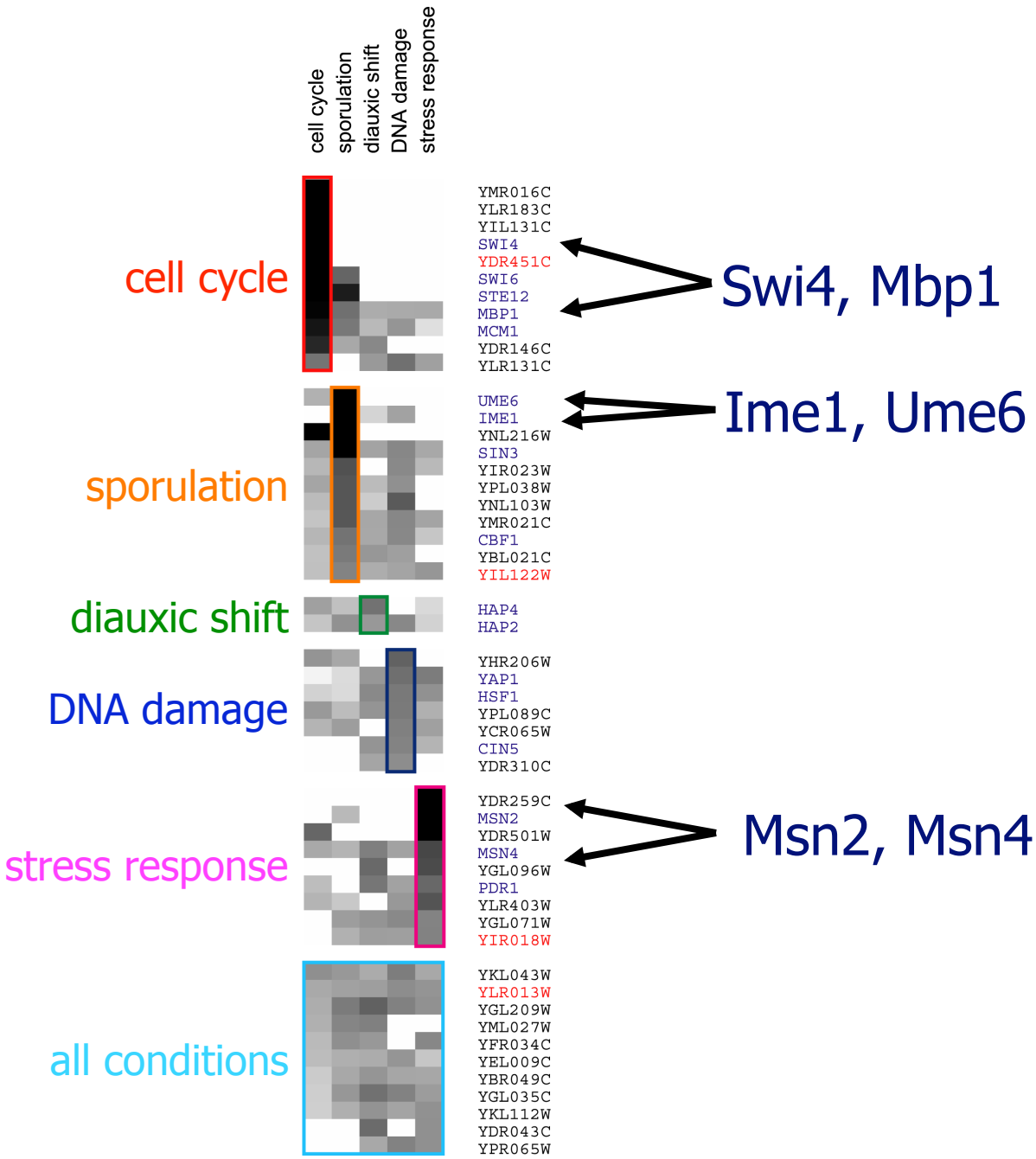
- Questions:
  - ◊ Do hubs stay the same or do they change over between conditions?
  - ◊ Do different TFs become important?
- Our Expectations
  - ◊ Literature:
    - Hubs are permanent features of the network regardless of condition
  - ◊ Random networks (sampled from complete regulatory network)
    - Random networks converge on same TFs
    - 76-97% overlap in TFs classified as hubs (*ie* hubs are permanent)

Luscombe et al. Nature 431: 308

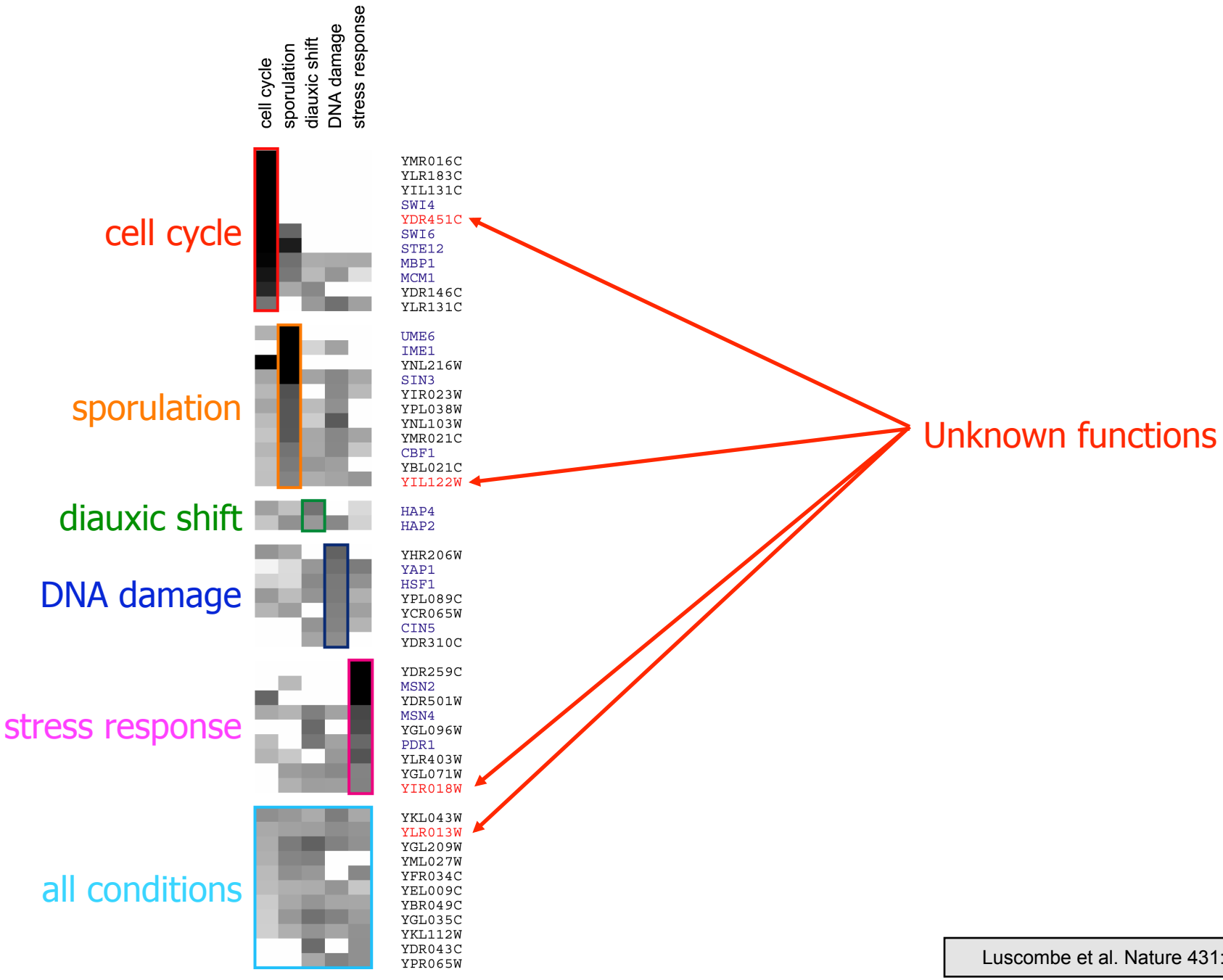


- Some permanent hubs
  - ◊ house-keeping functions
- Most are transient hubs
  - ◊ Different TFs become key regulators in the network
- Implications for condition-dependent vulnerability of network

Luscombe et al. Nature 431: 308



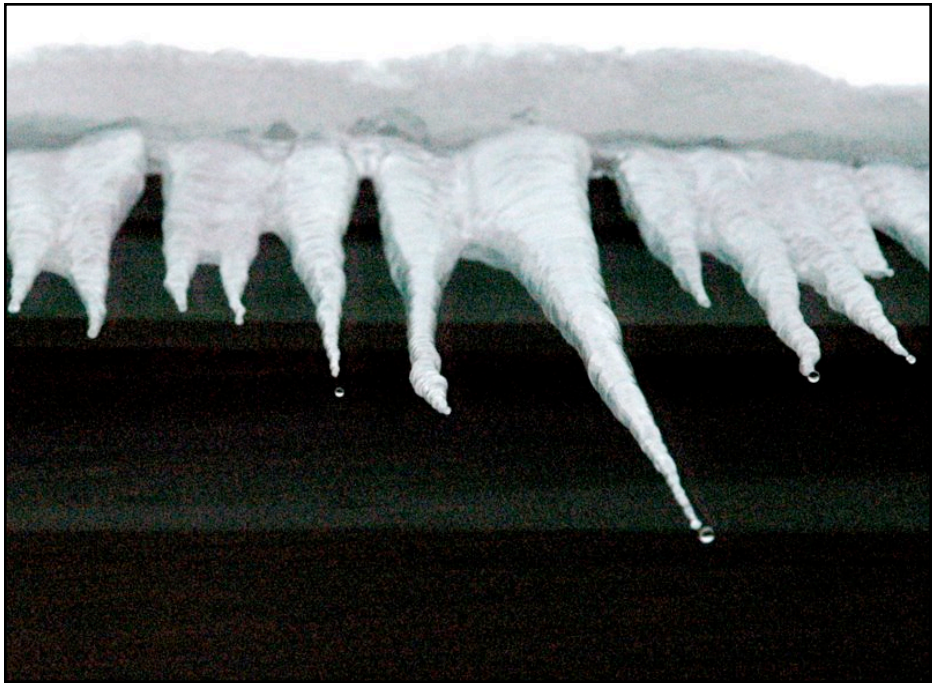
Luscombe et al. Nature 431: 308



Luscombe et al. Nature 431: 308

Network Dynamics #2: Environments

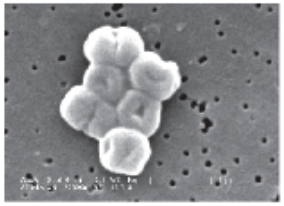
How do molecular networks change across environments?
What pathways are used more ?
Used as a biosensor ?



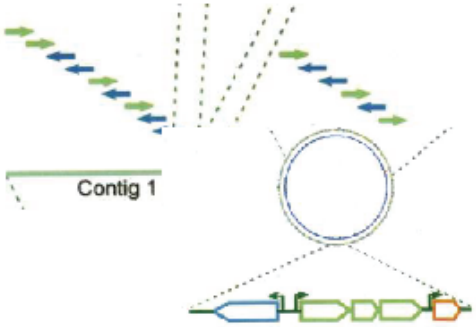
What is metagenomics?

Genomics Approach

Culture Microbes → Extract DNA → Sequence → Assemble and Annotate



ATCGTATA
CGCGAAG
ACGTCTGA
AGTGCTGCT

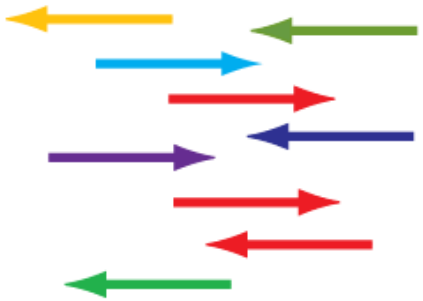


PROBLEM: Estimated that less than 1% can be cultured in the lab

Metagenomics Approach

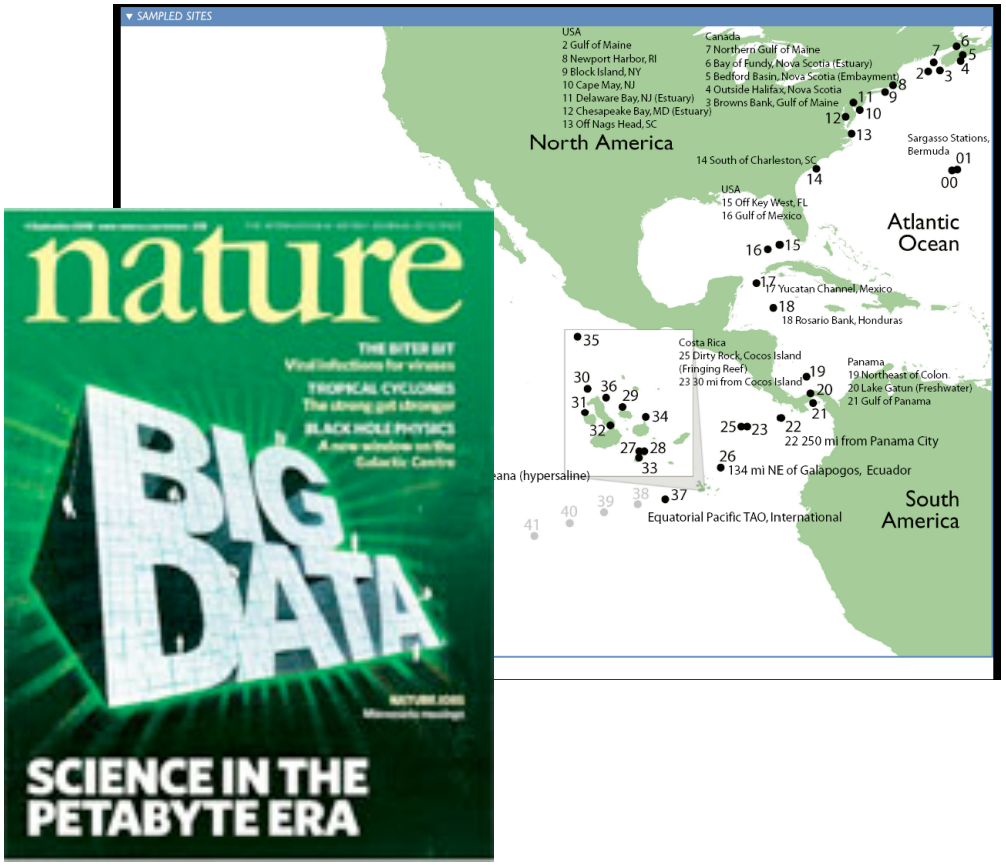
Collect Sample → Extract DNA → Sequence → Partially Assemble and Annotate

ATCGTGATAGATGATAGTAGA
ATGCTGCATGCATCTAGCACT
ACAGTAGCTAGCTACGTACTA
CAGCTGACTAGCTAGCTAGCT
ACGTAGCATGCTAGCTAGCAG
ACGTACGTAGCTAGCTAGCTAG
ACGTACGTACGTAGCTAGCATC
AGTCGACTGAGCCAGTGATGAT
ACGATGCATGAGCAGATGCTAC
AGATCGTAGCATGCTAGCATGCT
ACGTACGTAGCTAGCTAGCTAAG
AGCTAGCATGCTAGTAGCATGAG
ACGATGCTAGCTAGCTAGCTGATA
TCGATCAGCATGCTACGATGCAAG
ACGATCGATGCTAGCTAGCTAGCAT
AGCTAGCTAGTCAGCTAGCTAGATG



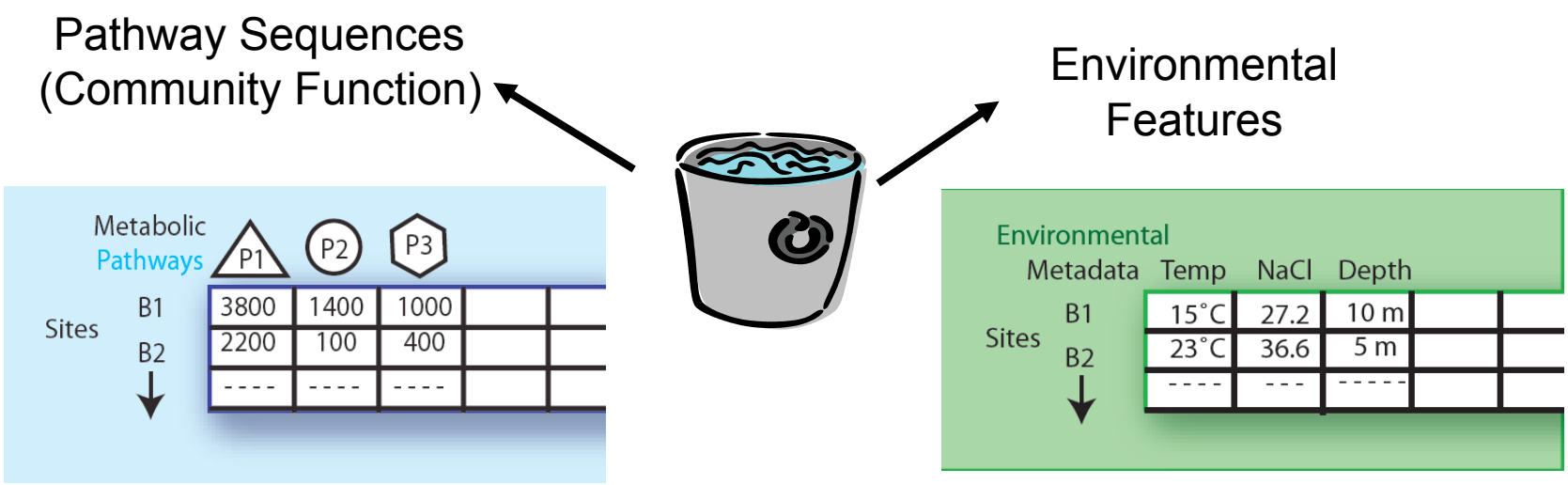
PROBLEM: Lose information about which gene belongs to which microbe.

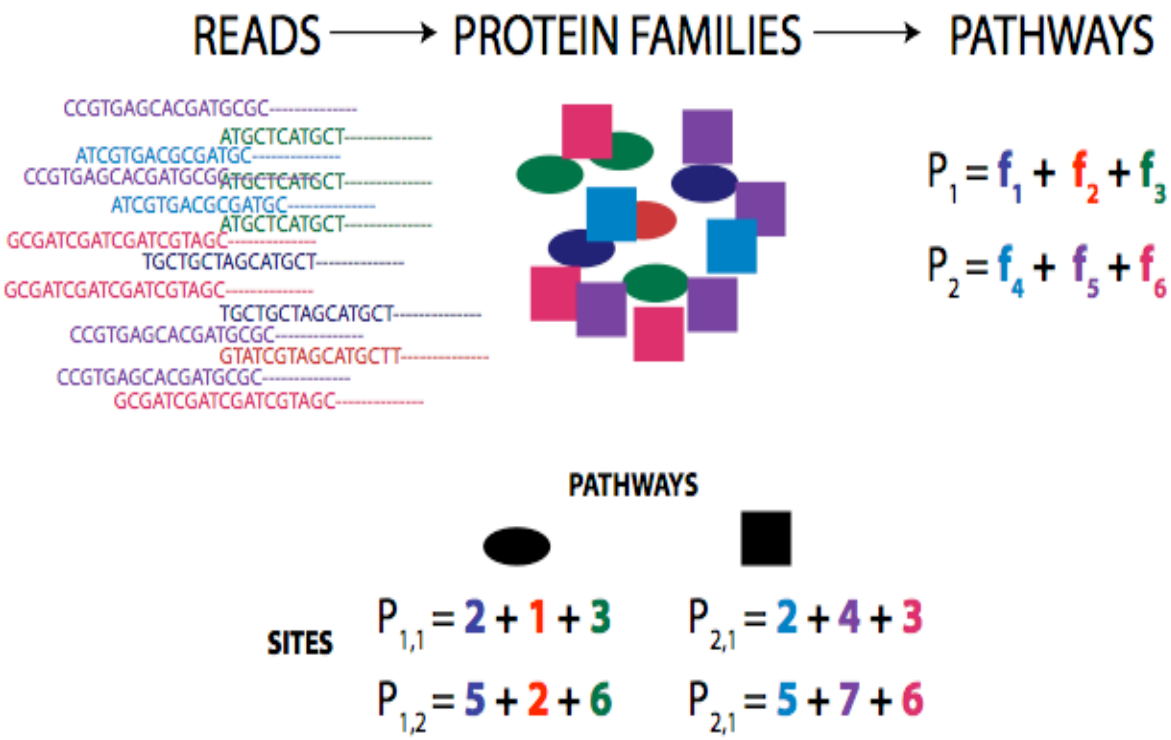
Global Ocean Survey Statistics (GOS)



6.25 GB of data
7.7M Reads
1 million CPU hours
to process

Rusch, et al., PLOS Biology 2007



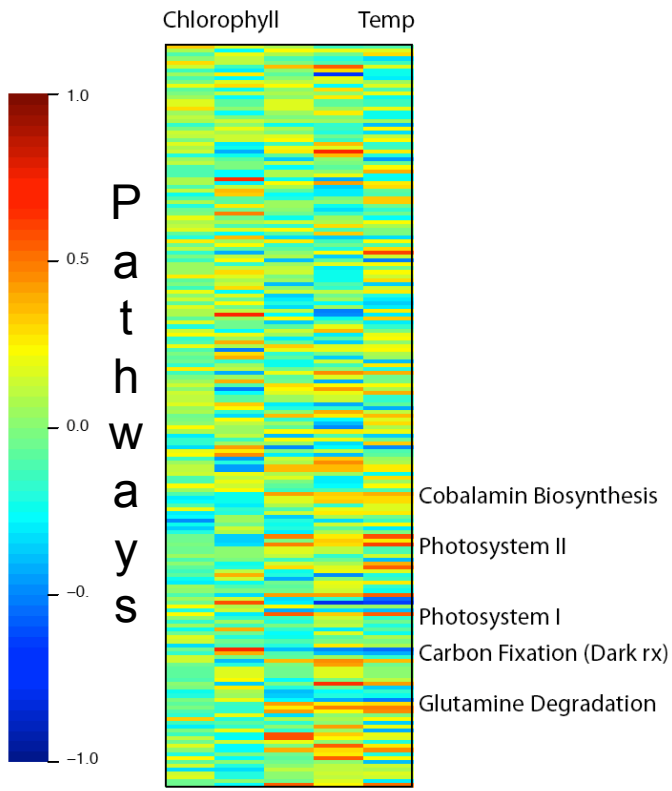


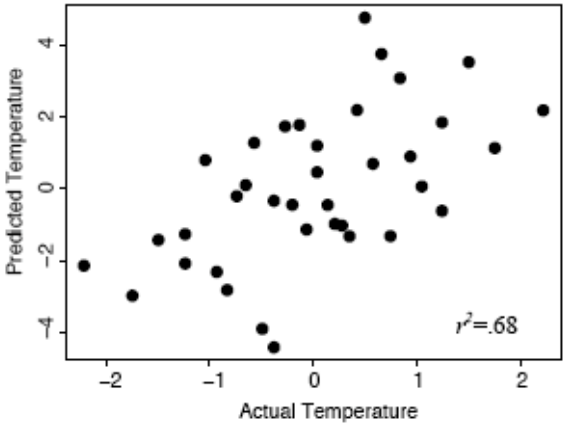
Expressing data as matrices indexed by site, env. var., and pathway usage

[Rusch et. al., (2007) PLOS Biology; Gianoulis et al., PNAS (in press, 2009]

Simple Relationships: Pairwise Correlations

Environmental Features

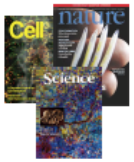




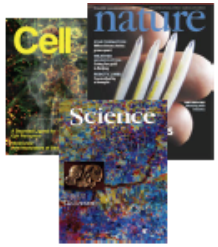
[Gianoulis et al., PNAS (in press, 2009)]

Canonical Correlation Analysis: Simultaneous weighting

Score	# of papers published
GRE	

Undergraduate Performance Index (UPI)	Graduate School Performance Index (GPI)
GRE GPA 	  

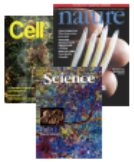
UPI = a GRE + b  + c GPA

GPI = a'  + b'  + c' 

[Gianoulis et al., PNAS (in press, 2009)]

Canonical Correlation Analysis: Simultaneous weighting

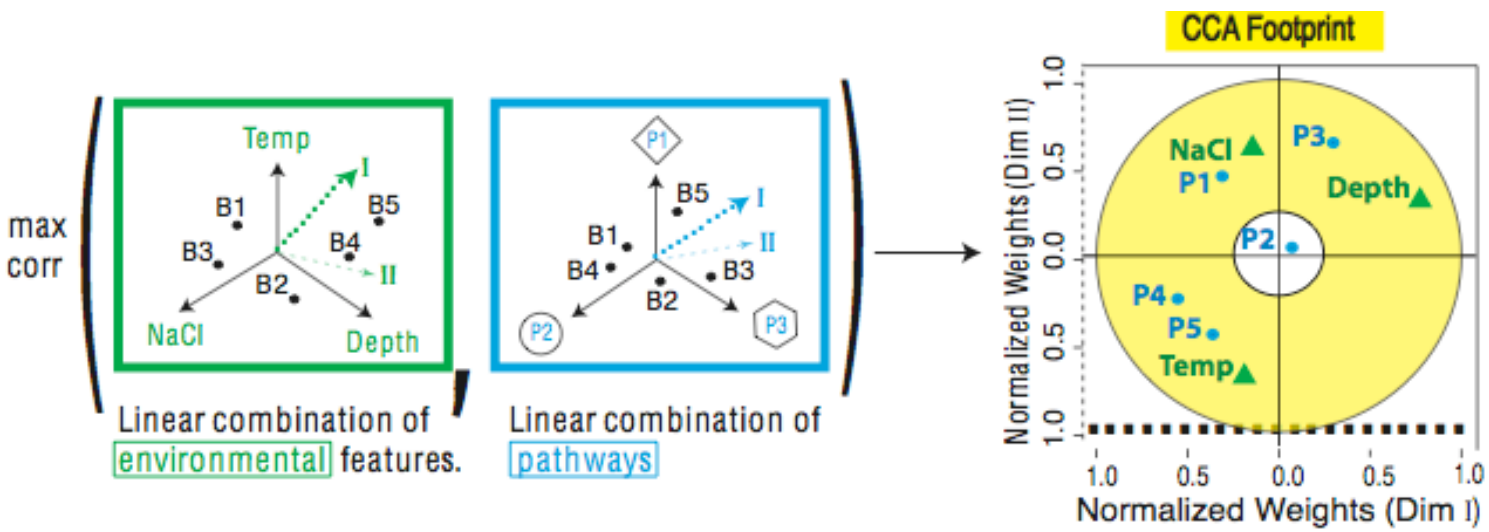
Score	# of papers published
GRE	

Undergraduate Performance Index (UPI)	Graduate School Performance Index (GPI)
GRE GPA 	  

Environmental Features	Metabolic Pathways
Temp etc	Photosynthesis etc
Chlorophyll	Lipid Metabolism

[Gianoulis et al., PNAS (in press, 2009)]

Environmental-Metabolic Space



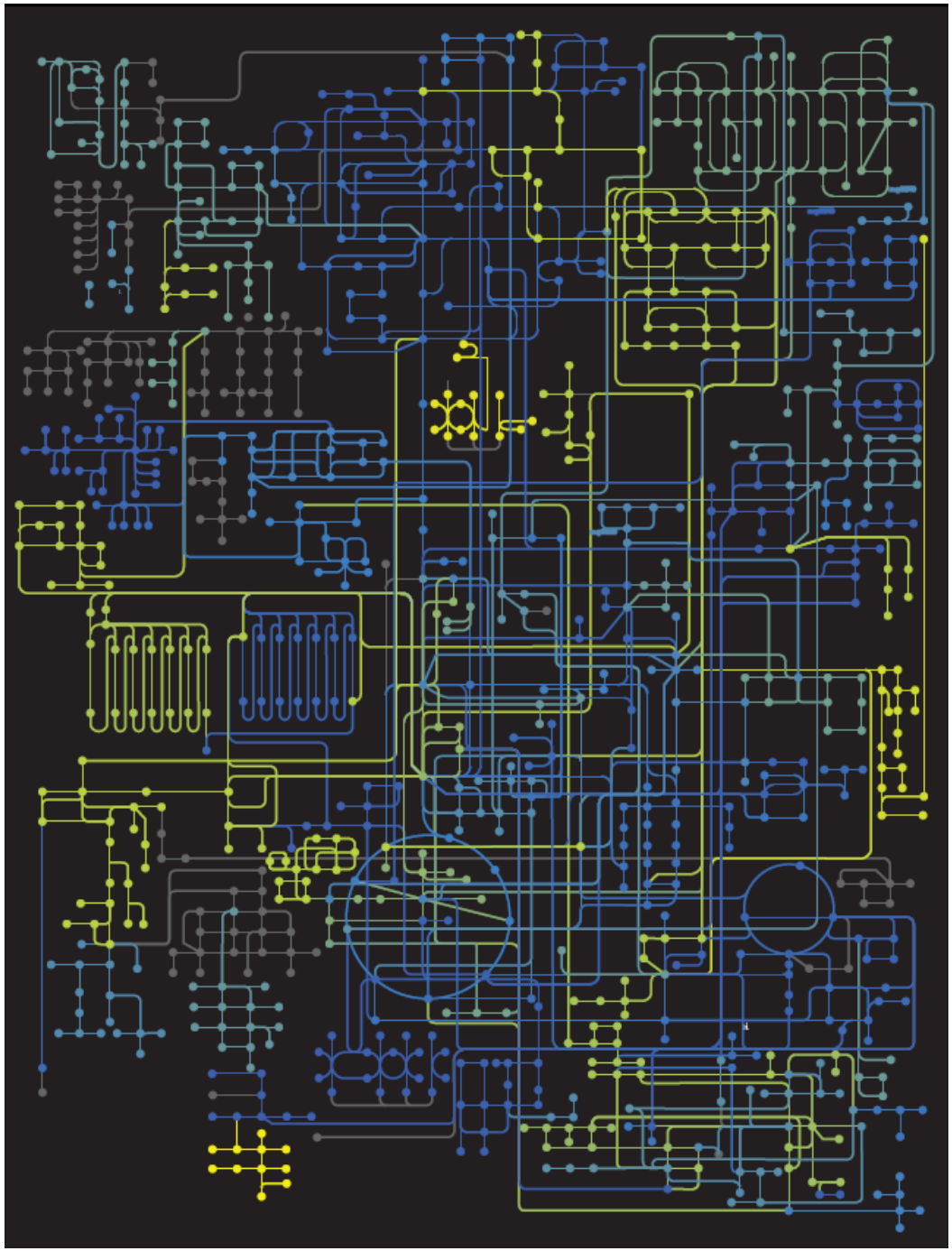
The goal of this technique is to interpret cross-variance matrices
We do this by defining a change of basis.

Given $X = \{x_1, x_2, \ldots, x_n\}$ and $Y = \{y_1, y_2, \ldots, y_m\}$

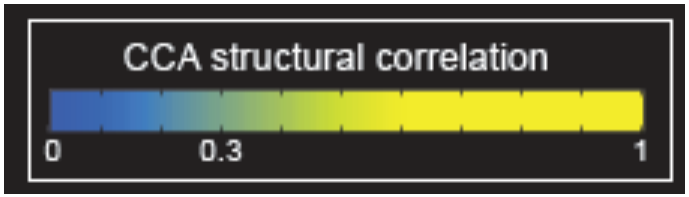
$$C = \begin{matrix} \Sigma_X & \Sigma_{X,Y} \\ \Sigma_Y & \Sigma_{Y,X} \end{matrix}$$

$$\max_{a,b} Corr(U,V) = \frac{a' \Sigma_{12} b}{\sqrt{a' \Sigma_{11} a} \sqrt{b' \Sigma_{22} b}}$$

[Gianoulis et al., PNAS (in press, 2009)]

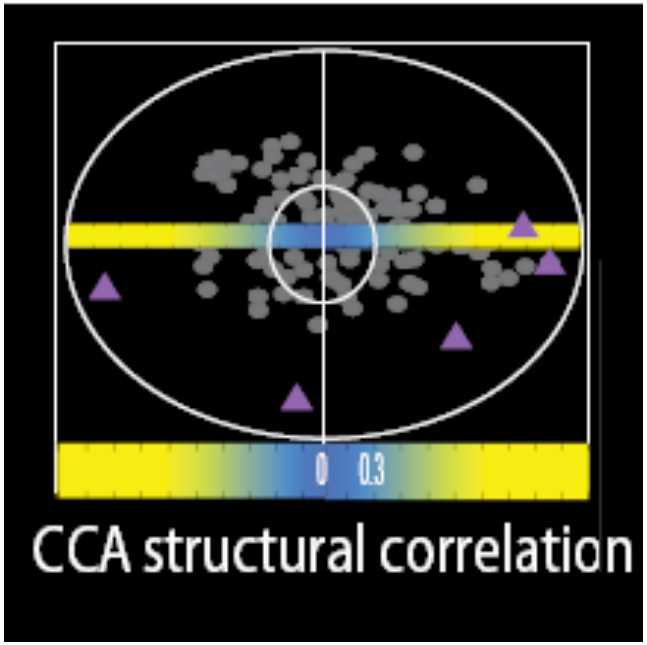


Strength of Pathway co-variation with environment



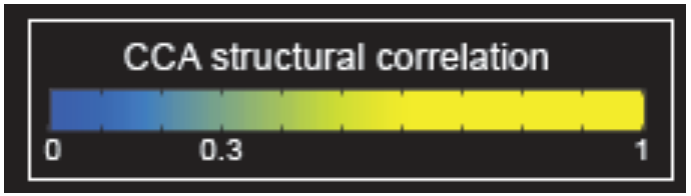
Environmentally invariant

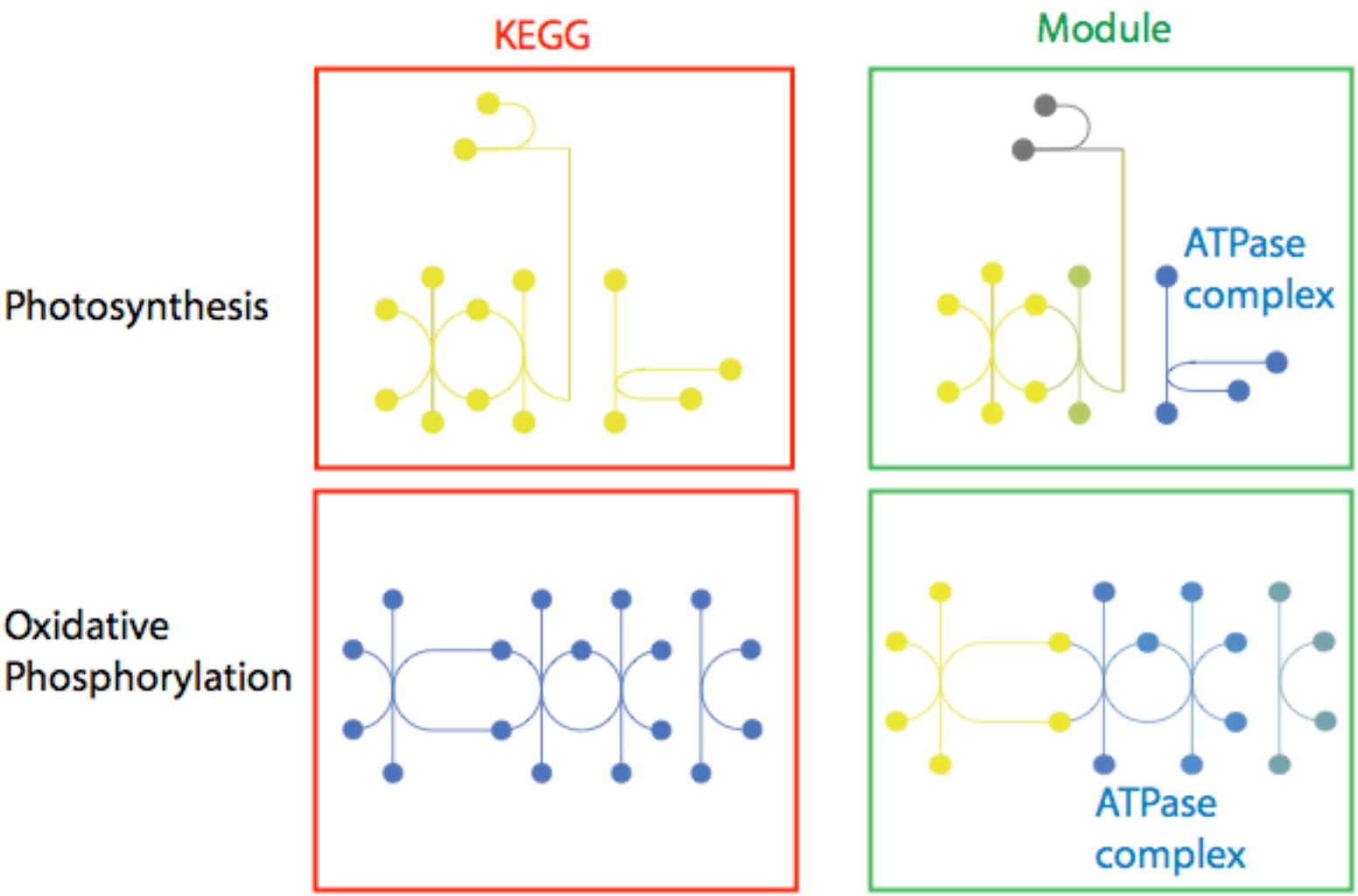
Environmentally variant



[Gianoulis et al., PNAS (in press, 2009)]

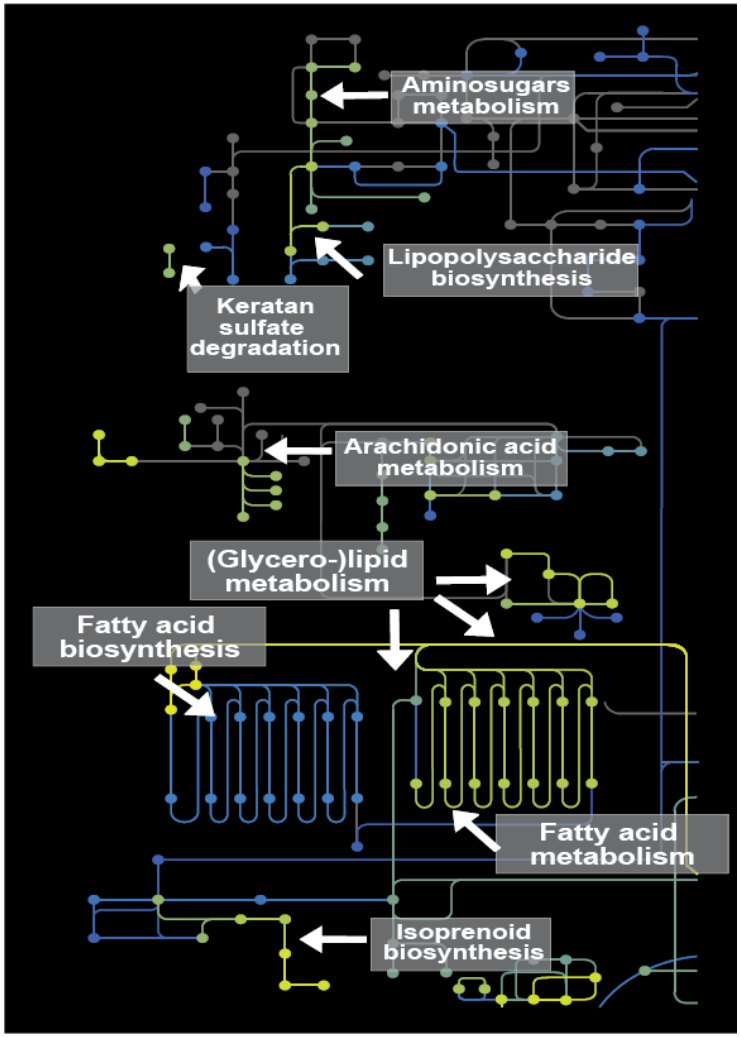
Conclusion #1: energy conversion strategy, temp and depth

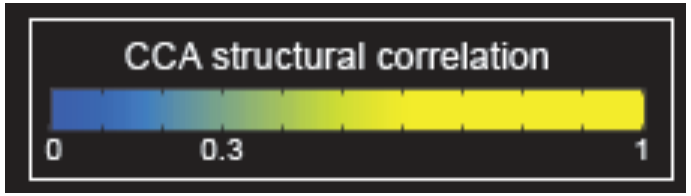




[Gianoulis et al., PNAS (in press, 2009)]

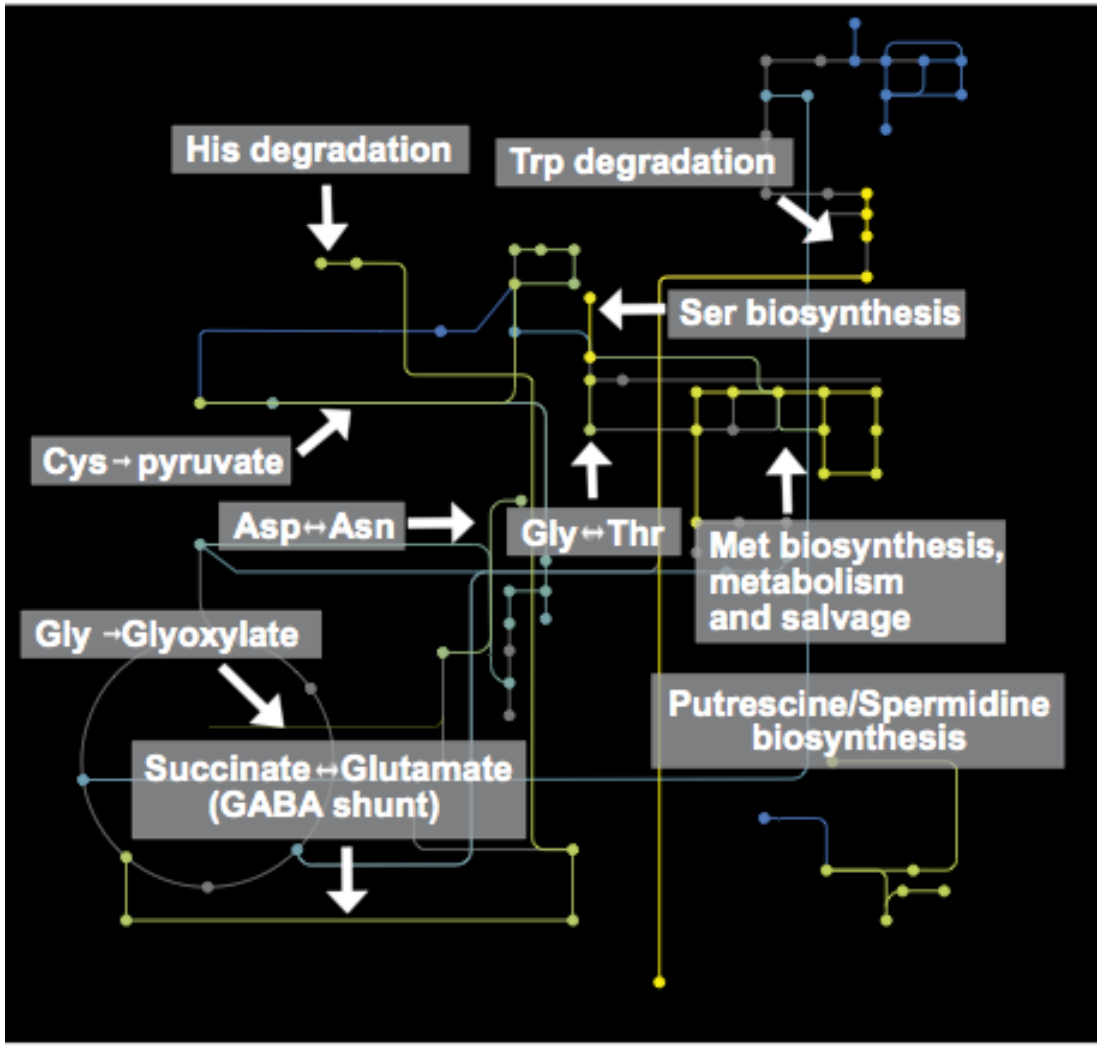
Conclusion #2: Outer Membrane components vary the environment





[Gianoulis et al., PNAS (in press, 2009)]

Conclusion #3: Covariation of AA biosynthesis and Import



Why is their fluctuation in amino acid metabolism? Is there a feature(s) that underlies those that are environmentally-variant as opposed to those which are not?

[Gianoulis et al., PNAS (in press, 2009)]

Conclusion #4: Cofactor (Metal) Optimization

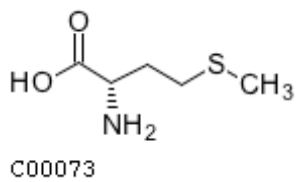
Methionine salvage, synthesis, and uptake, transport

IS DEPENDENT-ON

Methionine synthesis

Cobalamin biosynthesis

Cobalt transporters



Methionine

IS NEEDED FOR

Methionine degradation

S-adenosyl Methionine Biosynthesis (synthesize SAM one of the most important methyl donors)

Polyamine biosynthesis

RELIES ON

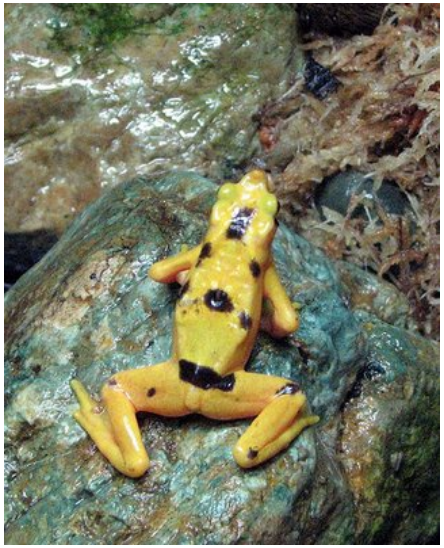
Methionine Salvage

Spermidine/Putrescine transporters

Arg/His/Ornithine transporters

[Gianoulis et al., PNAS (in press, 2009)]

Biosensors:
Beyond Canaries in a Coal Mine



[Gianoulis et al., PNAS (in press, 2009)]

Networks & Variation

Which parts of the network vary most in sequence?
Which are under selection, either positive or negative?

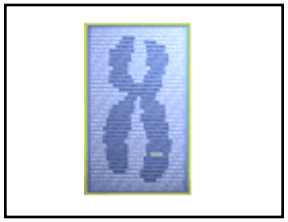
METHODOLOGY: MAP SNP AND CNV DATA ONTO ENSEMBL GENES, AND THEN MAP ENSEMBL GENES TO THE KNOWN INTERACTOME

ILLUSTRATIVE

Hapmap/Perlegen

SNPs

Database of Genomic Variants



CNVs + SDs

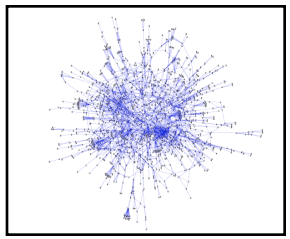
Map to ENSEMBL genes

Ensembl Genes

ENSG000XXXX:
rsSNP00XXX
CNV_XXX
DN/DS XXXX
Recombination rate

Map to proteins in the interaction network

Interactome



~30000 interactions from HPRD and Y2H screens

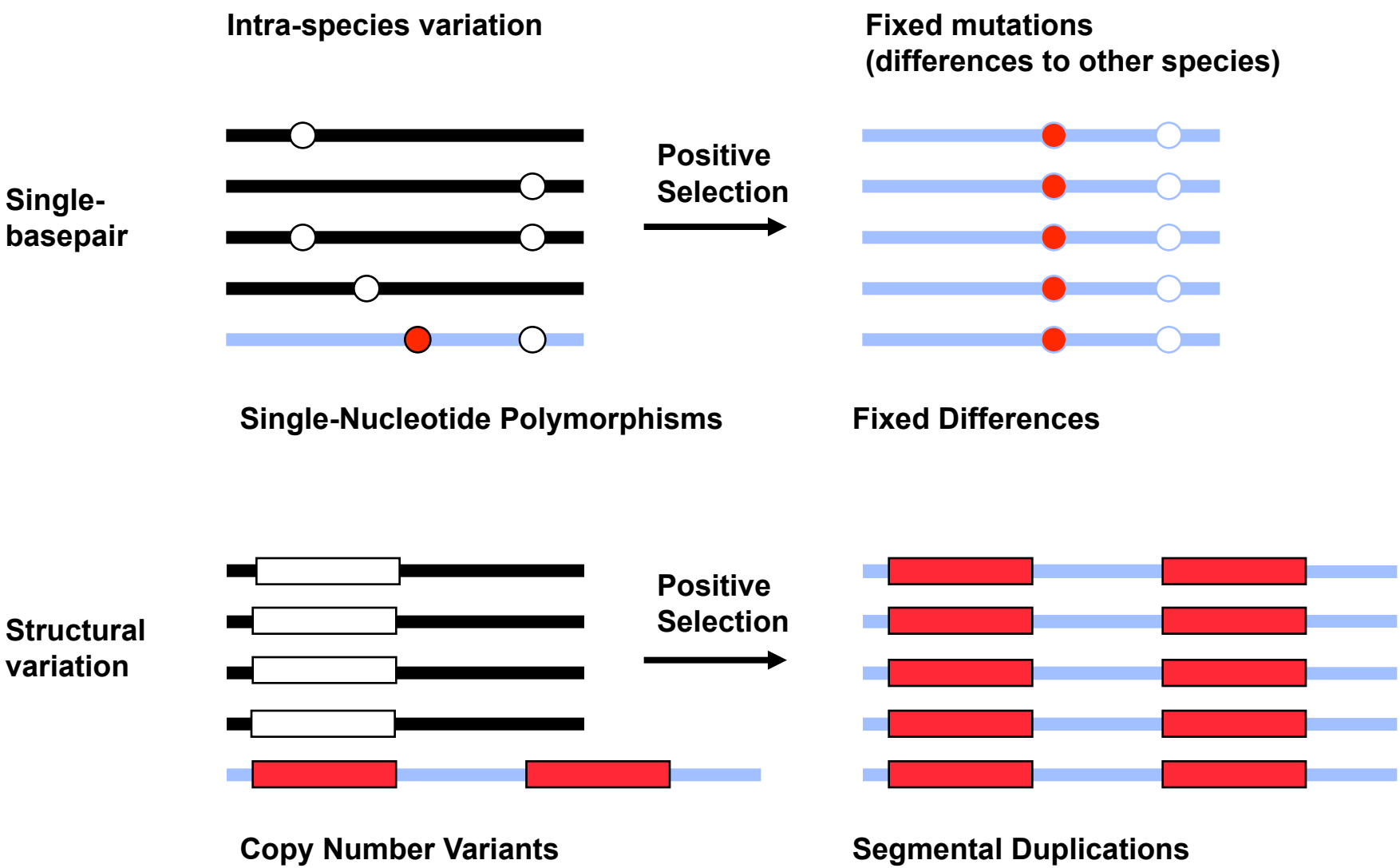
Result

- Dataset of network position / parameters (e.g. degree centrality or betweenness centrality) in relationship to SNPs, CNV's, recombination rates and positive selection tests

*From Nielsen et al. *PLoS Biol.* (2005) and Bustamante et al. *Nature* (2005)

Source: PMK

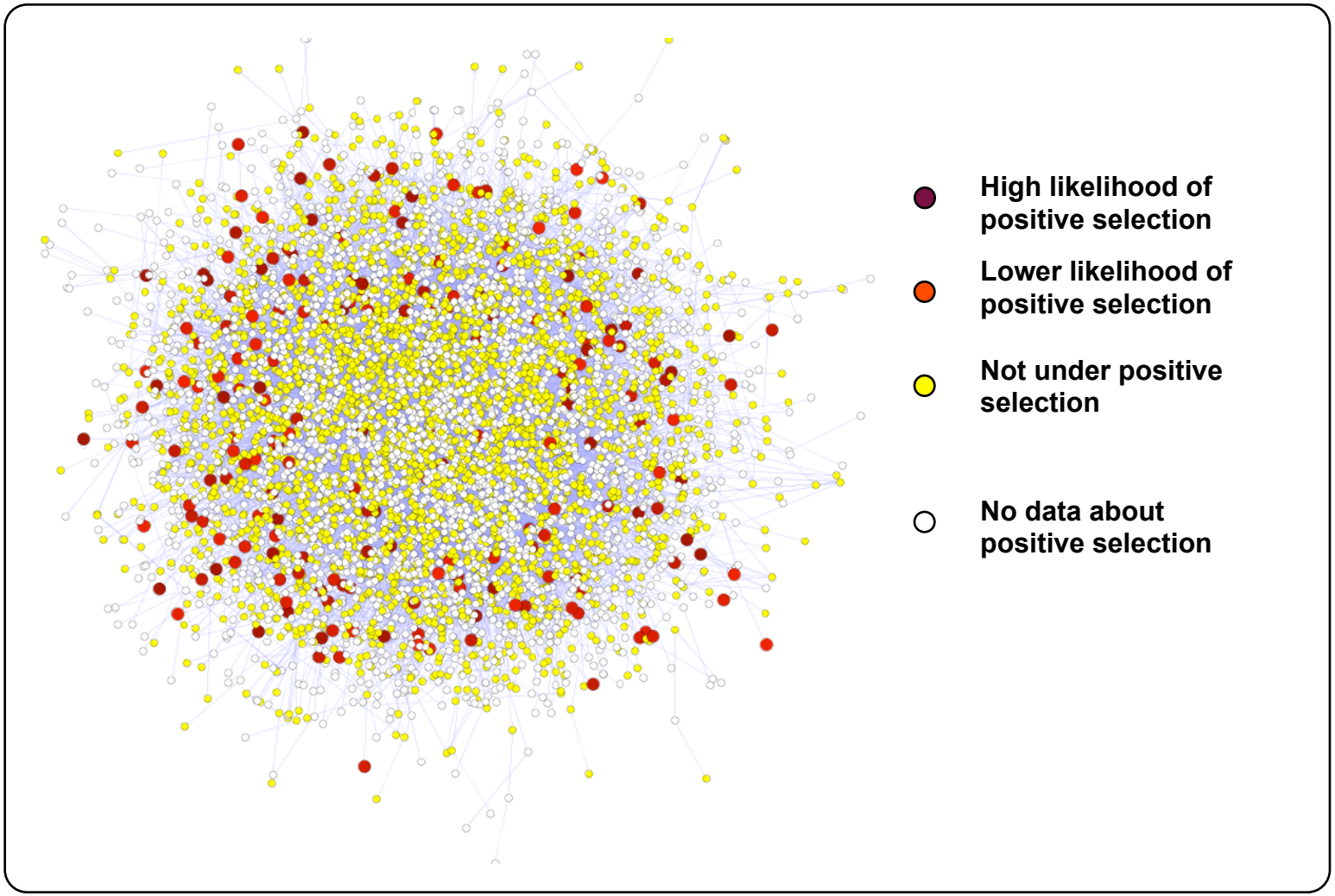
ADAPTIVE EVOLUTION CAN BE SEEN ON TWO DIFFERENT LEVELS



Source: PMK

POSITIVE SELECTION LARGELY TAKES PLACE AT THE NETWORK PERIPHERY

Positive selection in the human interactome

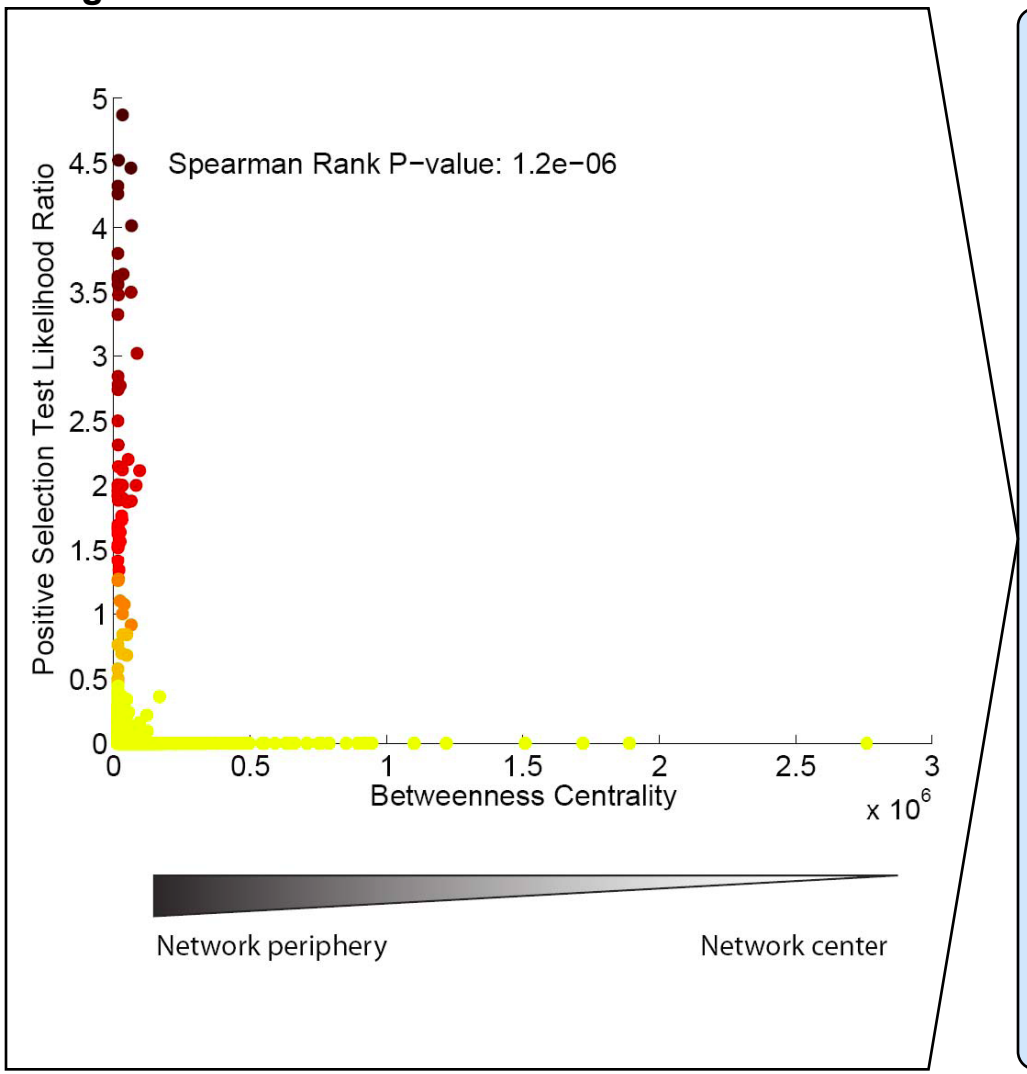


Source: Nielsen et al. *PLoS Biol.* (2005), HPRD, and Kim et al. PNAS (2007)

CENTRAL PROTEINS ARE LESS LIKELY TO BE UNDER POSITIVE SELECTION

Hubs

Degree vs. Positive Selection



Reasoning

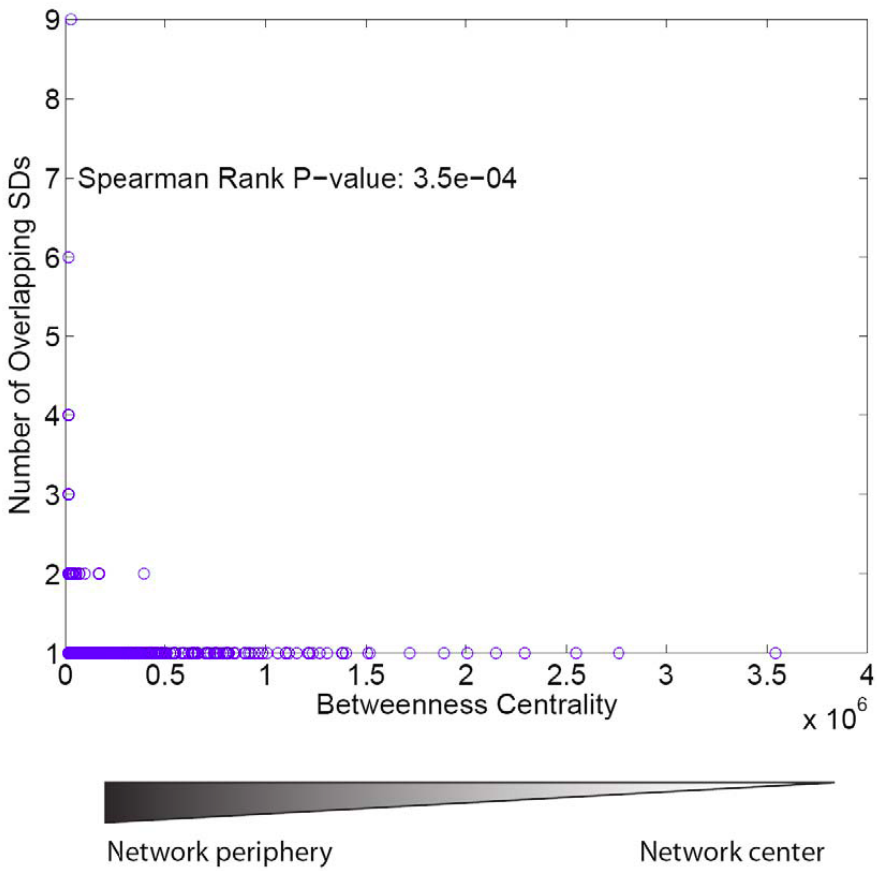
- Peripheral genes are likely to under positive selection, whereas hubs aren't
- This is likely due to the following reasons:
  - Hubs have stronger structural constraints, the network periphery doesn't
  - Most recently evolved functions (e.g. "environmental interaction genes" such as sensory perception genes etc.) would probably lie in the network periphery
- Effect is independent of any bias due to gene expression differences

*With a probability of over 80% to be positively selected as determined by Ka/Ks. Other tests of positive selection (McDonald Kreitmann and LDD) corroborate this result.

Source: Nielsen et al. *PLoS Biol.* (2005), Bustamante et al. *Nature* (2005), HPRD, Rual et al. *Nature* (2005), and Kim et al. PNAS (2007)

CENTRAL NODES ARE LESS LIKELY TO LIE INSIDE OF SDs

Centrality vs. SD occurrence



Reasoning

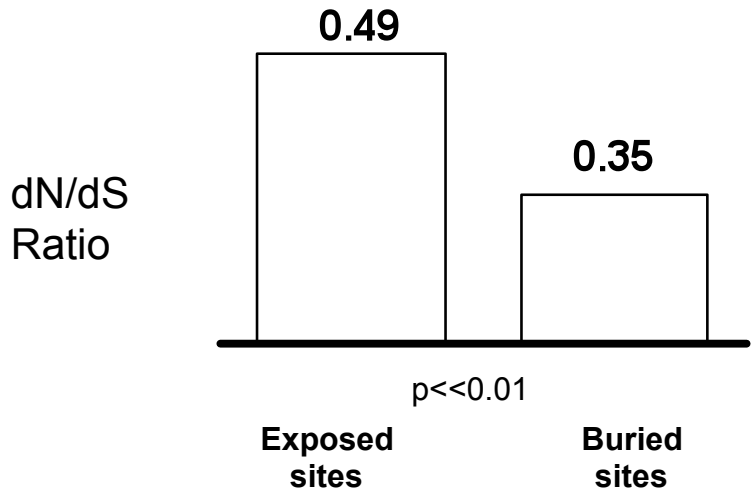
- This result also confirms our initial hypothesis – peripheral nodes tend to lie in regions rich in SDs.
- Since segmental duplications are a different mechanism of ongoing evolution, the less constrained peripheral proteins are enriched in them.
- Note that despite the small size of our dataset for known SD's we get significant correlations. It is to be expected that the correlations will get clearer as more data emerges*

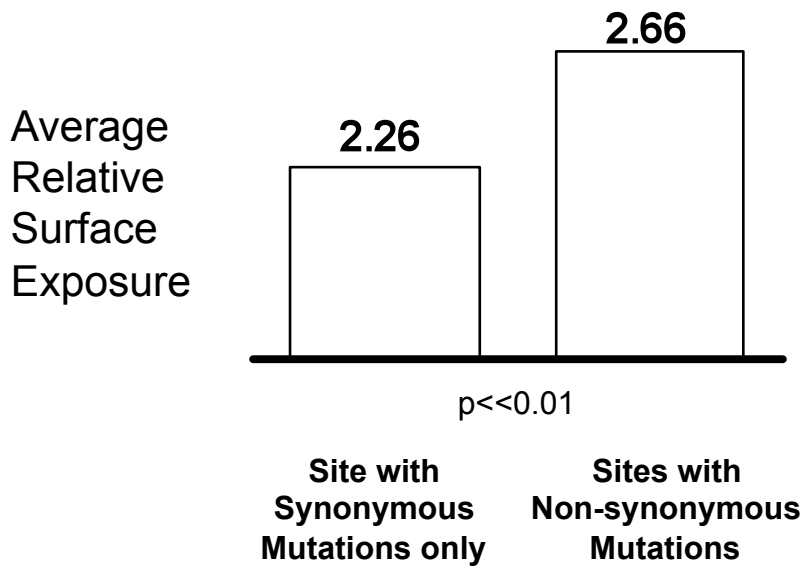
*Specifically, a number of the SDs are likely not fixed, but rather common CNVs in the reference genome

Source: Database of genetic variation, HPRD, Rual et al. *Nature* (2005), and Kim et al. PNAS (2007)

Why do we observer this? Perhaps central hub proteins are involved in more interactions & have more surface buried.

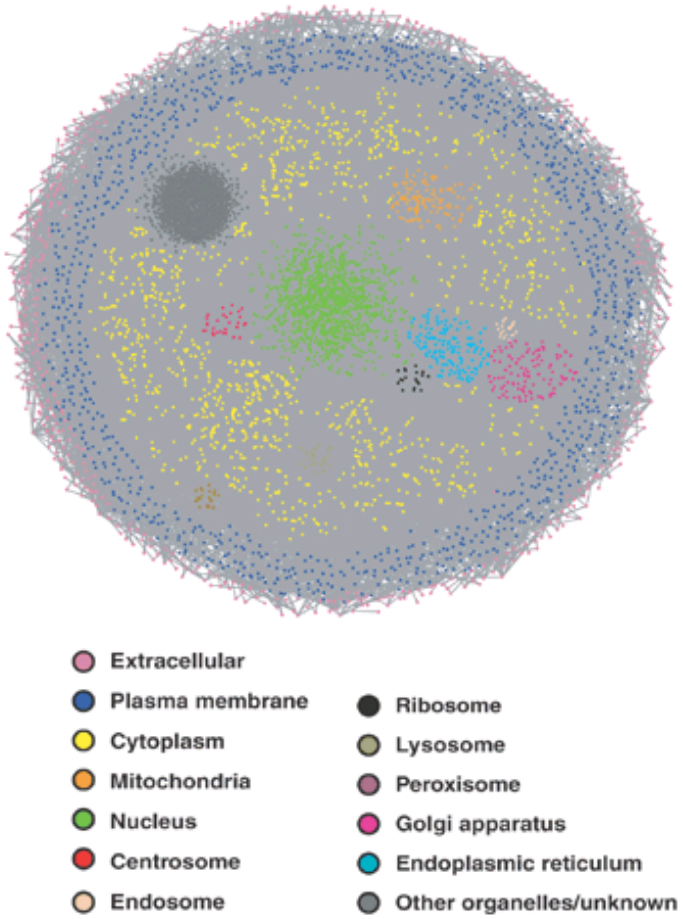
BURIED SITES ARE CONSERVED AND MUCH LESS LIKELY TO HARBOR NON-SYNONYMOUS MUTATIONS

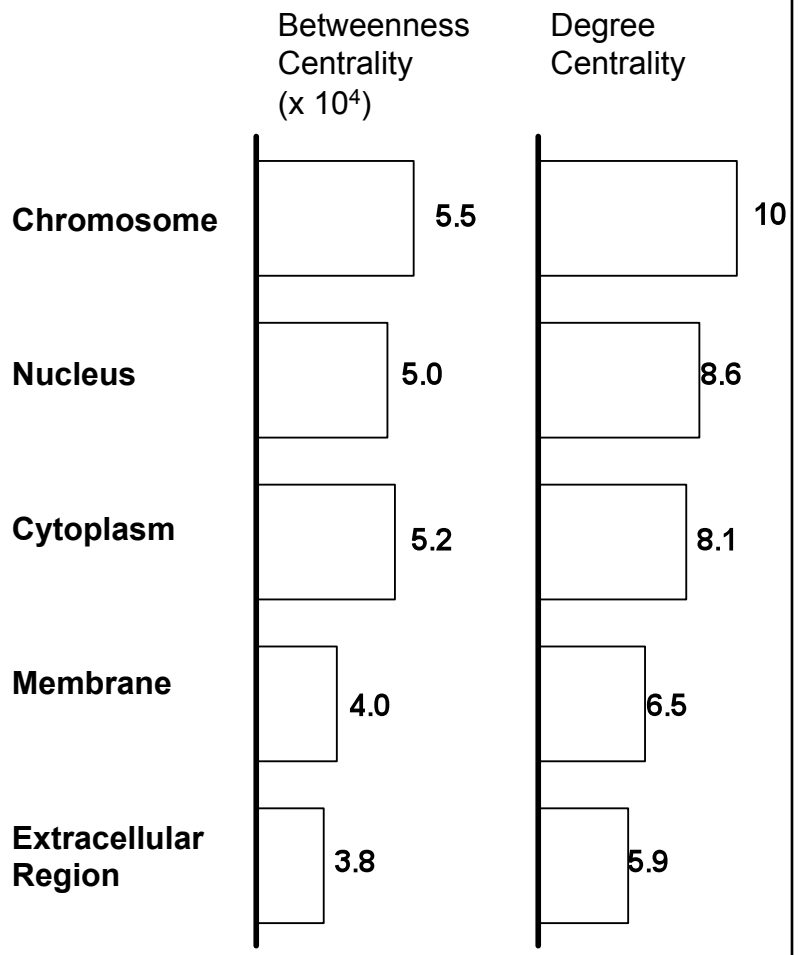




Source: Kim et al. PNAS (2007)

Another explanation: THE NETWORK PERIPHERY CORRESPONDS TO THE CELLULAR PERIPHERY





Source: Gandhi et al. (*Nature Genetics* 2006), Kim et al. PNAS (2007)

IS RELAXED CONSTRAINT OR ADAPTIVE EVOLUTION THE REASON FOR THE PREVALENCE OF BOTH SELECTED GENES AND SDs AT THE NETWORK PERIPHERY?

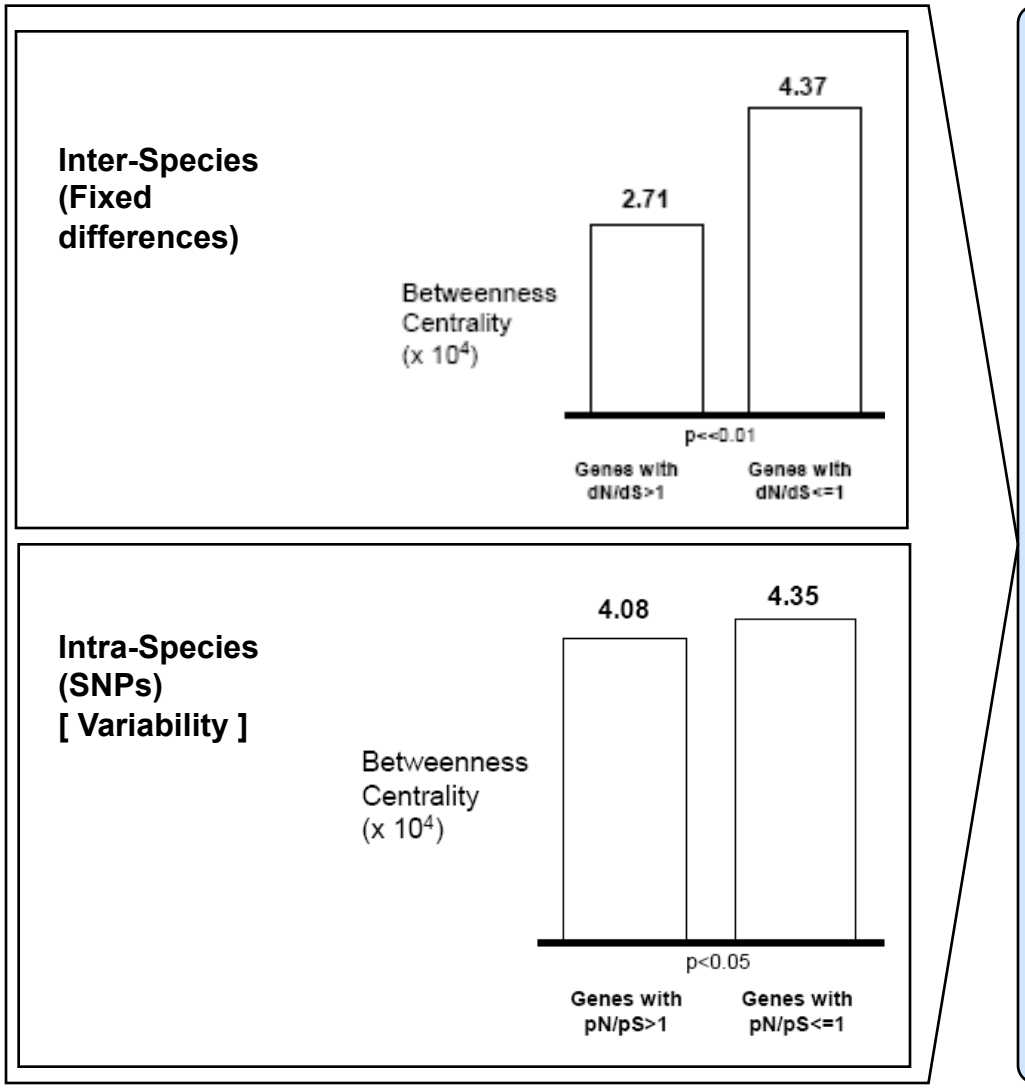
ILLUSTRATIVE

	Relaxed Constraint	Adaptive Evolution
Inter-Species Variation (Fixed differences)	• Increases inter-species variation – more variable loci are under less negative selection • Can be seen in higher Ka/Ks ratio or SD occurrence	• Increases inter-species variation – more variable loci are under less negative selection • Can be seen in higher Ka/Ks ratio or SD occurrence
Intra-Species Variation (Polymorphisms)	• Increases intra-species variation – for the very same reason • Can be seen in both SNPs or CNVs	• Should not have effects on intra-species variation

Source: Kim et al. PNAS (2007)

SOME, BUT NOT ALL OF THE SINGLE-BASEPAIR SELECTION AT THE PERIPHERY IS DUE TO RELAXED CONSTRAINT

Inter vs. Intra-Species Variation in Networks



Reasoning

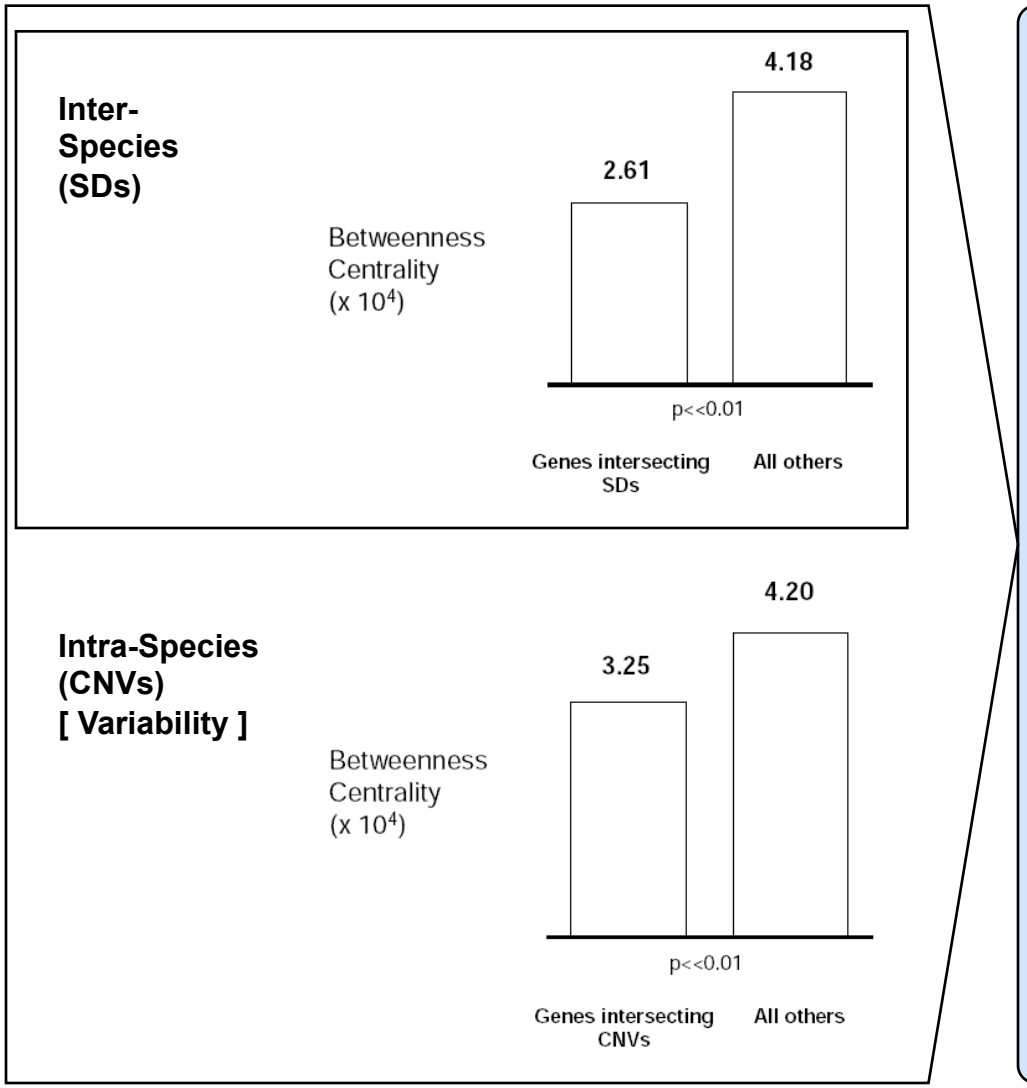
- There is a difference in **variability** (in terms of SNPs) between the network periphery and the center
- However, this difference is much smaller than the difference in **selection**
- This most likely means, that part of the effect we're seeing is due to relaxed constraint (and higher variability)
- But, not the entire effect*

*But it's hard to quantify

Source: Kim et al. (2007) PNAS

Similar Results for Large-scale Genomic Changes (CNVs and SDs)

Inter vs. Intra-Species Variation in Networks



Reasoning

- There a small difference in **variability** (in terms of CNVs) between the network periphery and the center
- But, there is a (as shown before) marked difference in fixed (and hence, presumably, **selected**) SDs at the network periphery and center

Source: Kim et al. (2007) PNAS

Outline: Molecular Networks

- Why Networks?
- Predicting Networks (yeast)
  - ◊ Propagating known information
- Network Structure: Key Positions (yeast)
  - ◊ Hubs & Bottlenecks
- Dynamics & Variation of Networks
  - ◊ Across cellular states (yeast)
  - ◊ Across environments (in prokaryotes)
- Protein Networks & Human Variation

Conclusions on Networks: Predictions & Structure

- Predicting Networks
  - ◊ Extrapolating from the Training Set
  - ◊ Principled ways of using known information in the fullest possible fashion
    - Prediction Propagation
    - Multi-level learning
- Centrality Measures in Protein Network
  - ◊ Hubs & Bottlenecks
  - ◊ Importance of later in regulatory networks

Conclusions: Network Dynamics across Cellular States

- Merge expression data with Networks
- Active network markedly different in different conditions
- Identify transient hubs associated with particular conditions
- Use these to annotate genes of unknown function

Conclusions: Networks Dynamics across Environments

- Developed and adapted techniques to connect quantitative features of environment to metabolism.
- Applied to available aquatic datasets, we identified footprints that were predictive of their environment (potentially could be used as biosensor).
- Strong correlation exists between a community's energy conversion strategies and its environmental parameters (e.g. temperature and chlorophyll).
- Suggest that limiting amounts of cofactor can (partially) explain increased import of amino acids in nutrient-limited conditions.

Conclusions: Connecting Networks & Human Variation

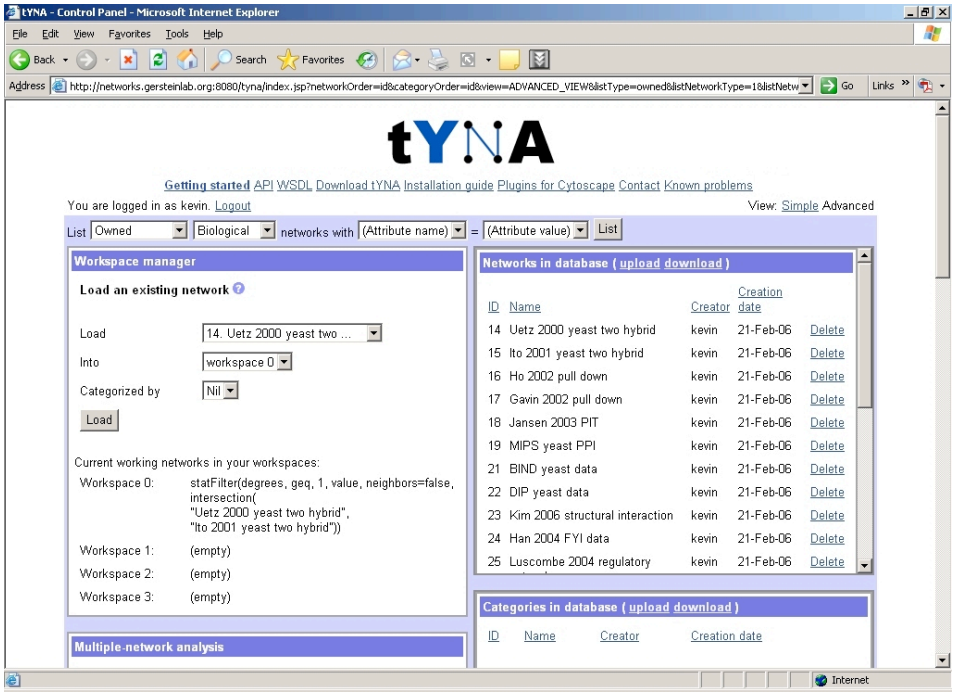
- We find ongoing evolution (positive selection) at the network periphery.
  - ◊ This trend is present on two levels:
    - On a sequence level, it can be seen as positive selection of peripheral nodes
    - On a structural level, it can be seen as the pattern of SDs that display significantly higher allele frequencies in non-central genes
  - ◊ 2 possible mechanisms for this : adaptive evolution at cellular periphery & relaxation of structural constraints at the network periphery
    - We show that the latter can only explain part of the increased variability,,,

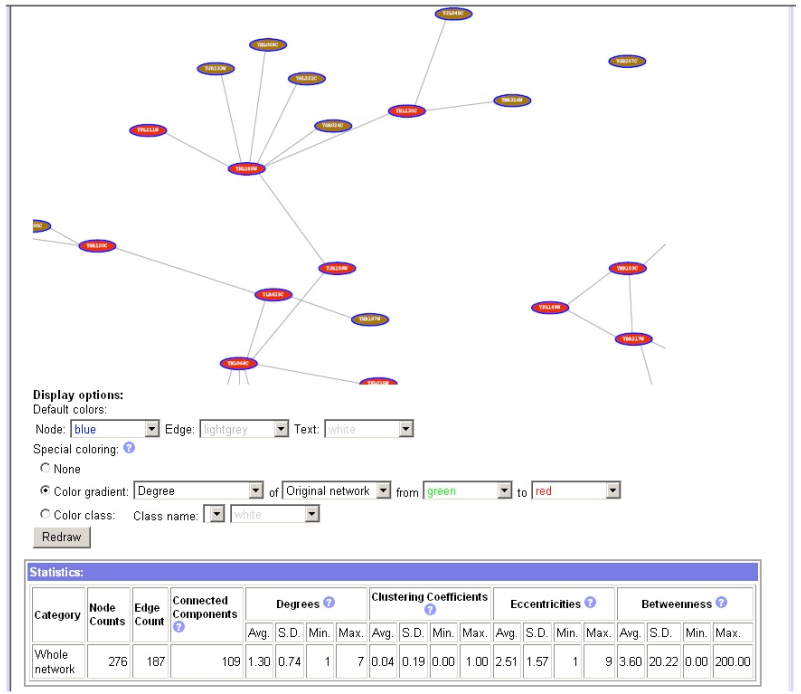
TopNet - an automated web tool

Topology of Networks

tYNA

(vers. 2 : "TopNet-like Yale Network Analyzer")



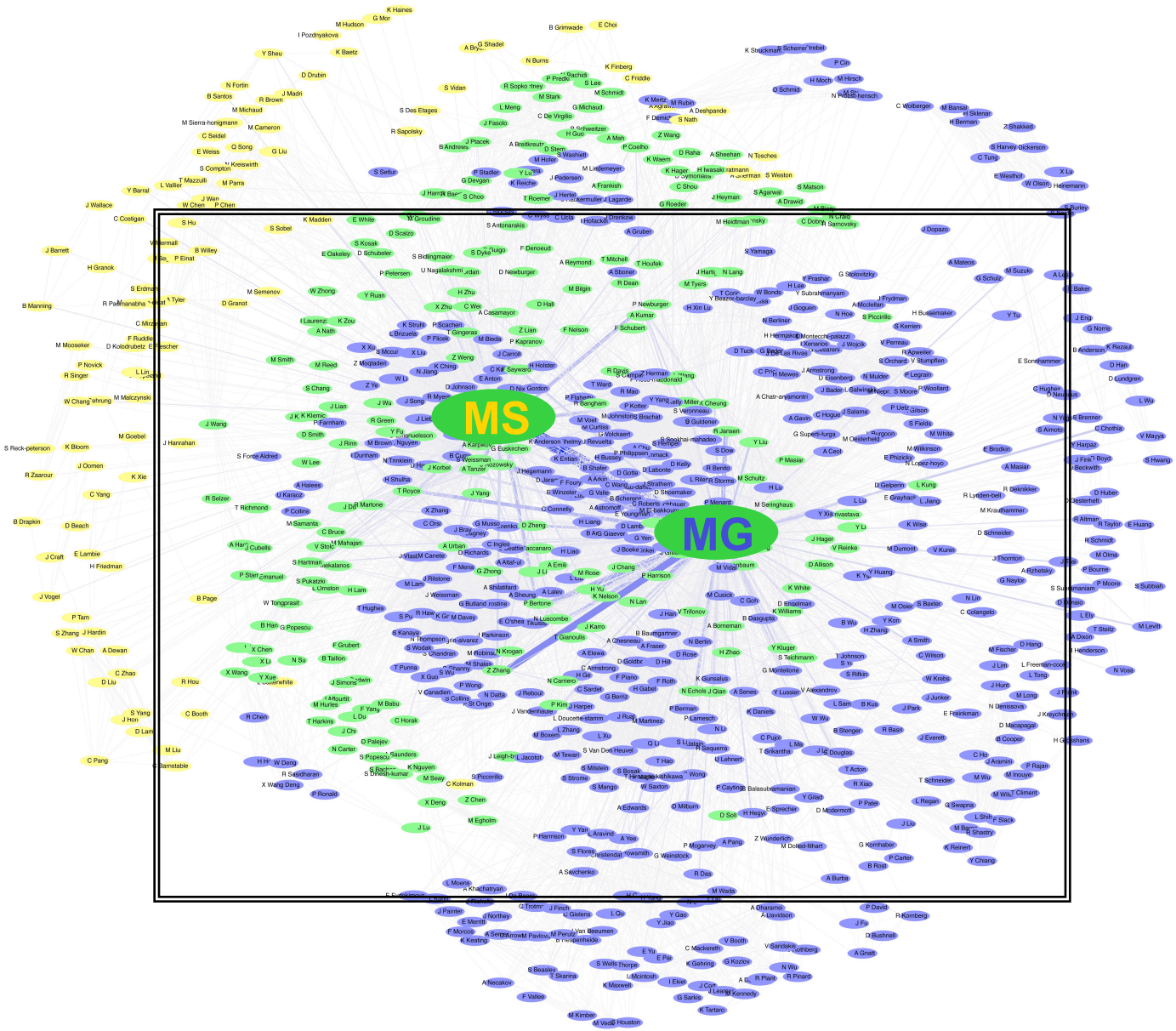


Normal website + Downloaded code (JAVA)
+ Web service (SOAP) with Cytoscape plugin

[Yu et al., NAR (2004); Yip et al. Bioinfo. (2006);
Similar tools include Cytoscape.org, Idekar, Sander et al]

Acknowledgements

Networks.GersteinLab.org



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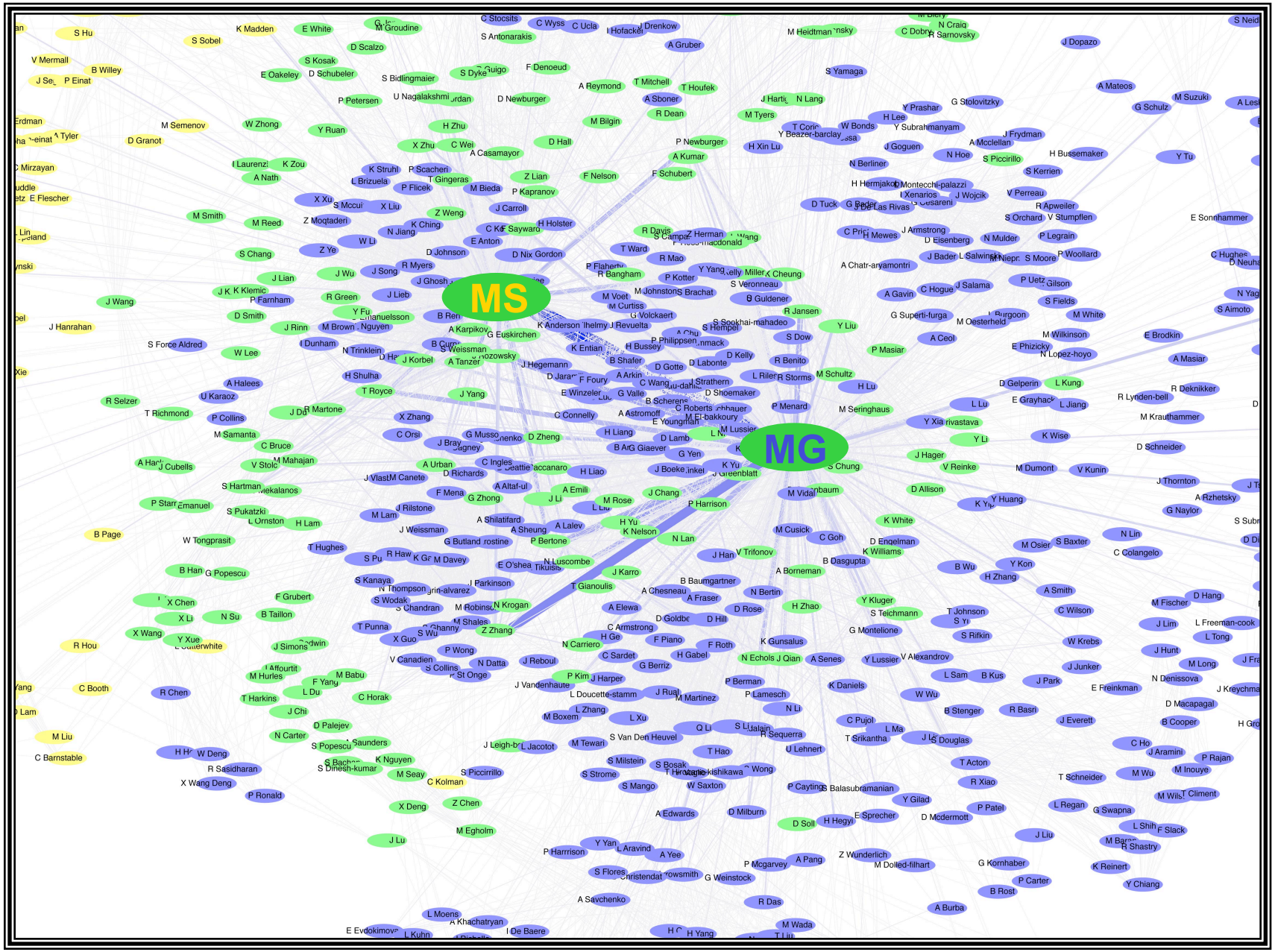

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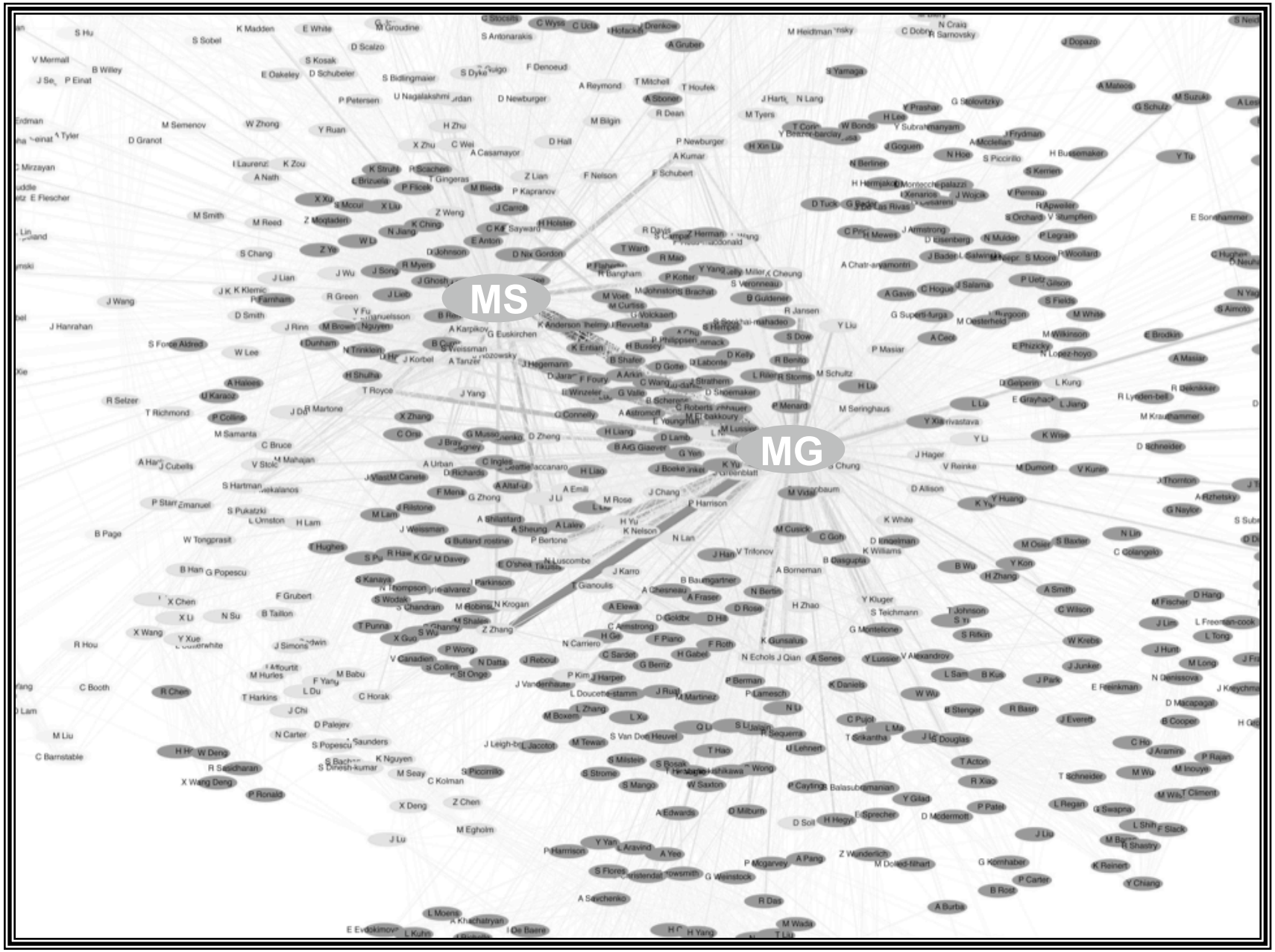
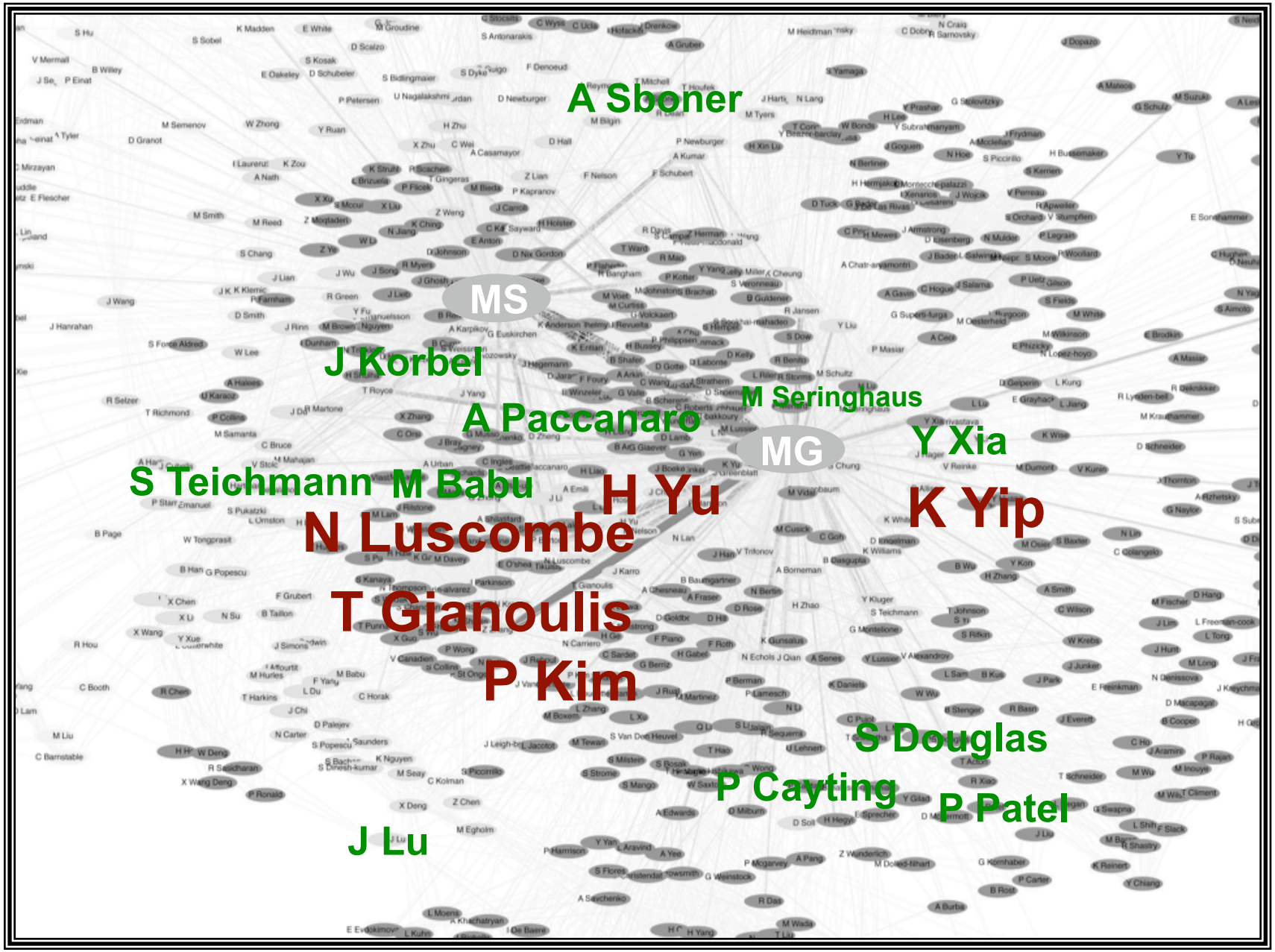


Acknowledgements

P Bork, J Raes

Networks.GersteinLab.org

Job opportunities currently for postdocs & students



More Information on this Talk

TITLE: Understanding Protein Function on a Genome-scale through the Analysis of Molecular Networks

SUBJECT: Networks

DESCRIPTION:
Ulam Lecture at Recomb 2009, 2009.05.18, 08:45-09:45; [I:**RECOMB09**]
(Long networks talk, incl. the following topics:
why networks w. **amsci*, funnygene***, net. prediction intro, **tse*, sandy*, metagenomics*, netpossel*, tyna* + topnet***, & **pubnet*** . Fits easily into 60′ w. 10′ questions. In particular, 5' to after GO DAG and then 11.5' to centraility discussion. PPT works on mac & PC and has many photos.)

(Paper references in the talk were mostly from Papers.GersteinLab.org. The above topic list can be easily cross-referenced against this website. Each topic abbrev. which is starred is actually a papers "ID" on the site. For instance,
the topic **pubnet*** can be looked up at
http://papers.gersteinlab.org/papers/pubnet)