

## METABOLIC PATHWAYS

Glycan Biosynthesis and Metabolism

Biodegradation of Xenobiotics

Nucleotide Metabolism

# Network Perspectives in Bioinformatics

Carbohydrate Metabolism

Lipid Metabolism

Metabolism of Other Amino Acids

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Amino Acid Metabolism

Energy Metabolism

Metabolism of Cofactors and Vitamins

Nishinomiya-Yukawa International & Interdisciplinary Symposium 2007

What is Life? Biosynthesis of Secondary Metabolites

2007/10/18

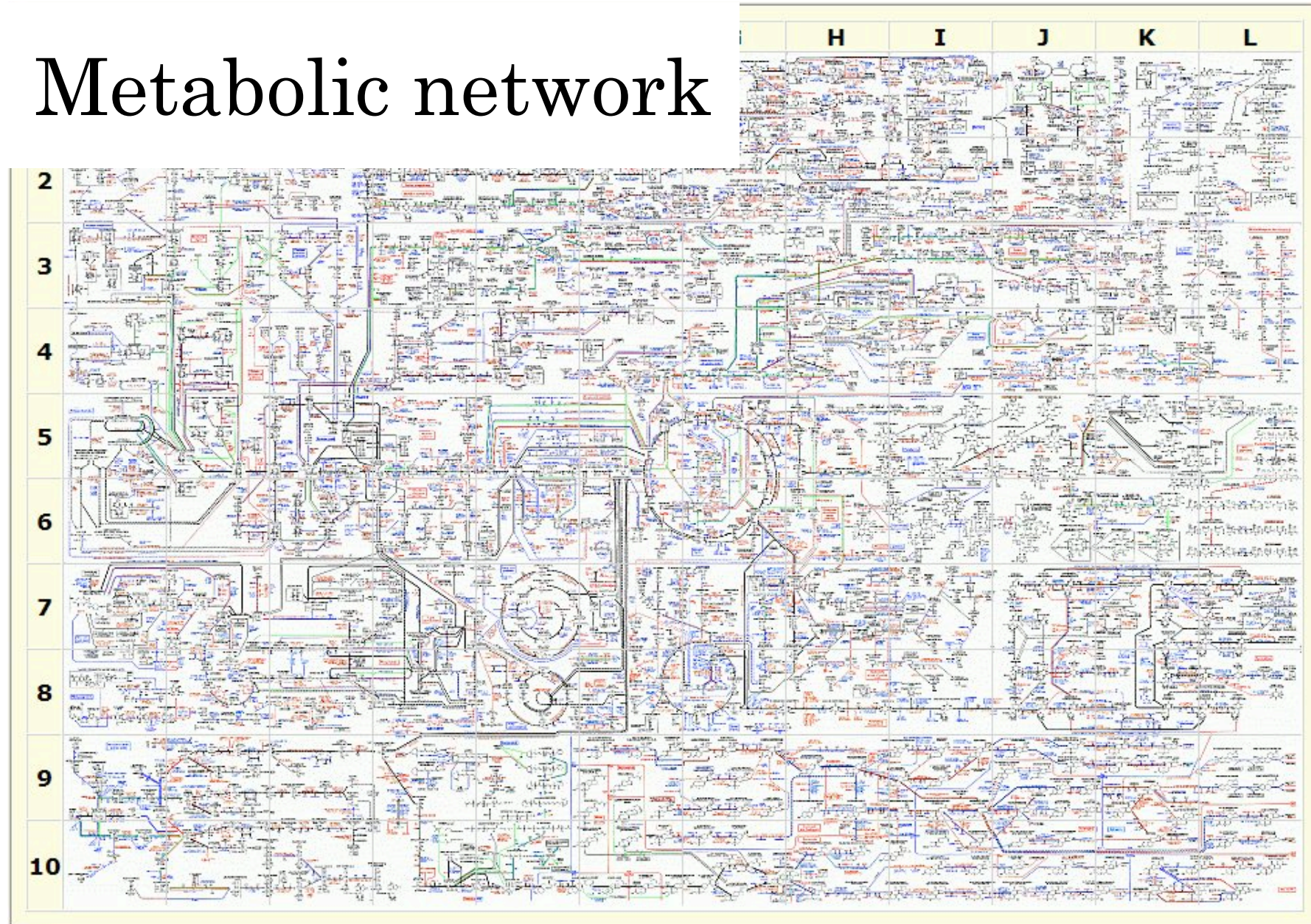
# Bioinformatics

- Large amount of omics data
  - Genomics, Transcriptomics, Proteomics, Interactomics, Metabolomics, etc.
- Development of various techniques for interpreting the data and solving biological problem, mainly on the molecular level

# What is Life?

- Autonomy?
- Interaction with others?
  
- Uptake of nutrients outside
  - Metabolism
- Sensing signals from outside
  - Signal transduction
- Replication

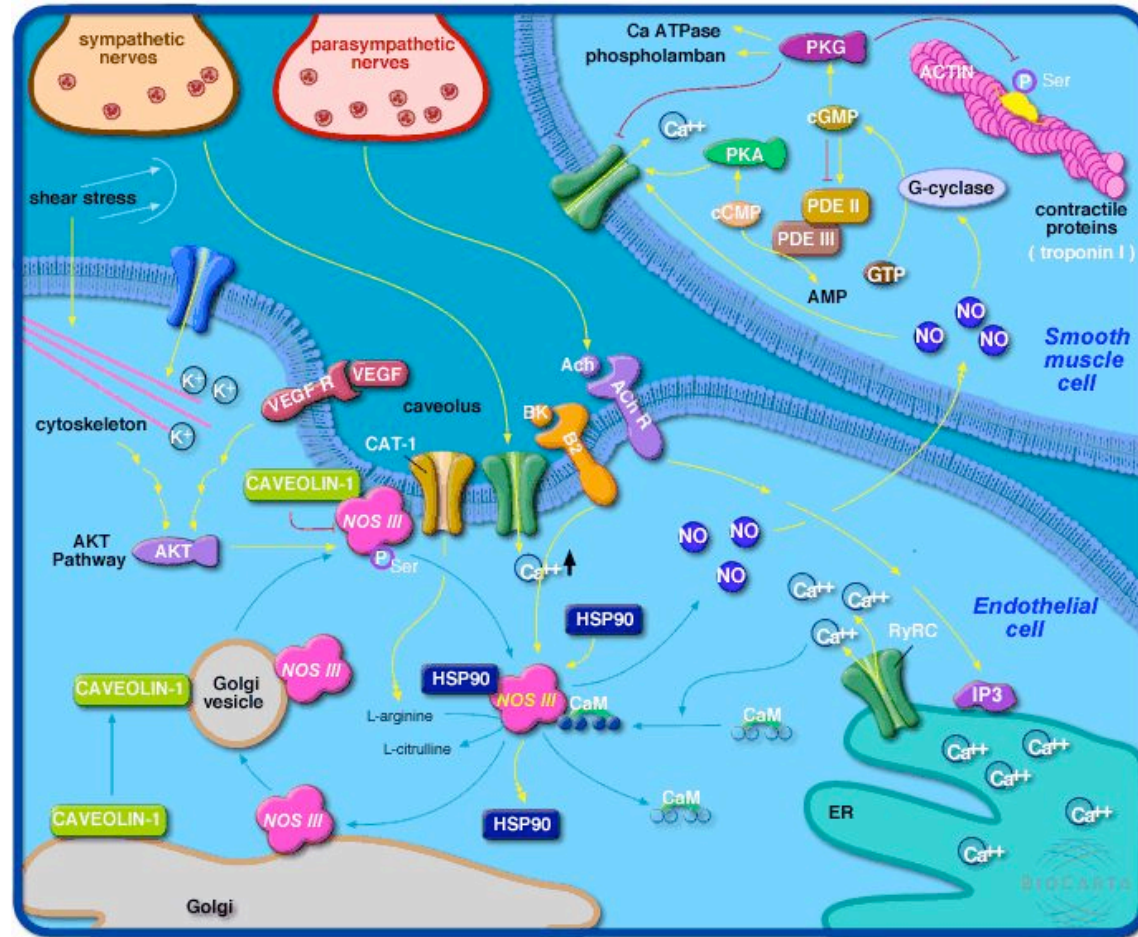
# Metabolic network



[http://www.expasy.org/cgi-bin/show\\_thumbnails.pl](http://www.expasy.org/cgi-bin/show_thumbnails.pl)

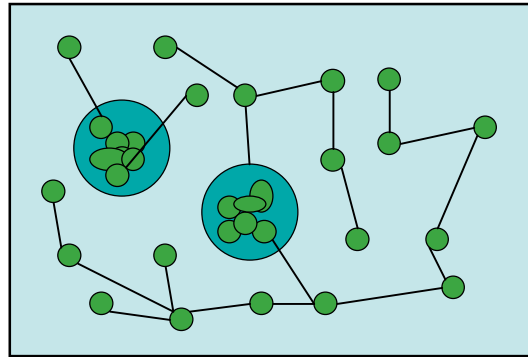
# Signaling network

Protein interaction network working in response to the signals from outside and within cells



# Network for understanding biological systems

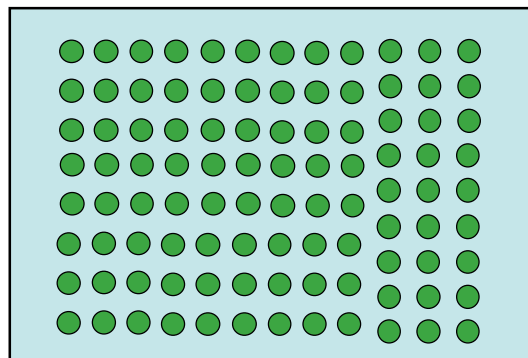
Biological system as a network of genes or gene products



Reductive approach



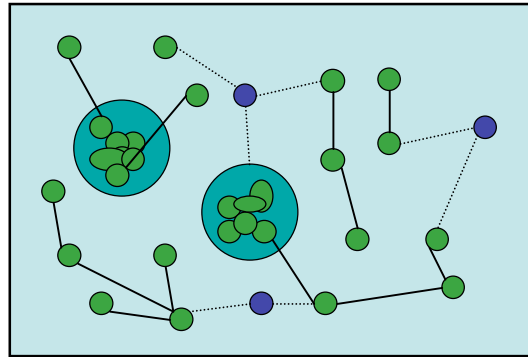
Synthetic approach  
(Bioinformatics)



Gene catalogs from genome projects

# Current Status of Functional Reconstruction

Biological system as a network of genes or gene products

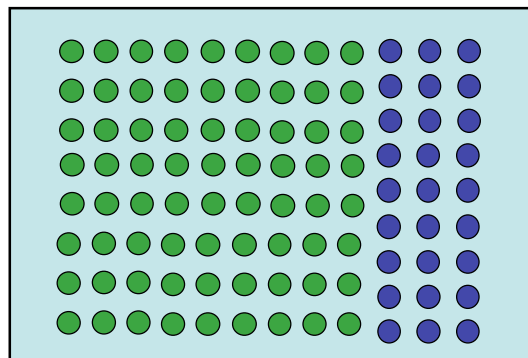


Missing enzymes in  
metabolic pathway

Reductive approach



Synthetic approach  
(Bioinformatics)



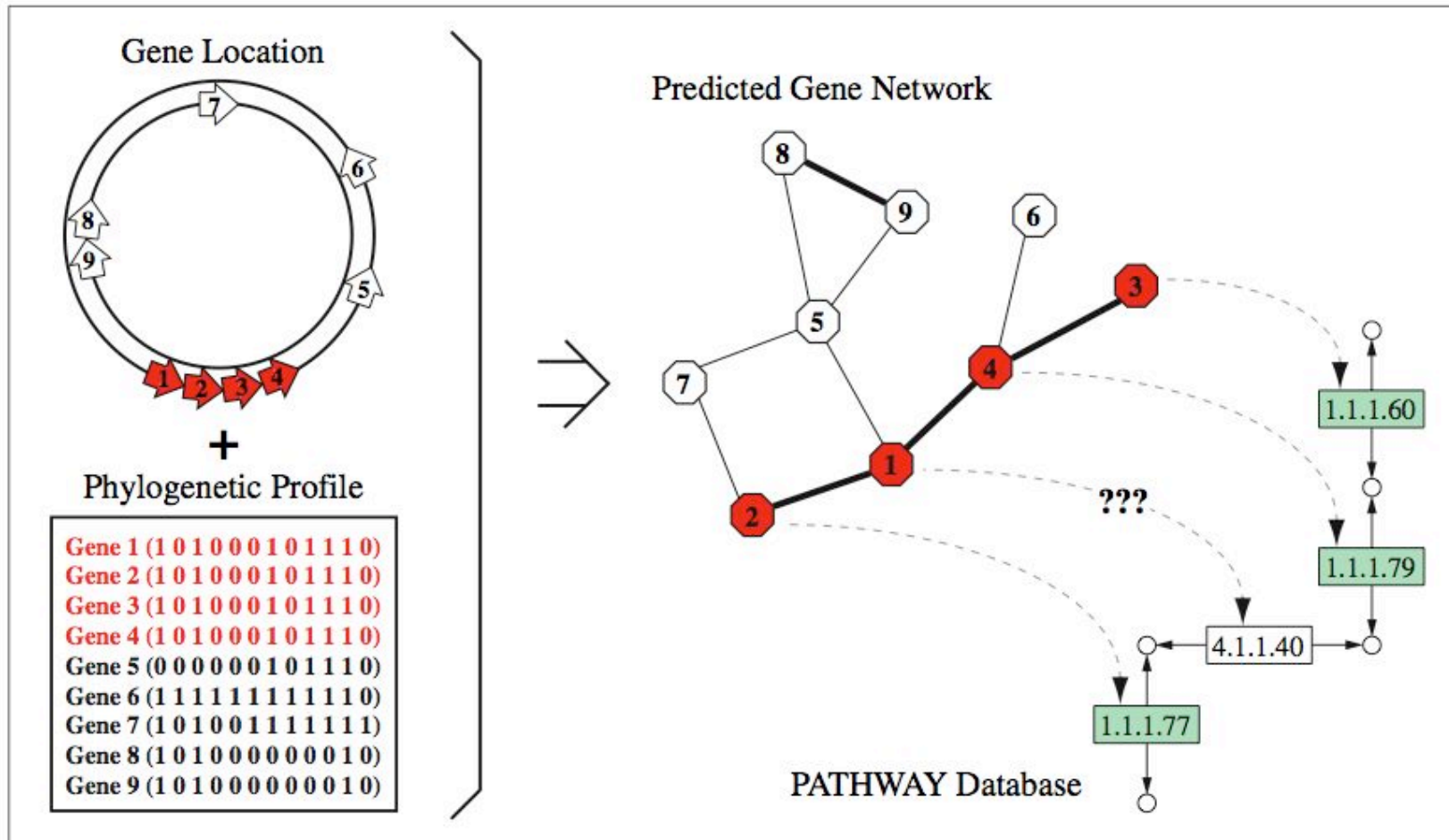
Genes with  
unknown function

Gene catalogs from genome projects





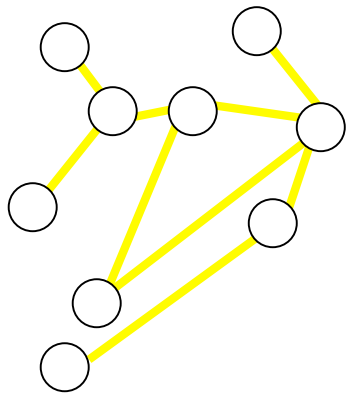
# Prediction of missing enzyme genes



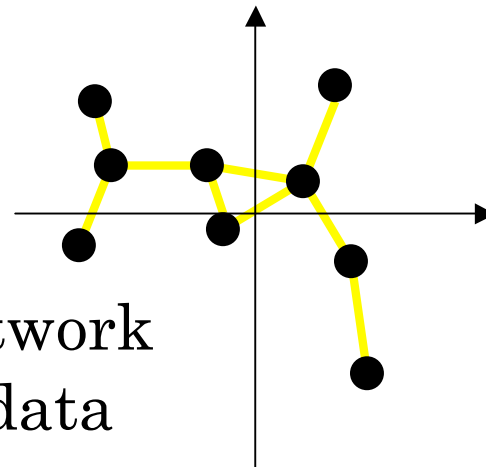
# Supervised approach 1/2

Step 1: Project the data into the feature space that explains the actual network

Original space



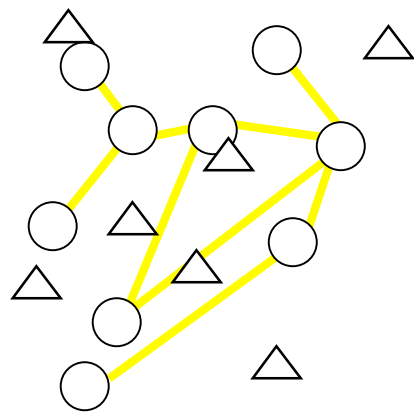
Feature space



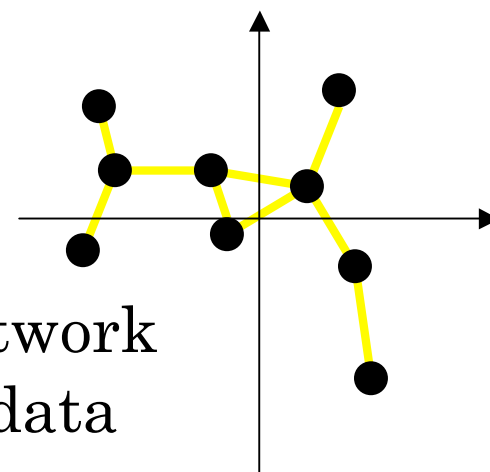
— : Actual network  
○ : Training data

# Supervised approach 2/2

Original space



Feature space

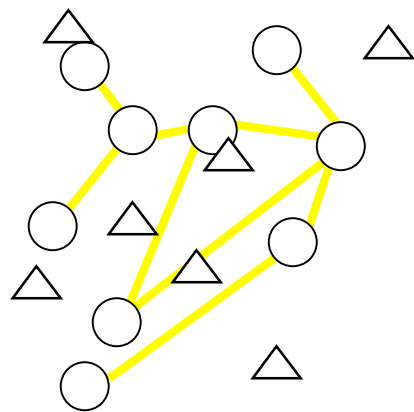


- : Actual network
- : Training data
- △ : Test data

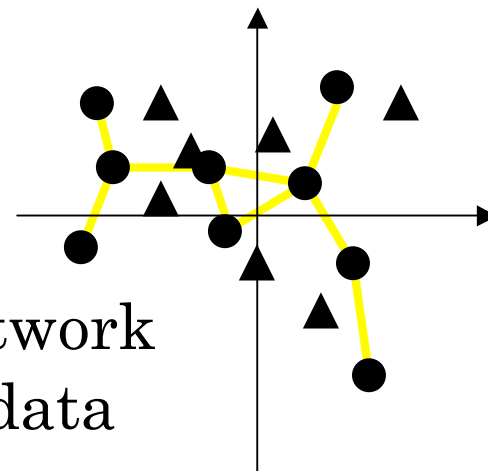
# Supervised approach 2/2

Step 2: Prediction of the interactions related to the test data

Original space



Feature space

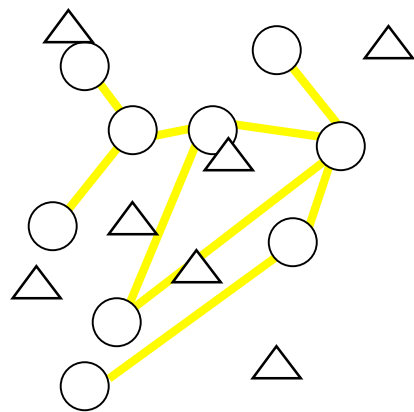


- : Actual network
- : Training data
- △ : Test data

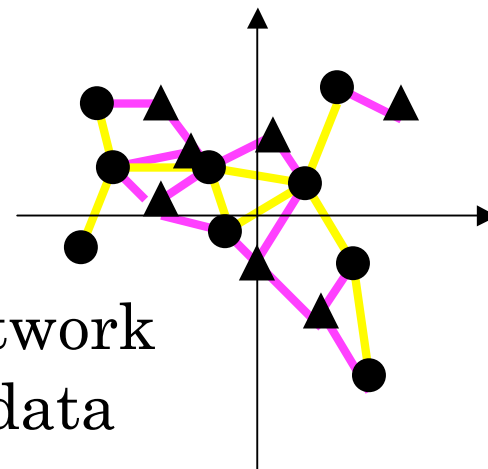
# Supervised approach 2/2

Step 2: Prediction of the interactions related to the test data

Original space

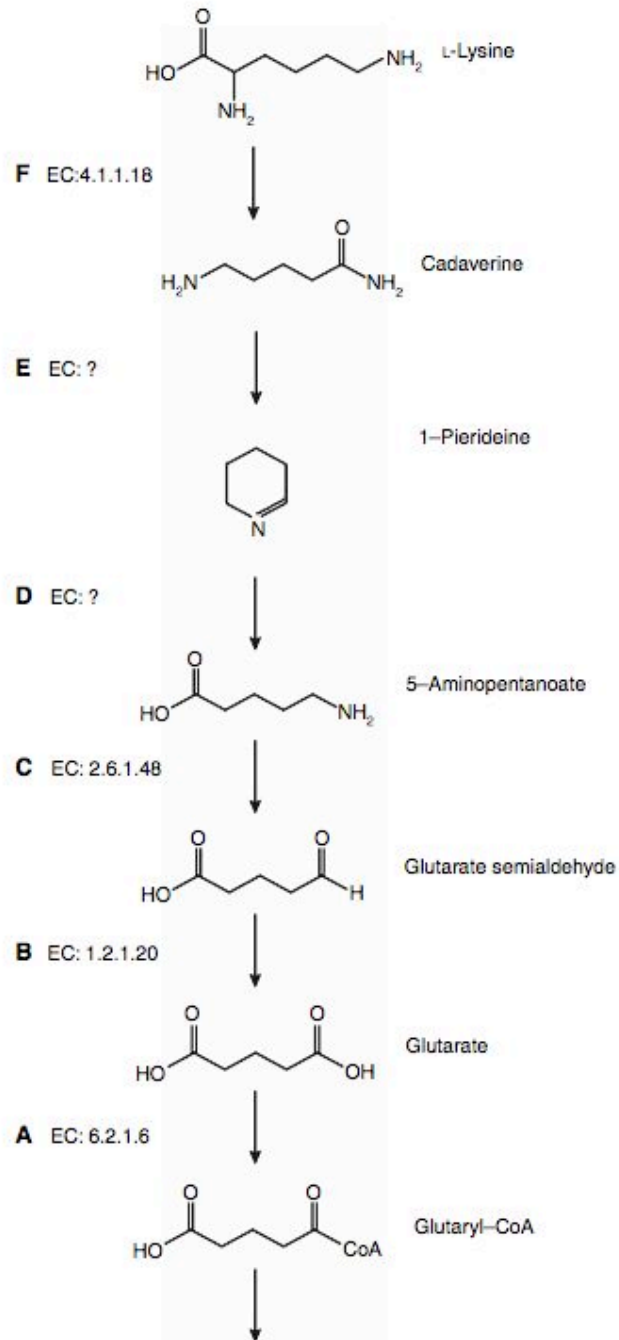


Feature space



- : Actual network
- : Training data
- △ : Test data

# Prediction of missing enzyme genes



Reaction

Candidate gene

Reaction	Candidate gene
A. EC:6.2.1.6	PA1589 (succinyl-CoA synthetase; EC 6.2.1.5)
B. EC:1.2.1.20	PA0265 (dehydrogenase; EC 1.2.1.16)
C. EC:2.6.1.48	PA0266 (amino-transferase; EC 2.6.1.19)
D. 5ami.1-pip	PA1576 (dehydrogenase; EC 1.1.1.31)
E. Cadav.Delta	not specified
F. EC:4.1.1.18	not specified

Yamanishi, et al. (2007) FEBS J. 274:2262

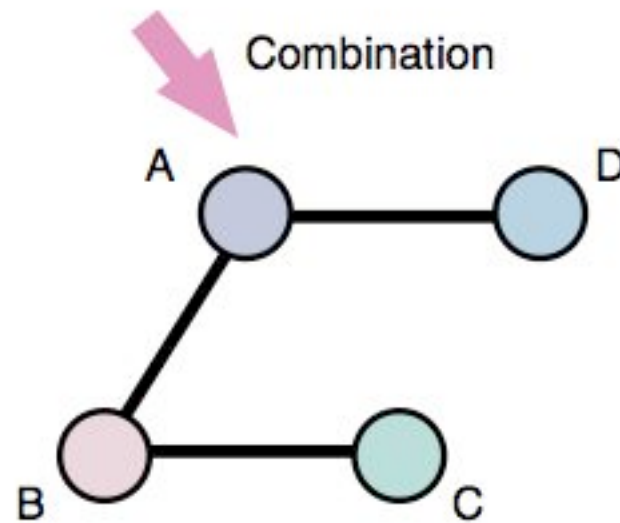
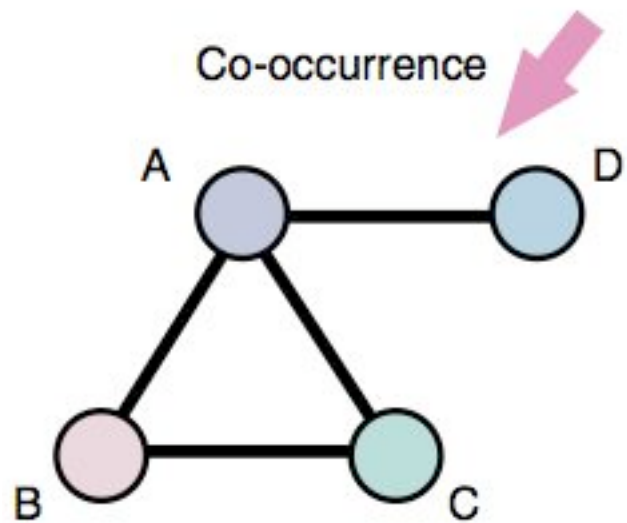
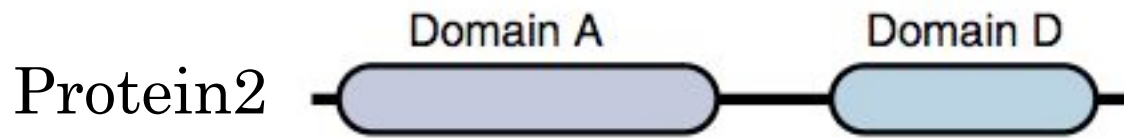
# Network Biology

- Power-law and scale-free distribution of node degree
- Robustness of the network
- Preferential or rich-get-richer model of evolution

# Topological analysis of biological network

- To elucidate how biological network has emerged
  - Metabolic network including activation and inhibition regulation -> network module
  - Signaling and transcription network
  - Domain combination network
- To analyze function of genes in terms of network

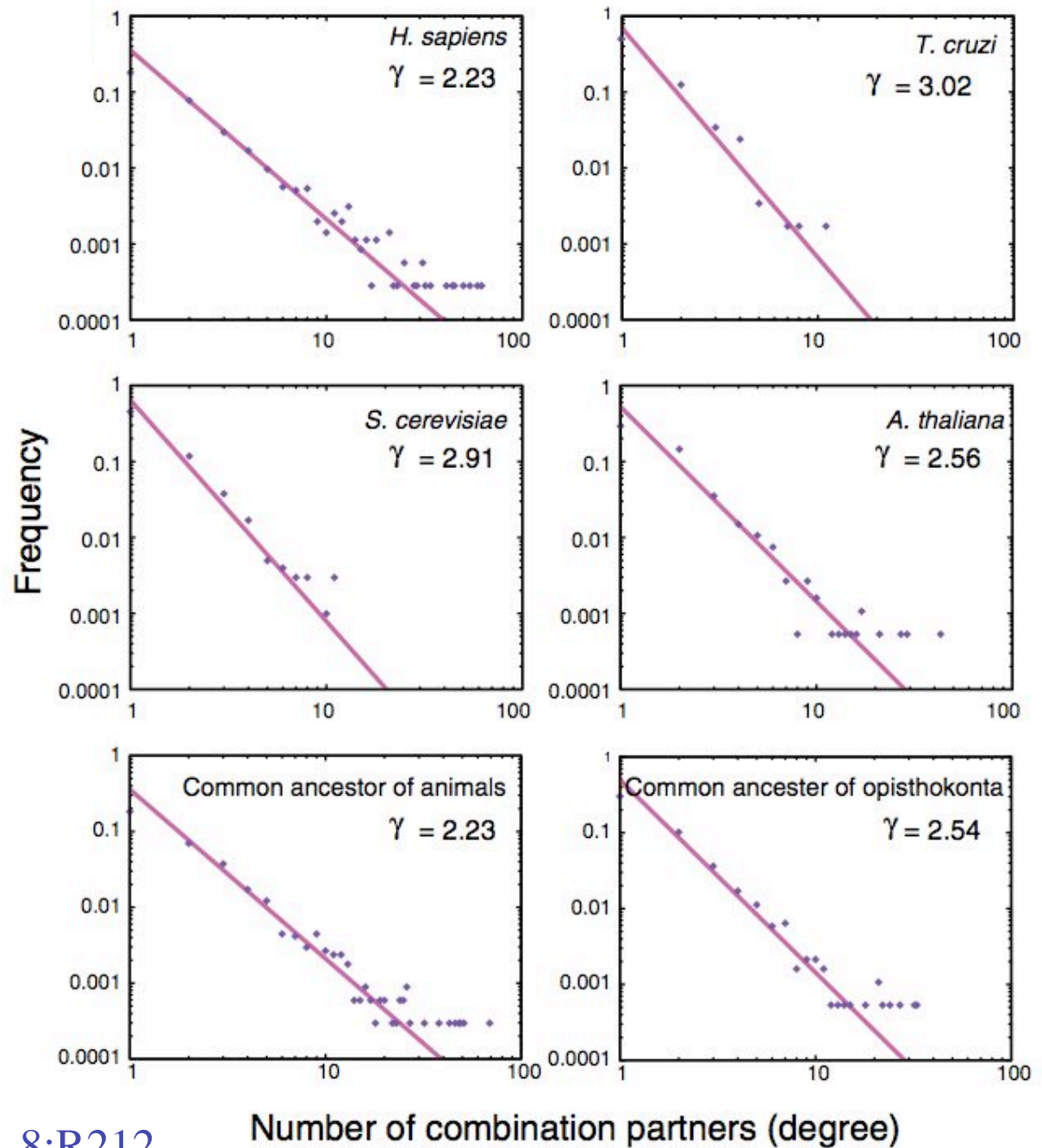
# Domain combination network



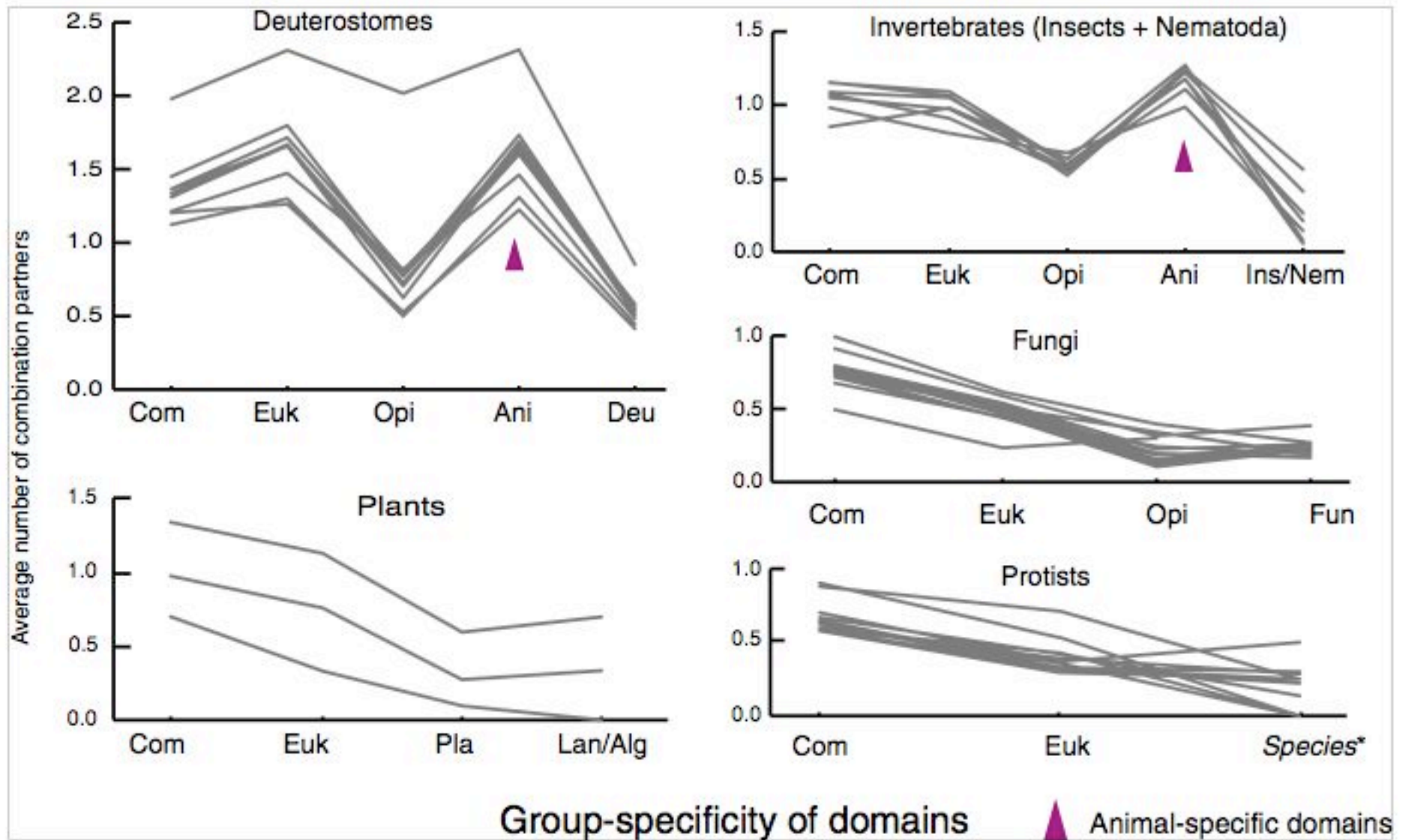
# Domain and its combination assignment to eukaryote proteomes

Category			Species	Specific domains (combinations)			Domains shared by prokaryotes			
Eukaryotes	Animals	Vertebrates	Mammals	<i>H. sapiens</i> <i>P. troglodytes</i> <i>M. musculus</i> <i>R. norvegicus</i> <i>C. familiaris</i>	116 (185)	*	235 (610)	407 (875)	**	1211 (225)
			Bird	<i>G. gallus</i>						
		Fishes	<i>D. rerio</i> <i>F. rubripes</i> <i>T. nigroviridis</i>	2 (40)						
		Ascidian	<i>C. intestinalis</i>	0 (188)						
		Insects	<i>D. melanogaster</i> <i>D. pseudoobscura</i> <i>A. gambiae</i> <i>A. mellifera</i> <i>B. mori</i>	22 (40)						
		Nematoda	<i>C. elegans</i> <i>C. briggsae</i>	73 (70)						
		Basidiomycetes	<i>C. neoformans</i> B-3501A <i>C. neoformans</i> JEC21	1 (10)						
	Fungi	Ascomycetes	<i>N. crassa</i> <i>M. grisea</i> <i>S. bayanus</i> <i>S. cerevisiae</i> <i>S. mikatae</i> <i>S. paradoxus</i> <i>K. lactis</i> <i>Y. lipolytica</i> <i>D. hansenii</i> <i>A. gossypii</i> <i>C. albicans</i> <i>C. glabrata</i> <i>S. pombe</i>	40 (46)	34 (55)	83 (70)	1439 (715)			
			Microsporidian	<i>E. cuniculi</i>	1 (0)					
			Amoebozoa	<i>D. discoideum</i> <i>E. histolytica</i>	5 (9)					
	Plants	Land plants	<i>C. hominis</i> <i>C. parvum</i> <i>P. falciparum</i> <i>P. yoelii</i> <i>T. annulata</i> <i>T. parva</i>	5 (9)						
			Euglenozoa	<i>L. major</i> <i>T. brucei</i> <i>T. cruzi</i>	4 (5)					
	Plants	Land plants	<i>A. thaliana</i> <i>O. sativa</i>	240 (178)	31 (30)					
		Red algae	<i>C. merolae</i>	8 (33)						
Prokaryotes										

Domain combination network shows a scale-free property

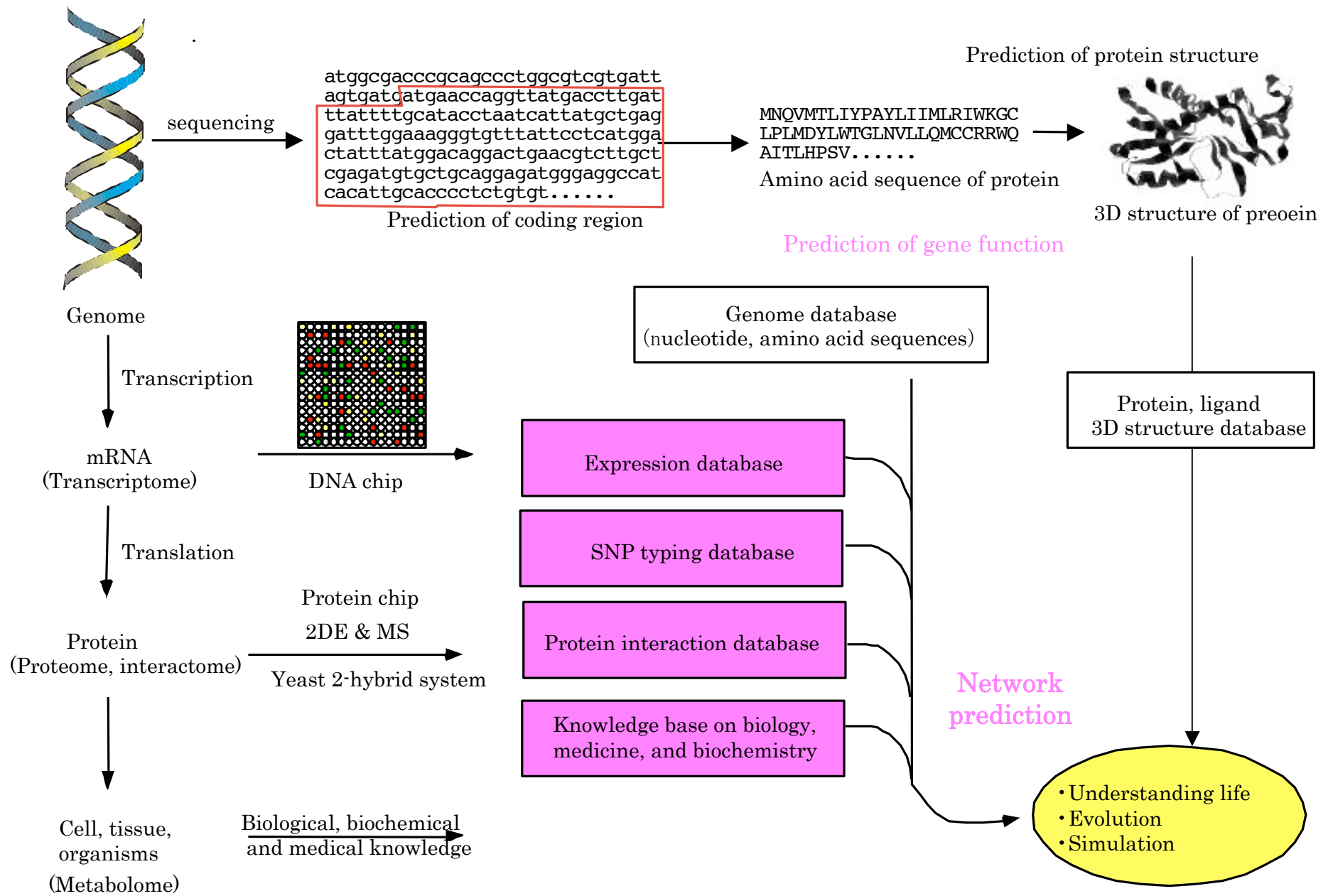


# Older domains have more partners with some exceptions



# Summary

- Importance of network in bioinformatics analysis
  - Function prediction
  - Domain network analysis
  - Functional modules in metabolic network
    - Yamada, et al. (2006) BMC Bioinformatics 7:130
    - Gutteridge, et al. (2007) BMC Bioinformatics 8:88
- What is Life?
  - What is not life?
    - What is or is not used in biological system in terms of protein network, domain network?



# Acknowledgement

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