Pathways, Networks and Systems

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Number of papers

	Submitted	Accepted	Percentage
Long	44	6	14%
Short	19	2	11%
Total	63	8	13%

Categorization of submitted papers

Network Structures   9

- Subgraph comparison (2)
- Graph kernel (1)
- Clustering (1)
- Scale-free, global topology (4)
- Visualization tool (1)

Network Inference   32

- Expression data (11)
- Proteomic data (5)
- Integrated data (4)
- Text data (1)
- Other data (5)
- Metabolic reconstruction (4)
- Database (2)

Network Dynamics   22

- Representation and reasoning (3)
- Modeling and simulation, biology (3)
- Modeling and simulation, methods (10)
- Metabolic flux analysis (4)
- Simulation tools (2)

Network structure analysis
 Graph comparison
  Chemical compound structure comparison
  Glycan structure comparison
  Pathway comparison
 Graph kernel
 Clustering
  Co-expression cluster
  Ortholog cluster
 Network computation
 Network modules
 Scale-free network

Network inference
  Chemical reaction network
    Reaction path prediction
    Metabolic reconstruction
  Gene regulatory network (from expression data)
    Boolean network
    Bayesian network
    Graphical Gaussian modeling
    S-system
    Differential equation models
  Protein ineraction network (from proteomic data)
    Comparative genomics
    Probabilistic models
    Kernel statistical analysis

Simulation

    Dynamics of molecular networks

        Biochemical systems theory

        Biochemical reaction simulation

        Genetic circuit analysis

        Metabolic flux analysis

        Probabilistic modeling

        Cell simulation

    Systems analysis

        Robustness analysis

        Systems of differential equations

        Metabolic control analysis

        Metabolic flux balance analsis

Network Structures

Local structural features

Long Paper #62
Mehmet Koyutürk, Ananth Grama, and Wojciech Szpankowski
An efficient algorithm for detecting frequent subgraphs in biological networks

Global structural features

Short Paper #56
Teresa Przytycka and Yi-Kuo Yu
Divergent evolutionary drift contradicts power law

Graph kernel

Long Paper #50
Koji Tsuda and William Stafford Noble
Learning kernels from biological networks by maximizing entropy

Network Inference

Integration - kernel method

Long Paper #50
Yoshihiro Yamanishi, Jean-Phillipe Vert, and Minoru Kanehisa
Protein network inference from multiple genomic data: a supervised approach

Expression data - probabilistic model

Long Paper #54
Iftach Nachman, Aviv Regev, and Nir Friedman
Inferring quantitative models of regulatory networks from expression data

Expression data - metabolic reconstruction

Long Paper #60
Peter Kharchenko, Dennis Vitkup, and George M. Church
Filling gaps in a metabolic network using expression information

Network Dynamics

Modeling and simulation

Short Paper #59
Tomer Shlomi and Eytan Ruppin
Constraint-based modelling of perturbed organisms: a ROOM for improvement

Representation and reasoning

Long Paper #64
Chitta Baral, Karen Chancellor, Nam Tran, Nhan Tran, Anna Joy, and Michael Berens
A knowledge based approach for representing and reasoning about signaling networks
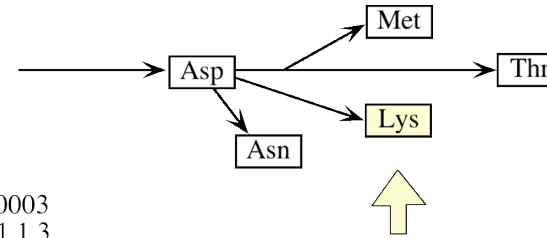

Database

Long Paper #56
Naohiko Heida, Yoshikazu Hasegawa, Yoshiki Mochizuki, Katsura Hirosawa, Akihiko Konagaya, and Tetsuro Toyoda
TraitMap: an XML-based genetic-map database combining multigenic loci and biomolecular networks
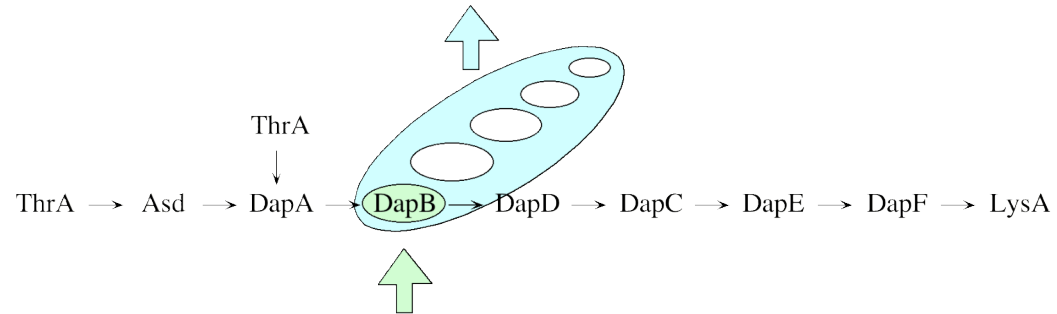
Level of Abstraction

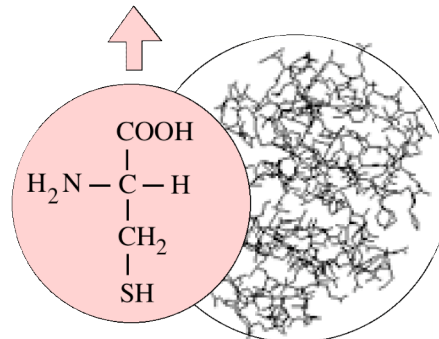**Network Levels**

(Pathway module network)

(Generic pathway)
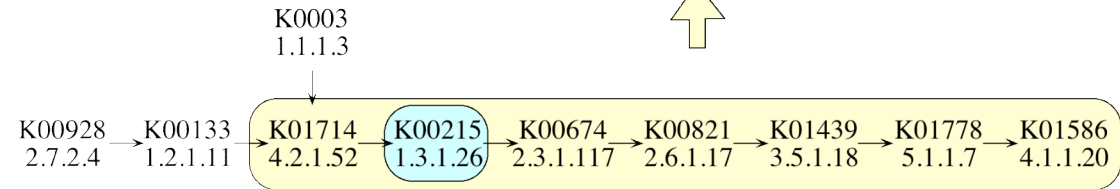
(Organism-specific pathway)

Sequence Level

Atomic Level

BRITE Inference
Network modules for inferring higher-order functions

N01100 Metabolism
 N01110 Carbohydrate Metabolism
  N00010 Glycolysis / Gluconeogenesis
  N00020 Citrate cycle (TCA cycle)
   M00021 Acetyl CoA + Oxaloacetate <--> 2-Oxo-glutarate
    K01647 citrate synthase [EC:2.3.3.1]
    K01681+K01682
    K00031 isocitrate
   M00022 2-Oxo-glu
    K00164 2-oxoglut
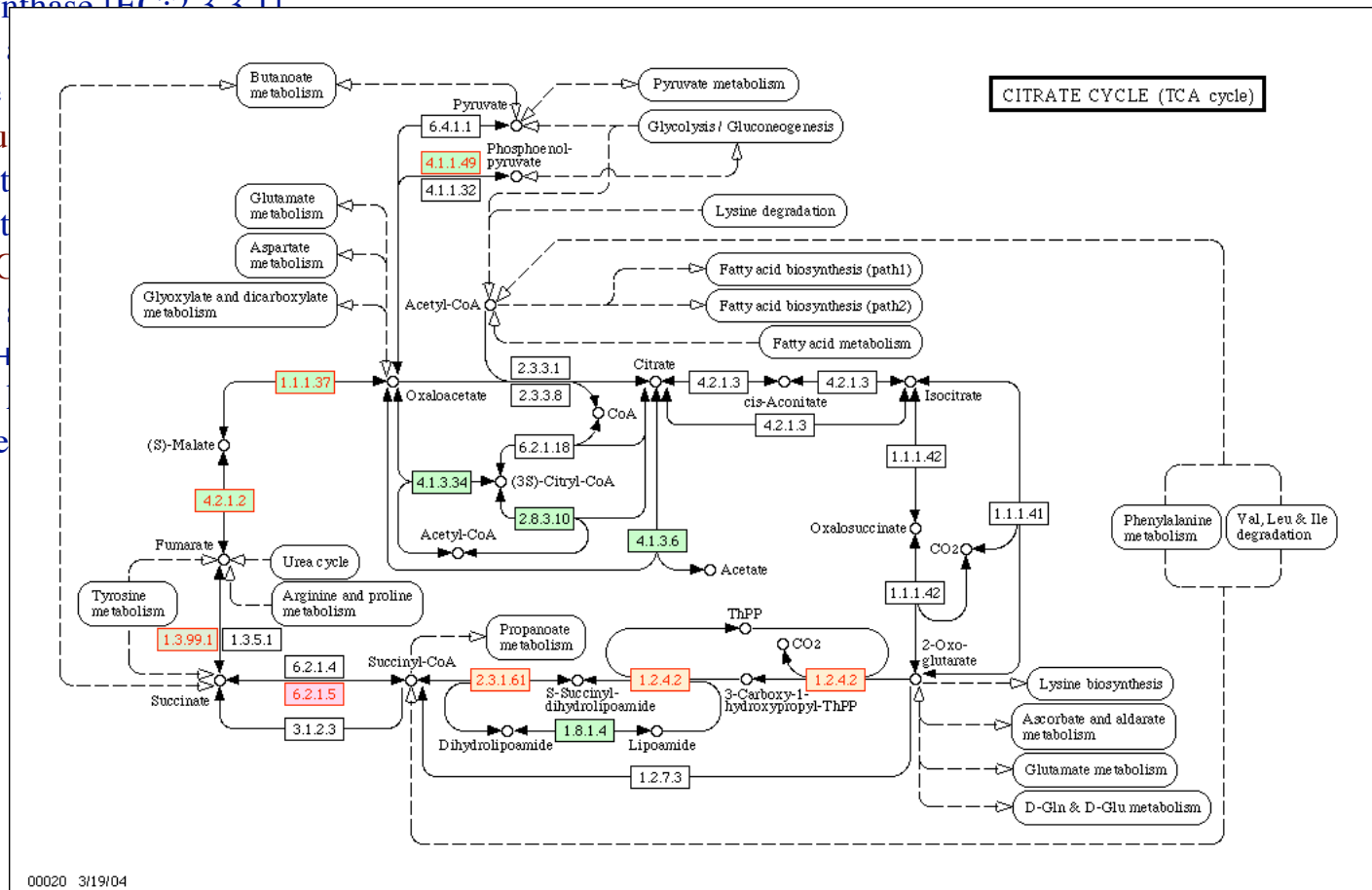   K00658 2-oxoglut
   M00023 Succinyl C
    K01902+K01903
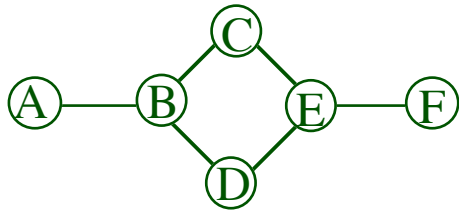   K00239+K00240+
    K01675 fumarate
    K00024 malate de

- Genome comparisons
- Co-expression information (operons, etc.)
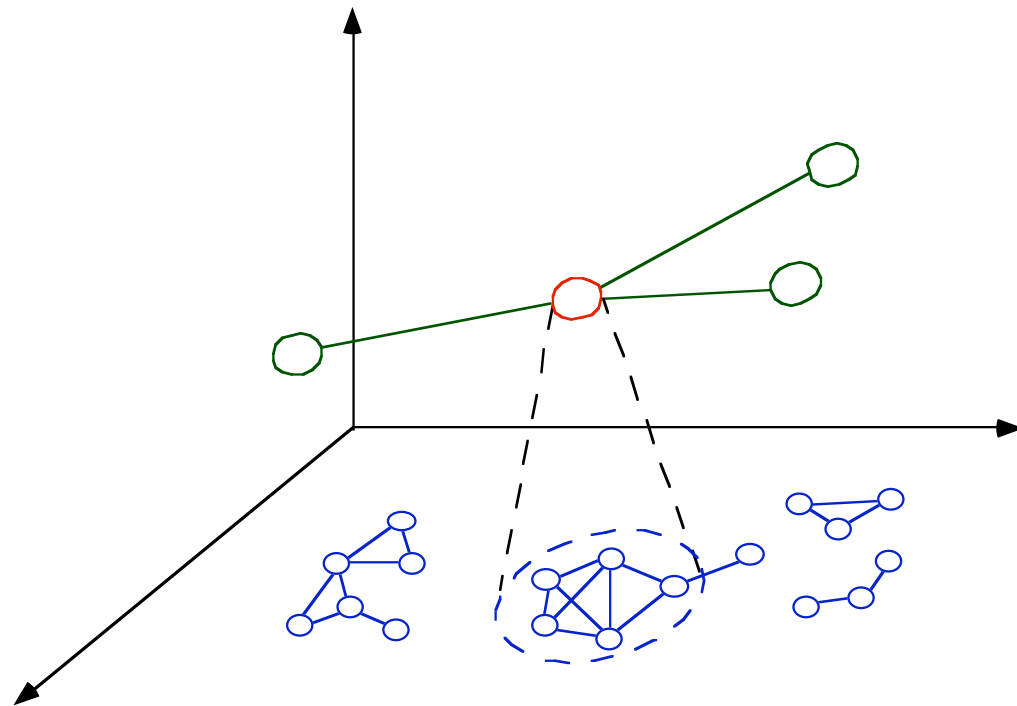- Continuous reaction steps between main compounds

Basic Concept (1)

Graph = Set of nodes and edges
        = Set of binary relations
Nested graph = Graph whose nodes can themselves be graphs
        → Level of abstraction, Ontology, Inference

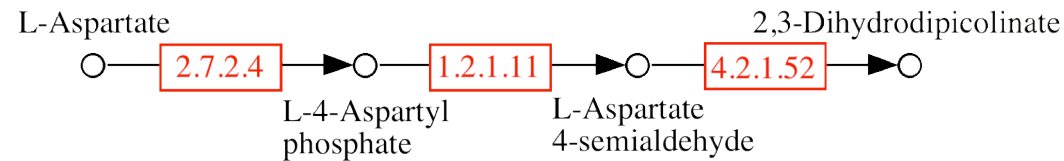|	A	B	C	D	E	F
A						
B	1					
C	0	1				
D	0	1	0			
E	0	0	1	1		
F	0	0	0	0	1	

Basic Concept (2)

Line graph = Graph derived by interchanging nodes and edges
→ Integration of genomics and chemistry

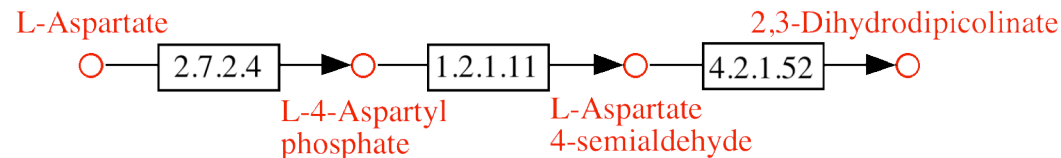Metabolic networks can be viewed in two complementary ways

Gene network (Protein network)
• nodes: enzymes (gene products), edges: compounds

Chemical network
• nodes: compounds, edges: enzymes (reactions)

Graph-based Integration of Complex Biological Objects

Networks
- Known pathway (such as in KEGG maps)
- Co-expression relations by microarray experiments
- Protein interaction data by two hybrid experiments
- Ortholog relations by comparative genomics
- Gene relations by synthetic lethal experiments

Structures
- 3D molecular structures
- 2D chemical structures
- Molecular sequences (nucleotide, amino acid, and carbohydrate)
- Gene orders on the chromosome

Kernel-based Integration of Complex Biological Objects

Kernel function

$$K(x, y) = f(x) \cdot f(y)$$

similarity measure of two objects x and y
obtained by mapping to the feature space f

Kernels for:
- Real-valued vectors - polynomial kernel, RBF kernel
- Strings (sequence)
- Trees (phylogenetic tree, glycan structure)
- Graphs (networks, compound structure)