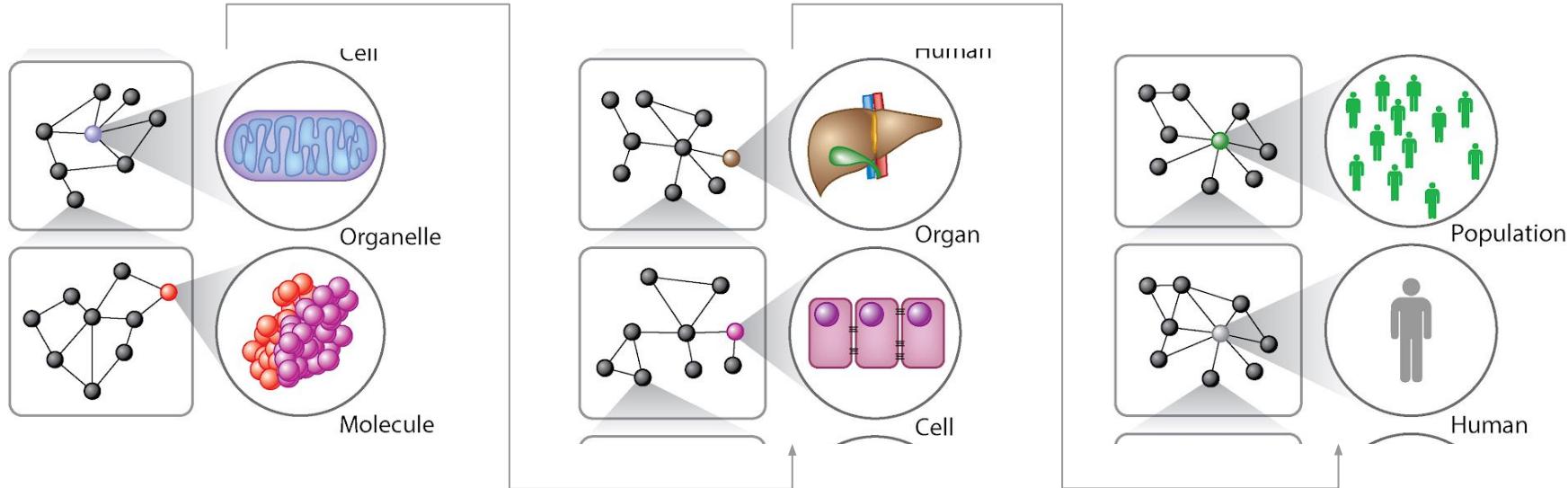


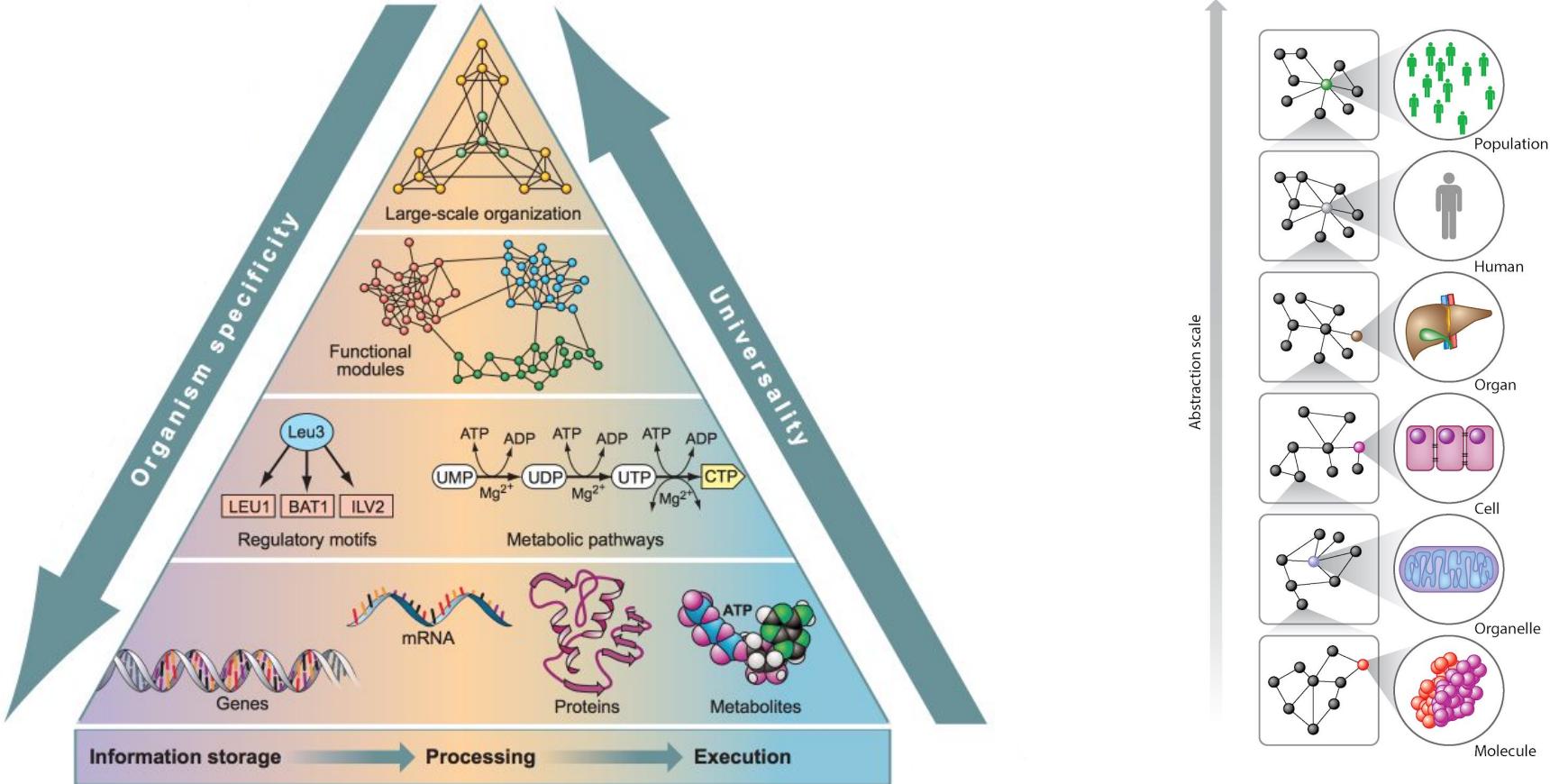
Large-scale biological networks

- Network topology
- Network motifs
- Condition-specific networks
- Network reconstruction
- Network propagation

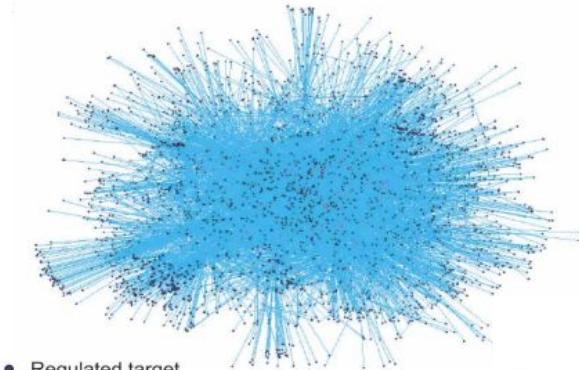
Layers of complexity and Network representations



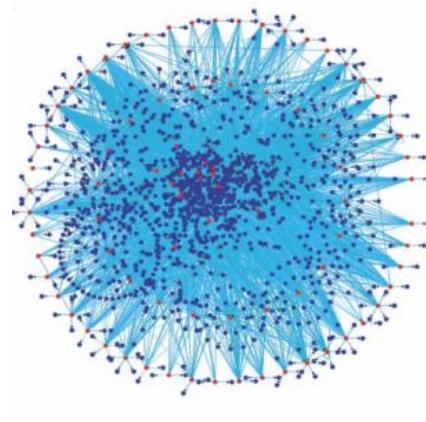
Layers of complexity and Network representations



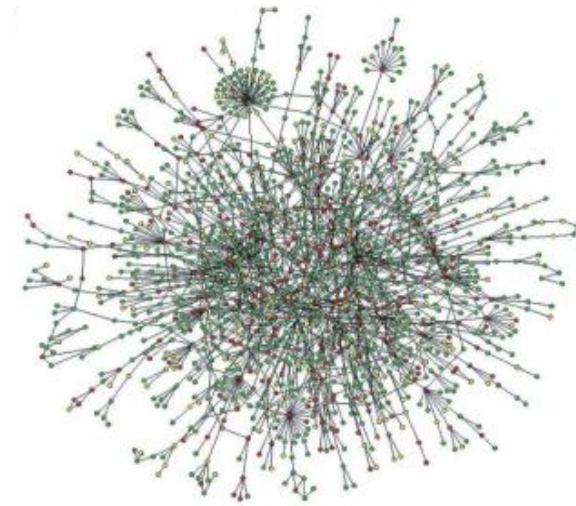
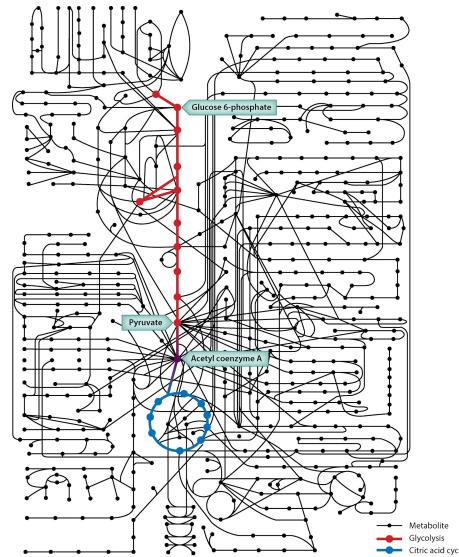
Molecular networks



- Regulated target
- Transcription factor

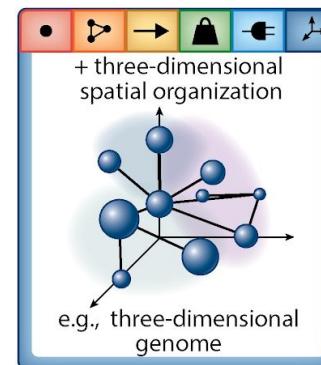
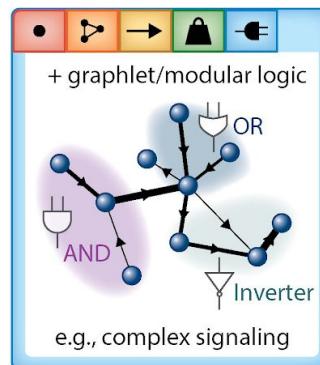
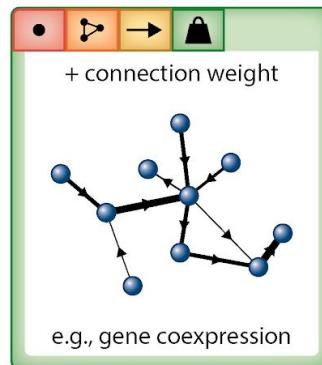
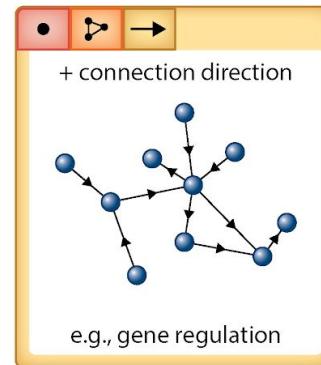
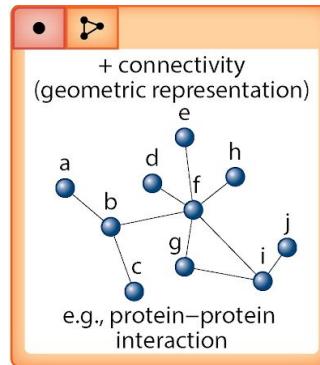
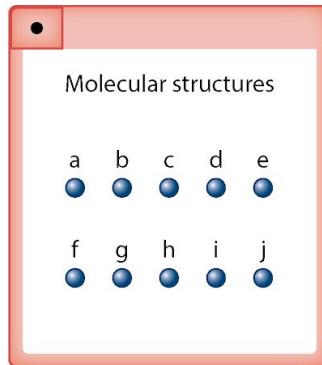


- Kinase
- Regulated target

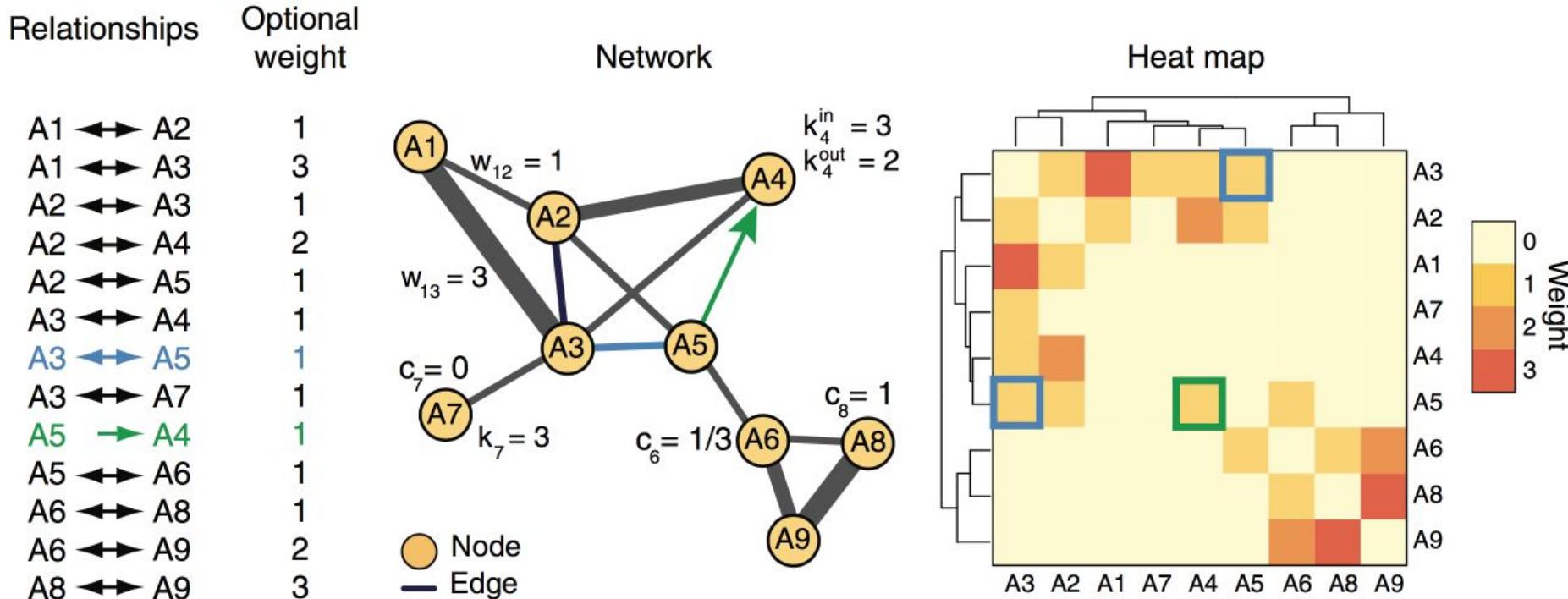


- Lethal
- Slow growth
- Unknown
- Non-lethal

Network description

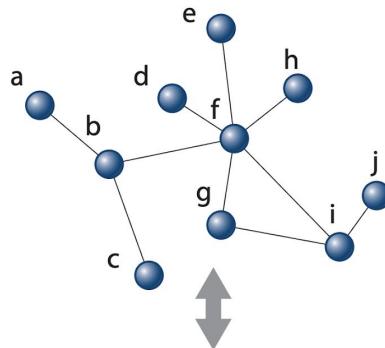


Network representations



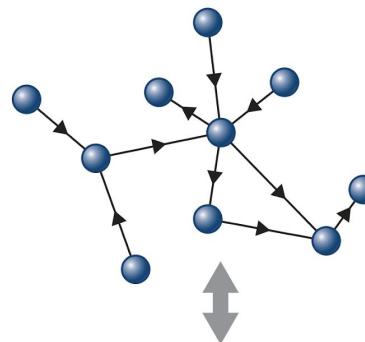
Network representations

Connectivity
e.g., protein–protein interaction



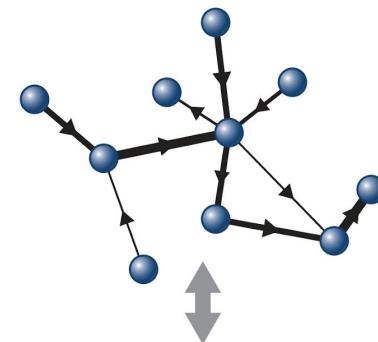
a	b	c	d	e	f	g	h	i	j
a	1								
b	1	1							
c	1								
d			1						
e				1					
f	1	1	1	1	1	1			
g				1					
h					1				
i						1	1		
j								1	

Connection direction
e.g., gene regulation



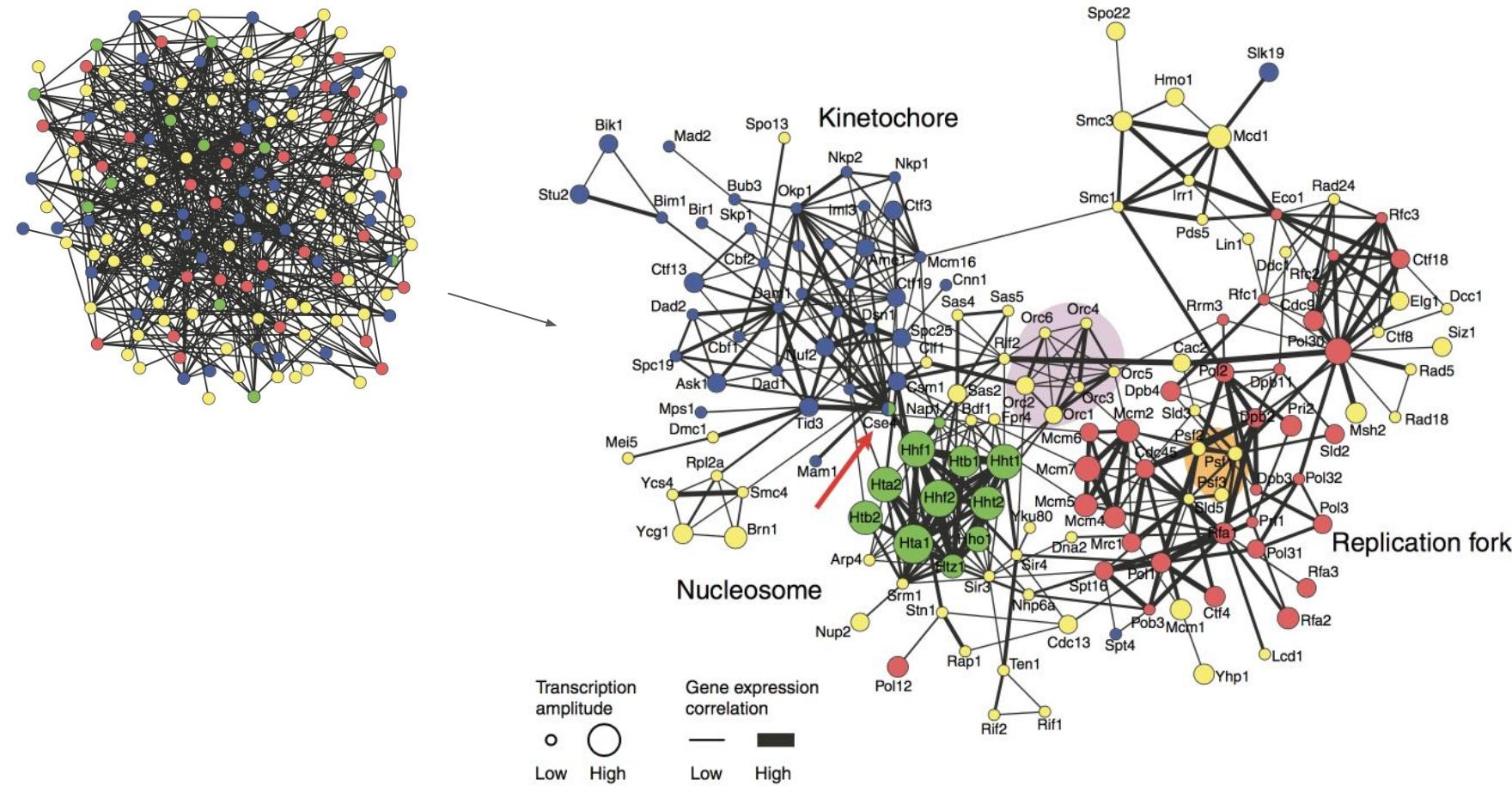
a	b	c	d	e	f	g	h	i	j
a	1								
b									
c	1								
d									
e									
f					1	1	1		
g						1			
h							1		
i								1	
j									

Connection weight
e.g., gene coexpression



a	b	c	d	e	f	g	h	i	j
a	3								
b									
c	1								
d									
e									
f					1	1	1		
g						1			
h							1		
i								1	
j									4

Network layout

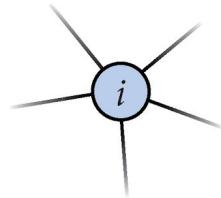


Network topology

Degree

$$d_i$$

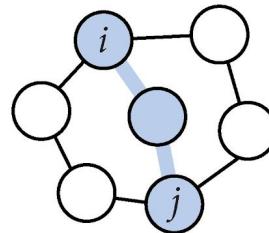
Number of nodes bound to node i



Shortest path distance

$$d_{ij} = \min\{|e_p| \subset E_{ij}\}$$

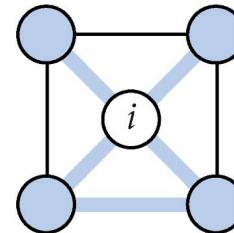
E_{ij} : all edge sets connecting nodes i and j



Clustering coefficient

$$c_i / \binom{n_i}{2}$$

c_i : edges connecting all n_i nodes bound to i

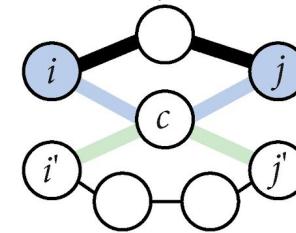


Betweenness centrality

$$b_c = \sum_i \sum_j I_{ij}/s_{ij}$$

s_{ij} : total number of shortest paths between i and j

I_{ij} : 1 if c is within path; 0 otherwise



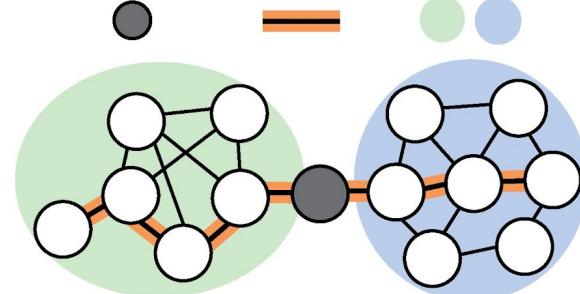
Bottleneck



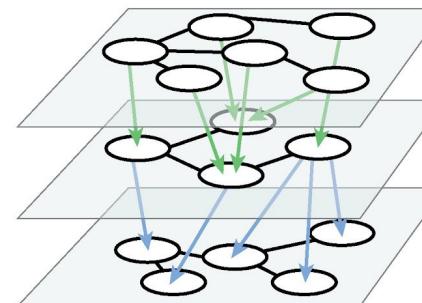
Diameter



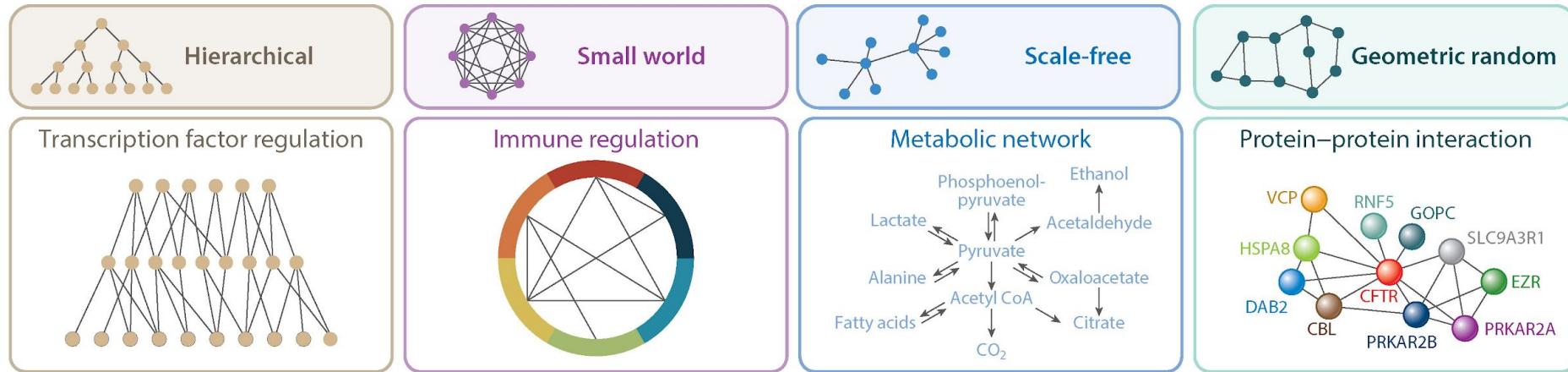
Modules



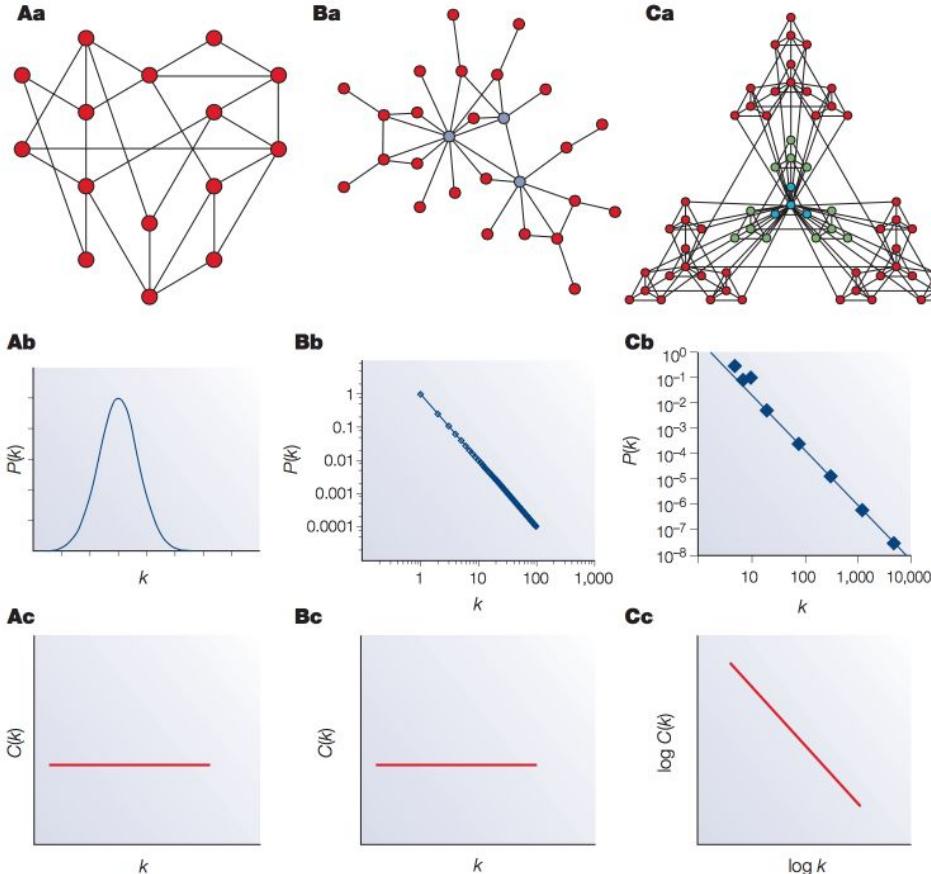
Network hierarchy



Large-scale network topology

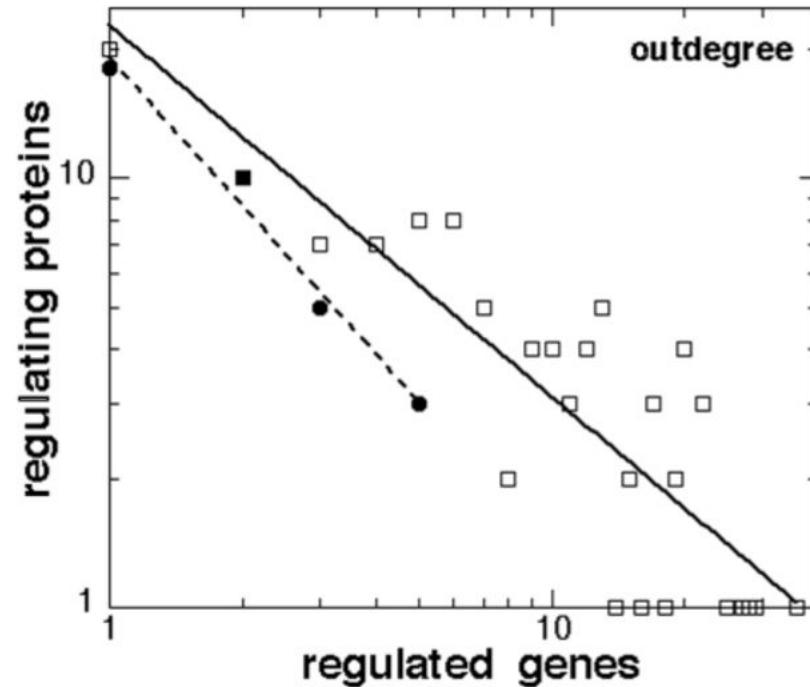
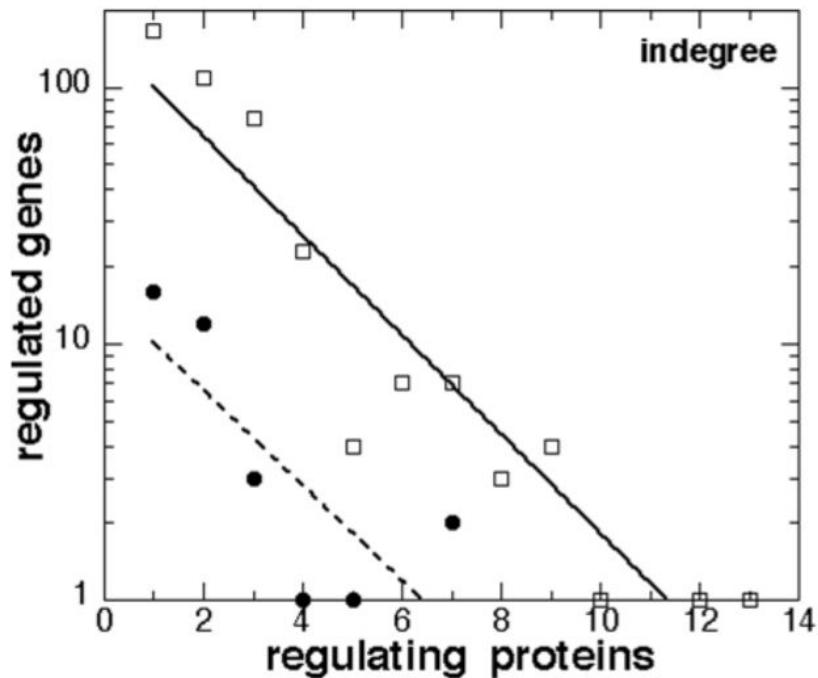


Network topology

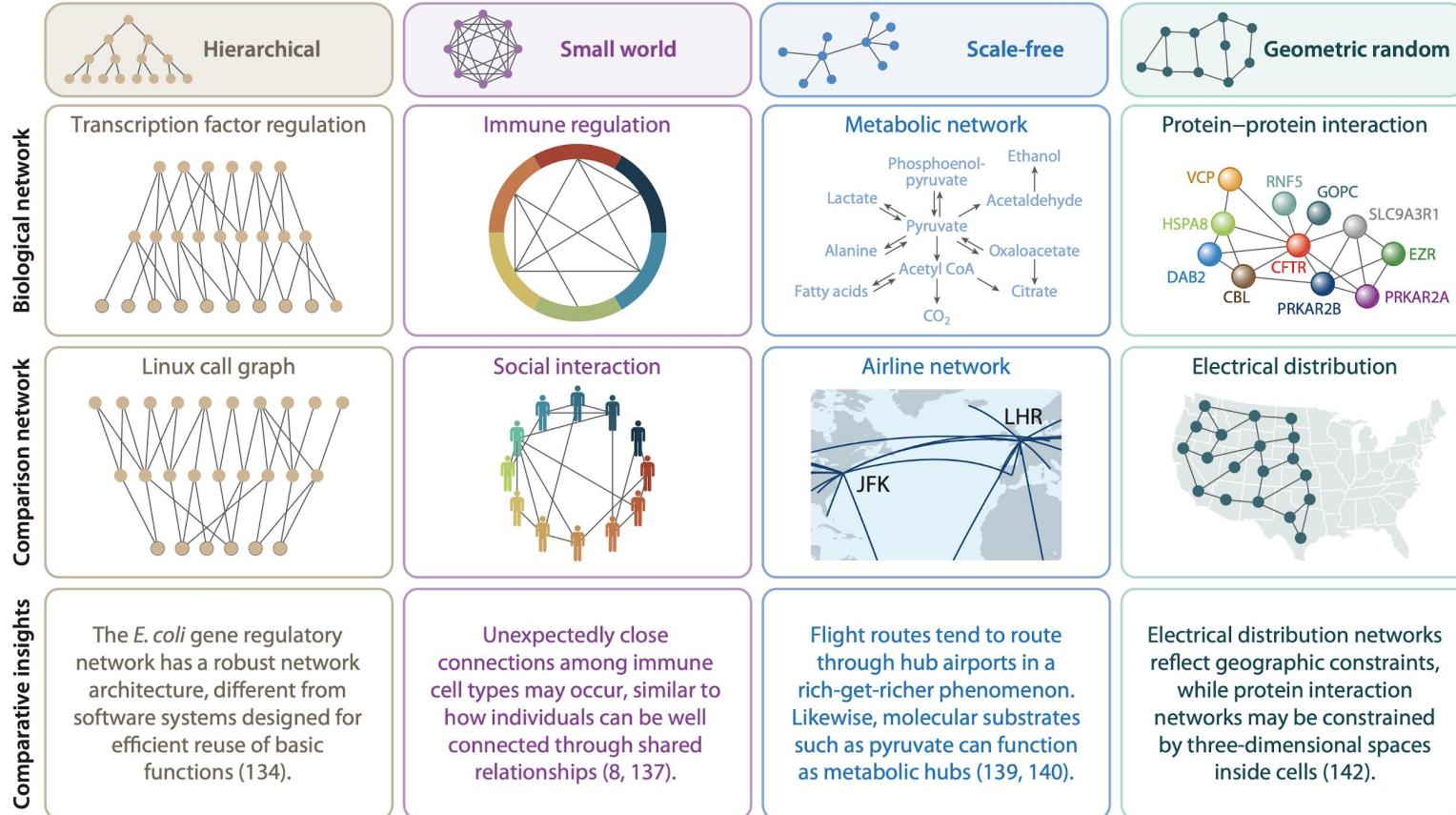


Network topology

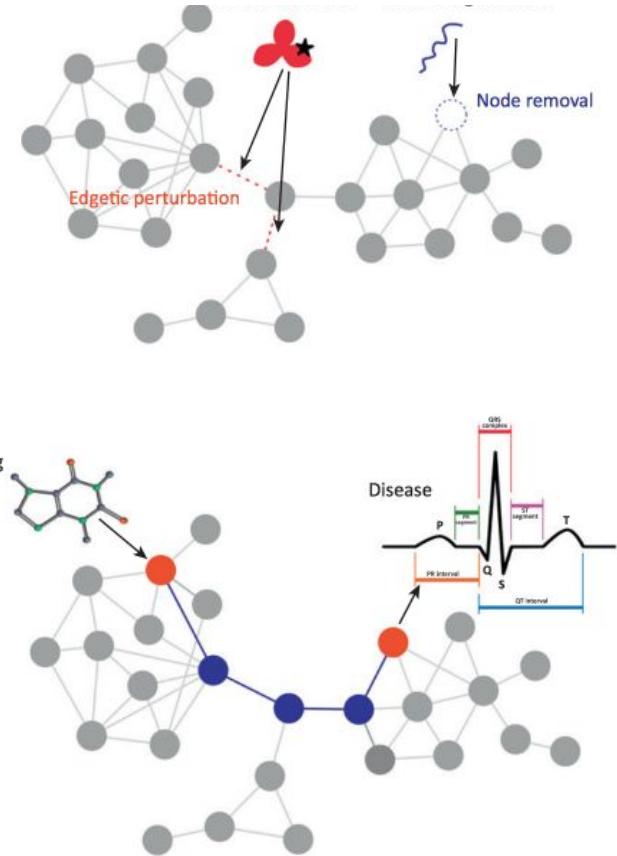
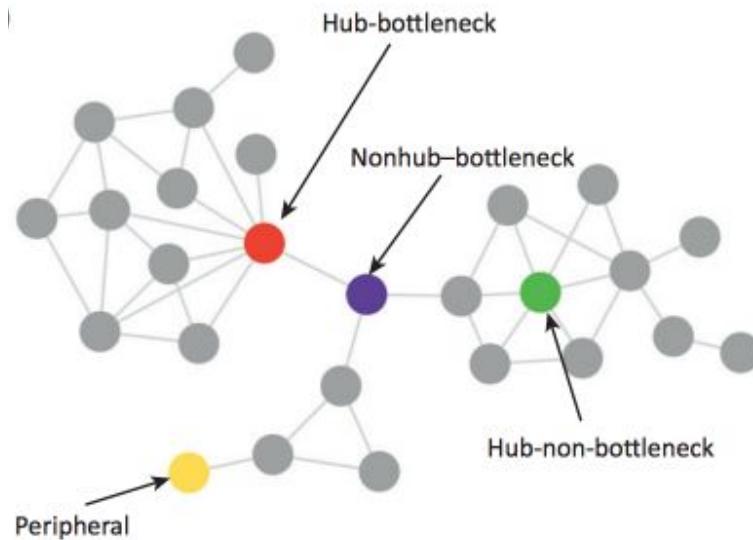
Yeast TF-target network



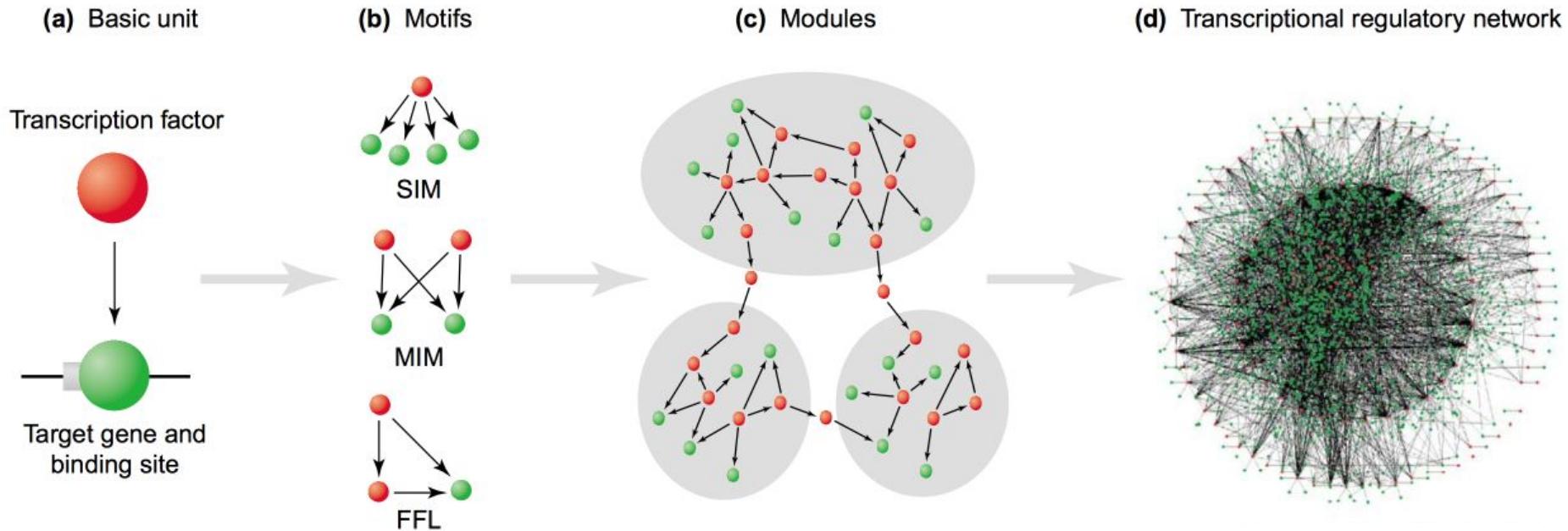
Network topology



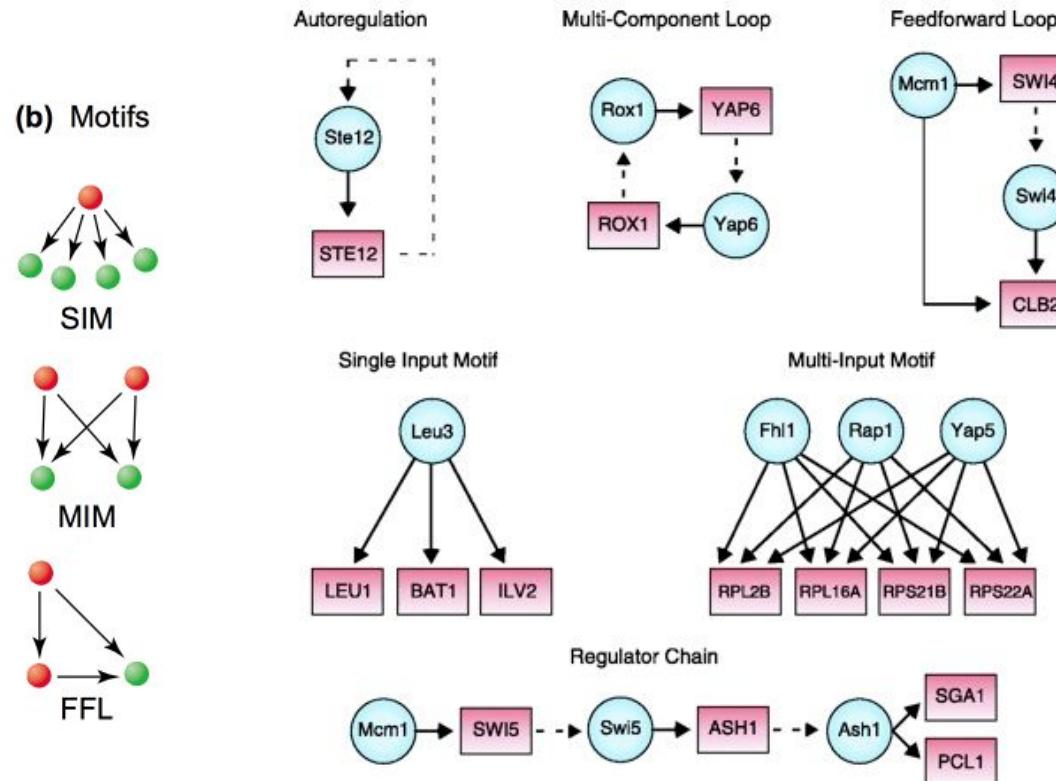
Network topology



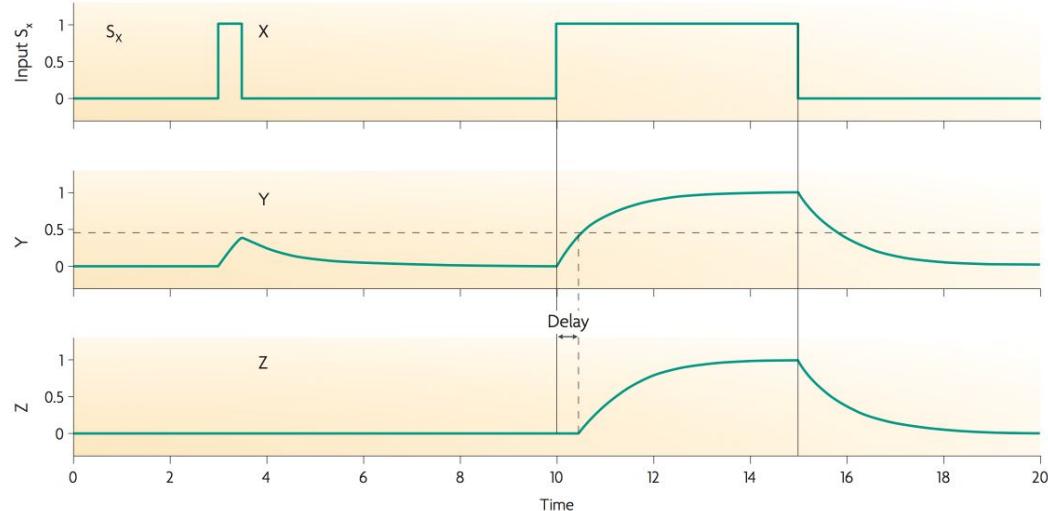
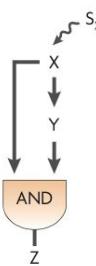
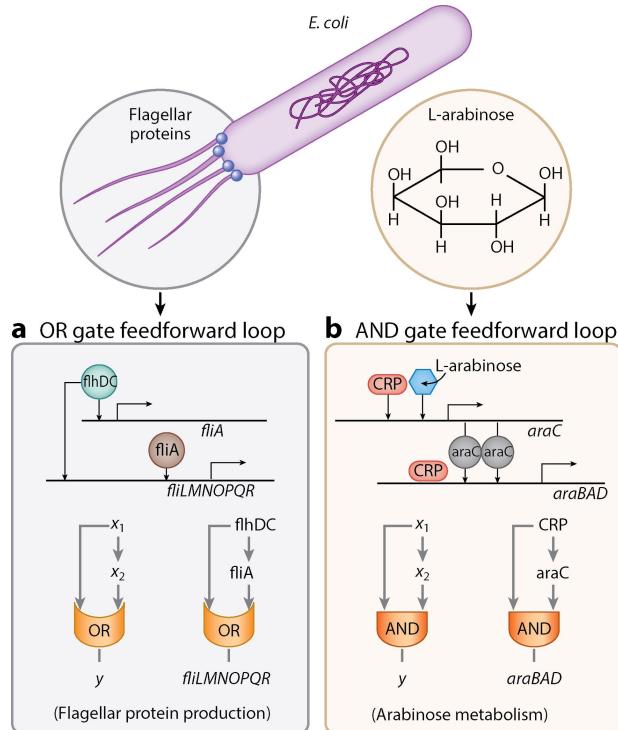
Network motifs



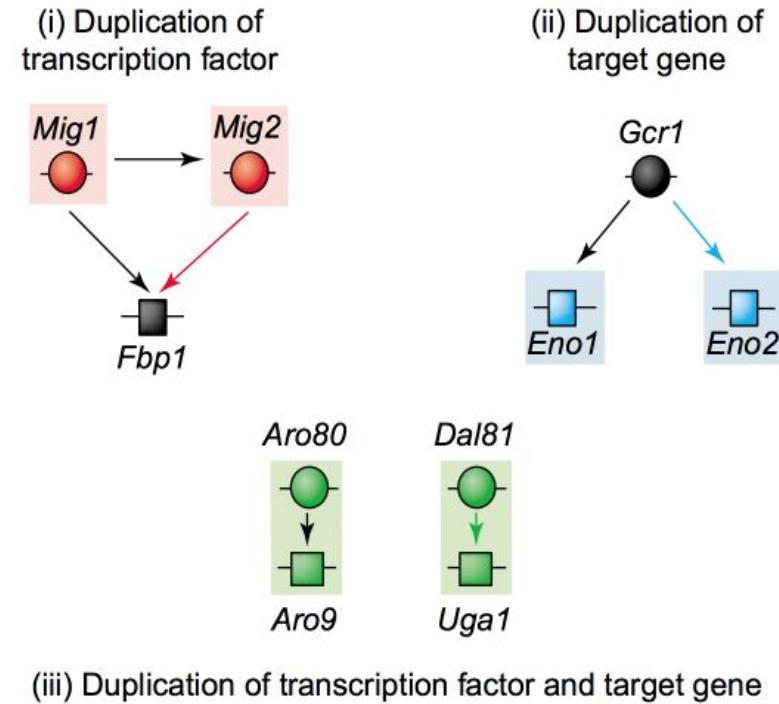
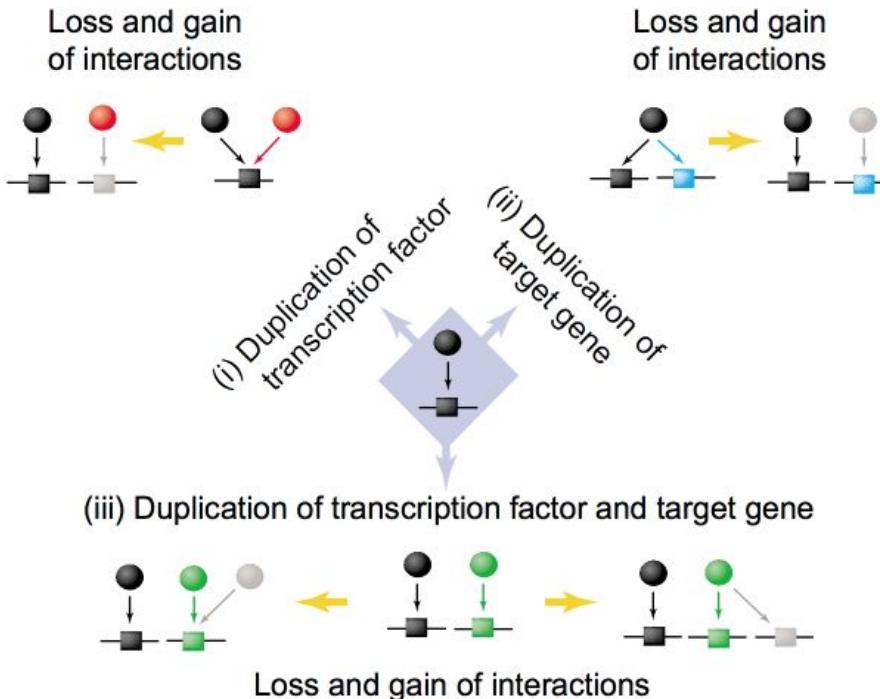
Network motifs



Network motifs

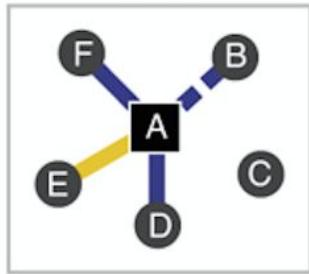


Network interactions evolve through time

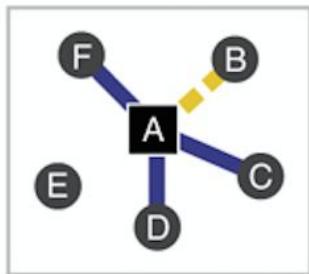


Network interactions are condition-specific

Condition ①



Condition ②



Interaction magnitude

Weak Significant

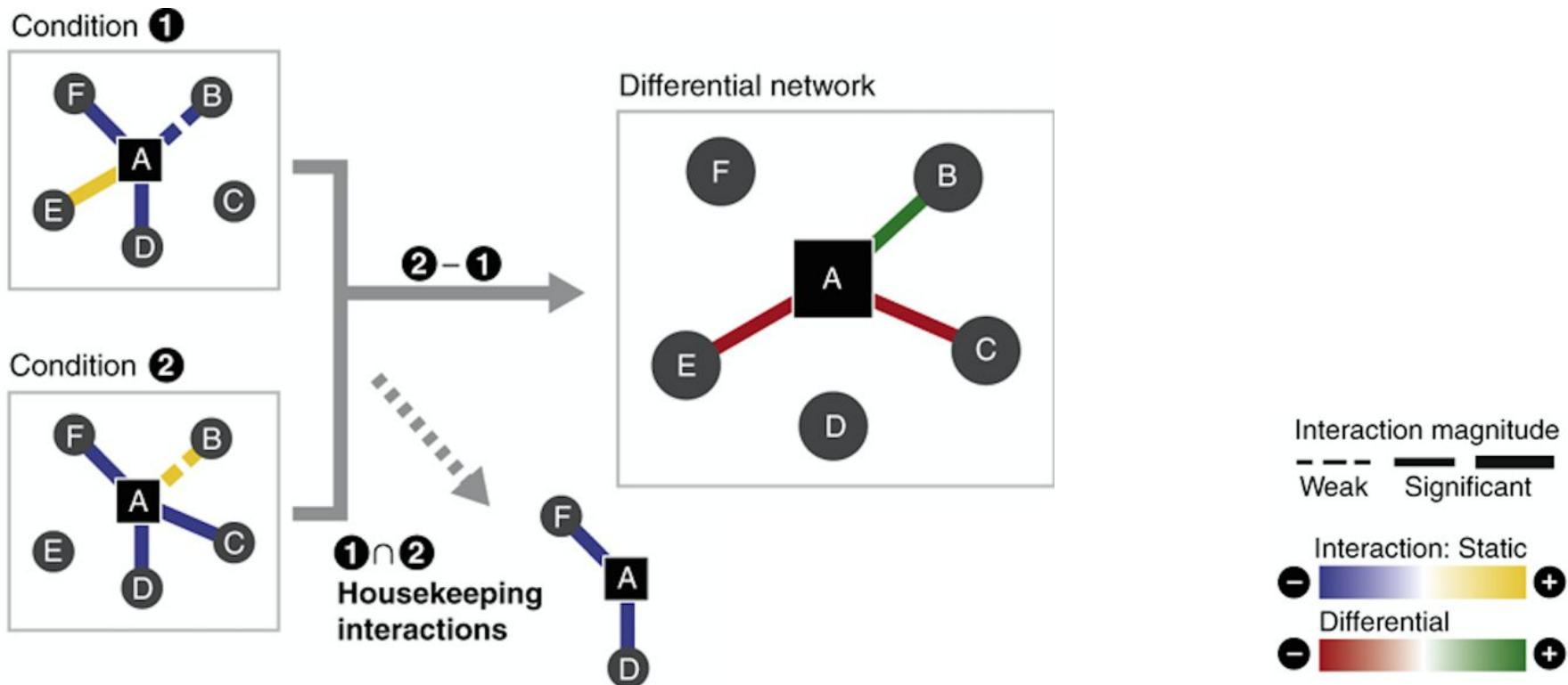
Interaction: Static

- +

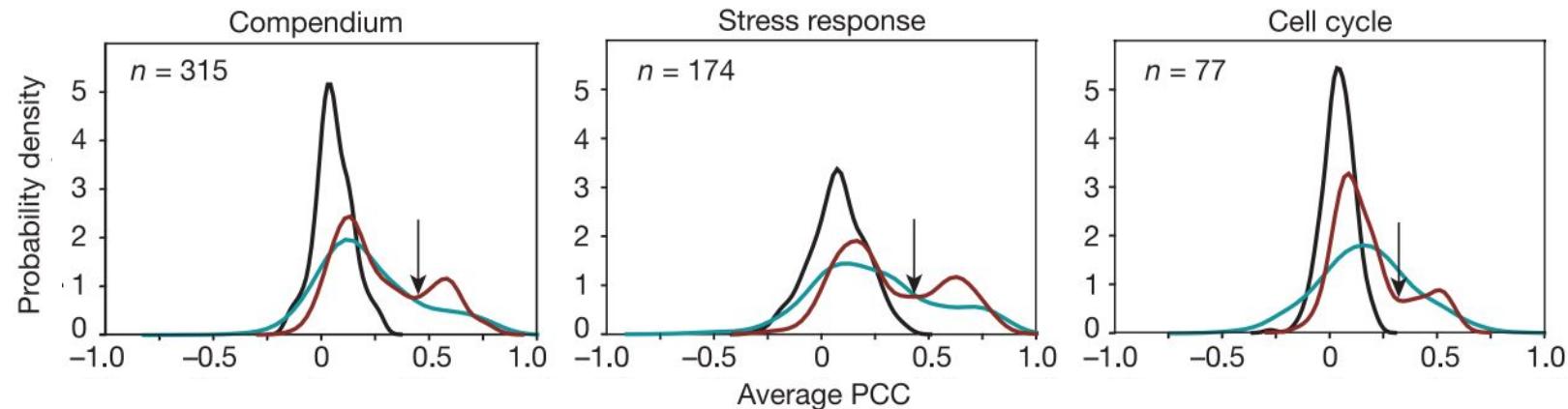
Differential

- +

Network interactions are condition-specific



Network interactions are condition-specific

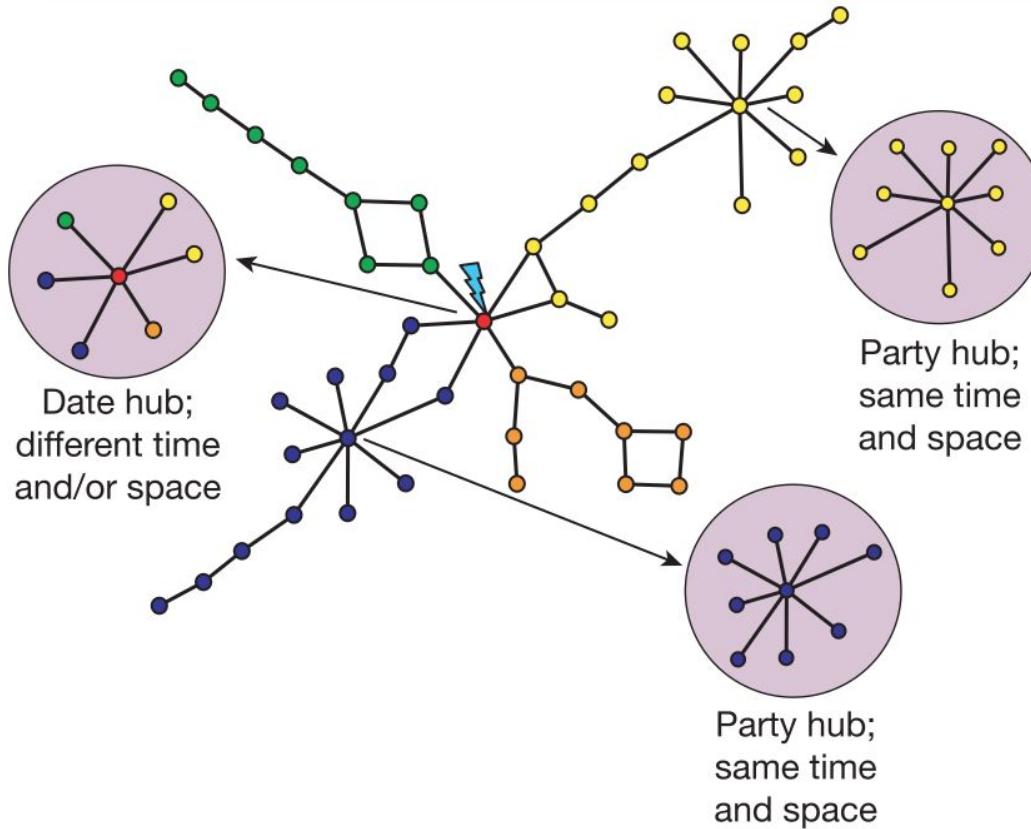


Red: Hub proteins

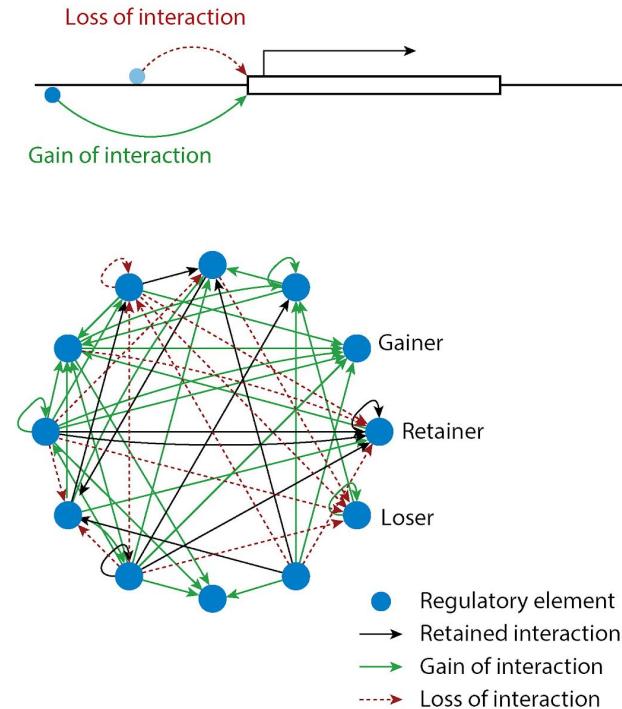
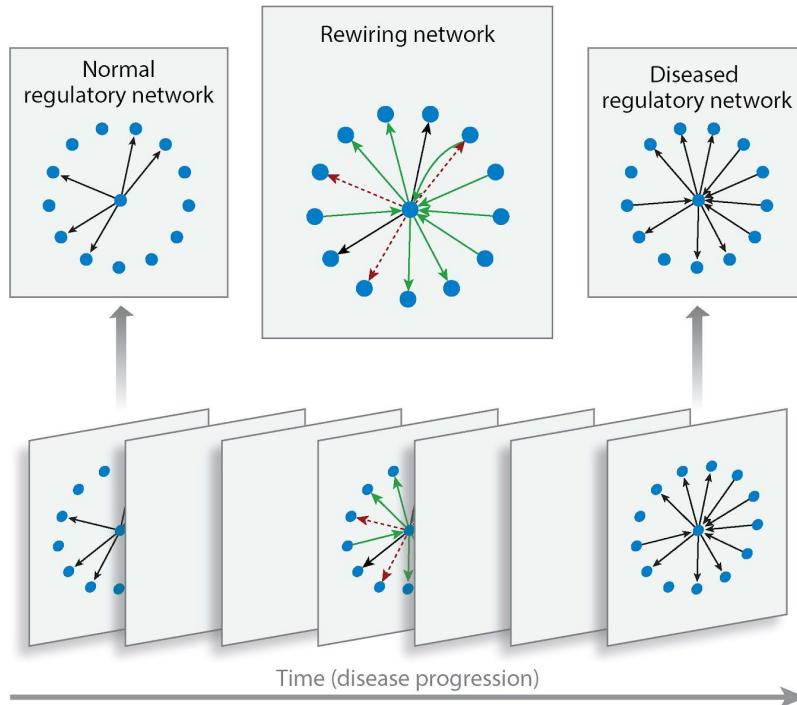
Cyan: Non-hub proteins

Black: Hubs in randomized networks

Network interactions are condition-specific



Network interactions are condition-specific



Network interactions are condition-specific

