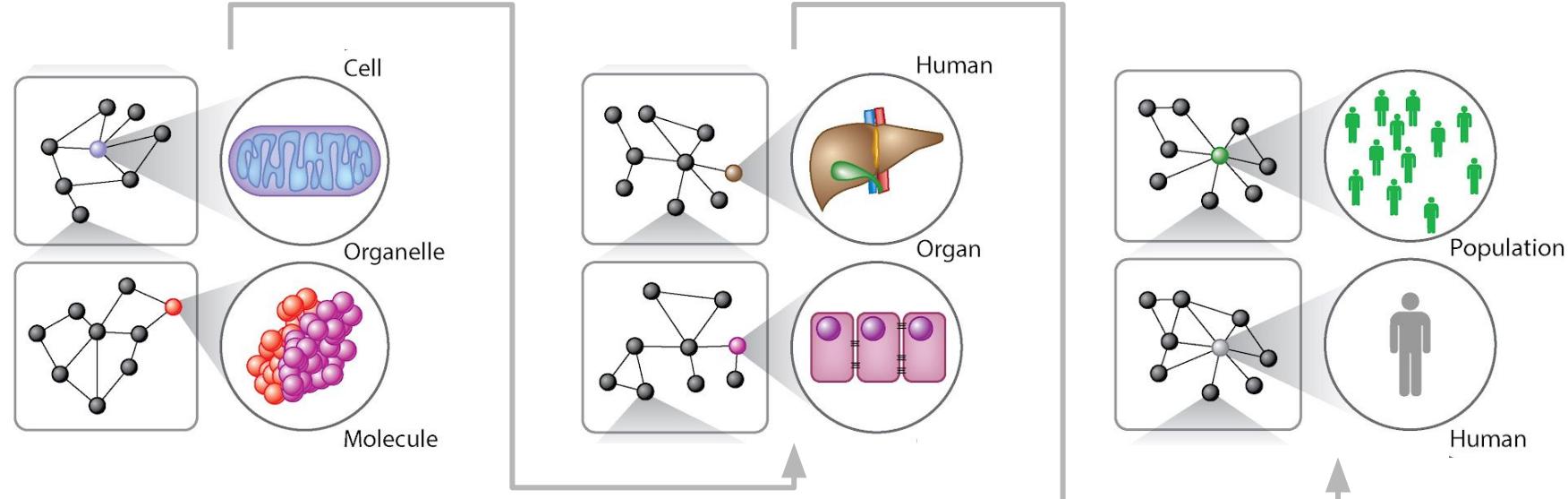


# Large-scale biological networks

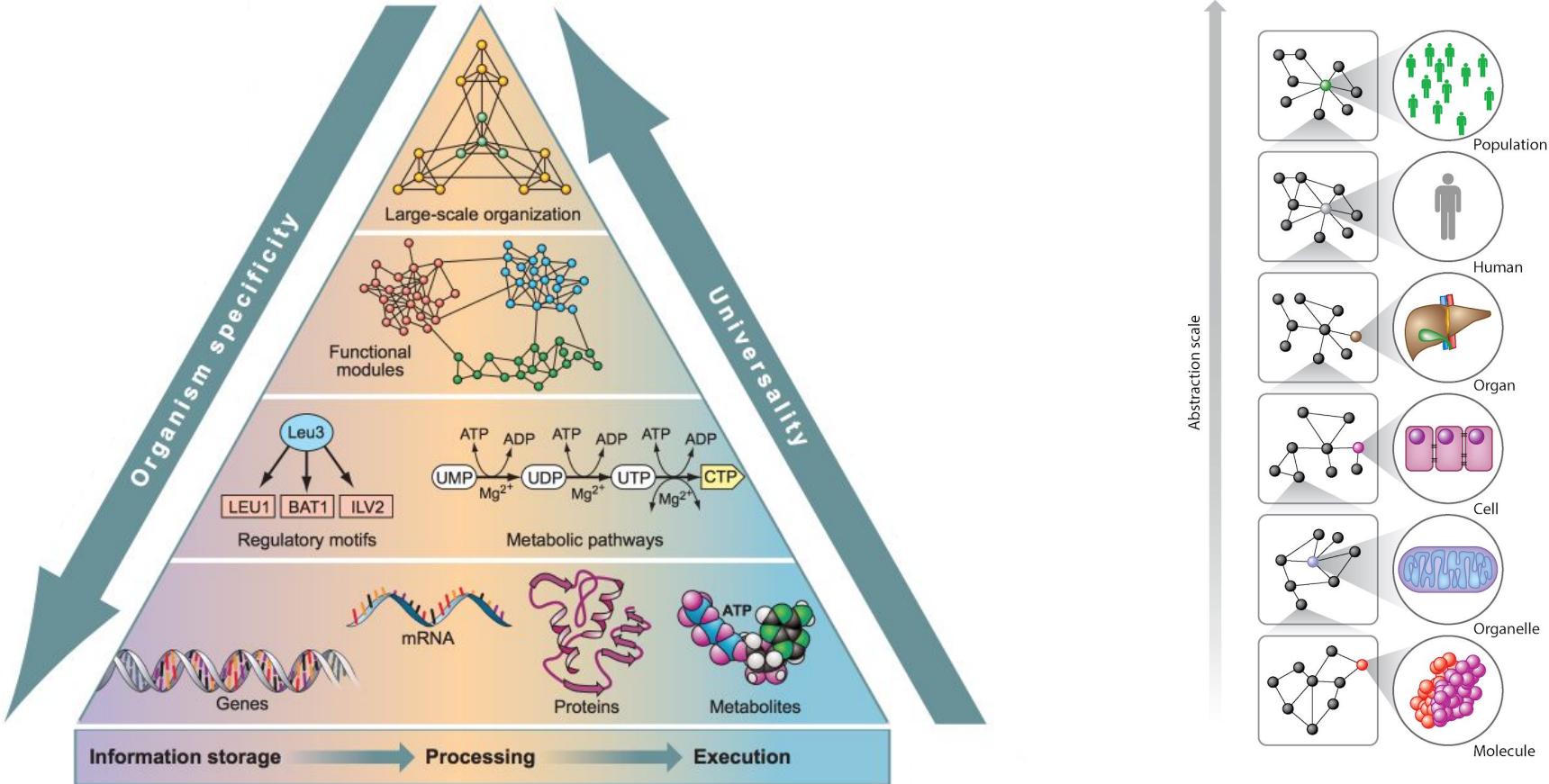
Network ...

- Topology
- Motifs
- Rewiring
- Reconstruction
- Propagation

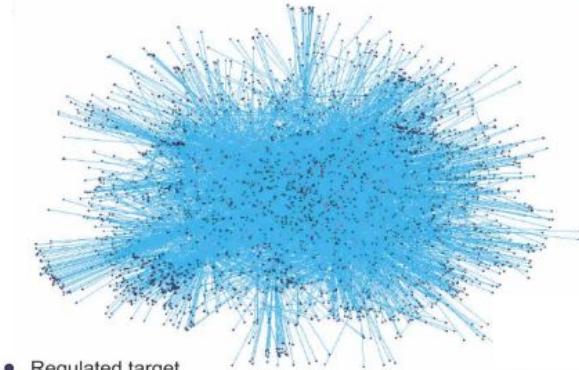
# Layers of complexity and Network representations



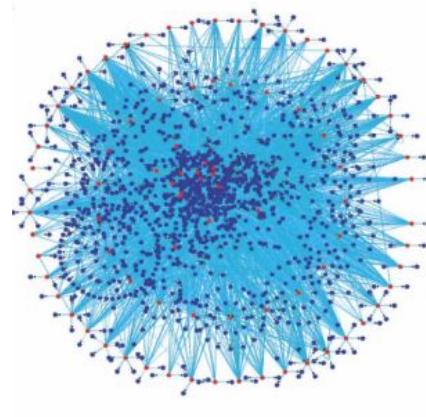
# Layers of complexity and Network representations



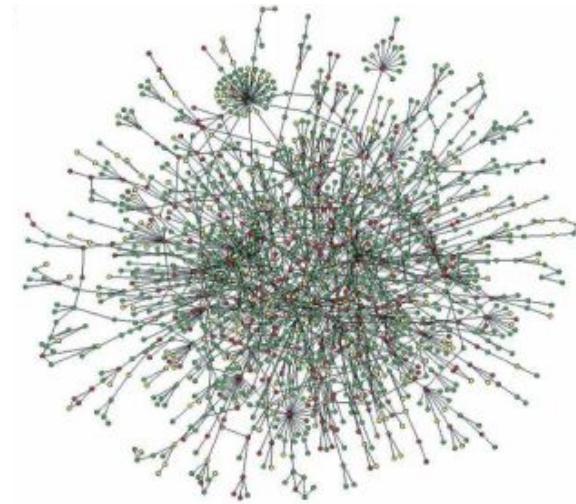
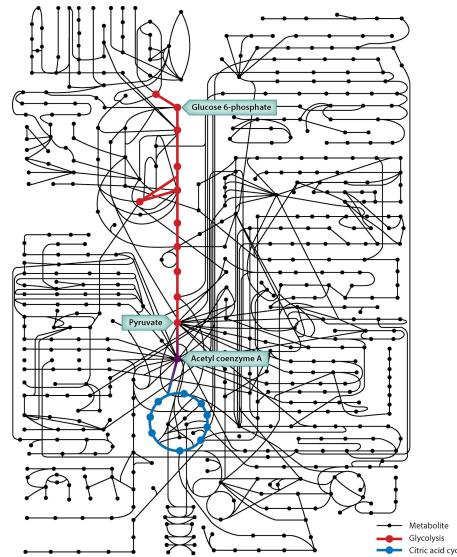
# Molecular networks



- Regulated target
- Transcription factor

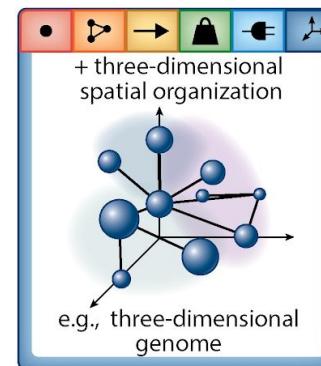
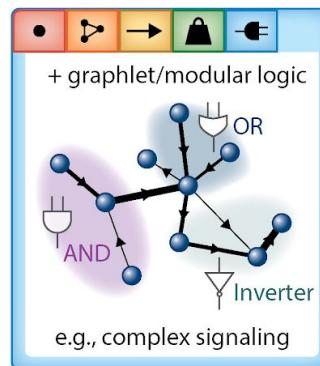
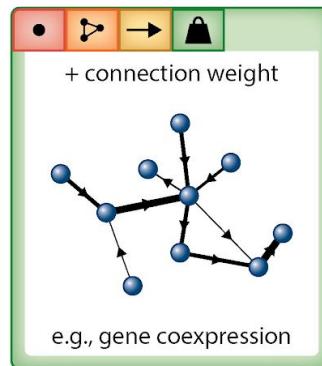
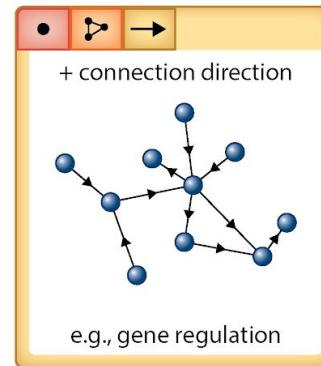
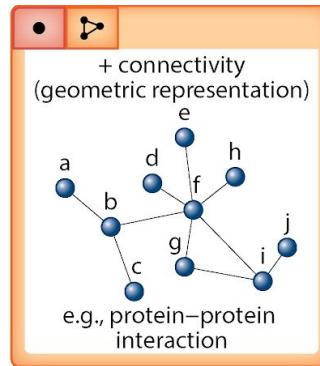
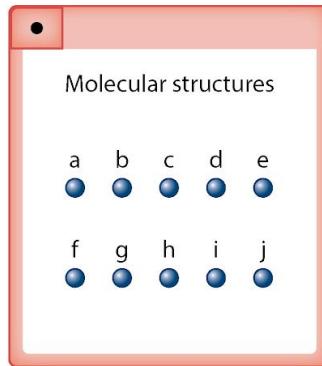


- Kinase
- Regulated target



- Lethal
- Slow growth
- Unknown
- Non-lethal

# Network description



# Network representations

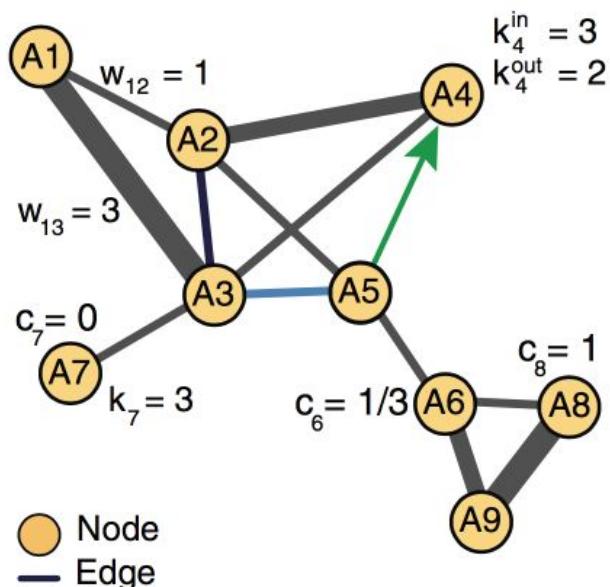
Edge list

Relationships    Weights

A1	↔	A2	1
A1	↔	A3	3
A2	↔	A3	1
A2	↔	A4	2
A2	↔	A5	1
A3	↔	A4	1
A3	↔	A5	1
A3	↔	A7	1
A5	→	A4	1
A5	↔	A6	1
A6	↔	A8	1
A6	↔	A9	2
A8	↔	A9	3

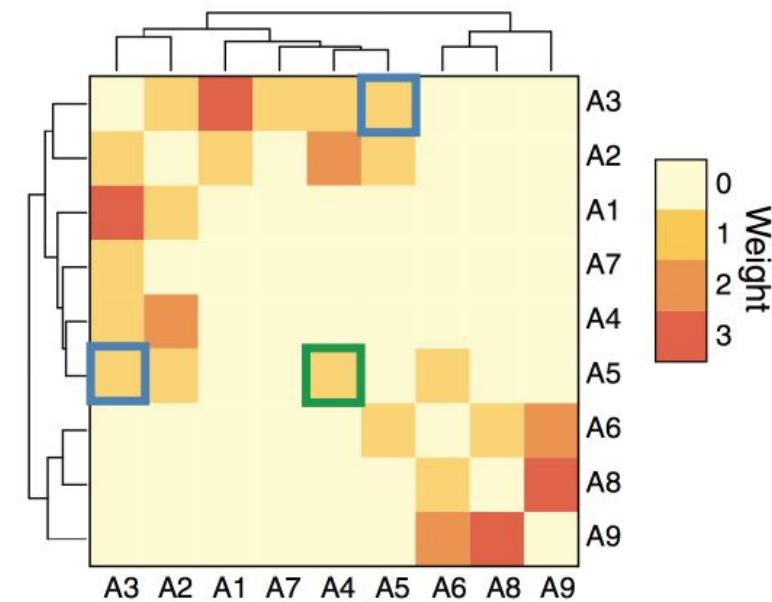
Graph

Network



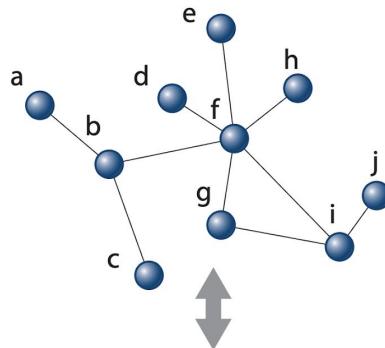
Adjacency matrix

Heatmap



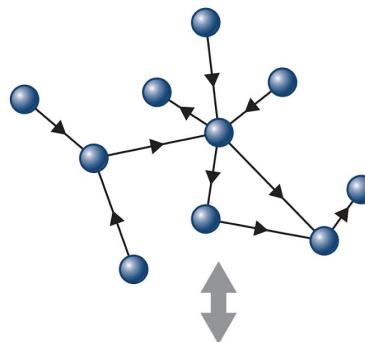
# Network representations

Connectivity  
e.g., protein–protein interaction



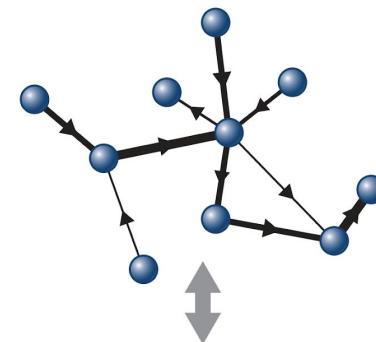
a	b	c	d	e	f	g	h	i	j
a	1								
b		1	1						
c			1						
d				1					
e					1				
f						1	1	1	1
g							1		
h								1	
i									1
j									

Connection direction  
e.g., gene regulation



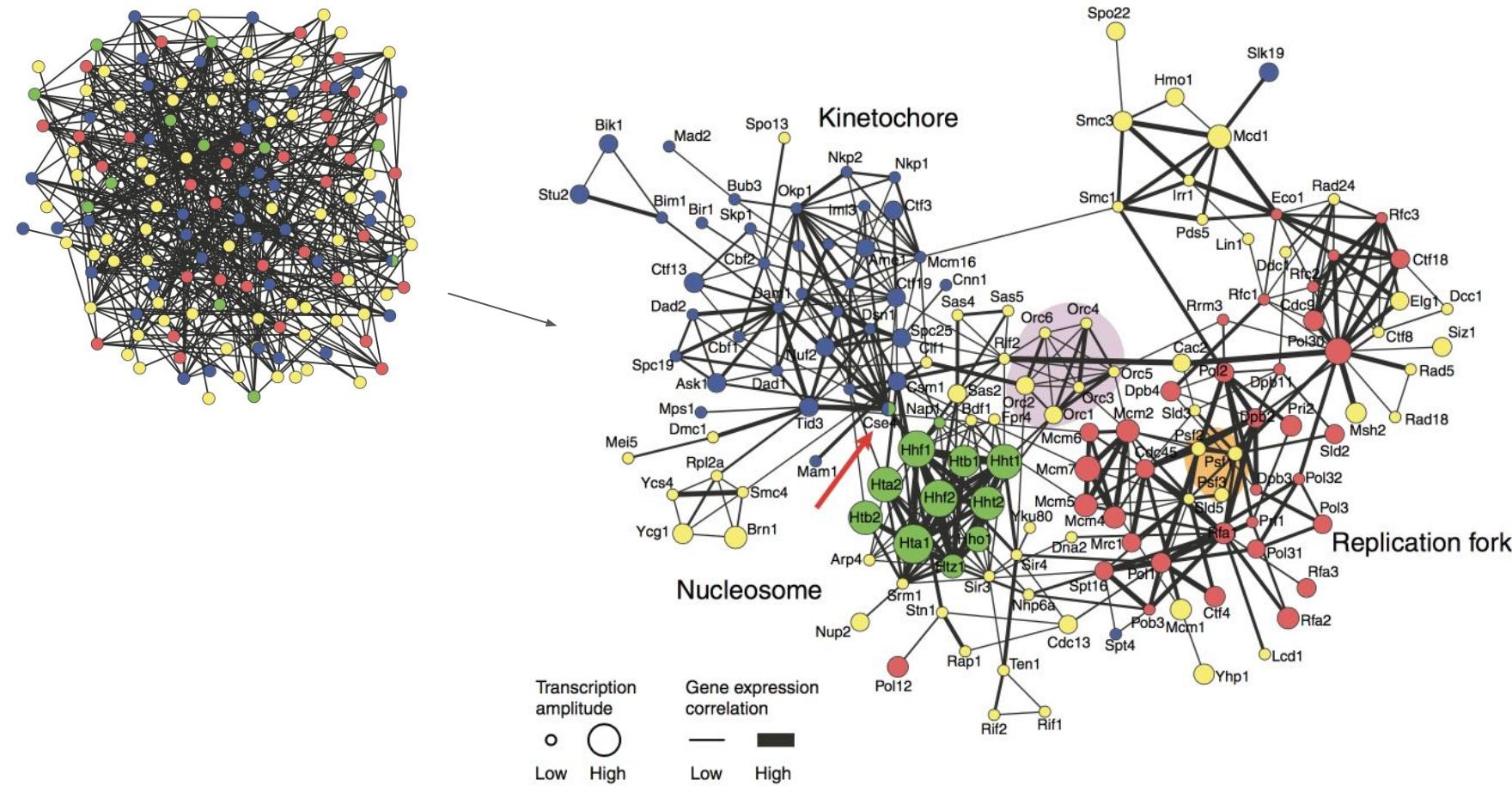
a	b	c	d	e	f	g	h	i	j
a	1								
b		1							
c			1						
d				1					
e					1				
f						1	1	1	1
g							1		
h								1	
i									1
j									

Connection weight  
e.g., gene coexpression



a	b	c	d	e	f	g	h	i	j
a	3								
b		4							
c	1								
d									
e									
f		1	3	1	3	1	3	1	3
g						2			
h							2		
i								4	
j									

# Network layout

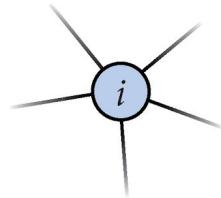


# Network topology

Degree

$$d_i$$

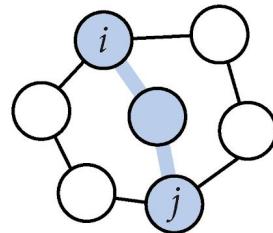
Number of nodes bound to node  $i$



Shortest path distance

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

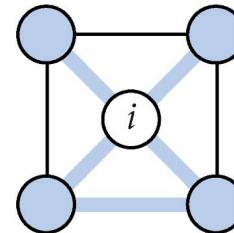
$E_{ij}$ : all edge sets connecting nodes  $i$  and  $j$



Clustering coefficient

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

$c_i$ : edges connecting all  $n_i$  nodes bound to  $i$

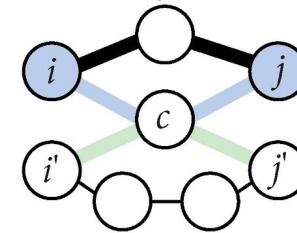


Betweenness centrality

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

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

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



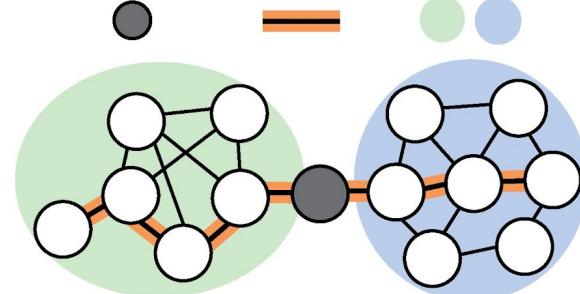
Bottleneck



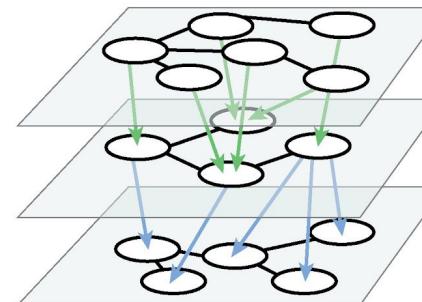
Diameter



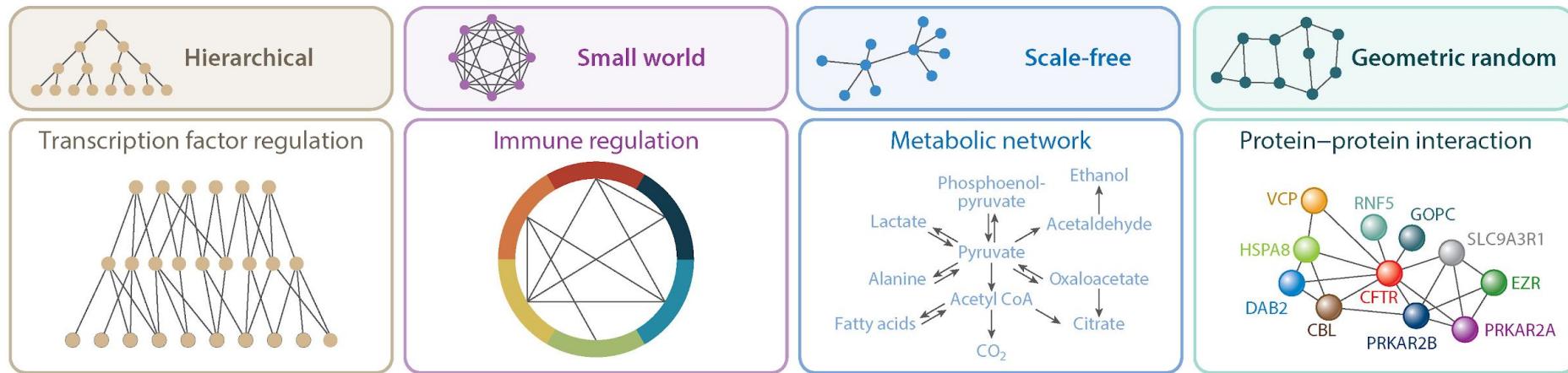
Modules



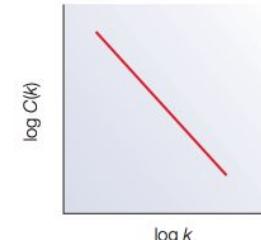
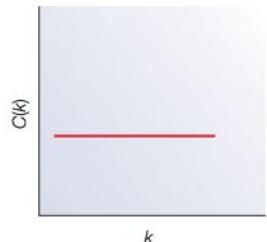
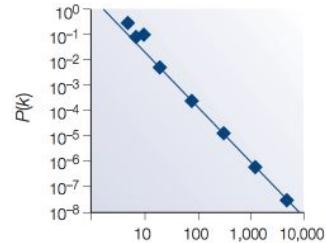
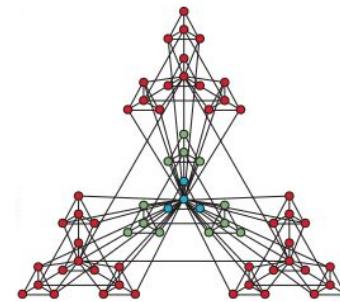
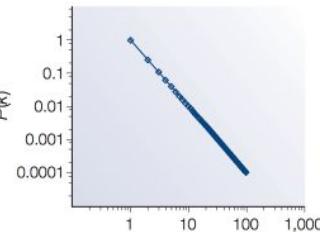
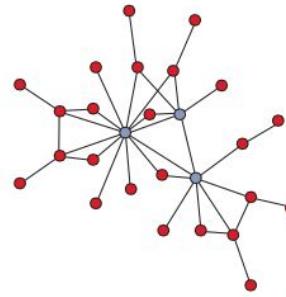
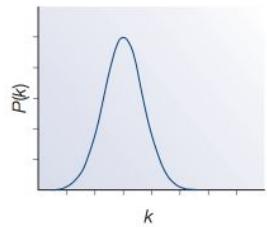
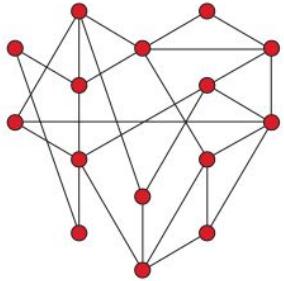
Network hierarchy



# Large-scale network topology



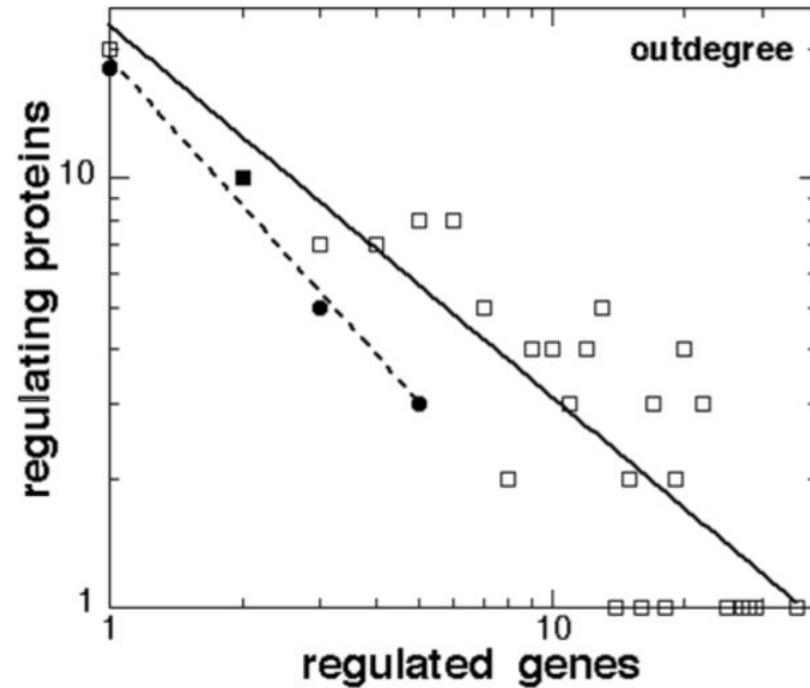
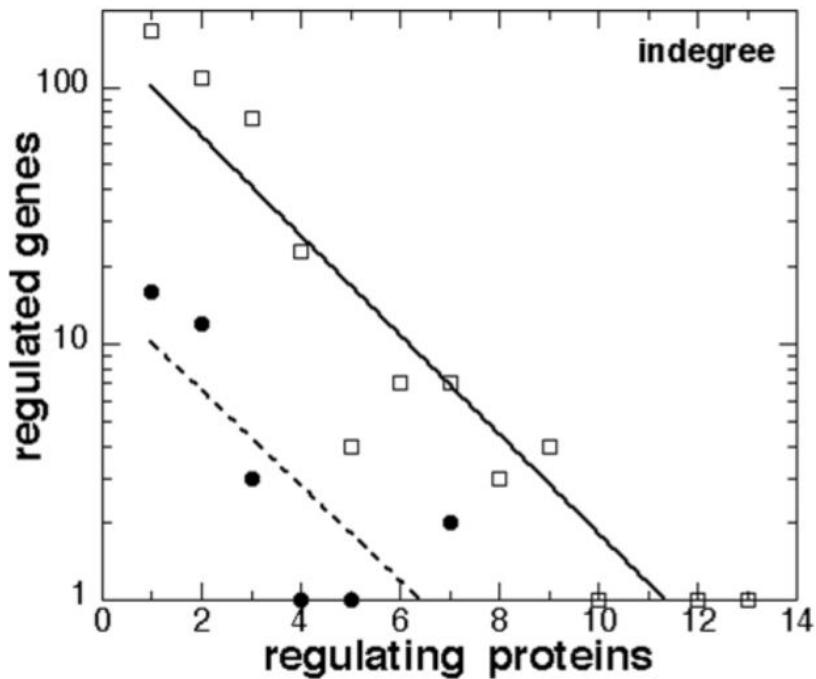
# Network topology



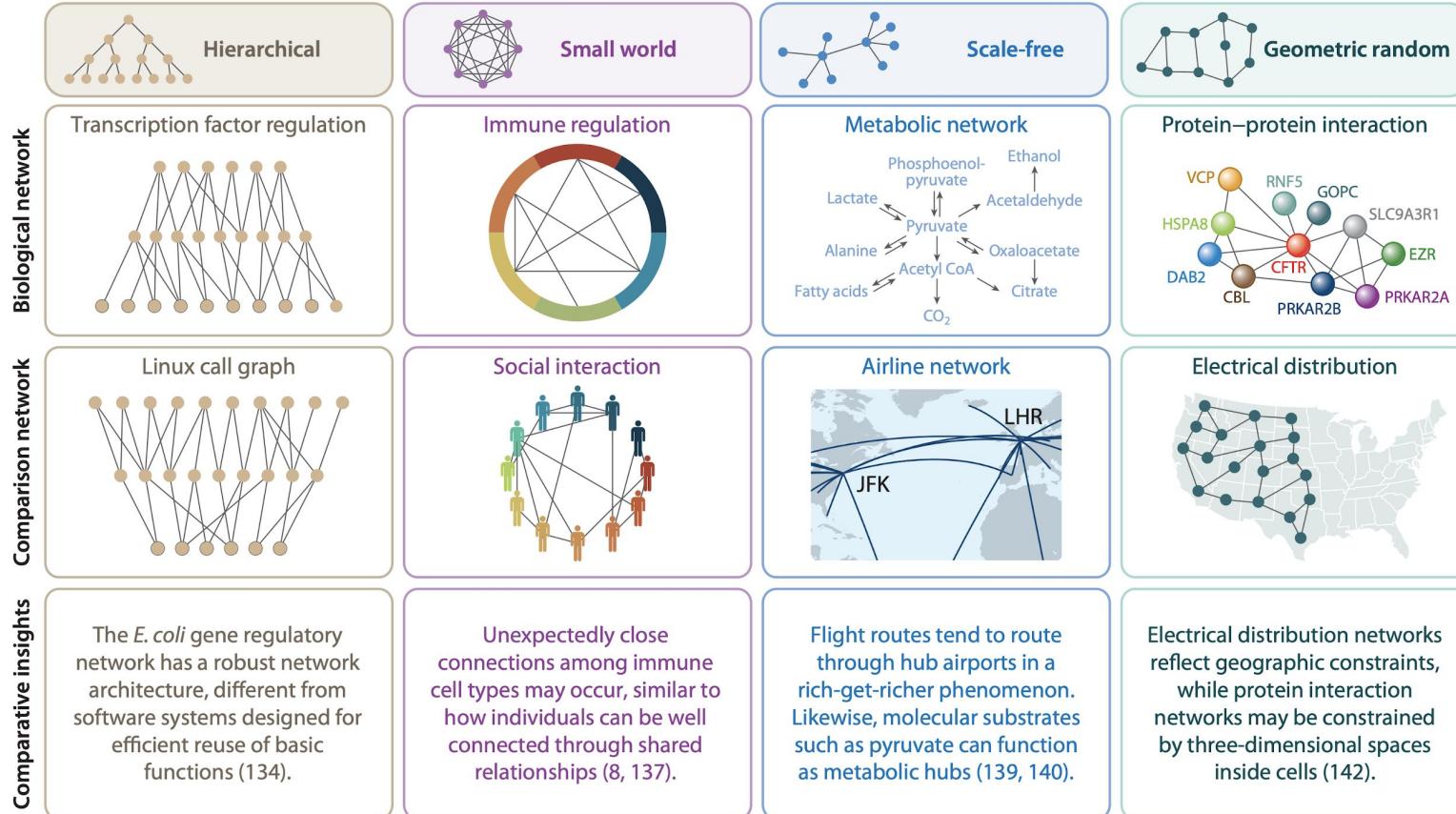
Barabasi, Oltvai (2004) Nat. Rev. Genet.

# Network topology

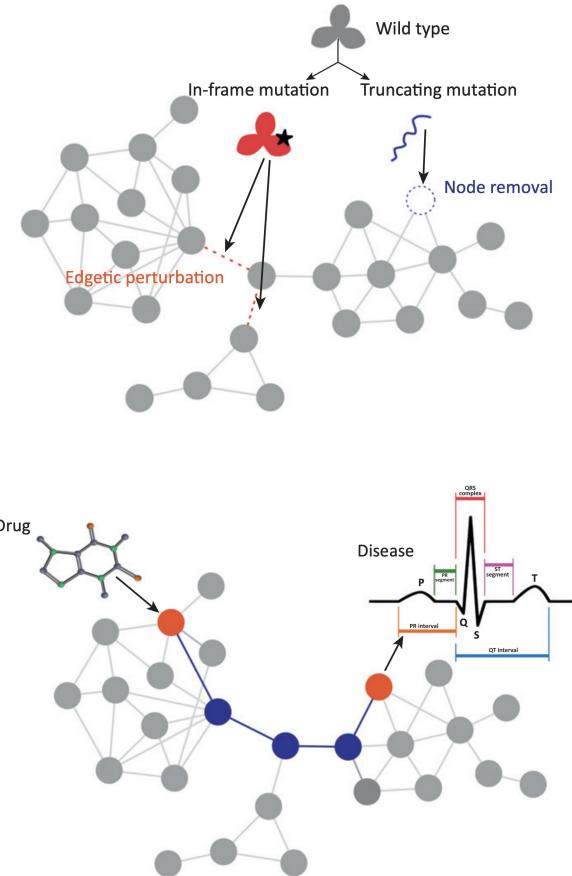
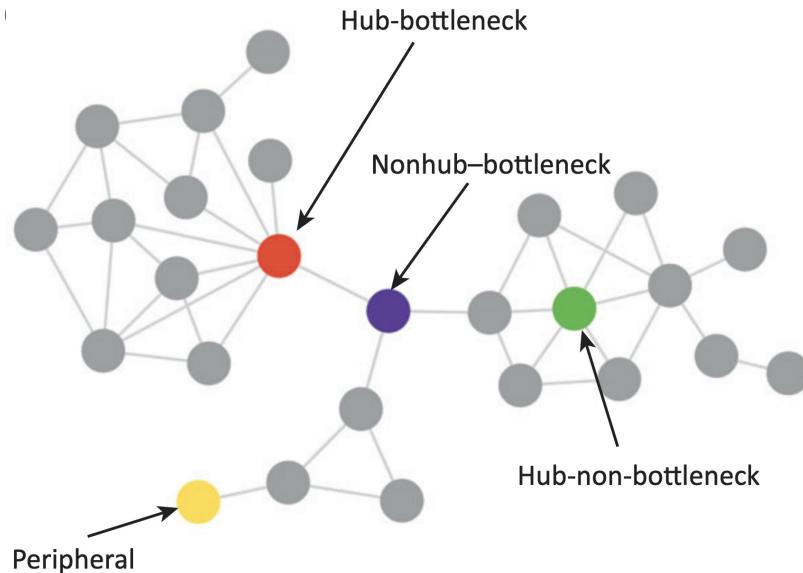
Yeast TF-target network



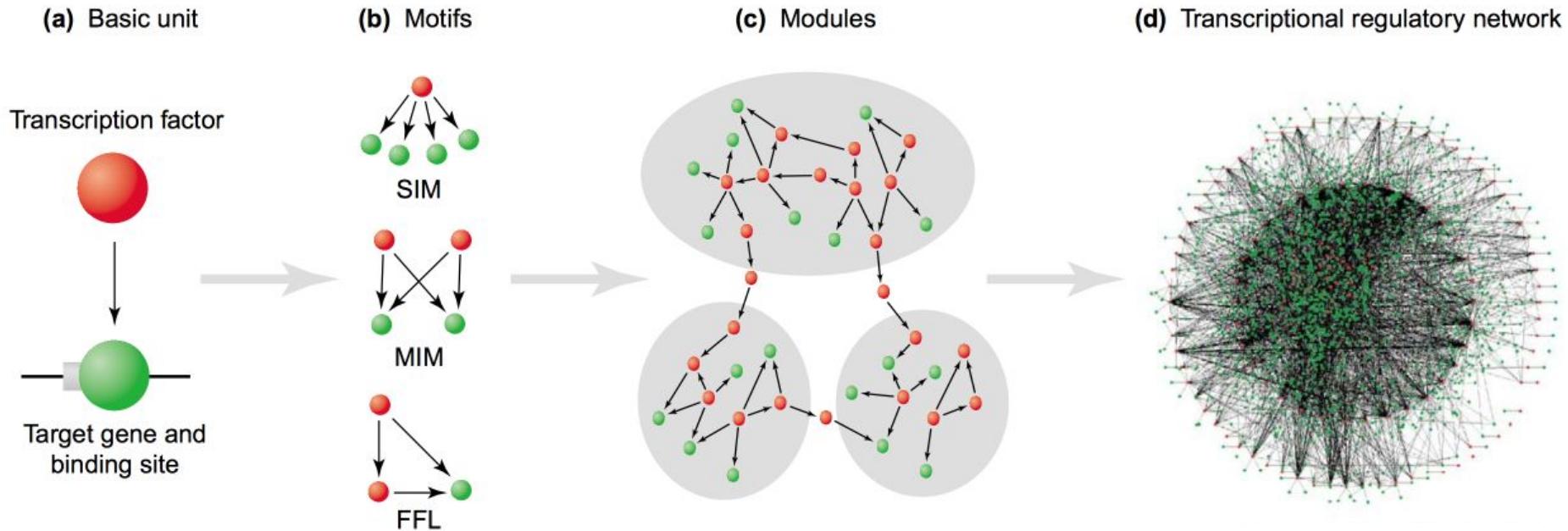
# Network topology



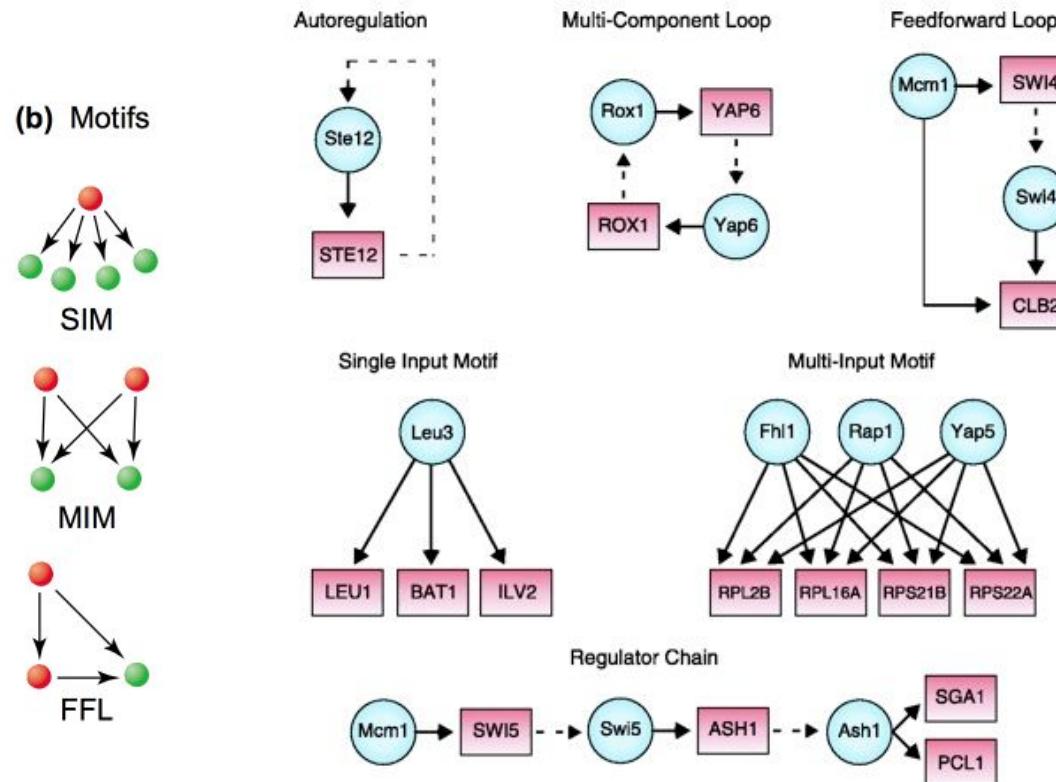
# Network topology



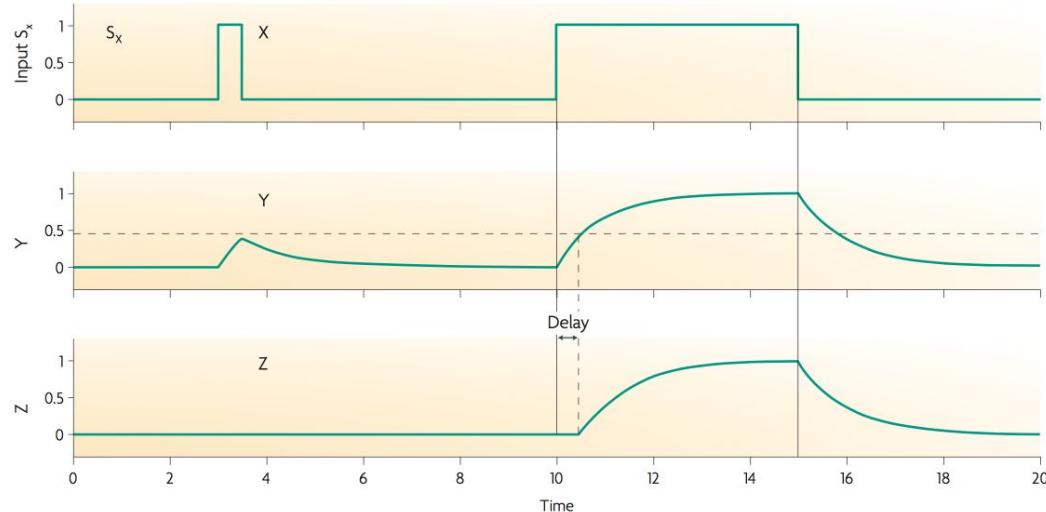
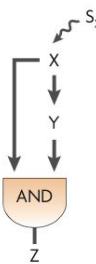
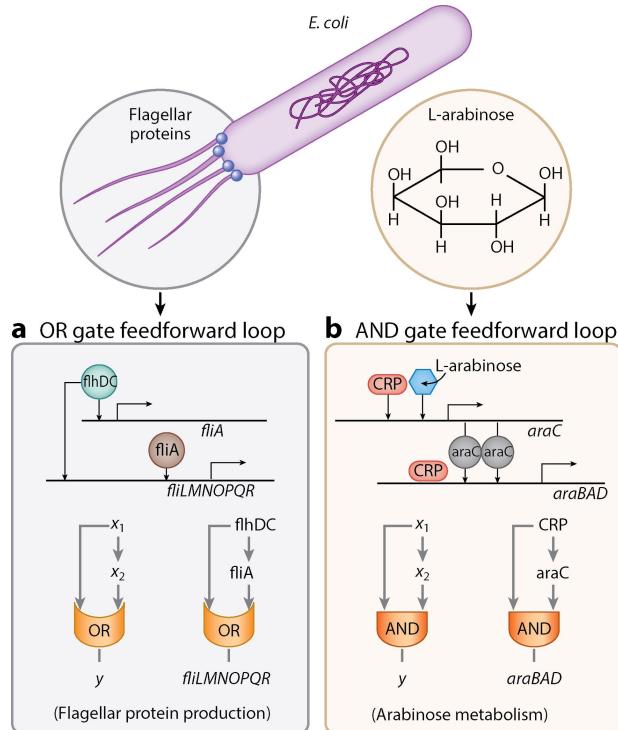
# Network motifs



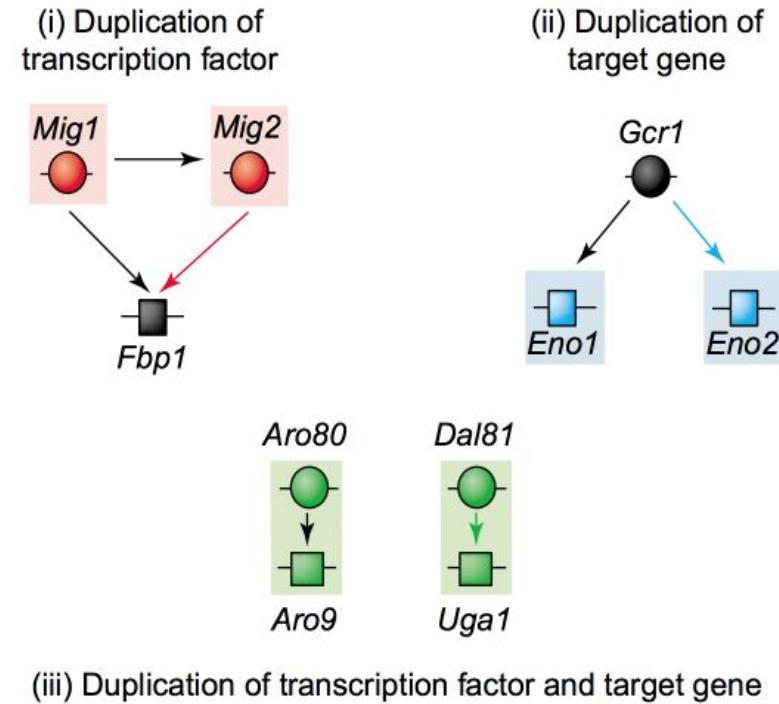
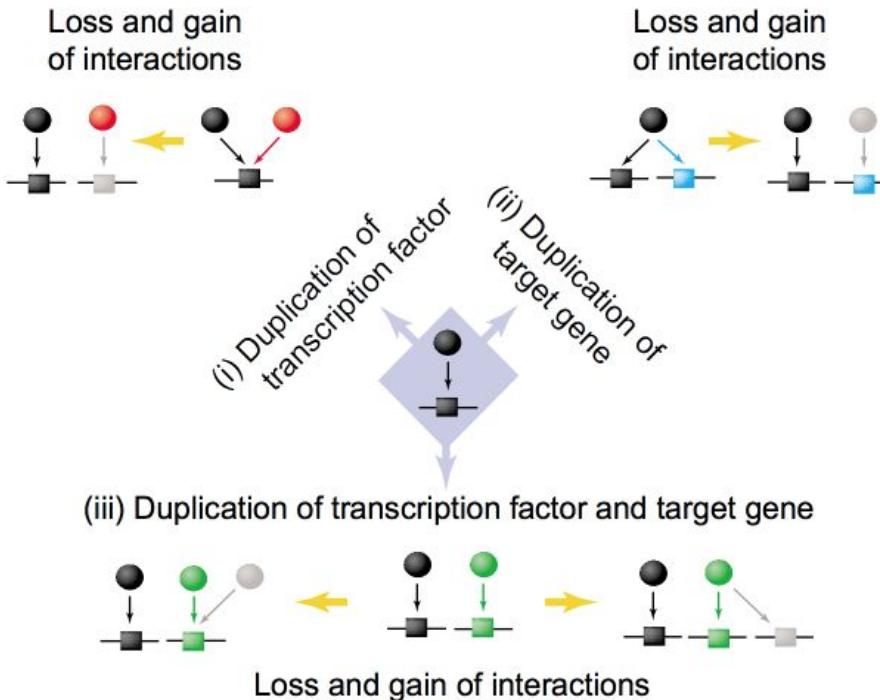
# Network motifs



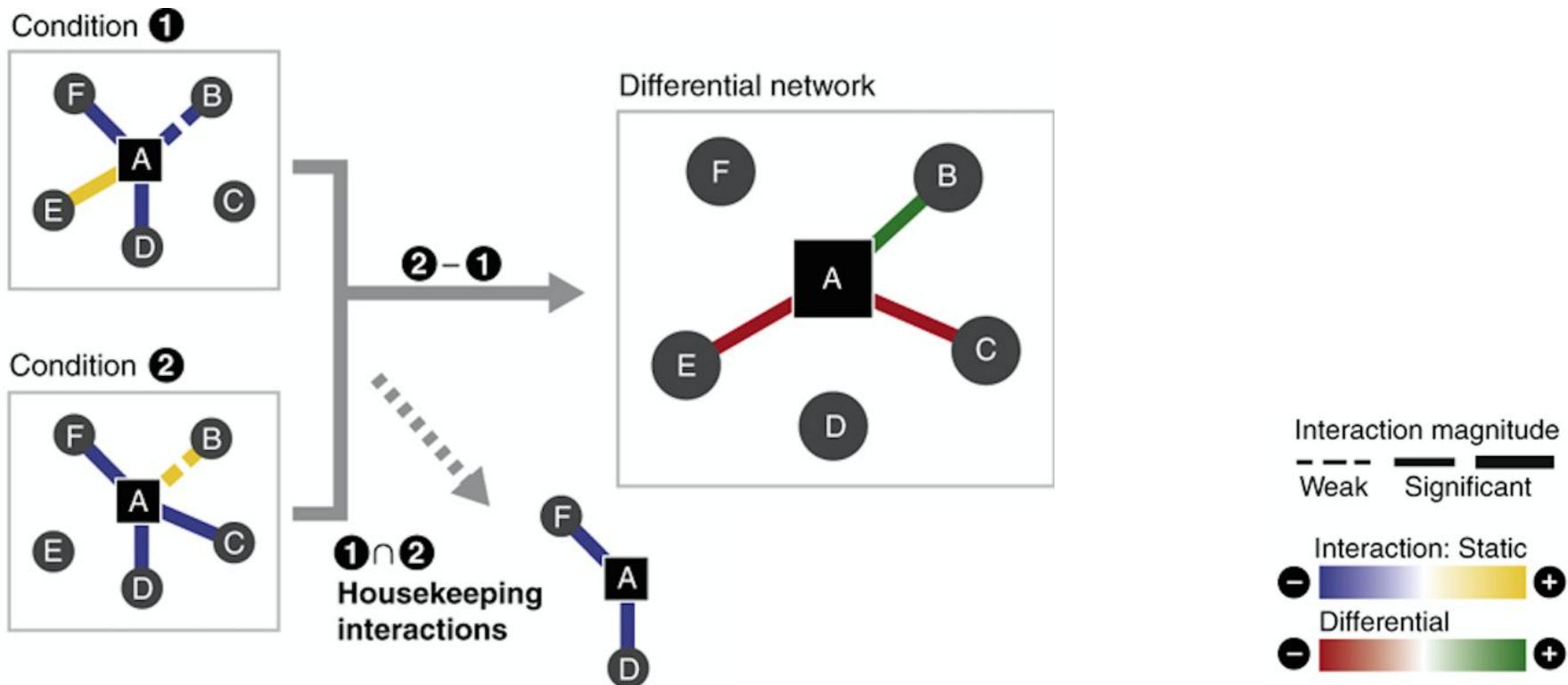
# Network motifs



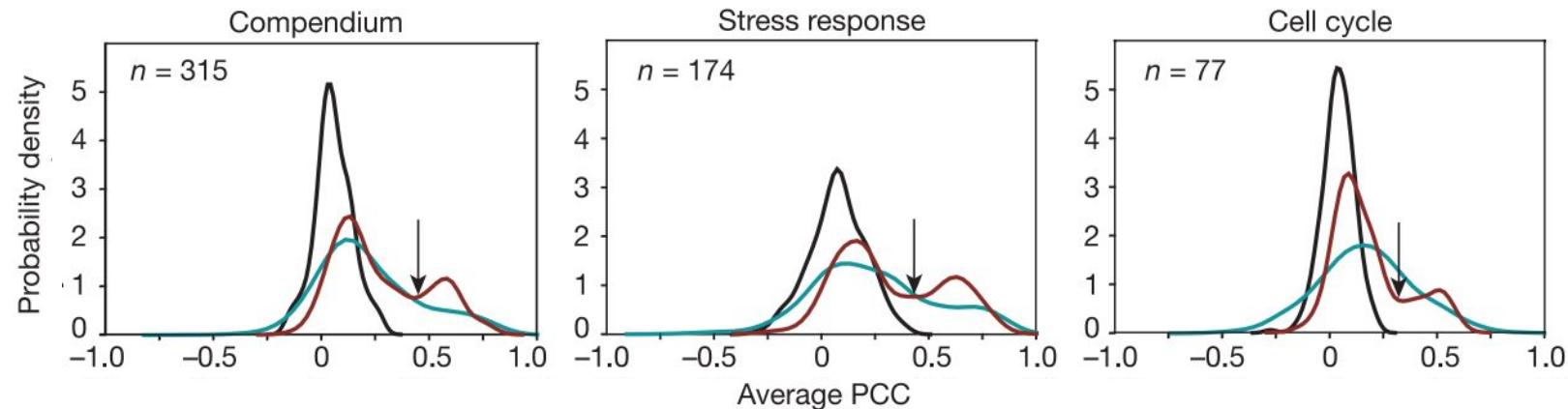
# Network interactions evolve through time



# Network interactions are condition-specific



# Network interactions are condition-specific

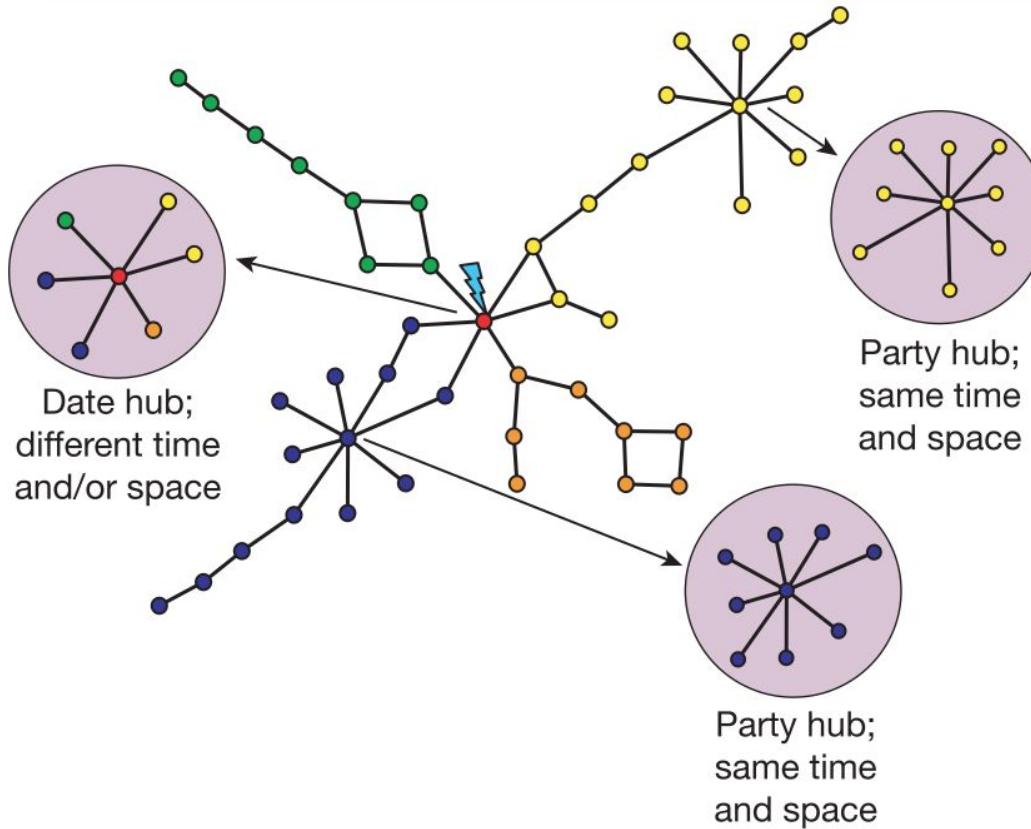


Red: Hub proteins

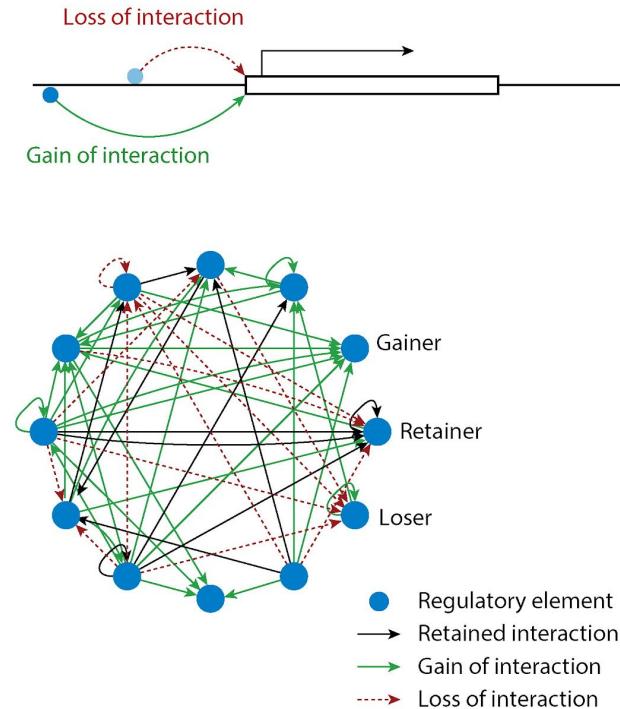
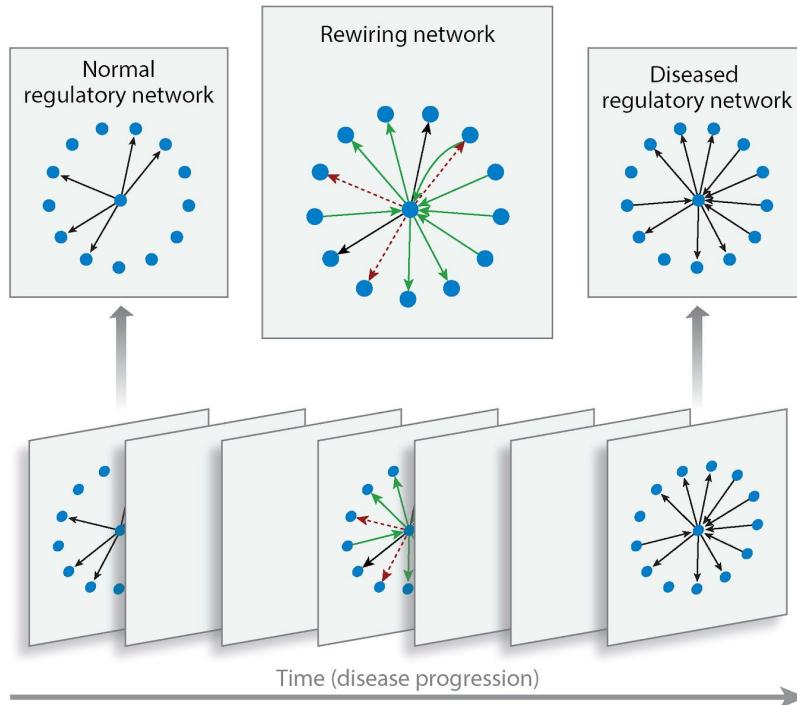
Cyan: Non-hub proteins

Black: Hubs in randomized networks

# Network interactions are condition-specific



# Network interactions are condition-specific



# Network interactions are condition-specific

