

# Biological networks (BIO 390, 09.11.2021)



University of  
Zurich<sup>UZH</sup>

**Session 1 (45 min):** Introduction to networks, and biological networks

**Session 2 (45 min):** Properties of networks



**Instructor:** Pouria Dasmeh

Postdoctoral Fellow, Institute for evolutionary biology and environmental studies,  
University of Zurich.

Long-term research fellow, Department of chemistry and chemical biology,  
Harvard University.



<https://github.com/dasmeh>

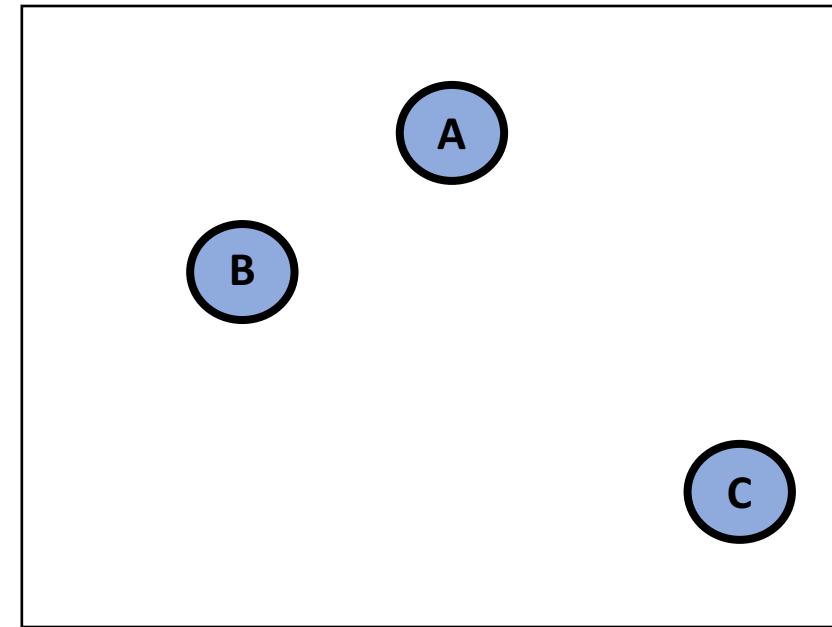
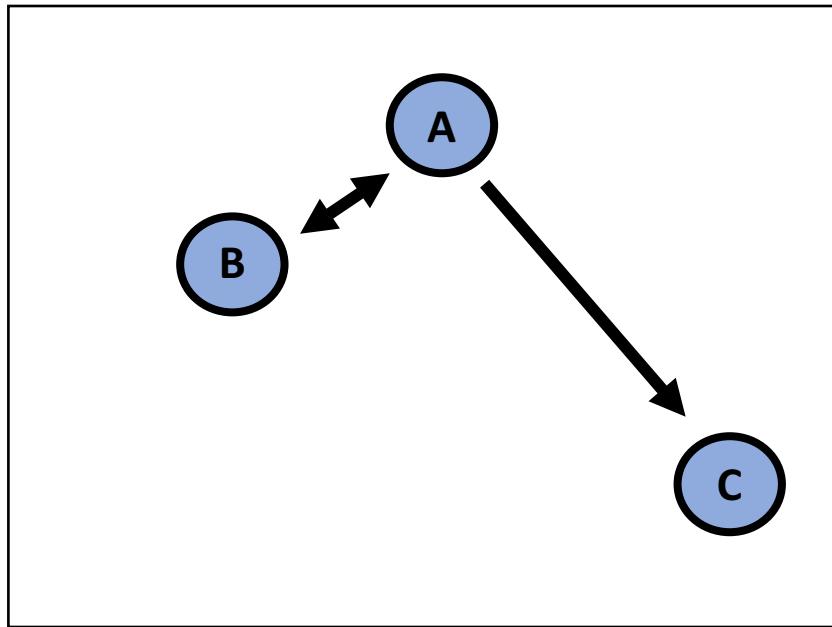


@PouriaDasmeh

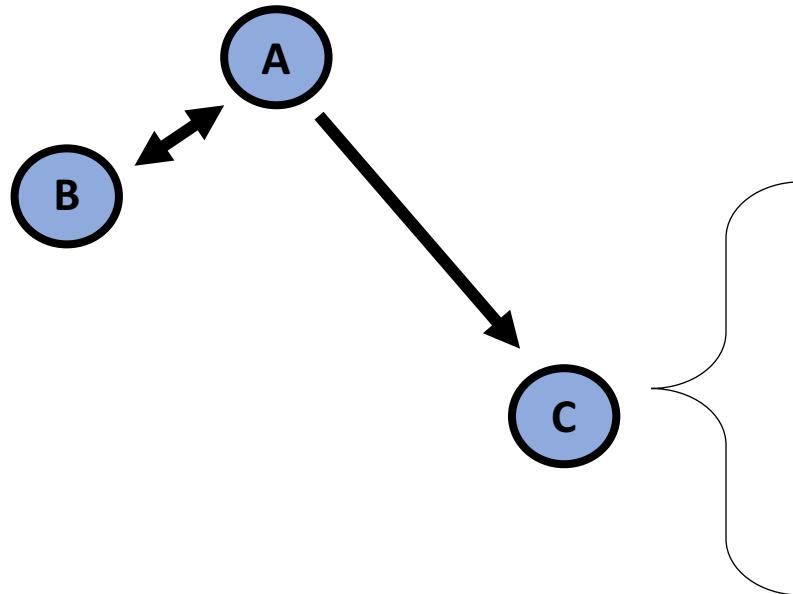
Pouria.dasmeh@uzh.ch

# What is a network?

Two or more components that can “interact” with each other



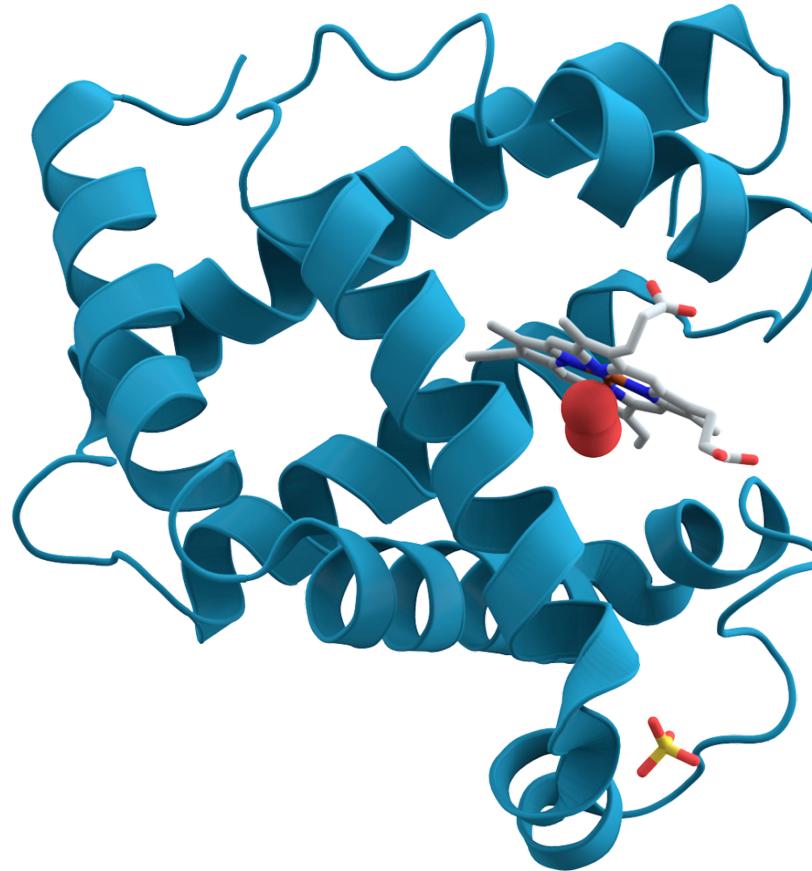
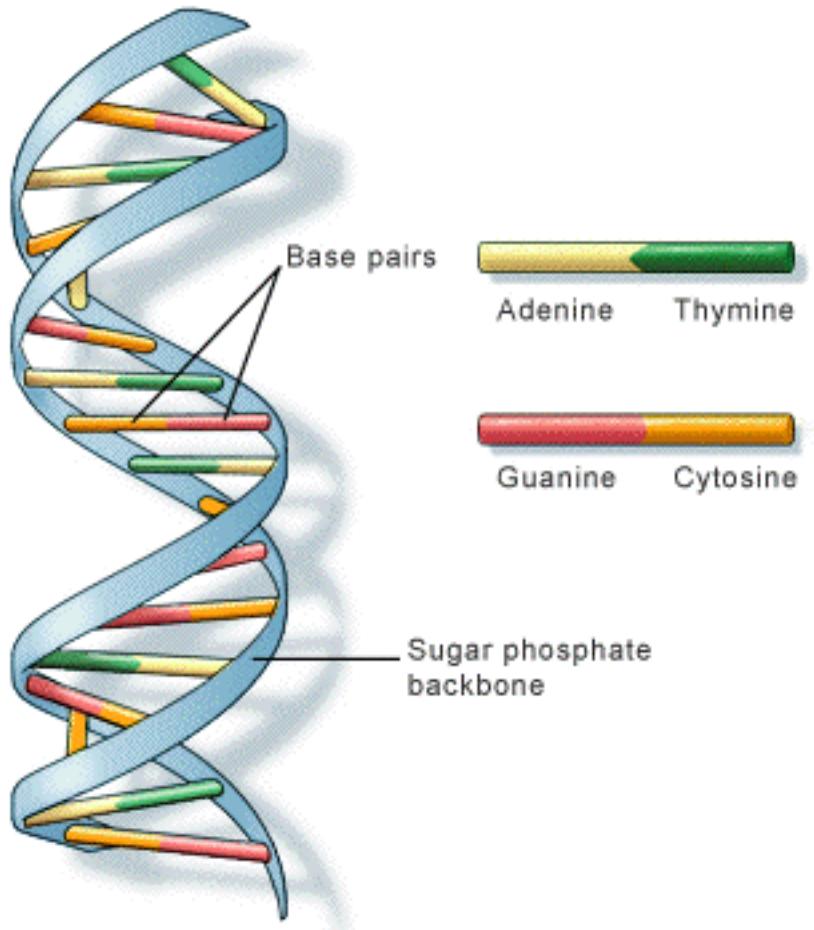
# Biological networks



Networks that apply to biological systems:

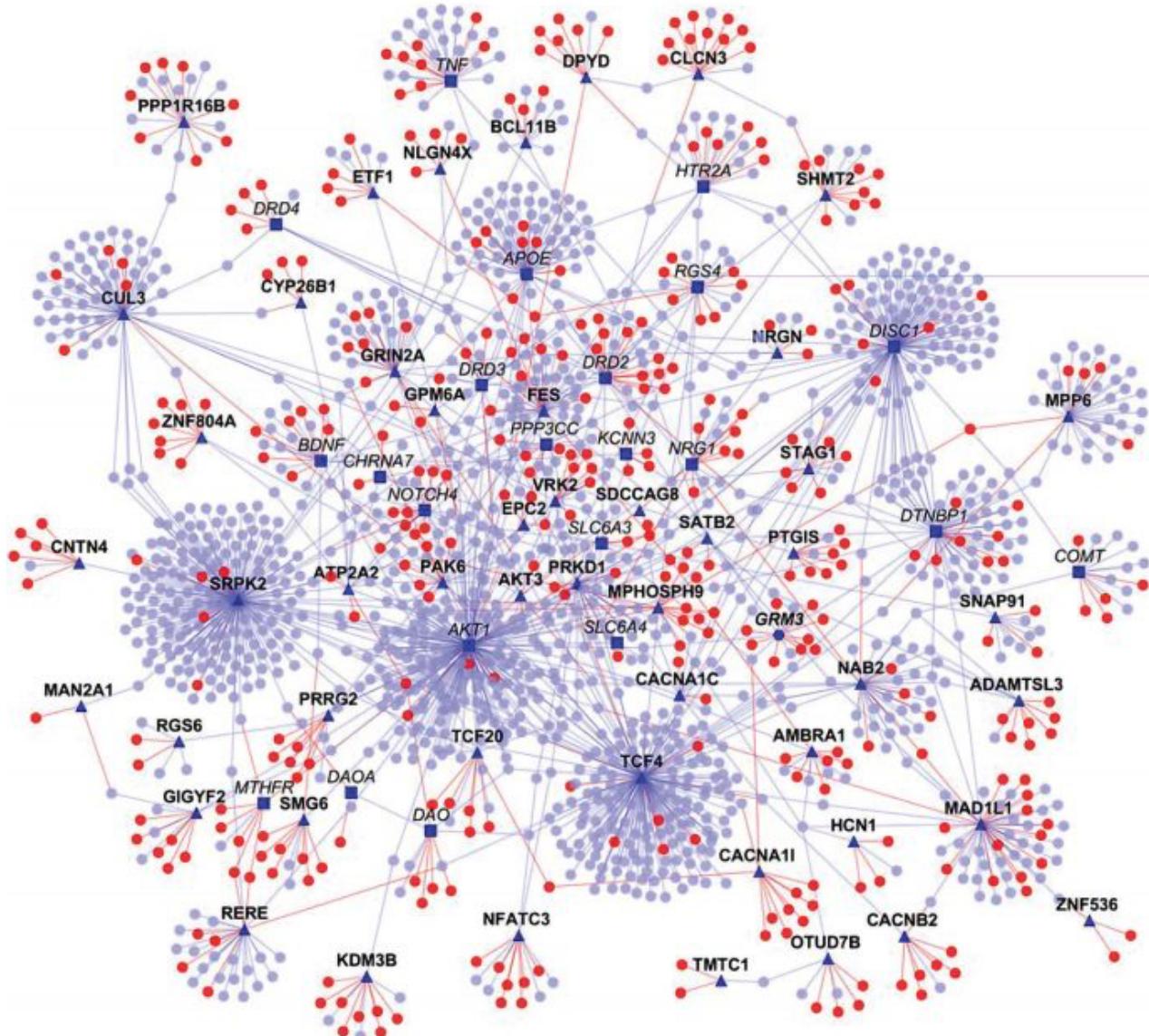
- 1) DNA
- 2) Protein
- 3) Cell
- 4) Organisms
- 5) .....

# DNA and Proteins



Chemical networks

# Protein-protein interaction network



# Welcome to STRING

Protein-Protein Interaction Networks

Functional Enrichment Analysis

ORGANISMS

14094

PROTEINS

67.6 mio

INTERACTIONS

>20 bln

SEARCH

© STRING CONSORTIUM 2021



SIB - Swiss Institute of Bioinformatics



CPR - Novo Nordisk Foundation Center Protein Research



EMBL - European Molecular Biology Laboratory

ABOUT

Content

References

Contributors

Statistics

INFO

Scores

Use scenarios

FAQs

Cookies/Privacy

ACCESS

Versions

APIs

Licensing

Usage

CREDITS

Funding

Datasources

Partners

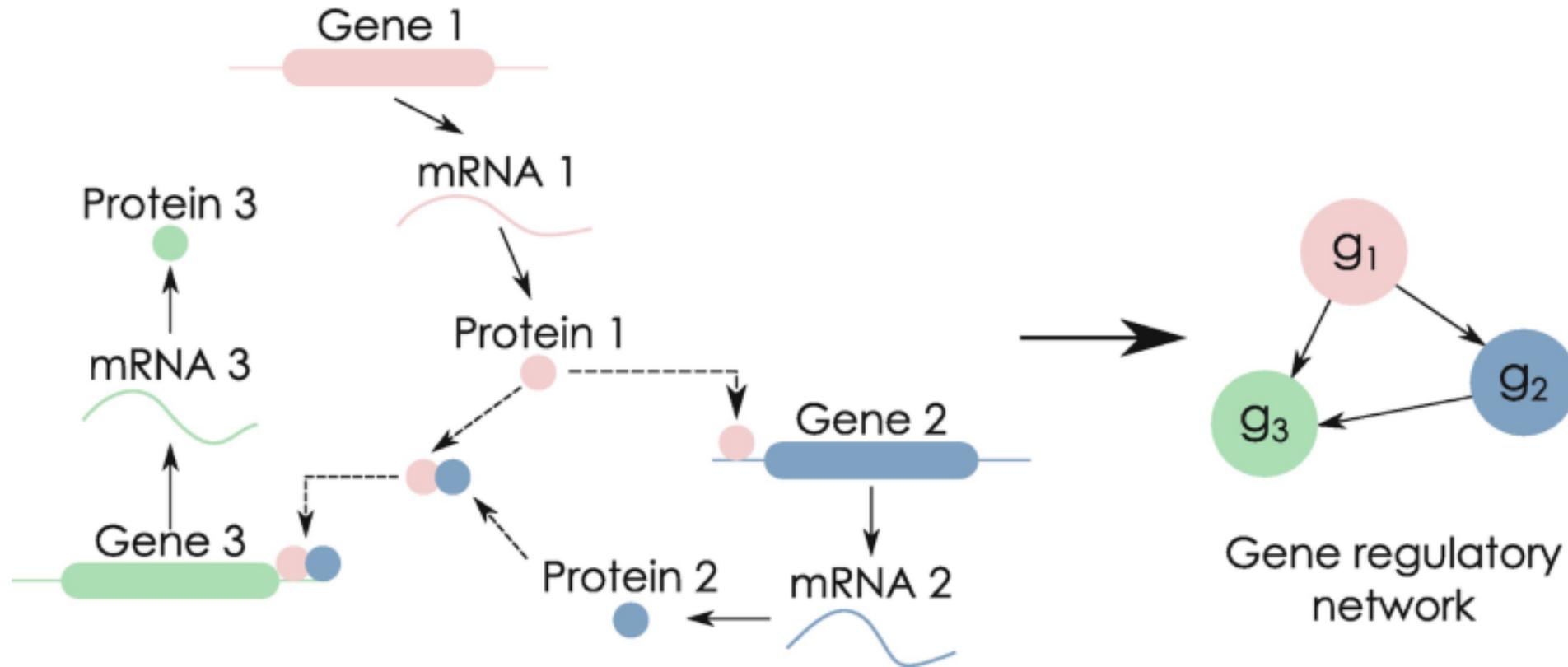
Software

## Database 1: STRING

Why do we have different tissues  
and cell types if we have only one DNA  
molecule?



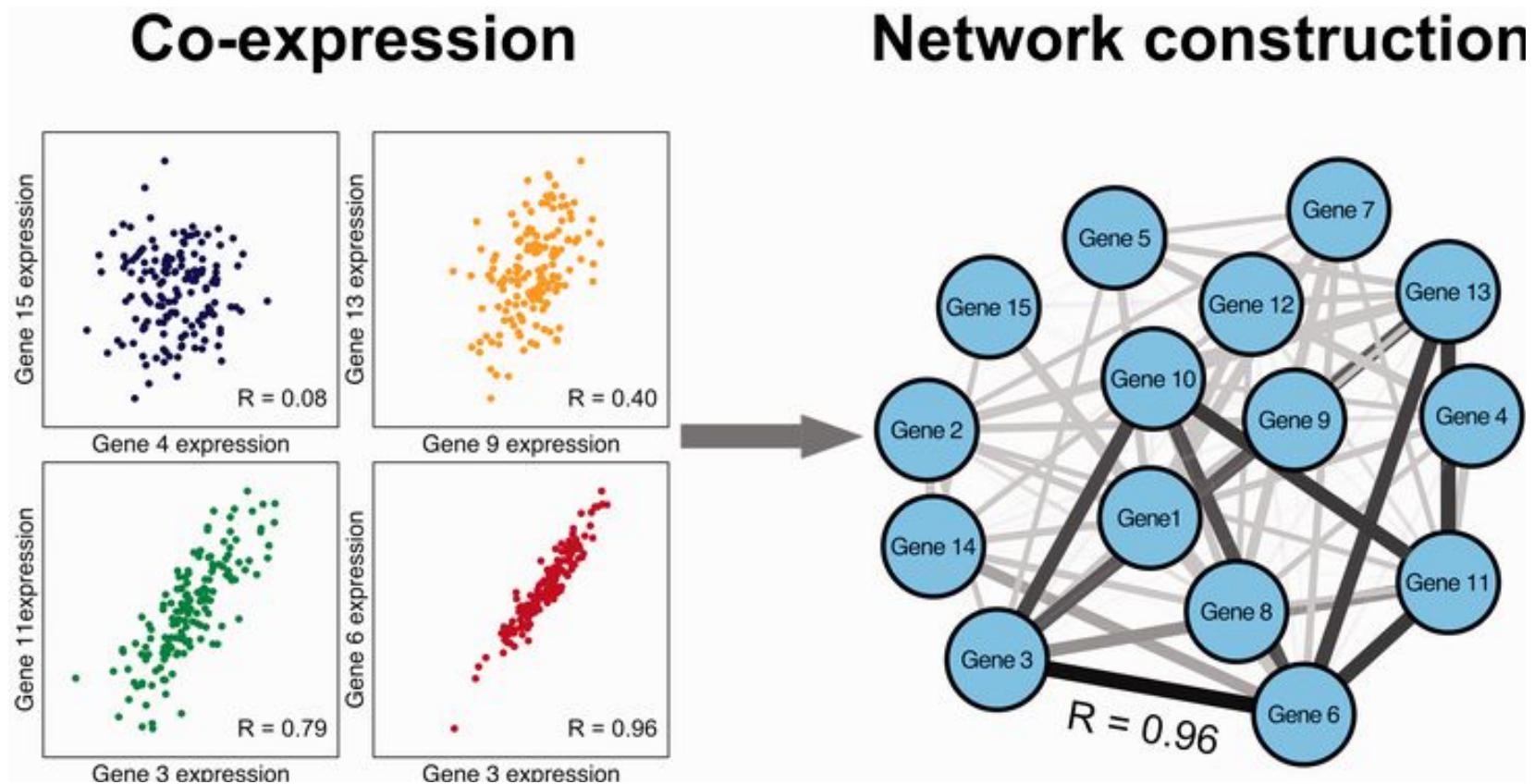
# Gene regulatory networks (DNA-protein interaction networks)



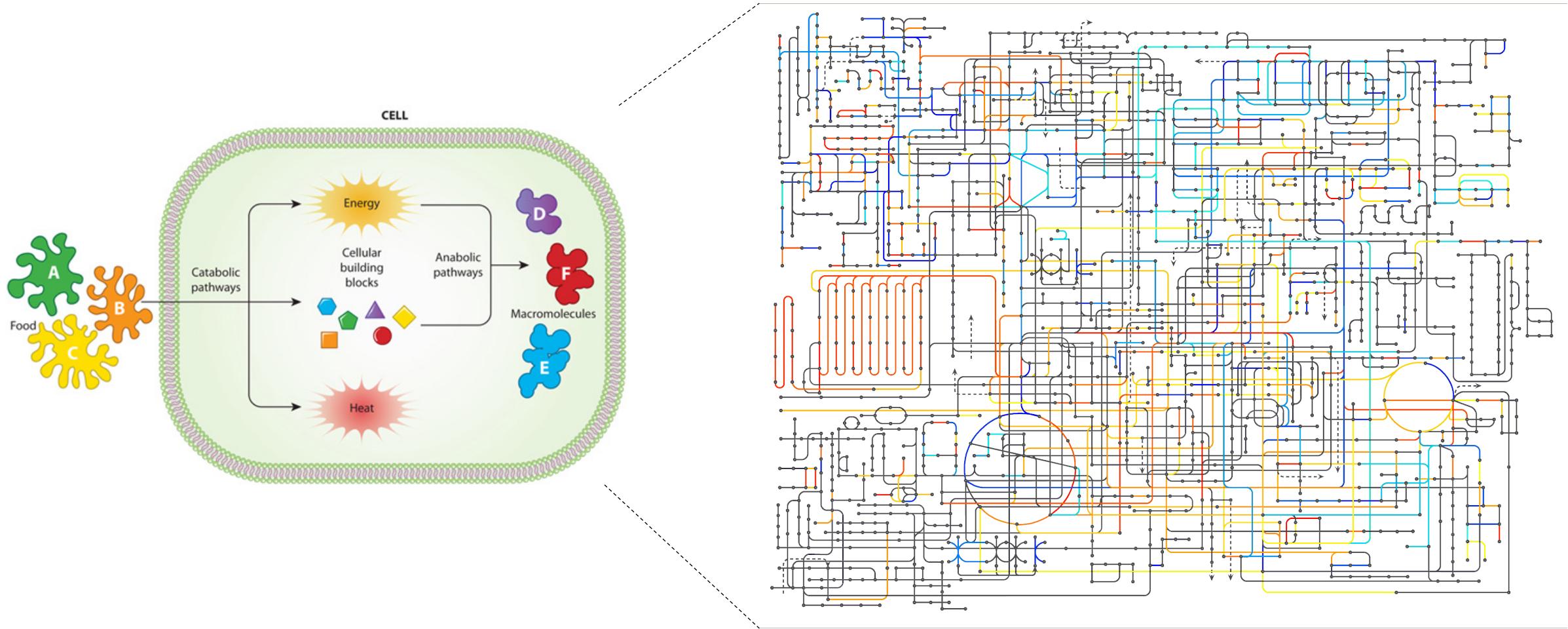
How to cells respond to stress  
conditions which enable them  
to survive ?



# Gene co-expression network



# Metabolic networks





# KEGG PATHWAY Database

Wiring diagrams of molecular interactions, reactions and relations

[KEGG2](#) [PATHWAY](#) [BRITE](#) [MODULE](#) [KO](#) [GENES](#) [COMPOUND](#) [DISEASE](#) [DRUG](#)

Select prefix

[map](#)

[Organism](#)

Enter keywords

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## Pathway Maps

**KEGG PATHWAY** is a collection of manually drawn pathway maps representing our knowledge of the molecular interaction, reaction and relation networks for:

### 1. Metabolism

[Global/overview](#) [Carbohydrate](#) [Energy](#) [Lipid](#) [Nucleotide](#) [Amino acid](#) [Other amino](#) [Glycan](#)  
[Cofactor/vitamin](#) [Terpenoid/PK](#) [Other secondary metabolite](#) [Xenobiotics](#) [Chemical structure](#)

### 2. Genetic Information Processing

### 3. Environmental Information Processing

### 4. Cellular Processes

### 5. Organismal Systems

### 6. Human Diseases

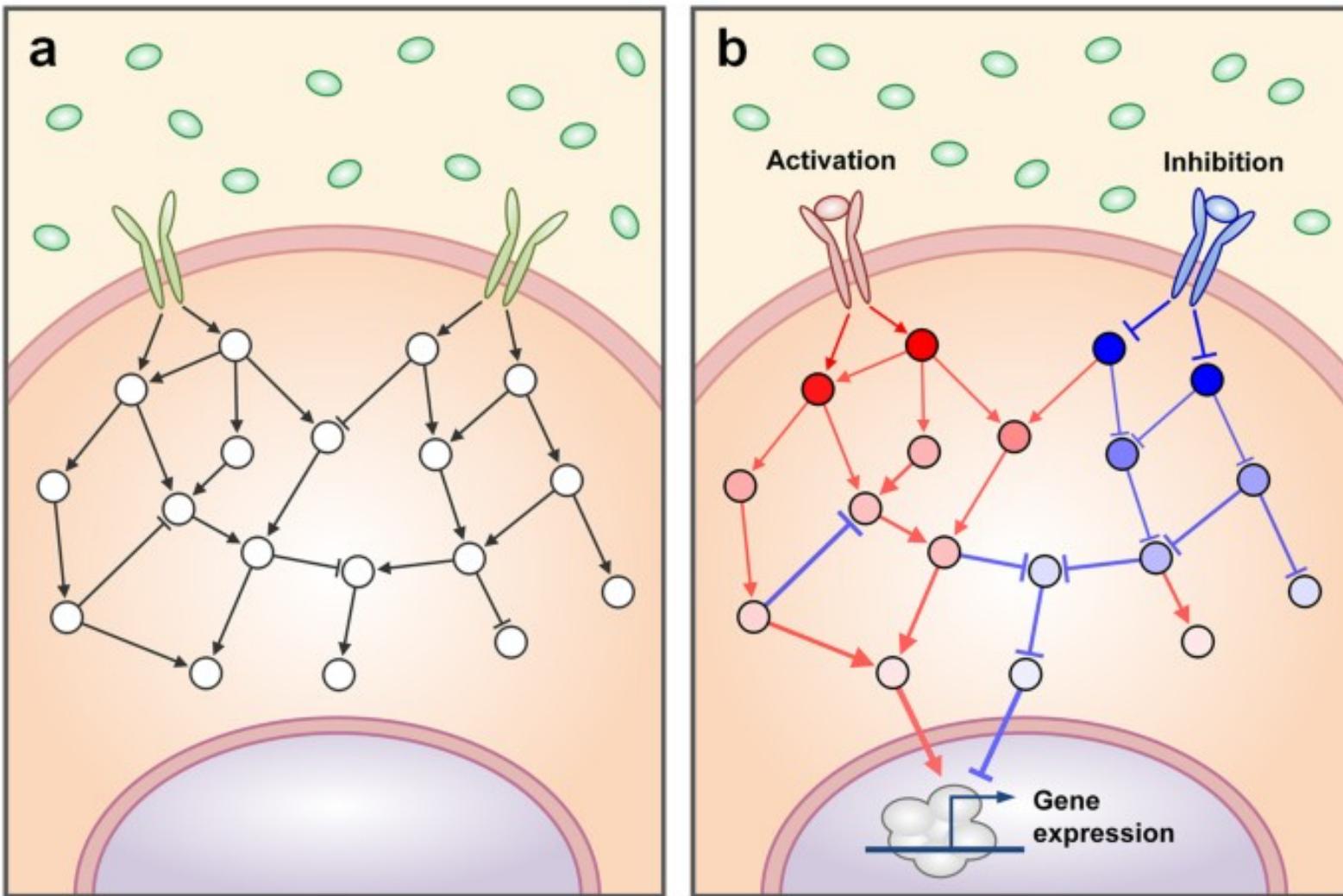
### 7. Drug Development

KEGG PATHWAY is the reference database for pathway mapping in **KEGG Mapper**.

(Obviously!) cells should communicate.  
How do they achieve this?



# Signaling networks

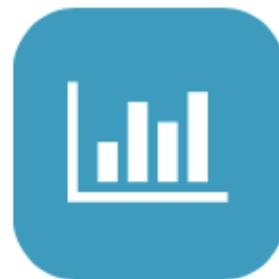


## Find Reactions, Proteins and Pathways

e.g. O95631, NTN1, signaling by EGFR, glucose

**Go!****Pathway Browser**

Visualize and interact with Reactome biological pathways

**Analysis Tools**

Merges pathway identifier mapping, over-representation, and expression analysis

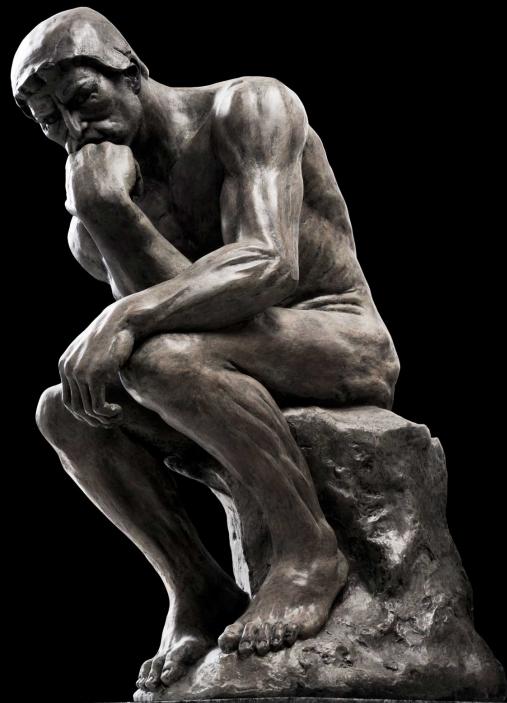
**ReactomeFIViz**

Designed to find pathways and network patterns related to cancer and other types of diseases

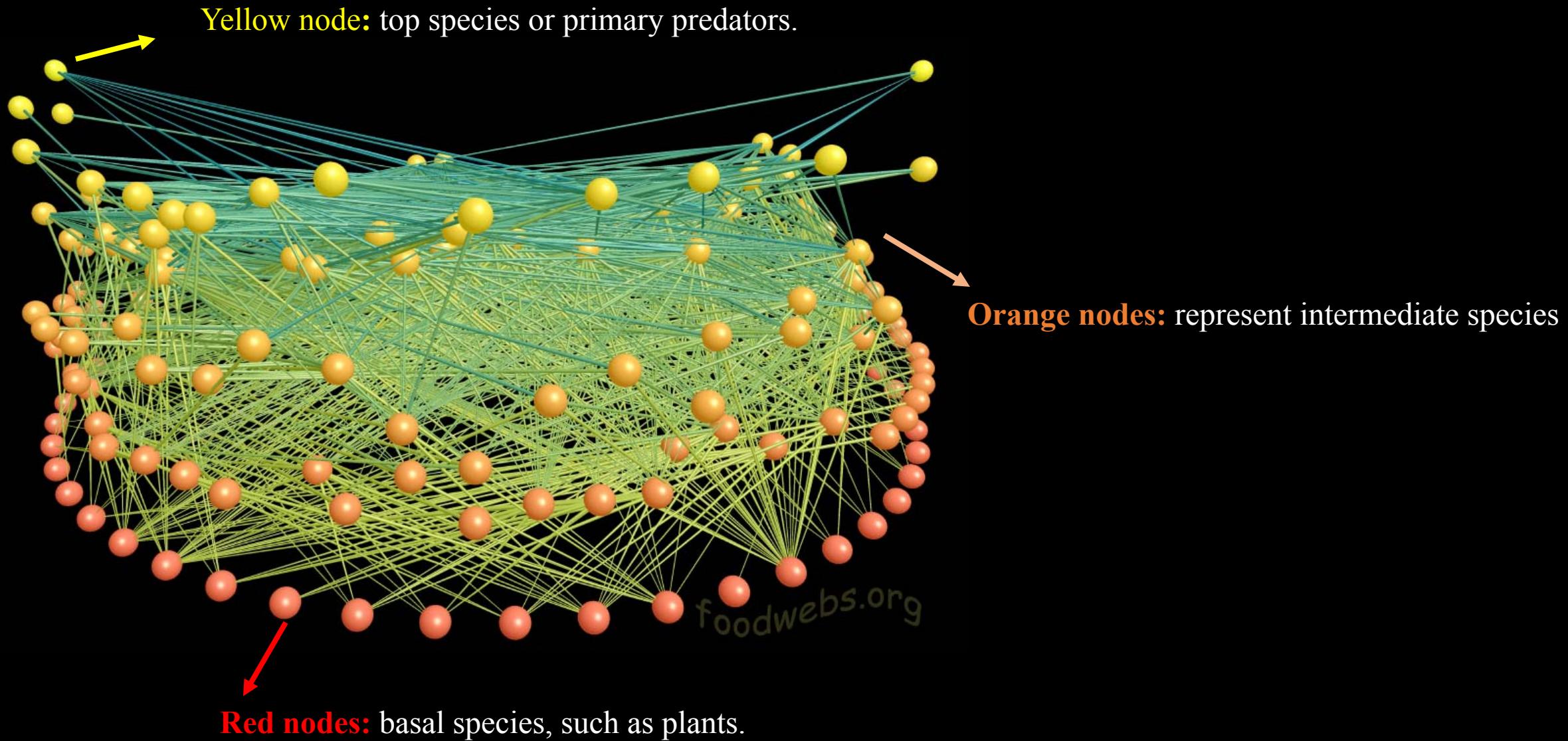
**Documentation**

Information to browse the database and use its principal tools for data analysis

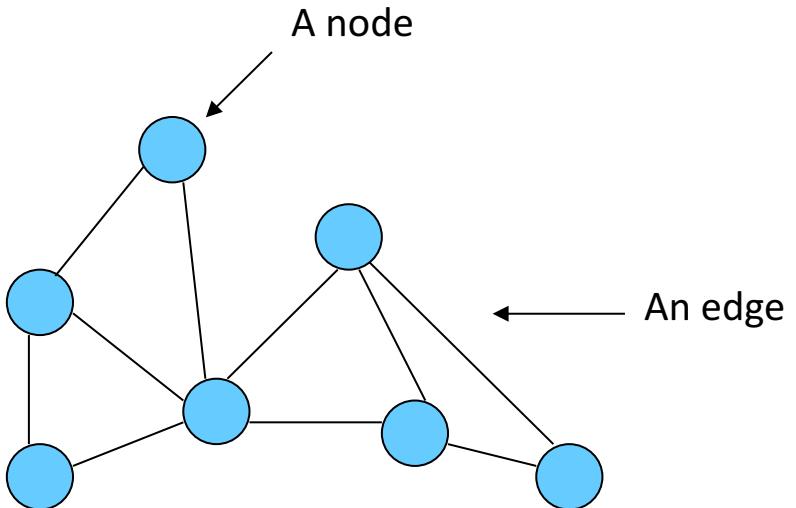
Any higher-level network to talk about?



## Food web



# Graphs

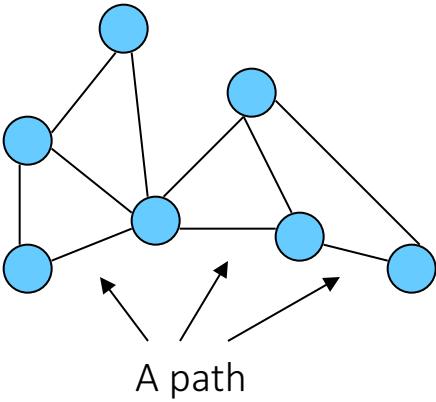


A graph  $G=(V,E)$  comprises  
a set  $V$  of nodes (vertices)  
a set  $E$  of edges

$$V = \{V_1, \dots, V_n\}$$
$$E = \{(V_i, V_j), \dots, (V_k, V_l)\}$$

Protein interaction networks are undirected graphs  
(Individual node pairs in  $E$  are unordered.)

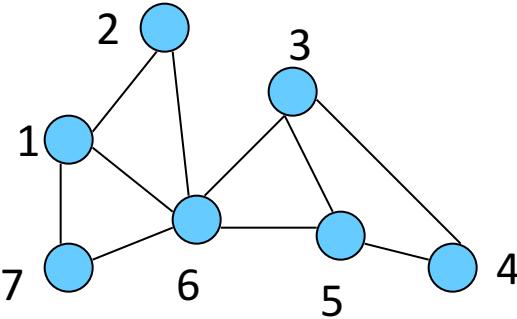
# Graphs



A path is a sequence of alternating nodes and edges in which no node is visited more than once

A geodesic is the shortest path between two nodes.

# Graphs can be represented by matrices

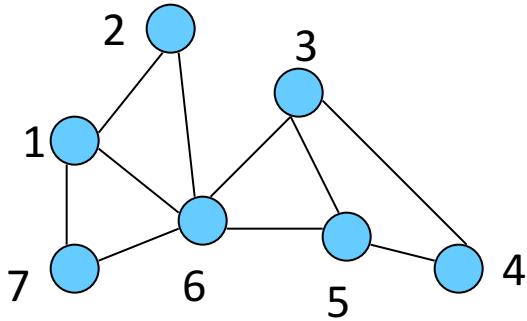


Adjacency matrix  $A=(a_{ij})$

$$\begin{array}{ll} a_{ij}=1 & (V_i, V_j) \in E \\ a_{ij}=0 & \text{otherwise} \end{array}$$

$$A = \begin{pmatrix} 0 & 1 & 0 & 0 & 0 & 1 & 1 \\ 1 & 0 & 0 & 0 & 0 & 1 & 0 \\ 0 & 0 & 0 & 1 & 1 & 1 & 0 \\ 0 & 0 & 1 & 0 & 1 & 0 & 0 \\ 0 & 0 & 1 & 1 & 0 & 1 & 0 \\ 1 & 1 & 1 & 0 & 1 & 0 & 1 \\ 1 & 0 & 0 & 0 & 0 & 1 & 0 \end{pmatrix}$$

## Degree distribution of graphs



The degree (connectivity)  $k_i$  of a node  $V_i$  is the number of edges incident with the node (e.g.,  $k_1=3$ ,  $k_6=5$ ).

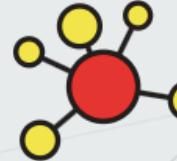
$$k_i = \sum_j a_{ij}$$

Graphs can be characterized according to their degree distribution  $P(k)$ , the fraction of nodes having degree  $k$ .

Class activity:

Determine the degree distribution of your network of friends ( $n=10$ )





# igraph – The network analysis package

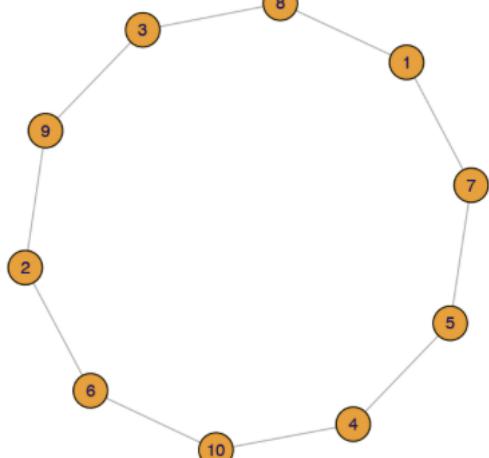
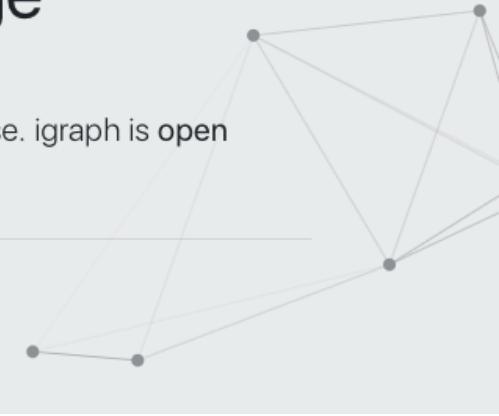
igraph is a collection of network analysis tools with the emphasis on efficiency, portability and ease of use. igraph is open source and free. igraph can be programmed in R, Python, Mathematica and C/C++.

igraph R package

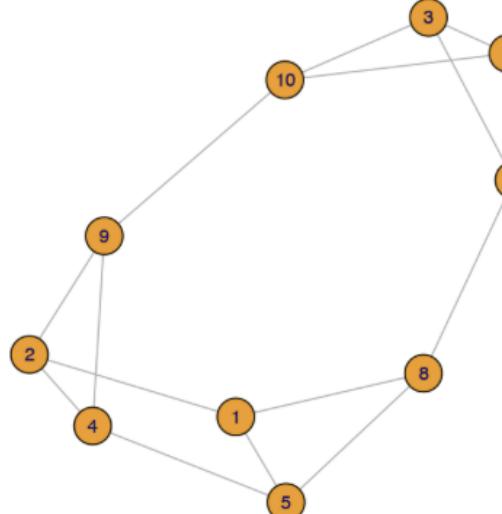
python-igraph

IGraph/M

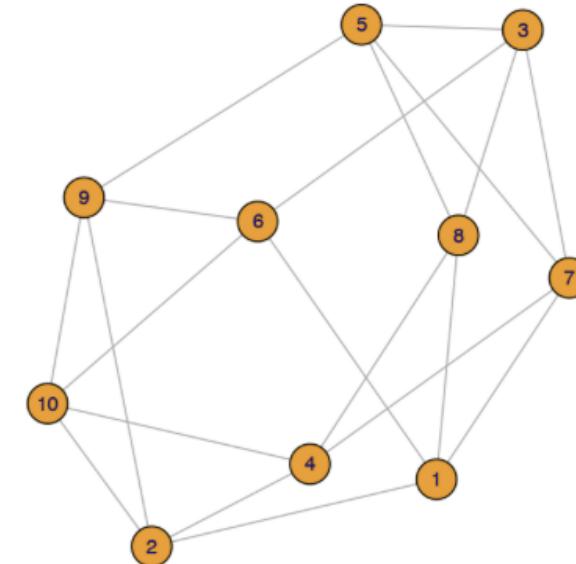
igraph C library



`plot(sample_k_regular(10, 2))`

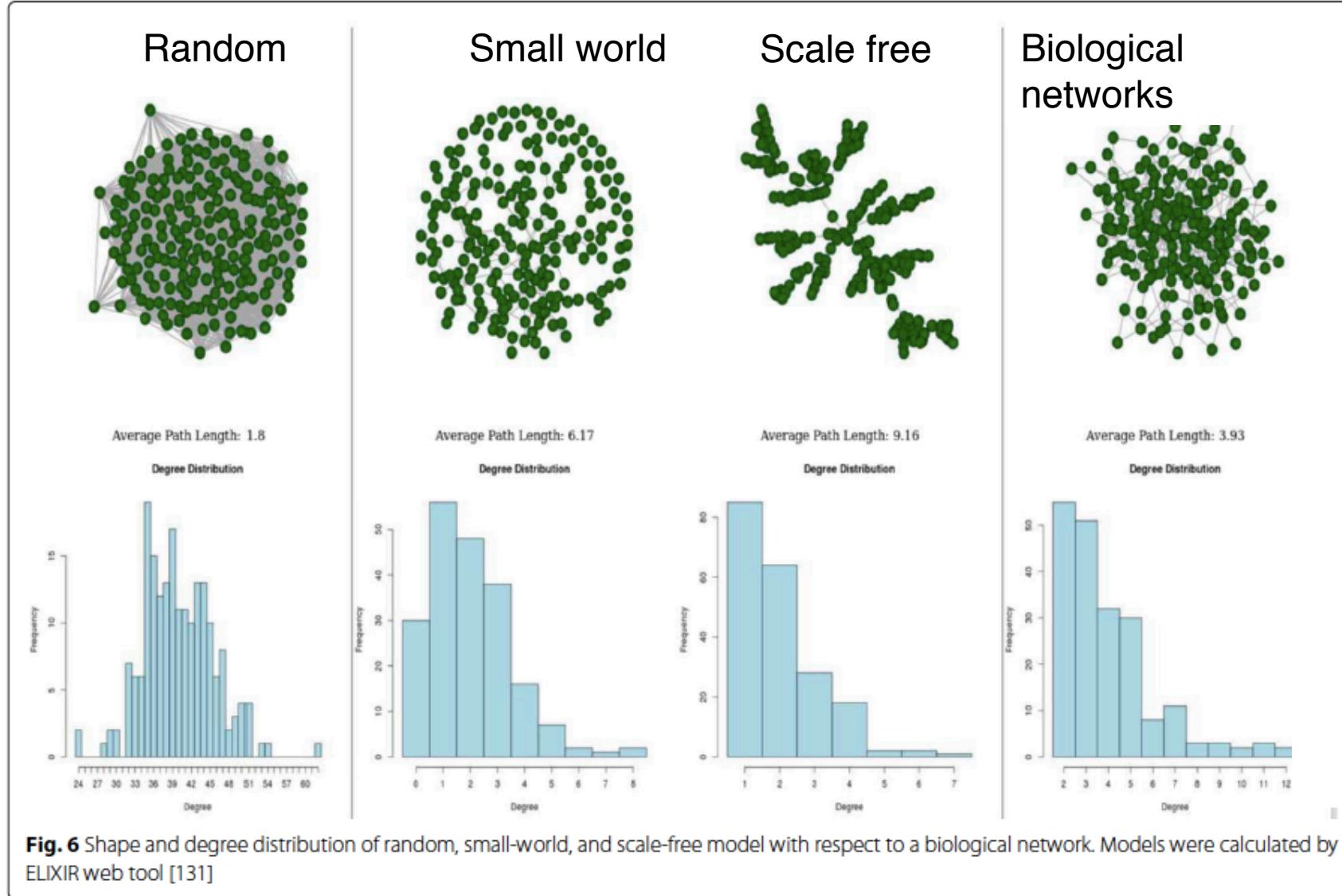


`plot(sample_k_regular(10, 3))`



`plot(sample_k_regular(10, 4))`

# Degree distribution can help us determine the type of network



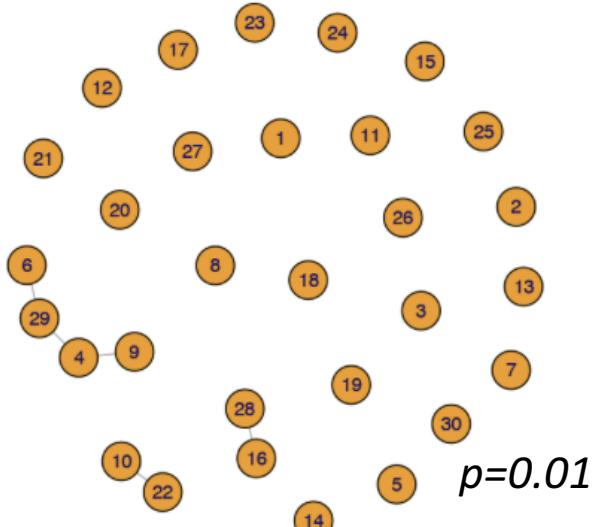
EURASIP Journal on  
Bioinformatics and Systems  
Biology 2017.1 (2017): 1-16.

# The random graph

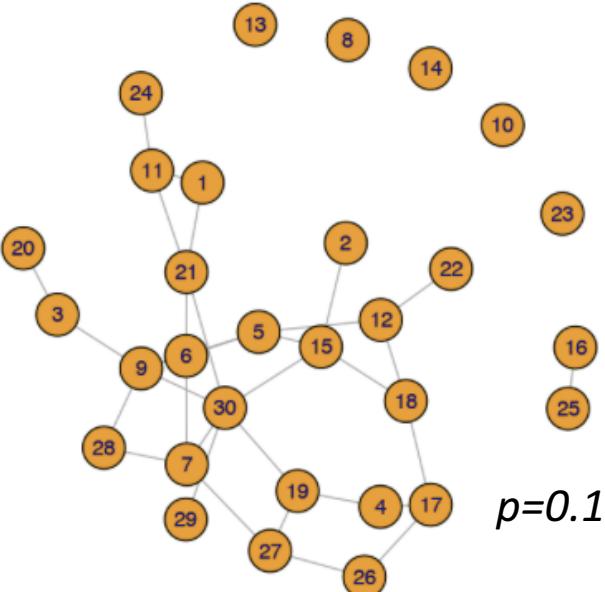
Erdős–Rényi model

$$P(k) = \binom{n-1}{k} p^k (1-p)^{n-1-k}$$

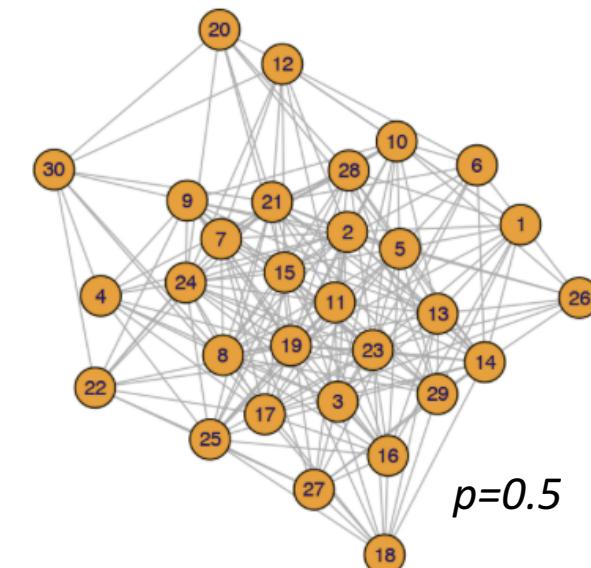
$$P(k) = e^{-\lambda} \frac{\lambda^k}{k!}$$



```
plot(sample_gnp(30, 0.01))
```

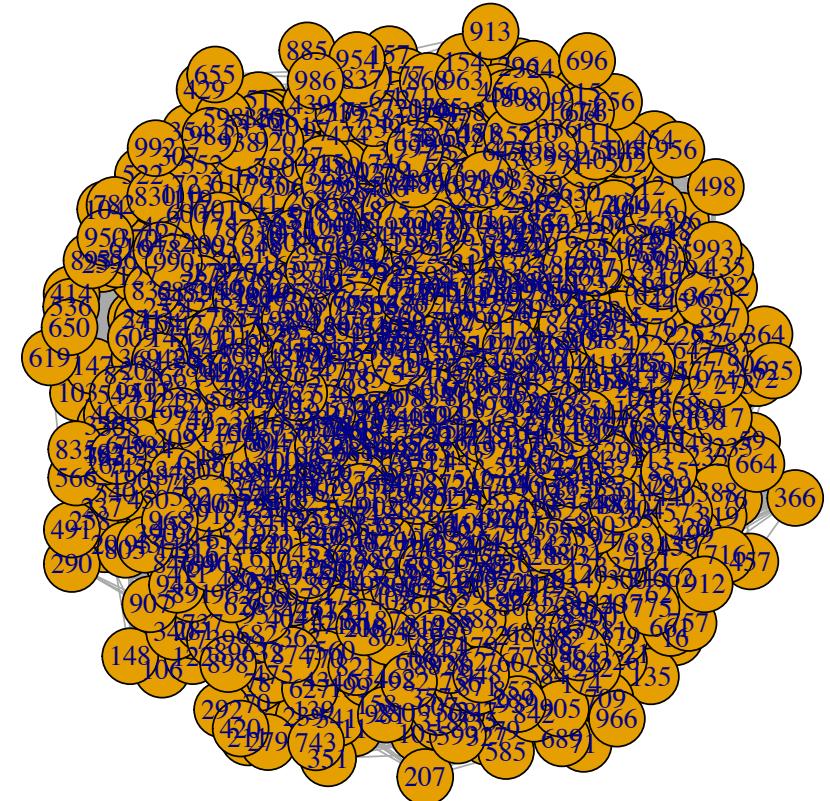
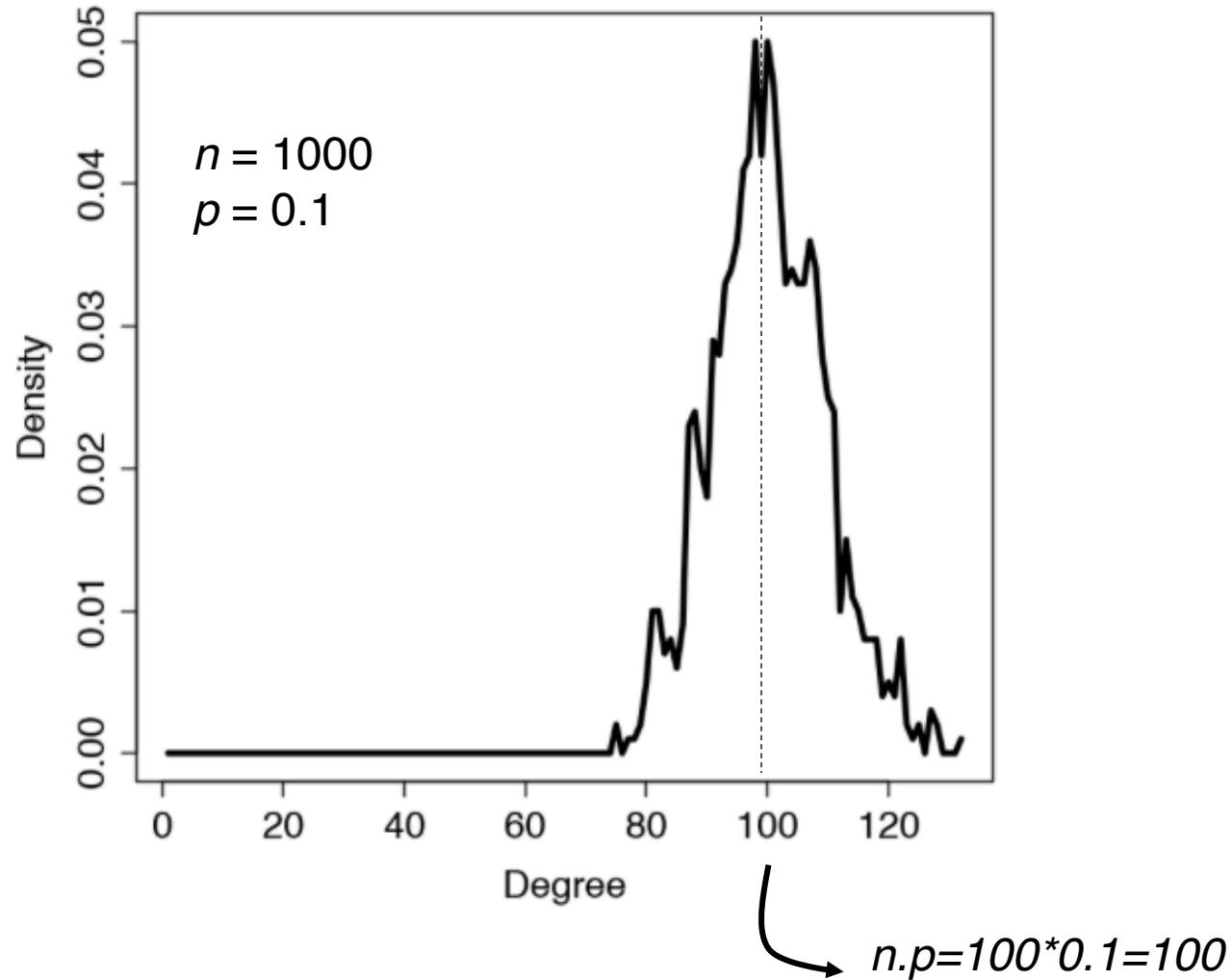


```
plot(sample_gnp(30, 0.1))
```

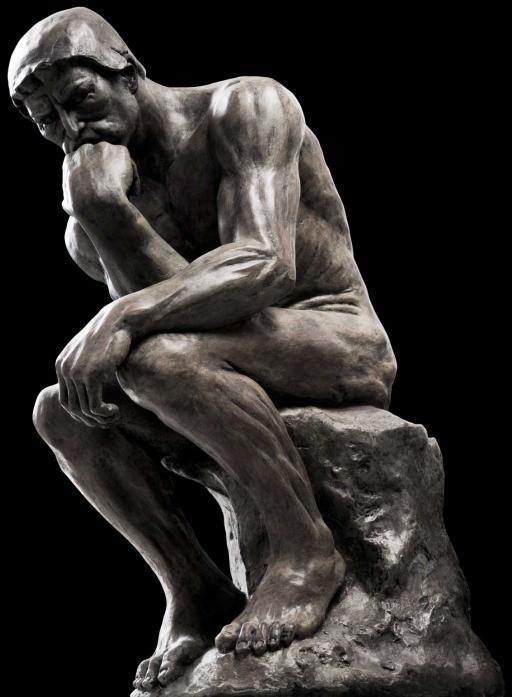


```
plot(sample_gnp(30, 0.5))
```

# The random graph

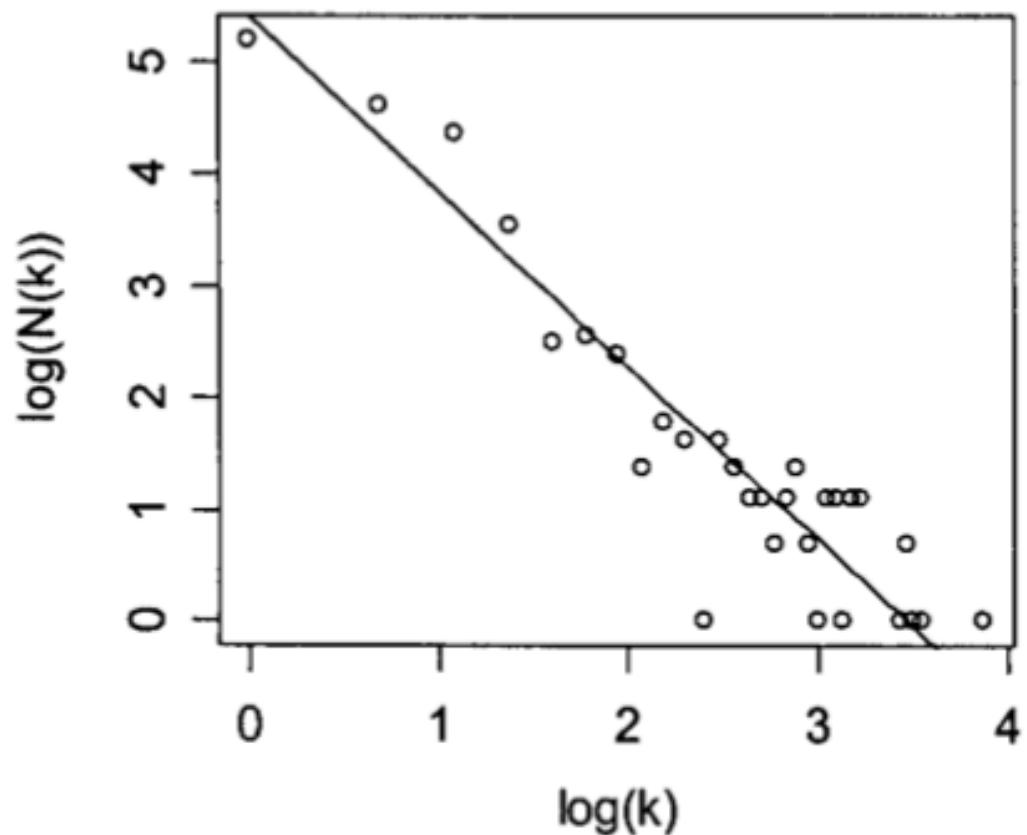


# Are biological networks random?



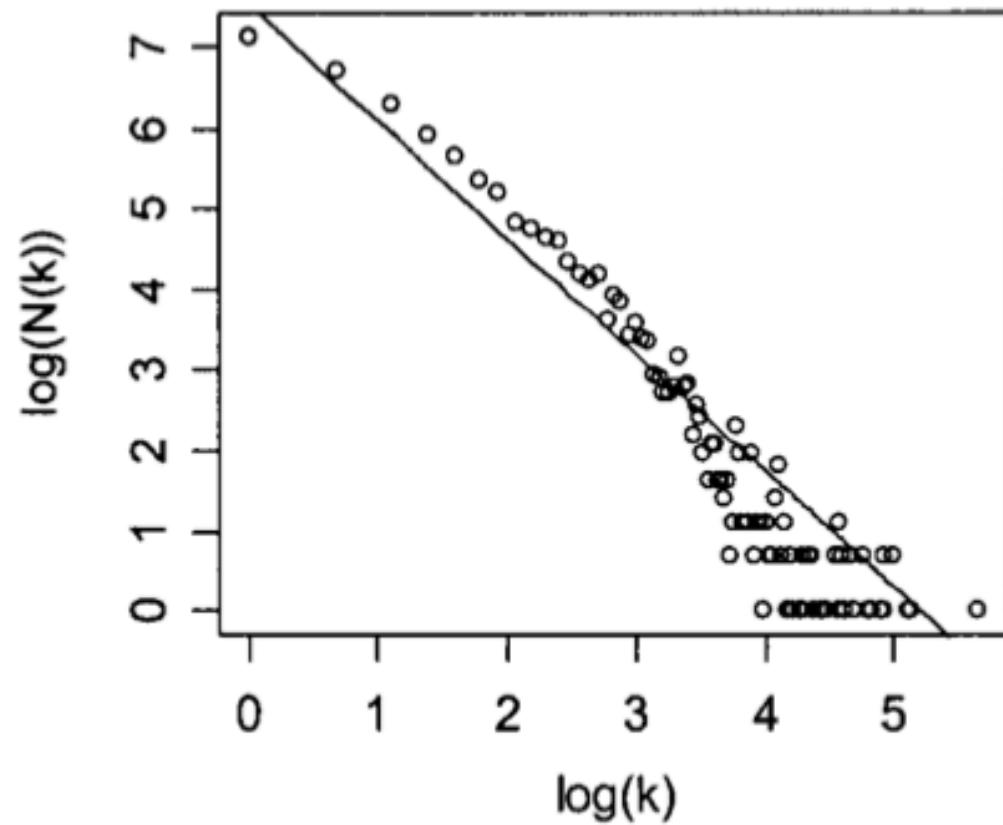
## Biological network are non-random

**Guelzim et al., 2002**



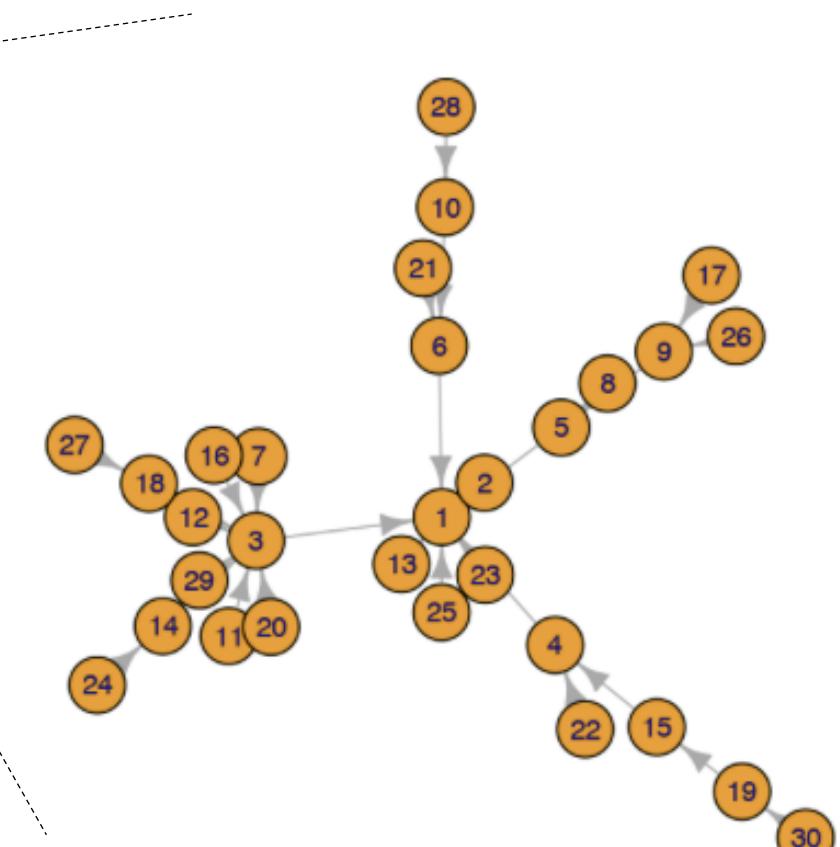
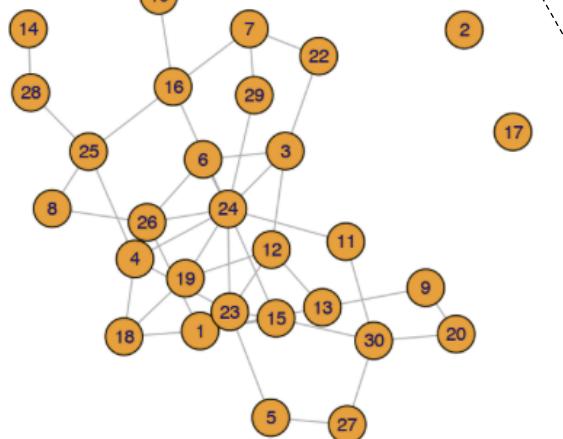
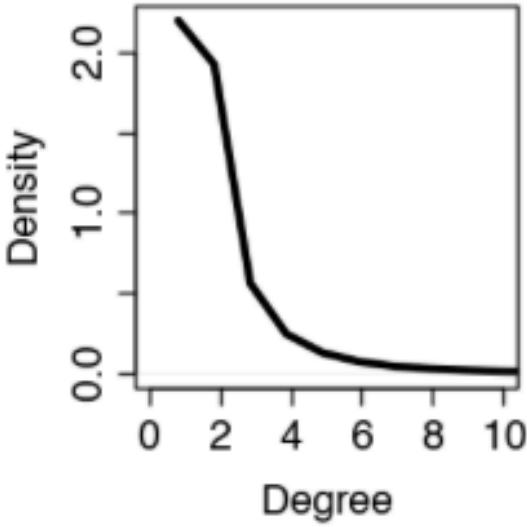
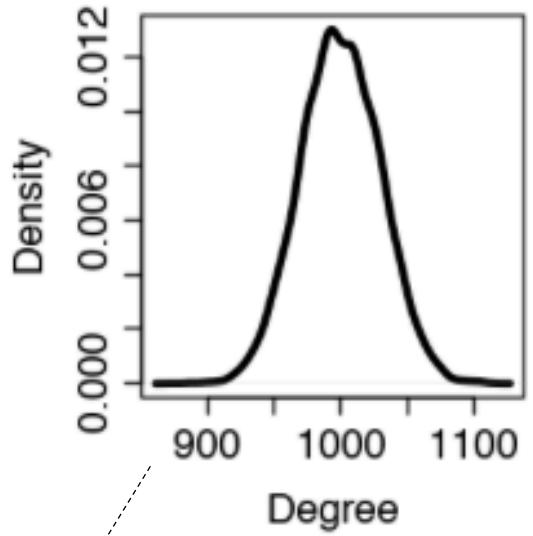
Transcriptional  
regulatory network

**Tong et al., 2004**



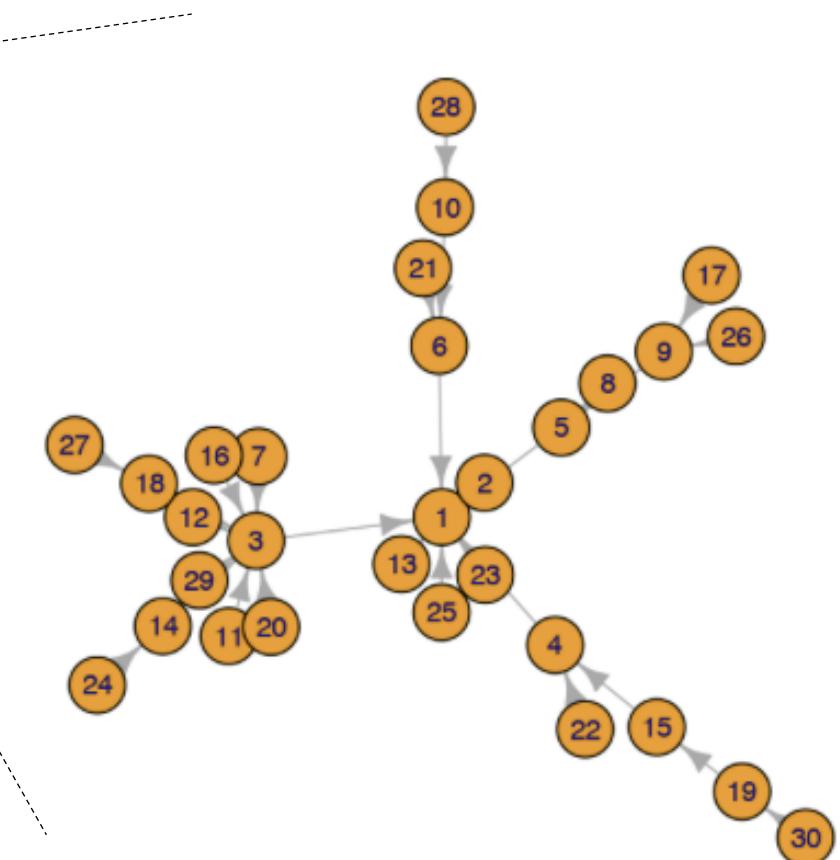
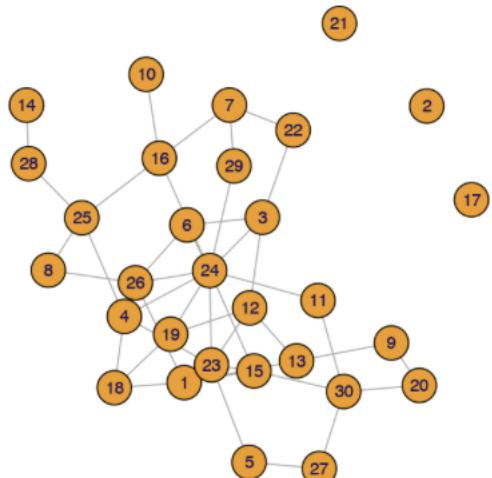
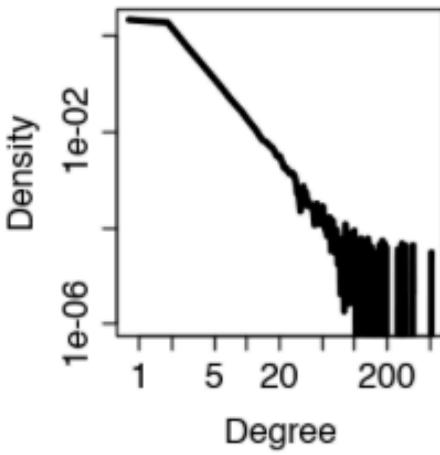
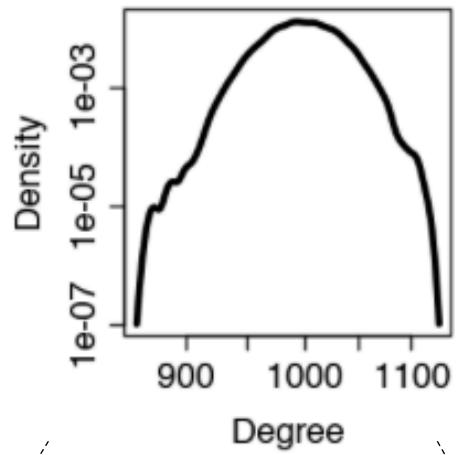
Genetic interaction  
network

# The random graph vs. scale-free graph



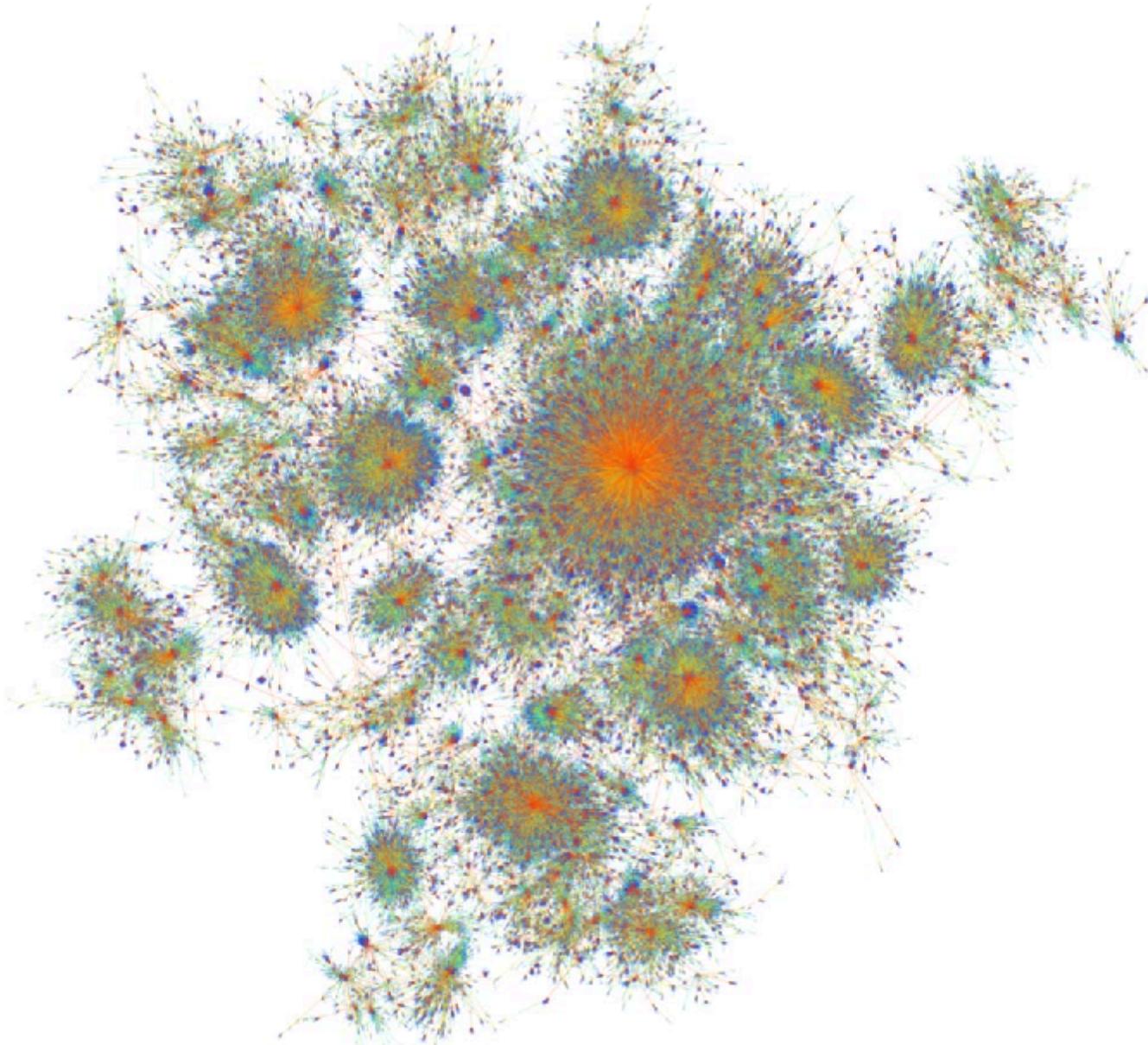
Linear-linear scale

# The random graph vs. scale-free graph



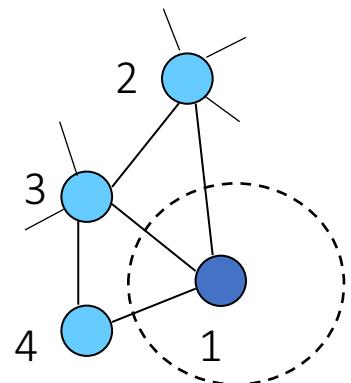
Log-log scale

## What is so special about scale-free networks?



# Nearest-neighbor degree of nodes

Average nearest neighbor degree of a node



$$k_1=3$$

$$k_2=5$$

$$k_3=5$$

$$k_4=2$$

$$k_{nn,1} = (1/3)(5+5+2) = 4$$

$$k_{nn,i} = \frac{1}{k_i} \sum_{j, \text{ nearest neighbors of } i} k_j$$

# Assortative vs. Disassortative networks

Average nearest neighbor degree of all nodes with degree  $k$

$$k_{nn,i} = \frac{1}{k_i} \sum_{j, \text{ nearest neighbors of } i} k_j$$

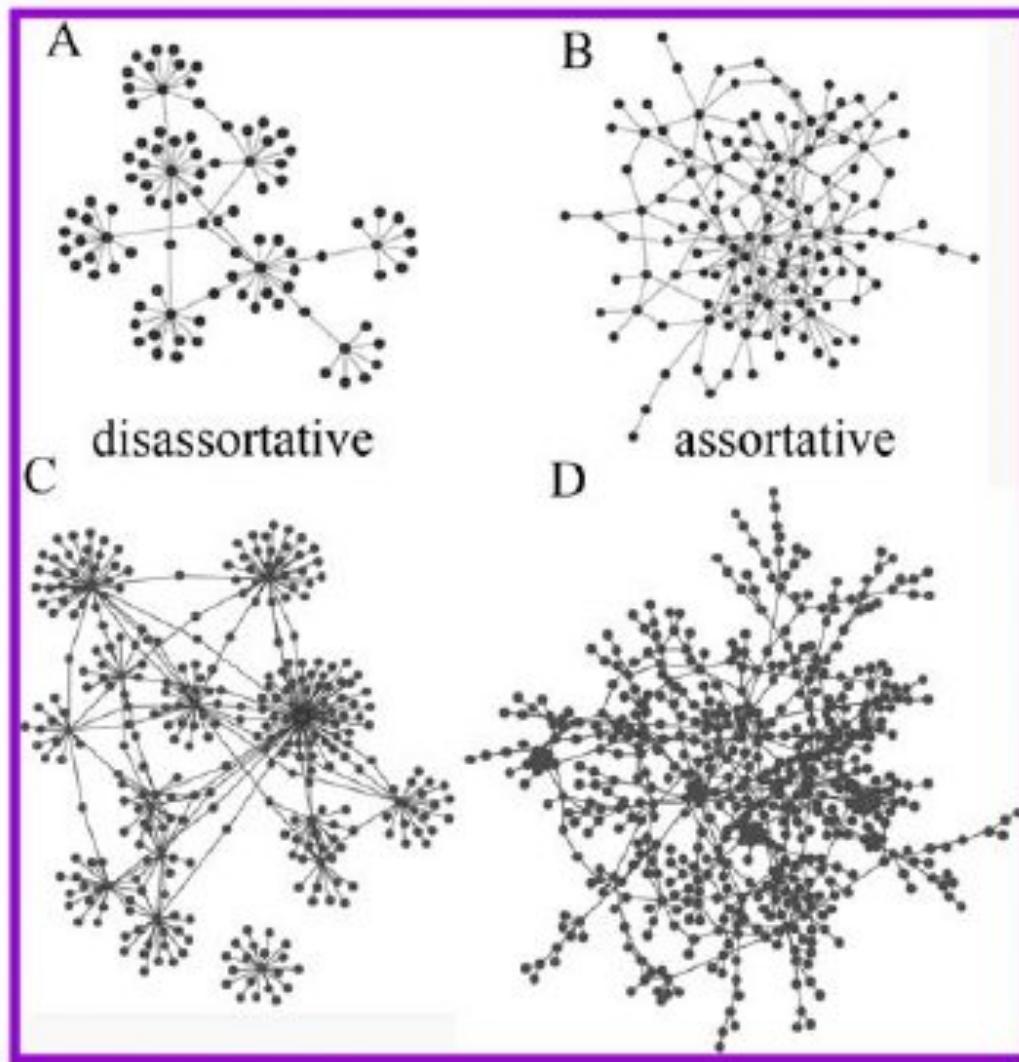
$N_k$ ...number of nodes with degree  $k$

$$k_{nn}(k) = \frac{1}{N_k} \left( \sum_{\text{nodes with degree } k} k_{nn,k} \right)$$

A graph is assortative if  $k_{nn}(k)$  increases with  $k$   
nodes connect to nodes of similar connectivity

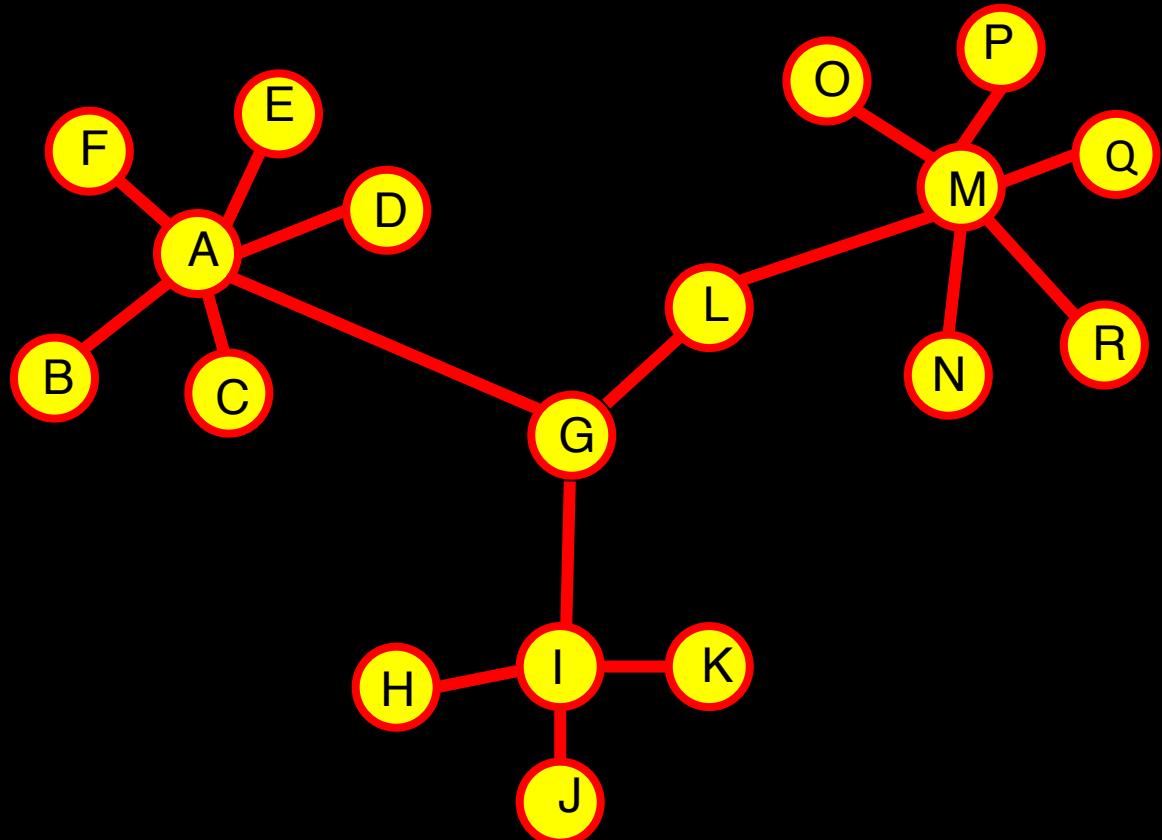
A graph is disassortive if  $k_{nn}(k)$  decreases with  $k$

## Assortative vs. Disassortative networks

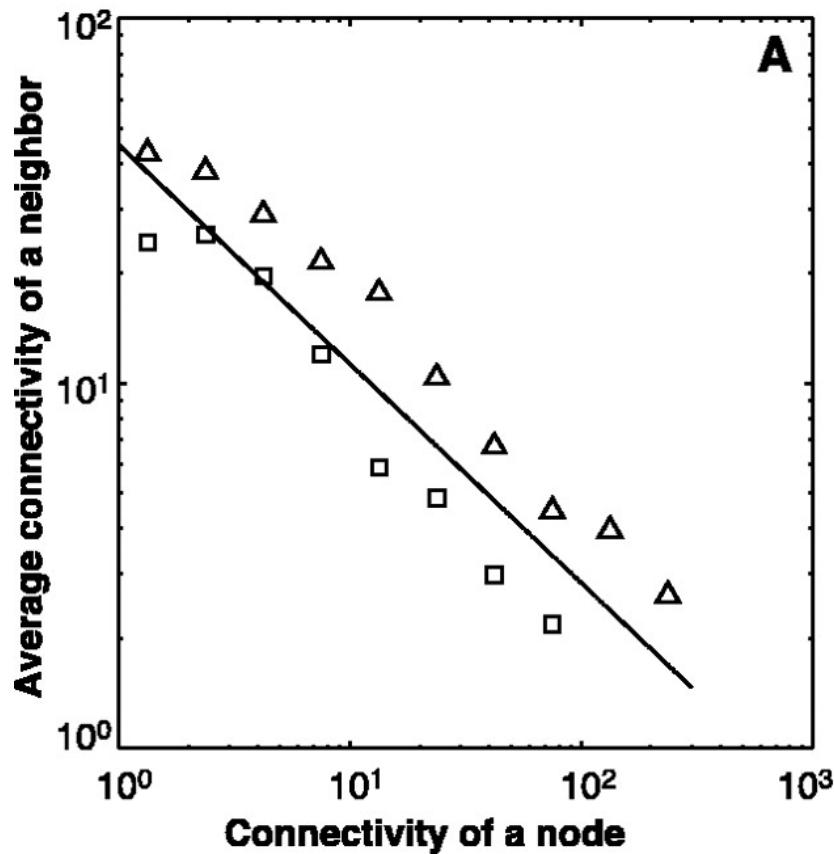


## Class activity:

With only three choices, how would you preserve or destroy the disassortative nature of the graph.



# Protein interaction networks are disassortative

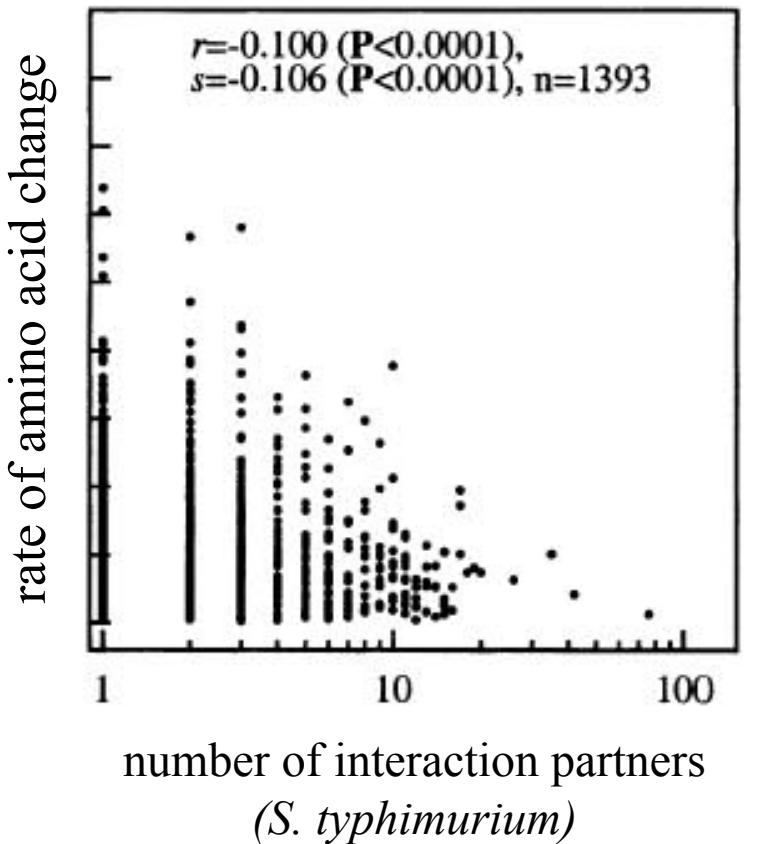


Plot of  $P_{nn}(k)$  against  $k$  for the yeast protein interaction network (triangles) and the transcriptional regulation network (squares)

Few interactions between hubs  
Many interactions between hubs and neighbors with low degree

Maslov and Sneppen, Science 2002

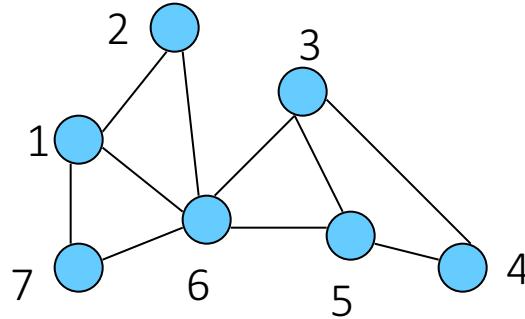
# Connectivity can effect the evolution of proteins!



**Highly connected proteins tolerate fewer amino acid substitutions in their evolution**

Hahn et al. Journal of Molecular Evolution 2004

## Measures of graph compactness: path length and diameter



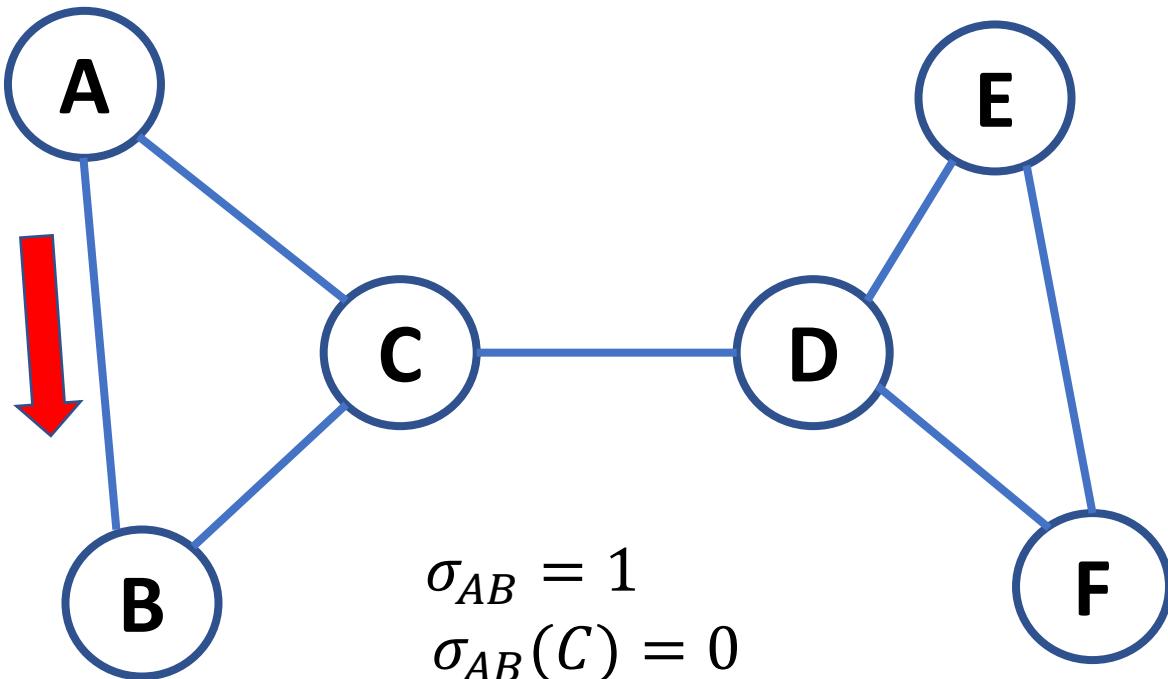
Matrix of shortest paths  $D=(d_{ij})$

$$D = \begin{pmatrix} 0 & 1 & 2 & 3 & 2 & 1 & 1 \\ 1 & 0 & 2 & 3 & 2 & 1 & 2 \\ 2 & 2 & 0 & 1 & 1 & 1 & 2 \\ 3 & 3 & 1 & 0 & 1 & 2 & 3 \\ 2 & 2 & 1 & 1 & 0 & 1 & 2 \\ 1 & 1 & 1 & 2 & 1 & 0 & 1 \\ 1 & 2 & 2 & 3 & 2 & 1 & 0 \end{pmatrix}$$

Connected graph:  $d_{ij} < \infty$  for all  $i, j$

## Betweenness centrality

Measure of centrality in a graph based on shortest path



$$\left. \begin{array}{l} \sigma_{uw} \\ \sigma_{uw}(v) \end{array} \right\}$$

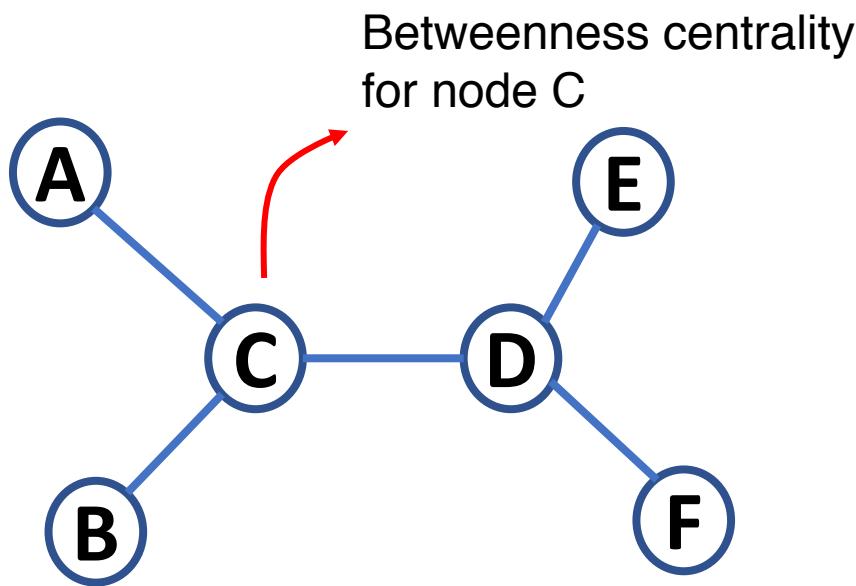
# of shortest path between nodes  
u and w

# of shortest path between nodes  
u and w that involve v

Betweenness centrality

$$= \frac{\sigma_{uw}(v)}{\sigma_{uw}}$$

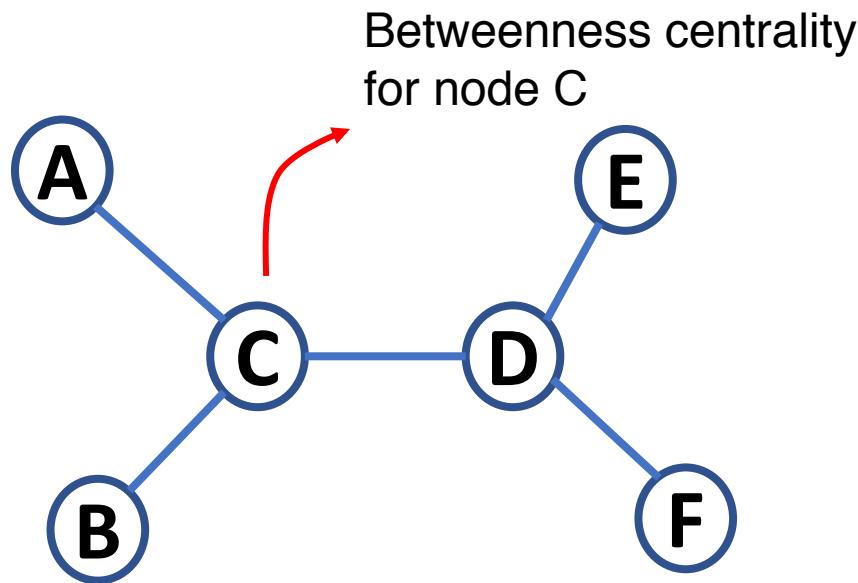
## Betweenness centrality



	$\sigma_{uw}$	$\sigma_{uw}(v)$	$\sigma_{uw}(v)/\sigma_{uw}$
(A,B)	1	0	0
(A,D)	1	1	1
(A,E)	1	1	1
(A,F)	1	1	1
(B,D)	1	1	1
(B,E)	1	1	1
(B,F)	1	1	1
(D,E)	1	0	0
(D,F)	1	0	0
(E,F)	1	0	0

Sum=6

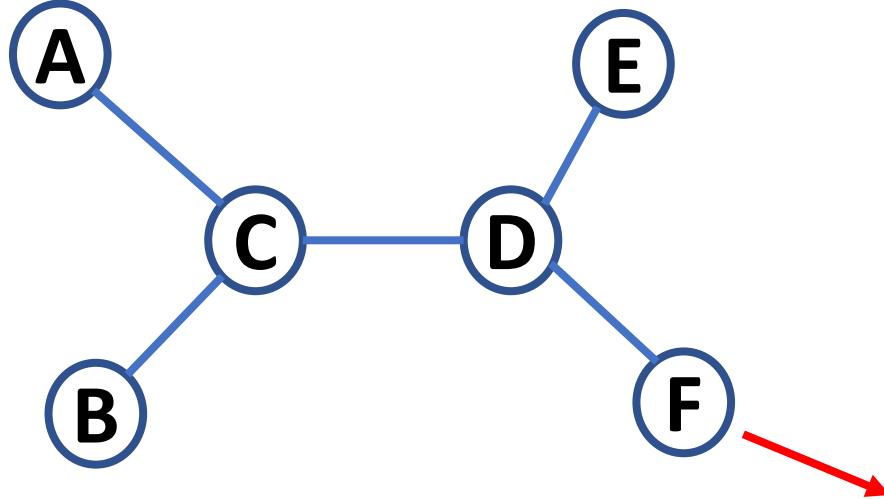
## Betweenness centrality



	$\sigma_{uw}$	$\sigma_{uw}(v)$	$\sigma_{uw}(v)/\sigma_{uw}$
(A,B)	1	0	0
(A,D)	1	1	1
(A,E)	1	1	1
(A,F)	1	1	1
(B,D)	1	1	1
(B,E)	1	1	1
(B,F)	1	1	1
(D,E)	1	0	0
(D,F)	1	0	0
(E,F)	1	0	0

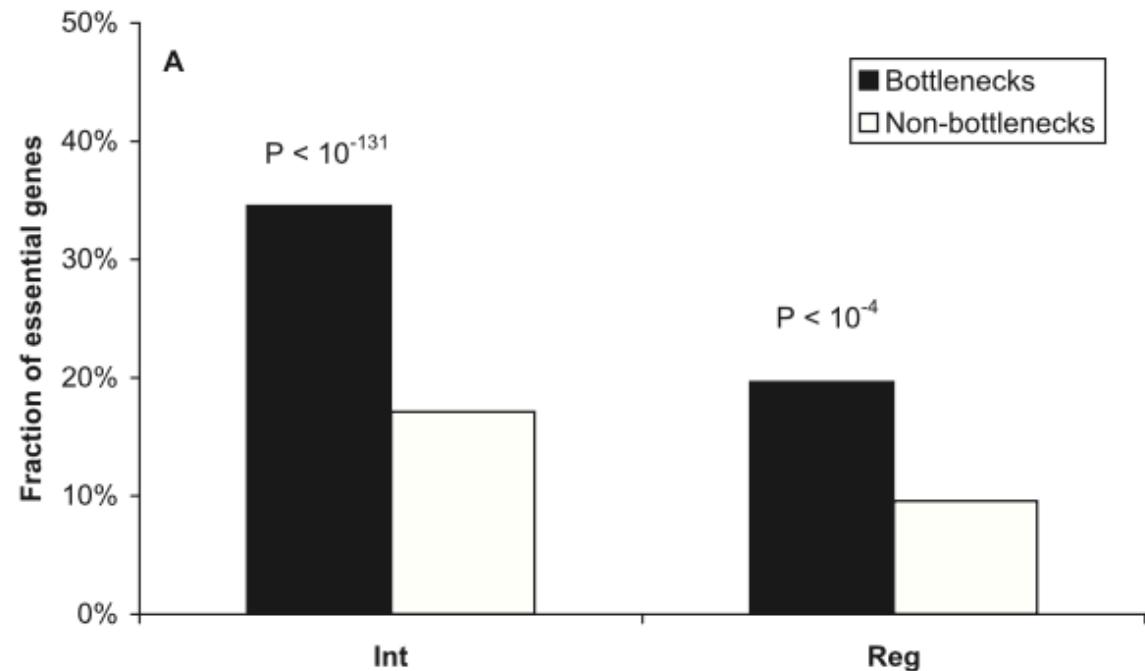
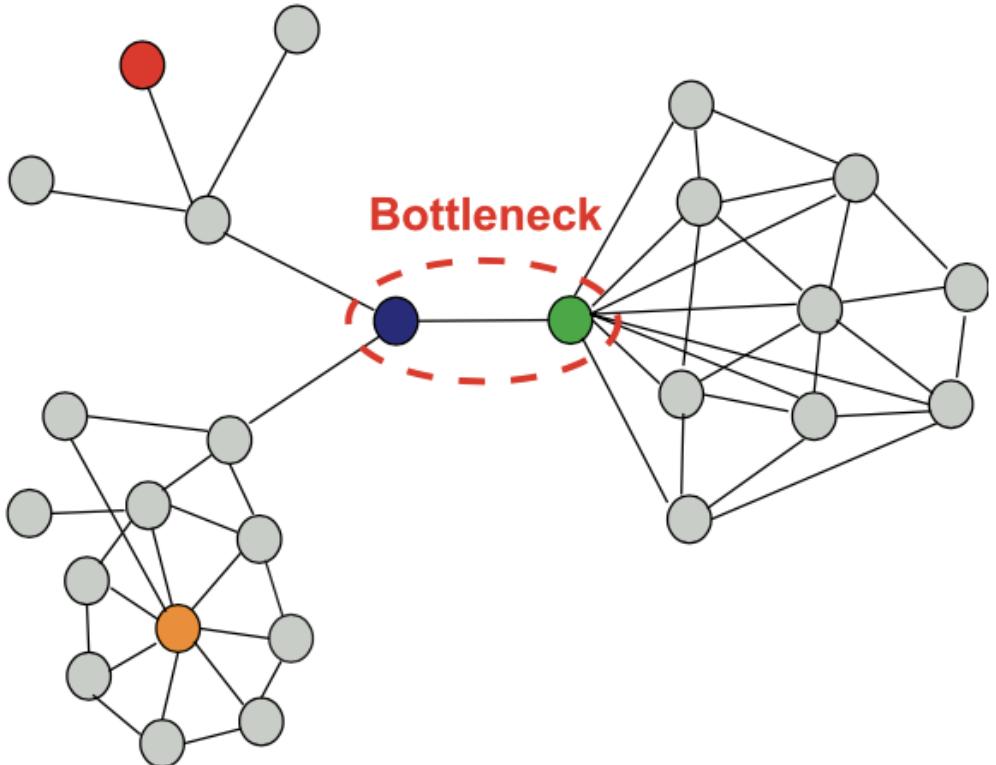
Sum=6

## Betweenness centrality



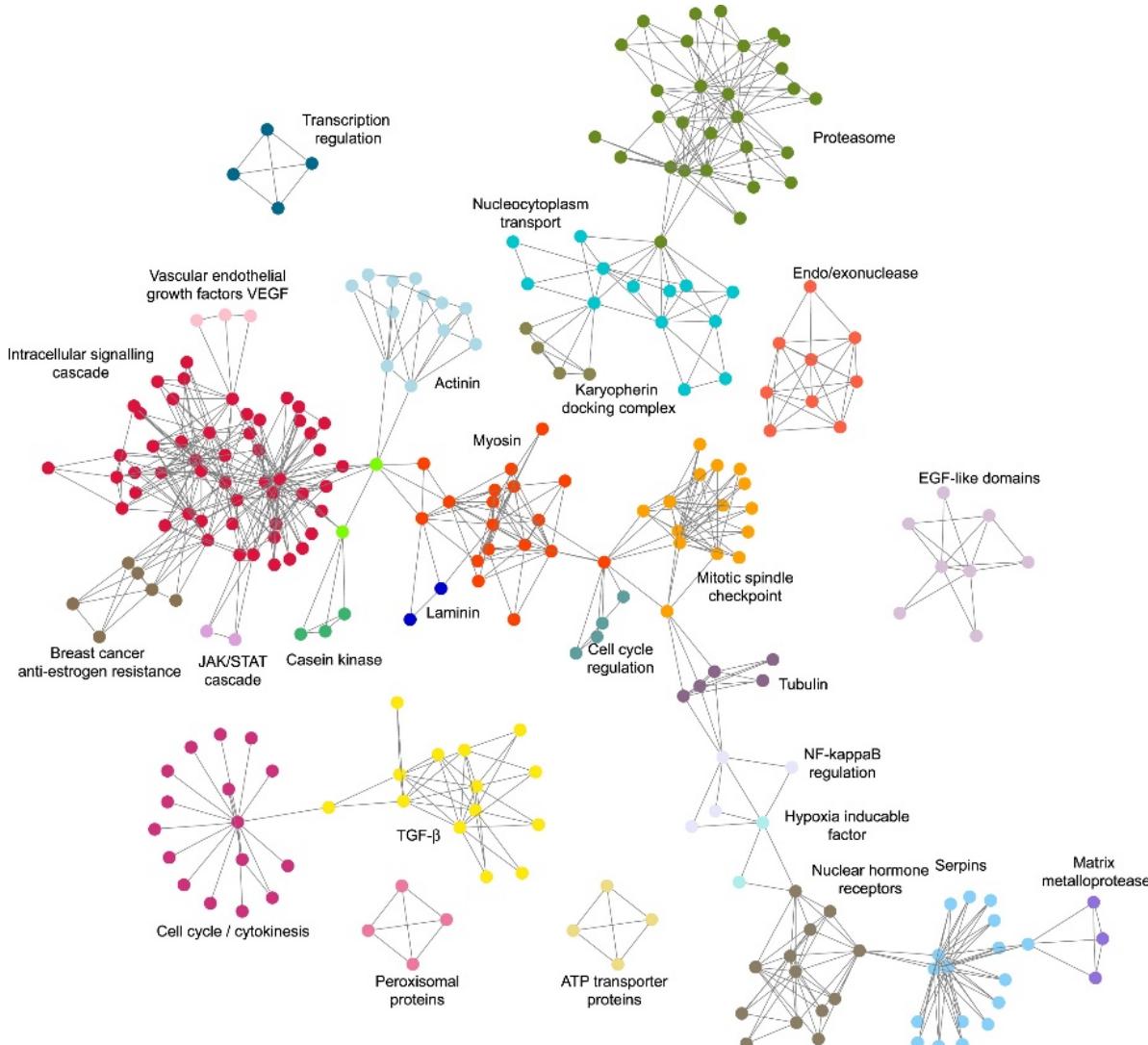
What is the betweenness centrality of the node F ?

# Bottlenecks have high betweenness centrality scores



Proteins with high betweenness scores  
tend to be more essential

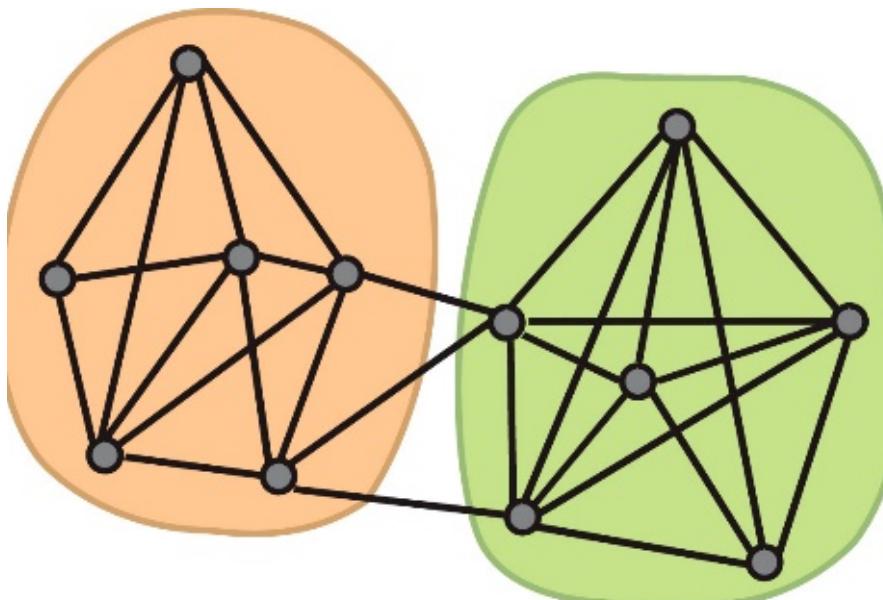
# Graphs can be subdivided into “communities”



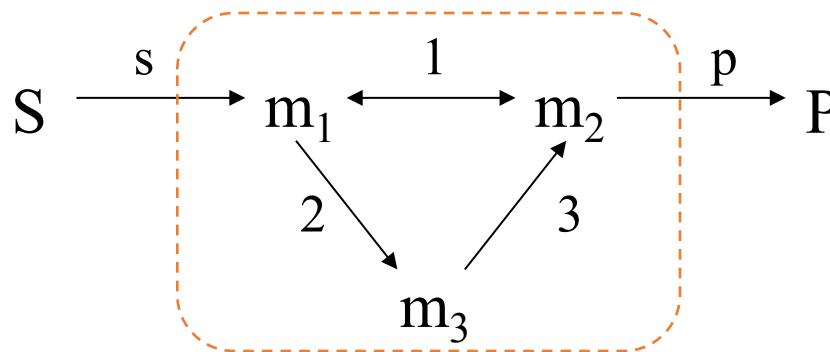
Community structure of a rat protein interaction network

## Graphs can be subdivided into “communities”

In a graph that can be subdivided into communities (clusters, modules) nodes fall into groups that share more edges with each other than with nodes outside the community



## We can do calculations with graphs



A chemical reaction network

Metabolite concentrations  $m_i$  change according to the equations

$$\frac{dm_1}{dt} = v_s - v_1 - v_2$$

$$\frac{dm_2}{dt} = v_1 + v_3 - v_p$$

$$\frac{dm_3}{dt} = v_2 - v_3$$

$$\frac{d\vec{m}}{dt} = \mathbf{S}\vec{v}$$

$$\mathbf{S} = \begin{pmatrix} 1 & -1 & -1 & 0 & 0 \\ 0 & 1 & 0 & 1 & -1 \\ 0 & 0 & 1 & -1 & 0 \end{pmatrix}$$

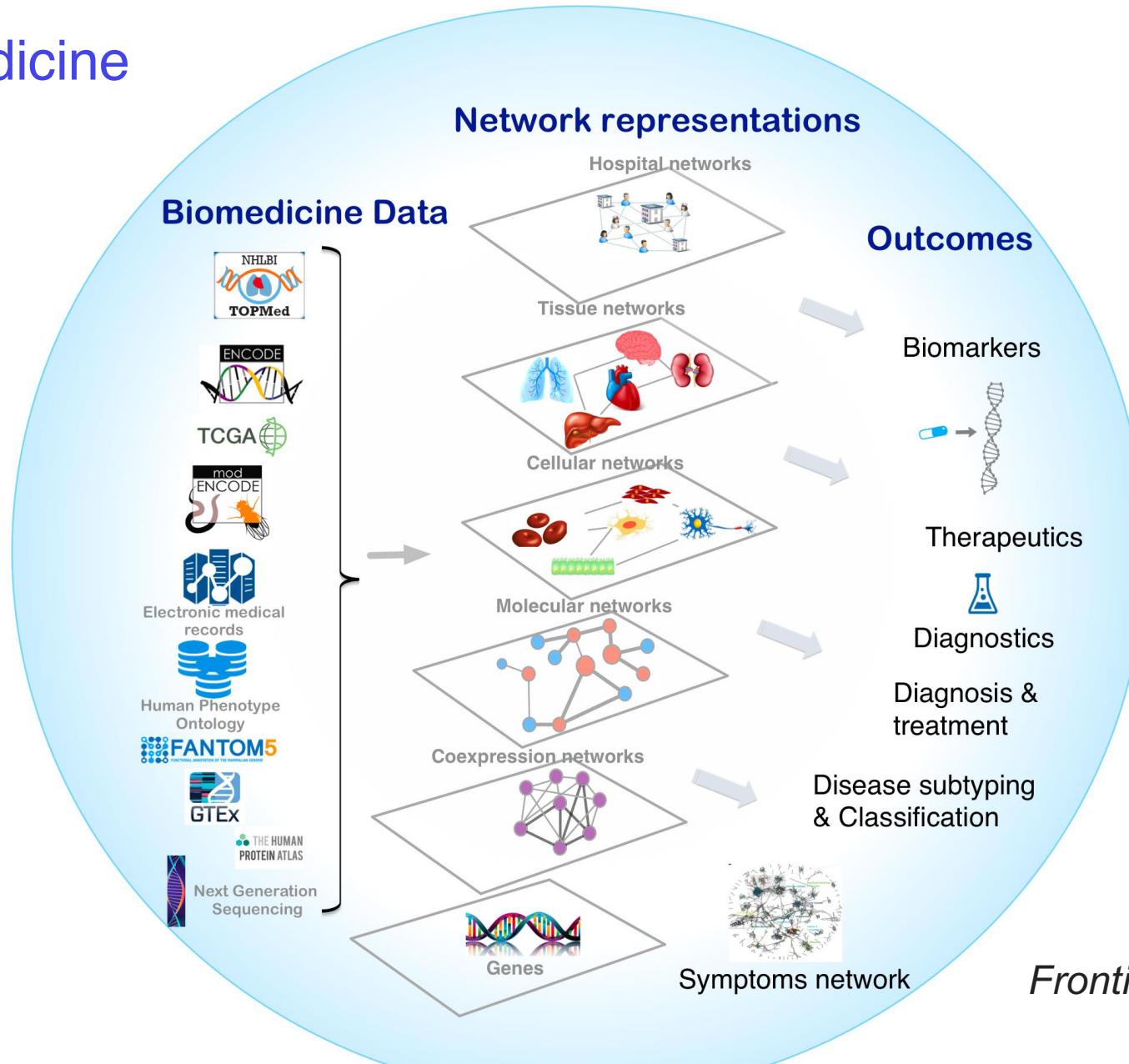
Stoichiometry matrix

$v_i$  metabolic flux through reaction i

$$\vec{v} = (v_s, v_1, v_2, v_3, v_p)^\top$$

Rows: metabolites  
Columns: reactions

# Network medicine



*Frontiers in Genetics* 10 (2019): 294.

## Concluding remarks

- Networks are everywhere! Biological systems also behave as interconnected networks.
- Several mathematical approaches and disciplines such as graph theory helps us model networks.
- We don't just visualize networks. We also use networks for:
  - Quantitative analyses
  - Predictions (Bayesian graph networks)
- Don't overlook the experimental approaches to build networks!
- Network theory can be used for diagnosis (Network medicine)

## Exam questions

