

# Biological network analysis

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SciLifeLab



# Overview

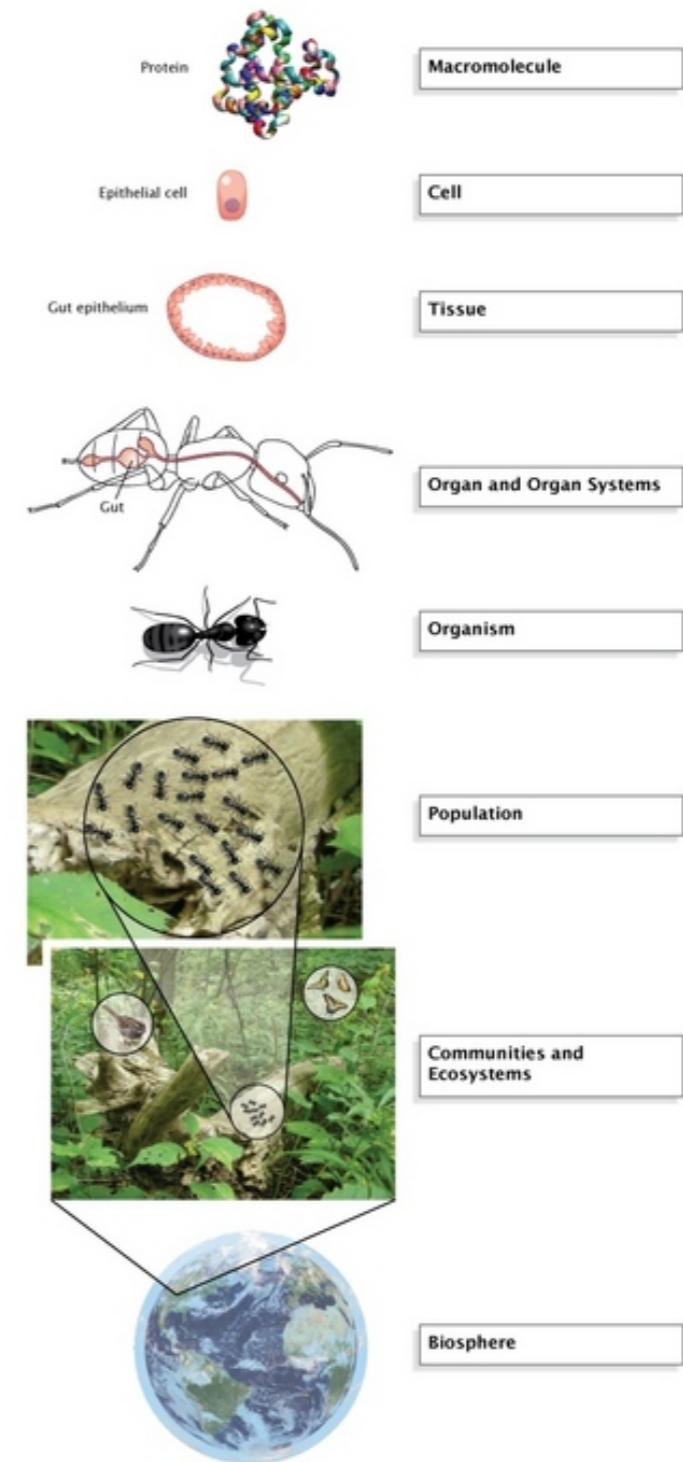
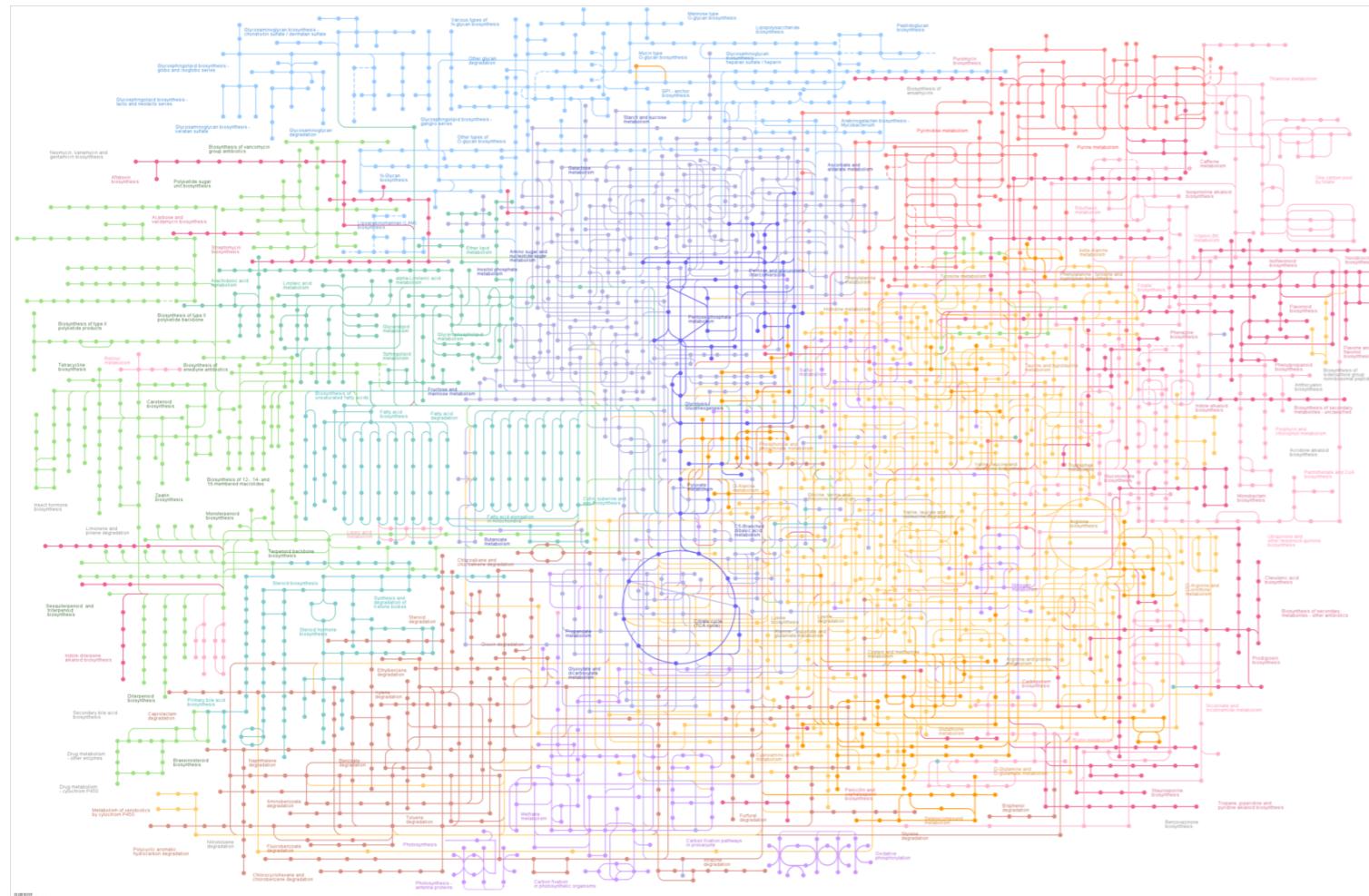
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1. Introduction to network analysis
2. Terminology
3. Network construction
4. Key network properties
5. Community analysis
6. Visualization
7. Workshop

# Introduction

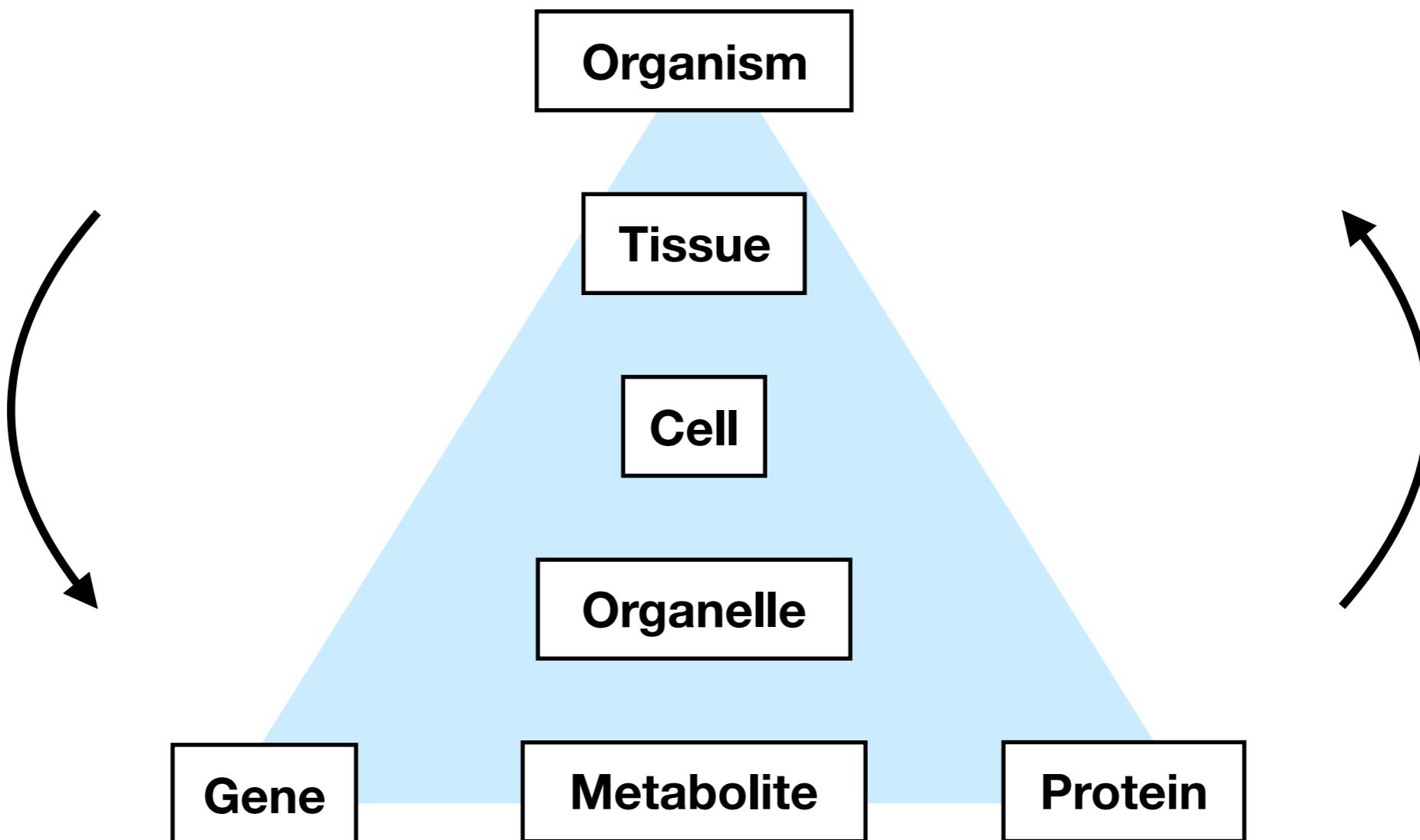
- [\*\*1. Introduction\*\*](#)
- [\*\*2. Terminology\*\*](#)
- [\*\*3. Network construction\*\*](#)
- [\*\*4. Key properties\*\*](#)
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# Biological complexity under attack



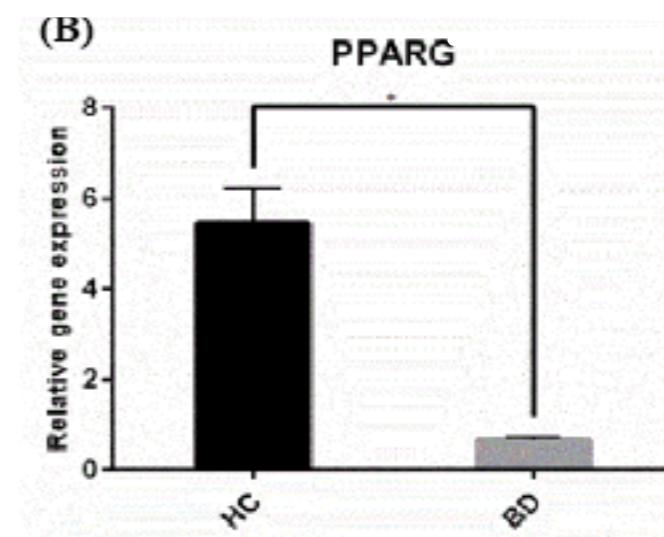
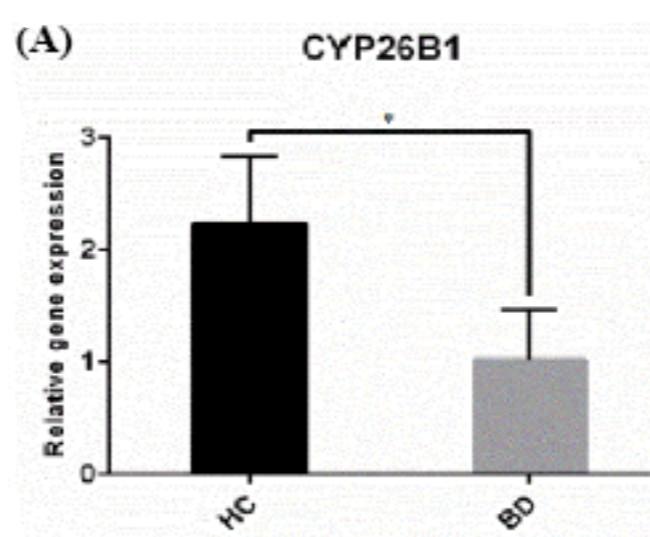
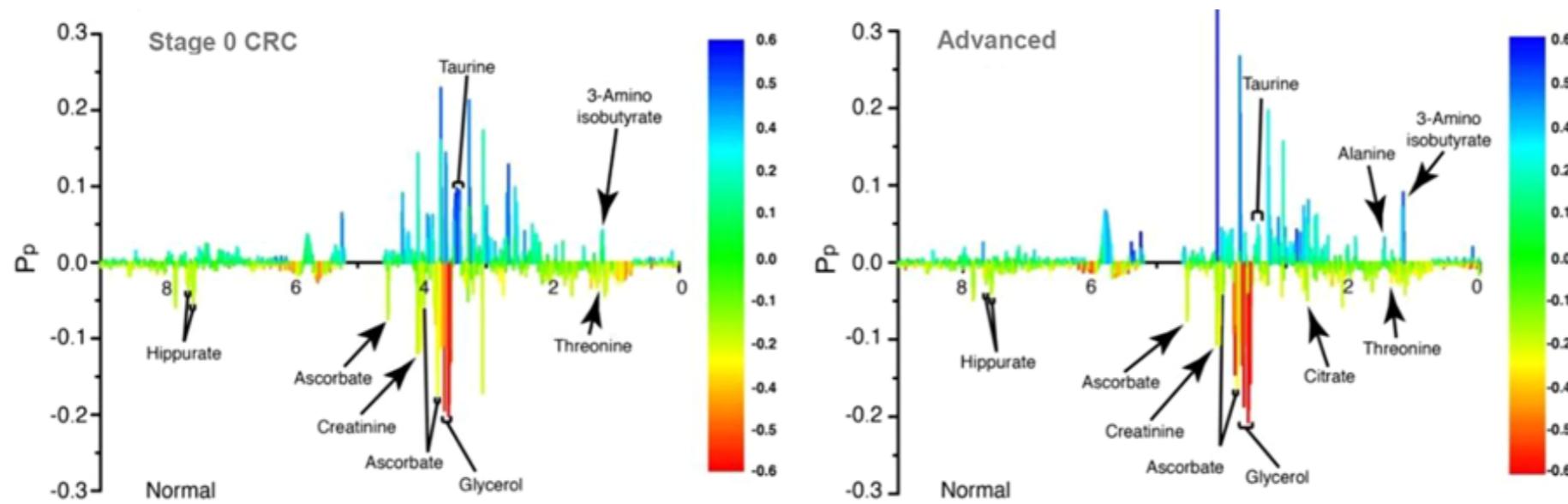
# How to tackle biological complexity?

Moving from reductionist approaches towards global characterisations



# How to tackle biological complexity?

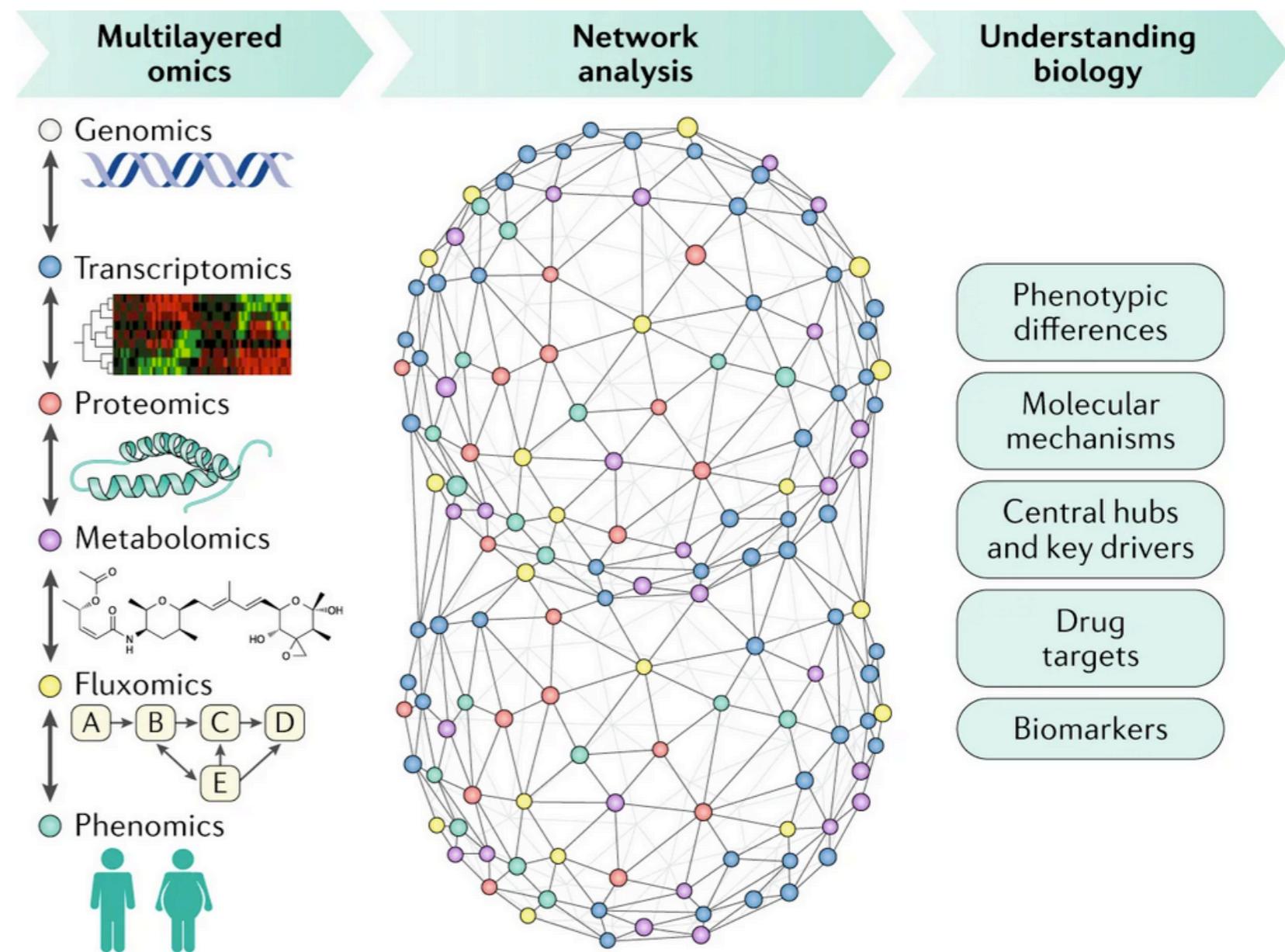
Moving beyond reductionist approaches



# How to tackle biological complexity?

Integrative approaches, and global patterns

- Feature association
- Modeling
- Network analysis



# What are networks?

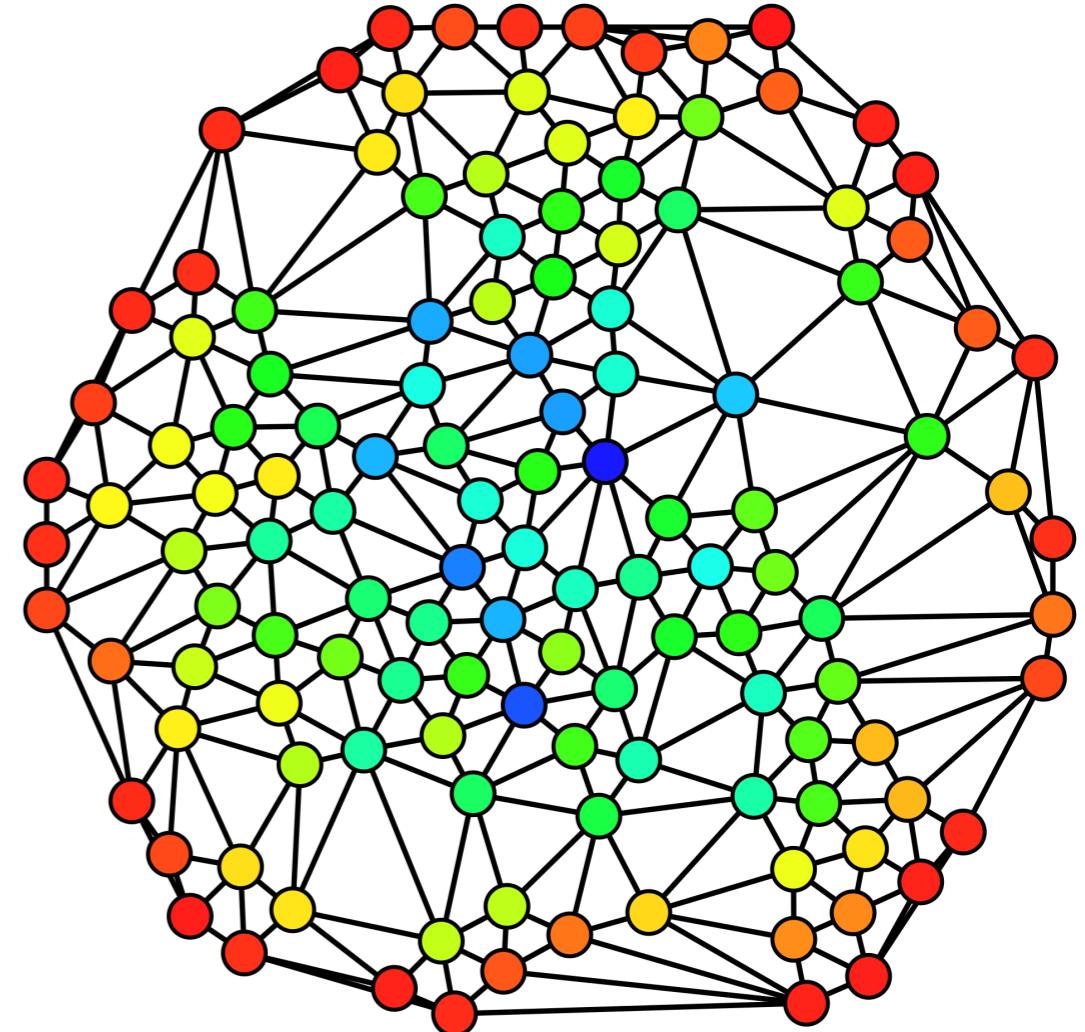
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Networks are representations of complex systems

Permit defining and studying global properties of interacting components

Give us insight not easily achieved by other approaches:

- Comprehensive
- Coordinated



# What are networks?

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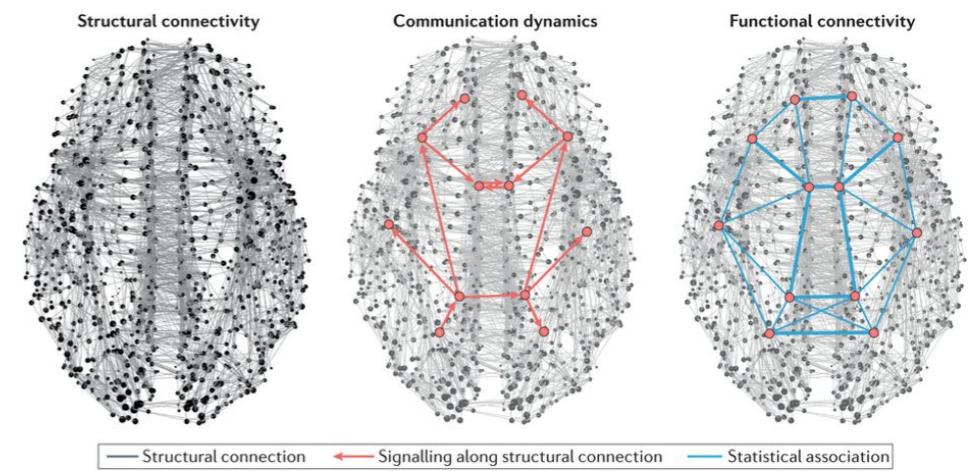
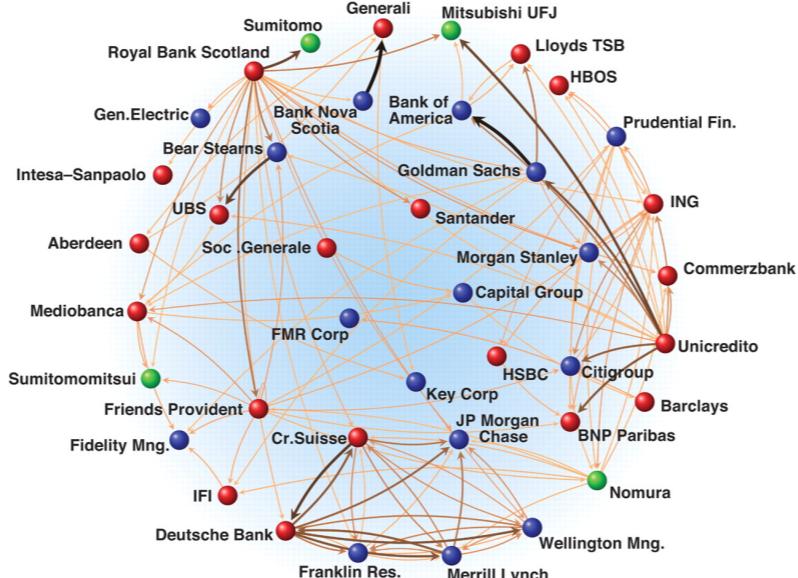
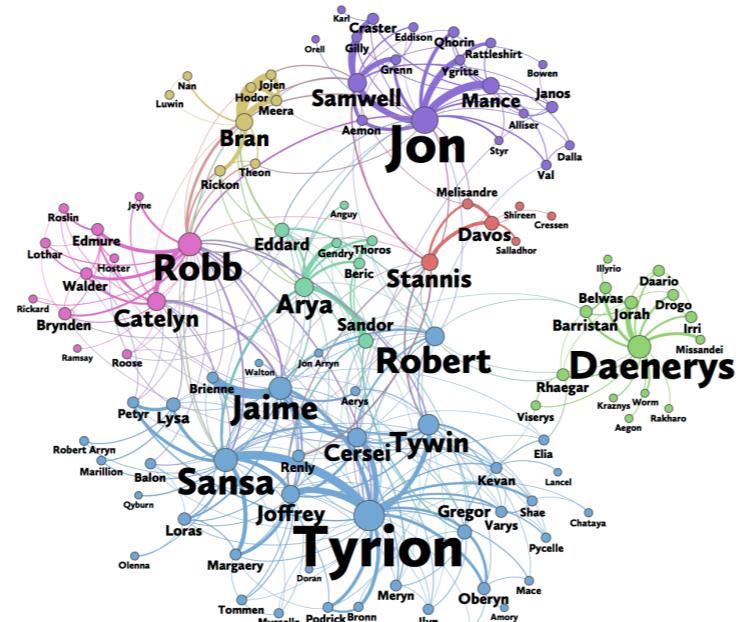
# What are networks?

## Social

# Economic

# Communication

# Neuronal



# What are biological networks?

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# What are biological networks?

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Protein - Protein interaction (PPI) networks

Transcription-factor regulatory networks

Gene - gene co-expression networks

Signal transduction networks

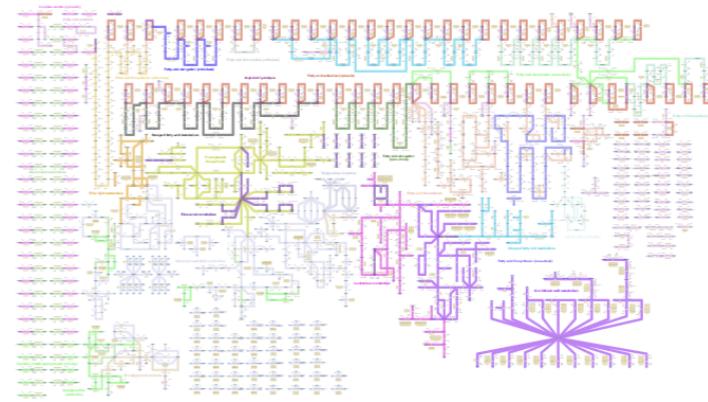
Transcription-Factor Regulatory networks

Drug-disease association networks

Aim  
**Functional characterisations**

# What are biological networks?

Metabolite - Enzyme - Signal - Genes (GEMs)

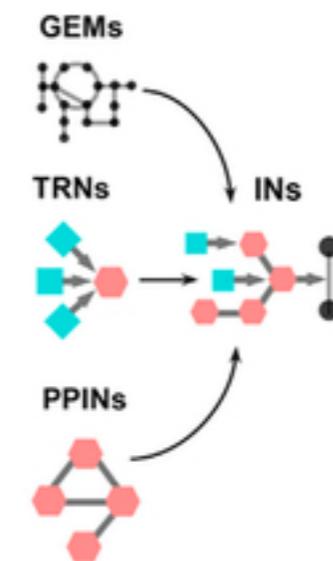
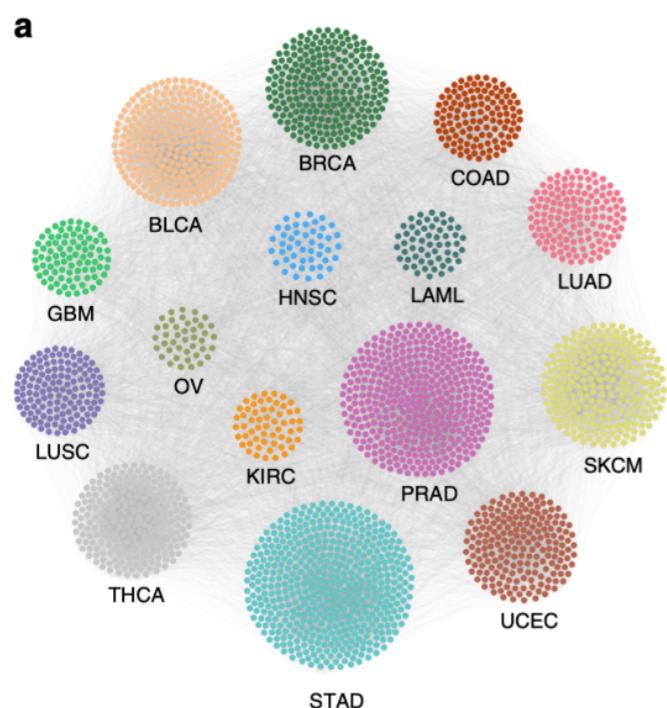
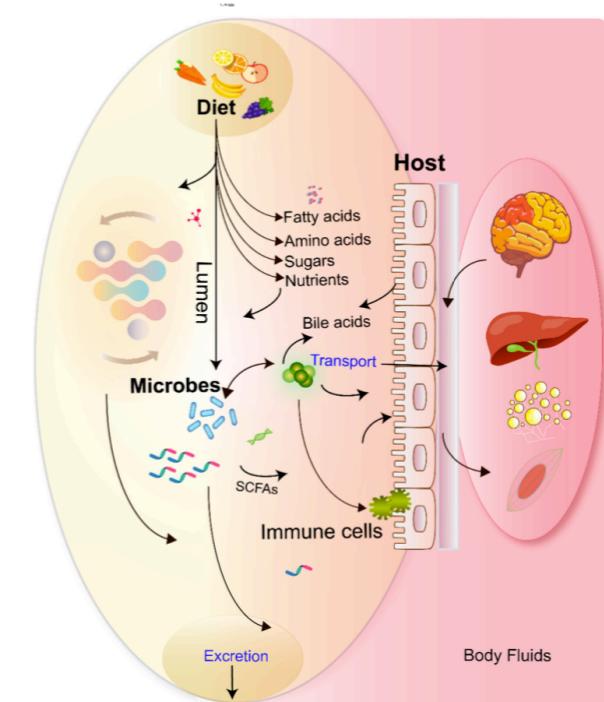
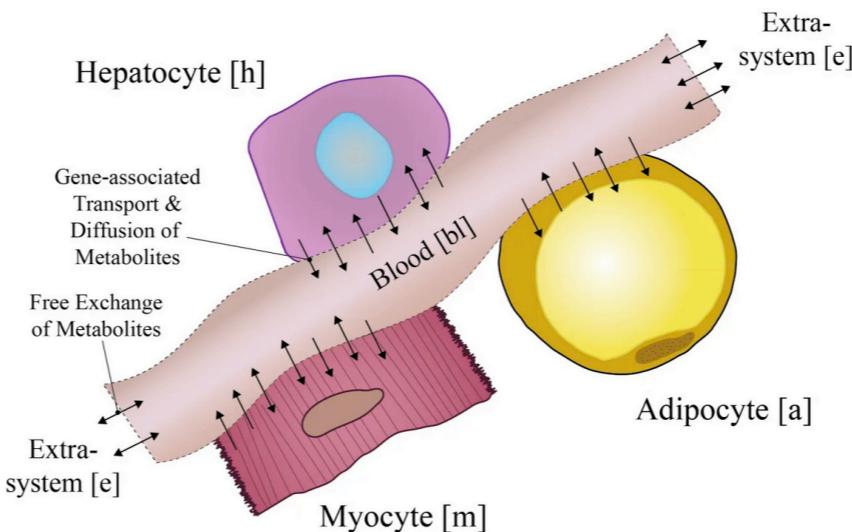


Multi-tissue networks

Multi-species networks

Cancer-disease networks

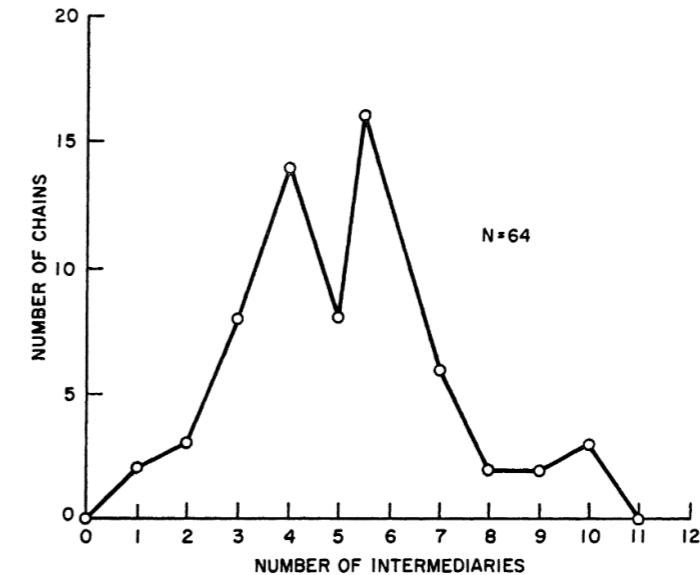
Integrated networks



# Small world

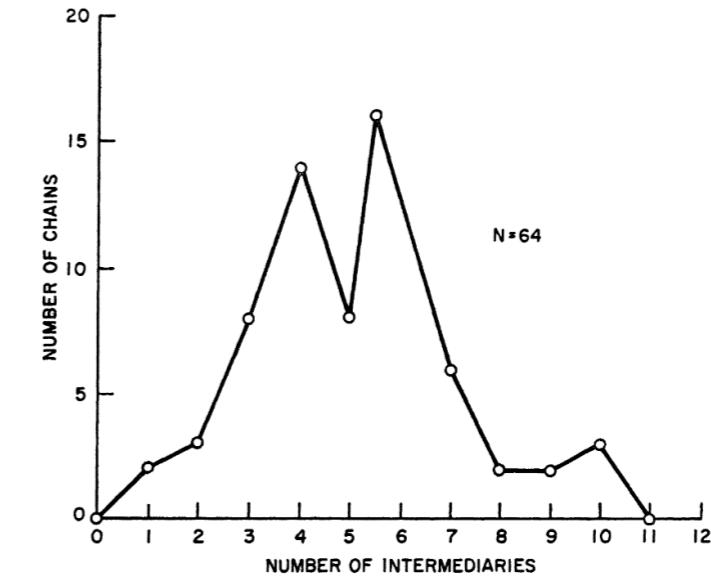
Stanley Milgram (1967) - 6 degrees

- 64 / 296 letters successful

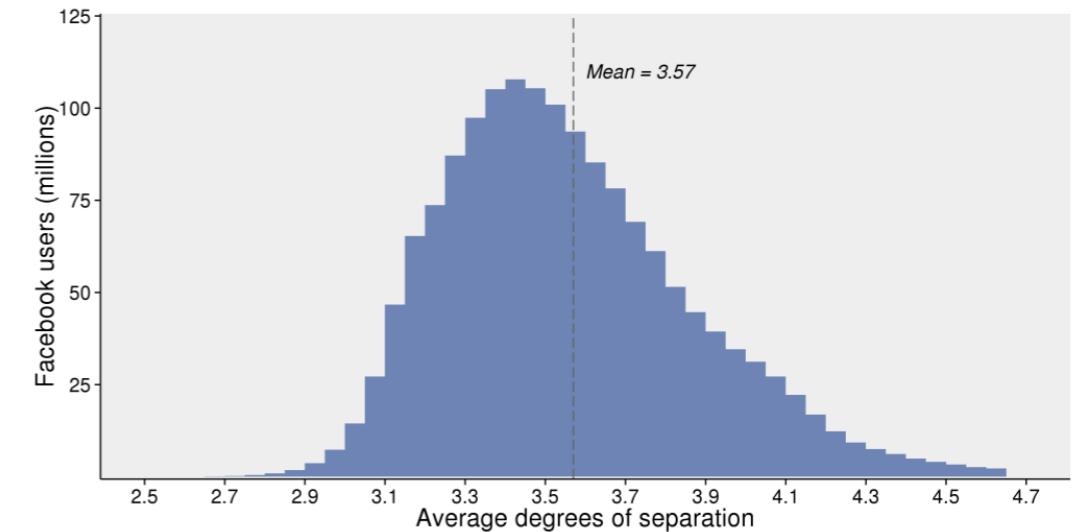


# Small world

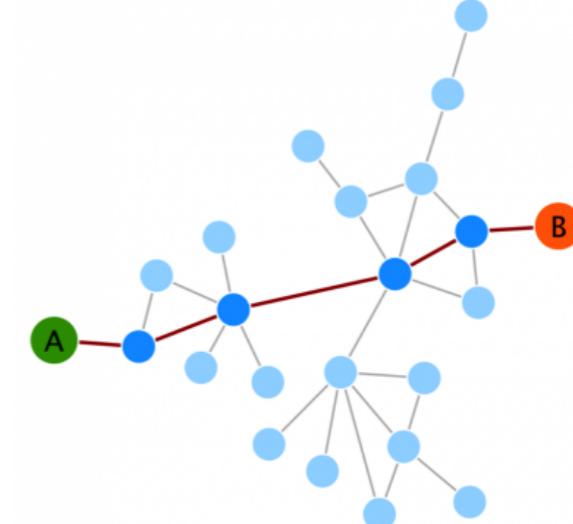
Stanley Milgram (1967) - 6 degrees



Backstrom et al. (2016) - 3.6 degrees



Biological Networks



# Why look at network topology?

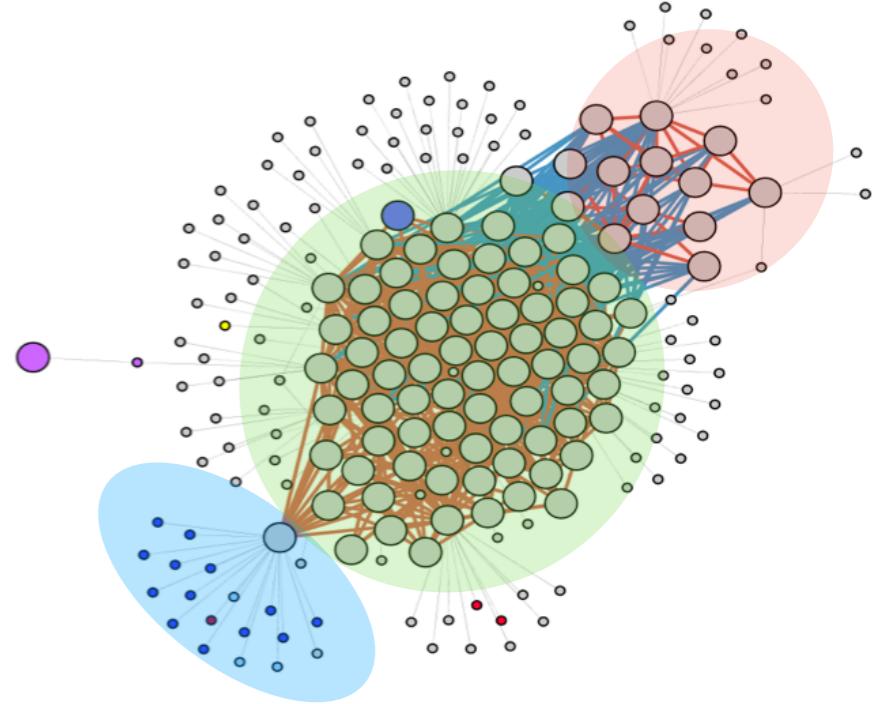
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Use networked systems to identify:

- Identify global / local patterns
- Identify functional properties
- Make predictions

Examples:

- How associated are the elements of my network?
- What are its first-hand associated elements?
- What are the groups of closely-associated elements in my network?
- What are their functional relationships?
- What are the "weakest" links in the network?



# What is my biological network?

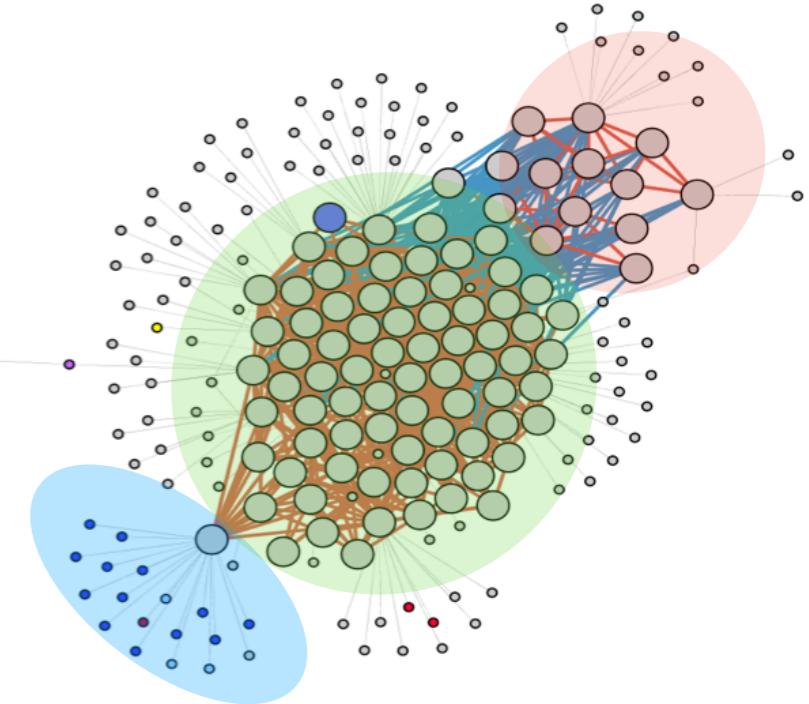
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Any association matrix may be translated to a network format

Many standard analyses may be employed regardless of data type

...but care must be taken in generating the network

Some of the functional analyses depend on annotation



# Limitations

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Sample size

False discovery

*~requires high throughput*

(further discussed in following lectures)

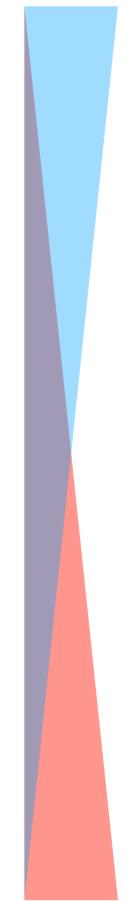
# Terminology and initial properties in graph analysis

1. Introduction
- 2. Terminology**
3. Network construction
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# Motivation

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What modeling formalism suits your data and biological question?

	Pros	Cons	Details
<b><u>Kinetic models</u></b>	Detailed Quantitative Dynamic / Steady state	Small Requires detailed parameterization	
<b><u>Stoichiometric</u></b>	Large Semi-quantitative Steady state	Static	
<b><u>Topological</u></b>	Large Only topological information	No dynamic properties	<b>Size</b>

# Graphs, nodes, edges

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Graph G consists of a set of **nodes** (V) interconnected by **edges** (E)

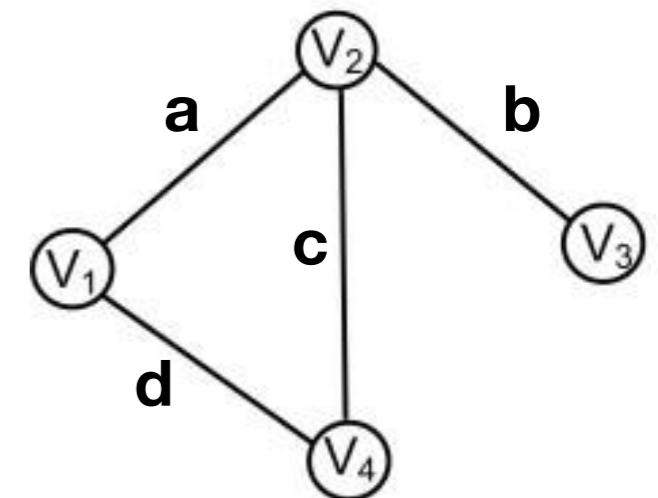
$$G = (V, E)$$

$$V=\{v_1, v_2, v_3, v_4\}$$

$$E=\{a, b, c, d\}$$

Nodes sometimes called **vertices**

Two connected nodes are called **neighbours**, **adjacent**, or **end-nodes**



# Simple vs multigraphs

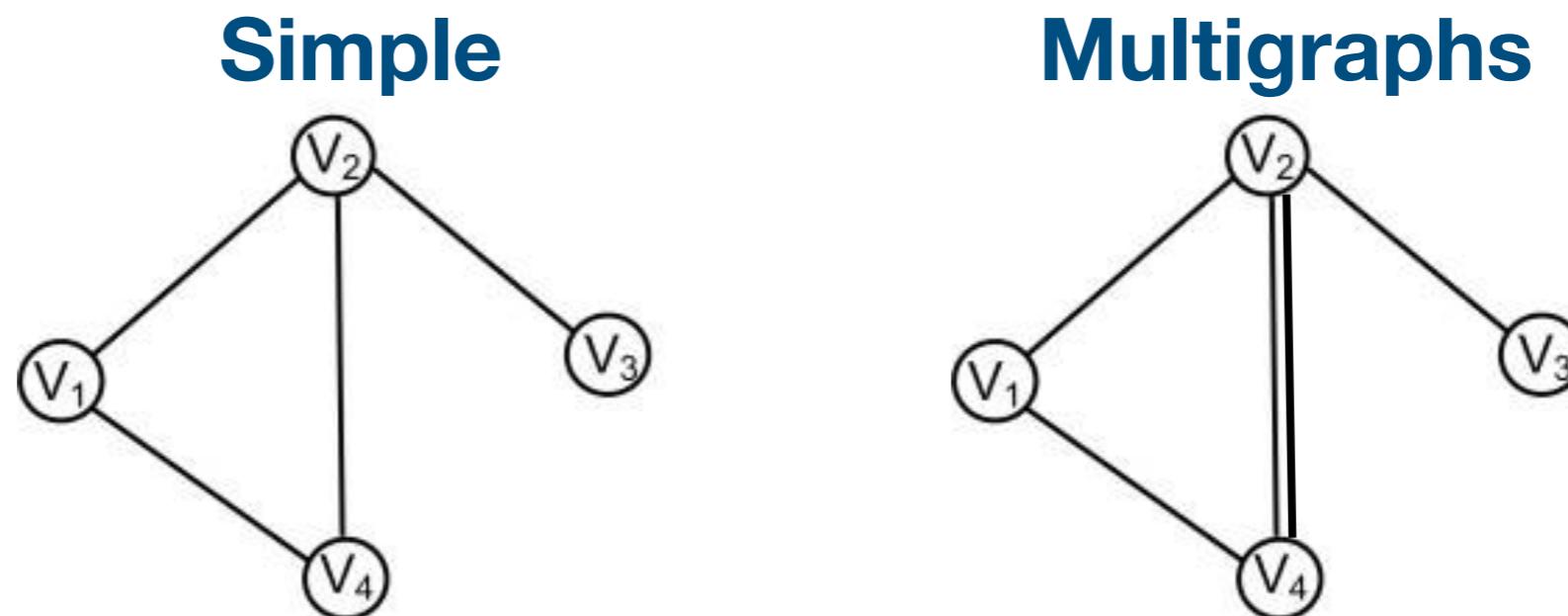
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**Multigraphs** contain parallel edges

**Multi-edged** connections indicate different properties

Example: PPI

- Experimental evidence for interaction
- Co-expression



# Hypergraphs

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**Hypergraphs** contain edges that connect any number of nodes

**Reaction 1:**  $A \rightarrow B + C$

**Reaction 2:**  $B + C \rightarrow D$

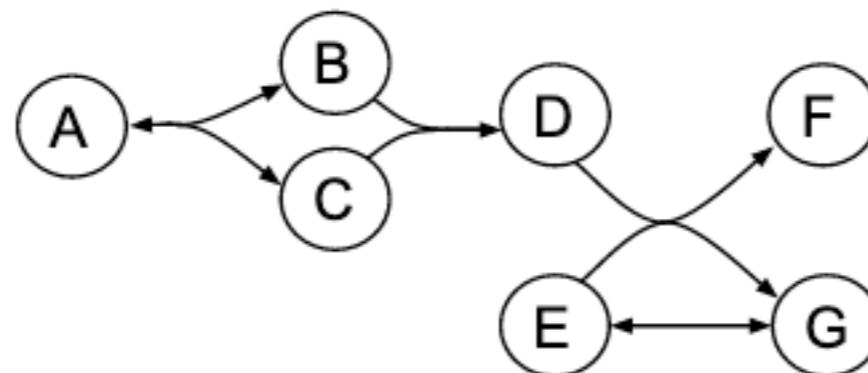
**Reaction 3:**  $D + E \rightarrow F + G$

**Reaction 4:**  $E \rightarrow G$

**Reaction 5:**  $B + C \rightarrow A$

**Reaction 6:**  $G \rightarrow E$

(a) Reaction network



# Directed vs undirected graphs

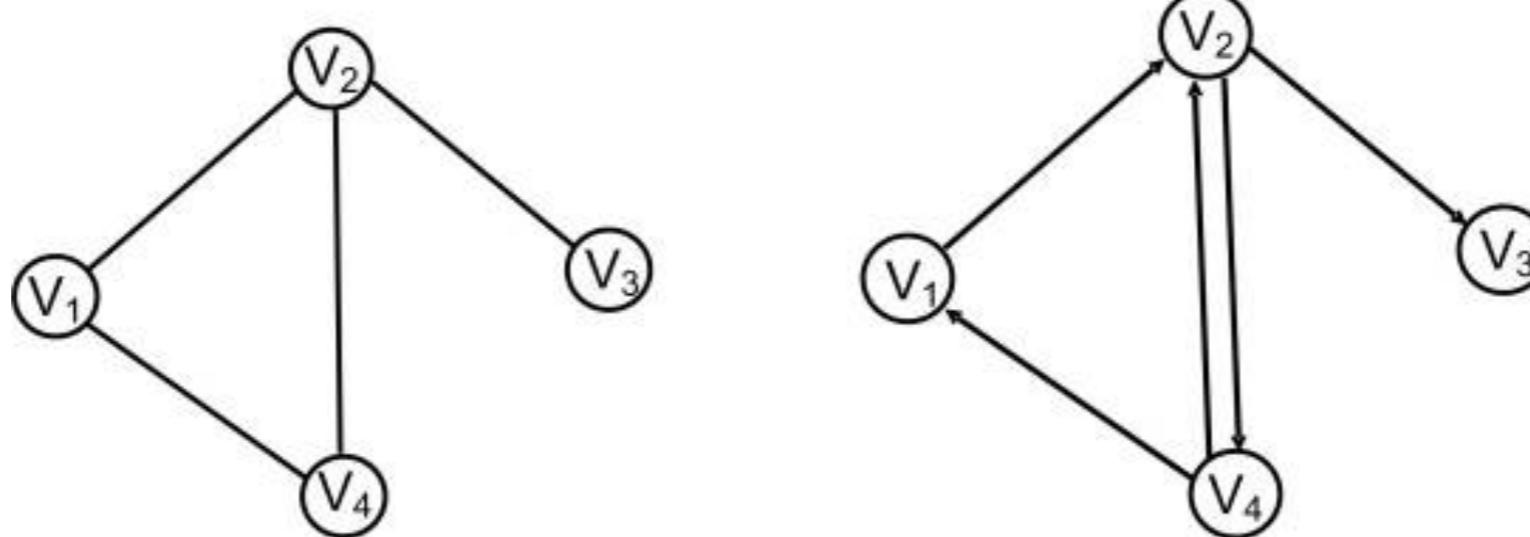
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**Directed graphs** is given by an ordered triple

$$G = (V, E, f)$$

**f** : function mapping an element in **E** to the ordered pair of vertices in **V**

$$E = \{ (v_1, v_2), (v_2, v_3), (v_2, v_4), (v_4, v_1), (v_4, v_2) \}$$

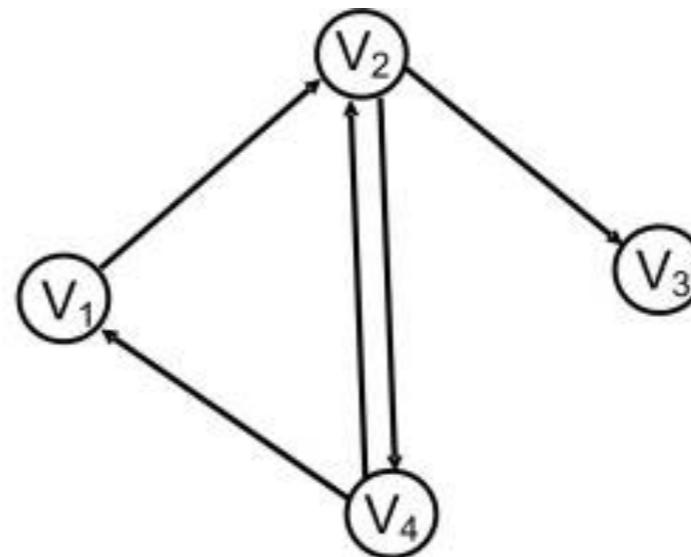
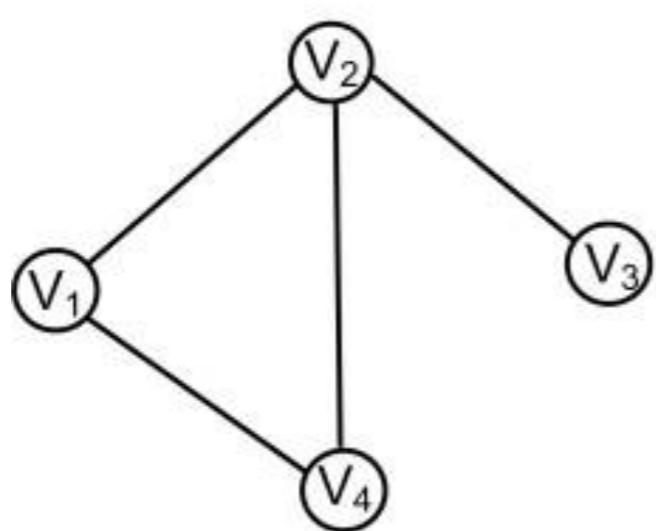


# Directed vs undirected graphs

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Examples:

- **Undirected graphs:** co-expression networks
- **Directed graphs:** metabolic networks



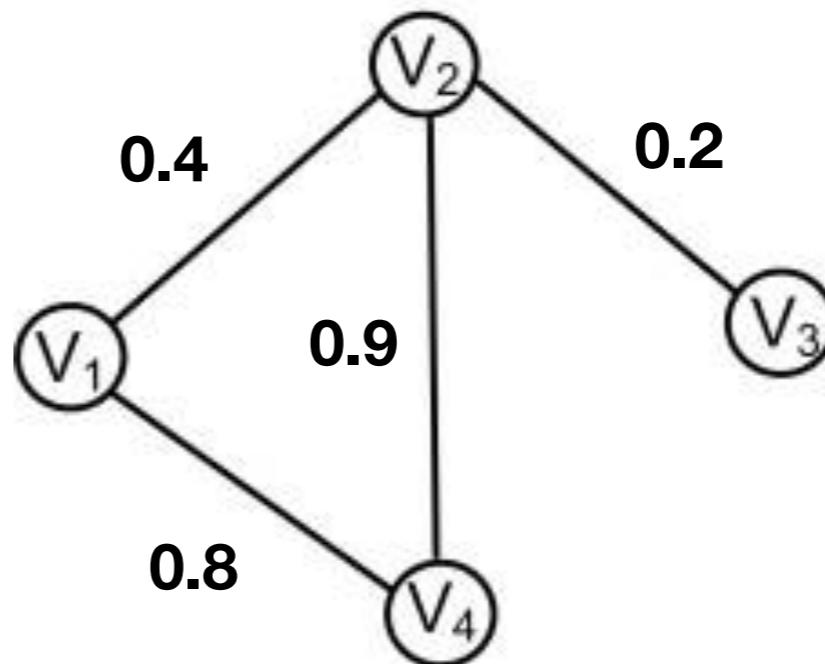
# Weighted vs unweighted graphs

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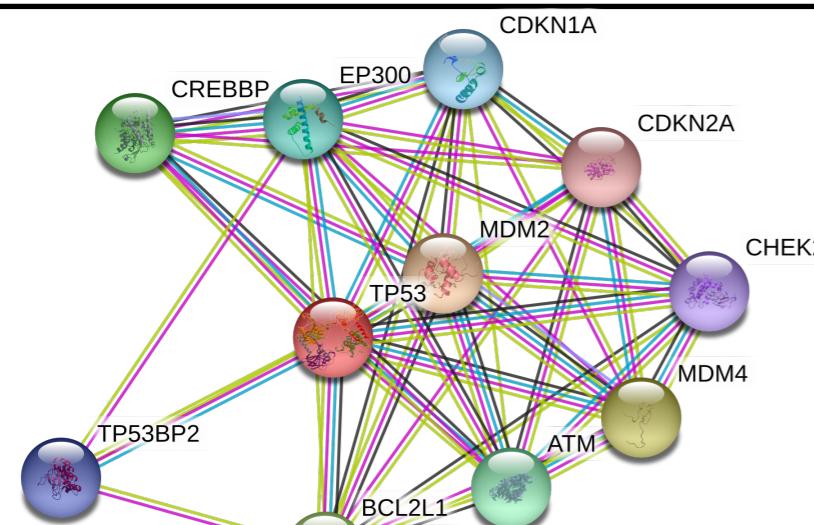
**Weighted edges** associate a value to an interaction between two nodes. Usually give the confidence in the interaction.

Negative weights?

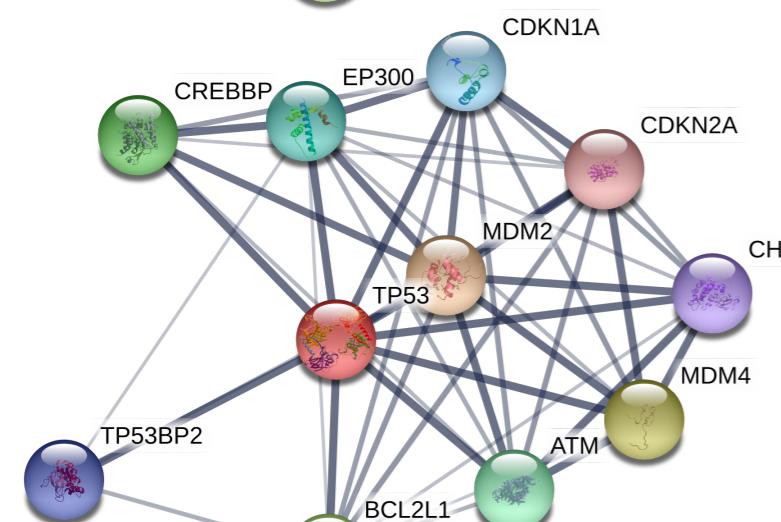
E.g. weighted co-expression networks



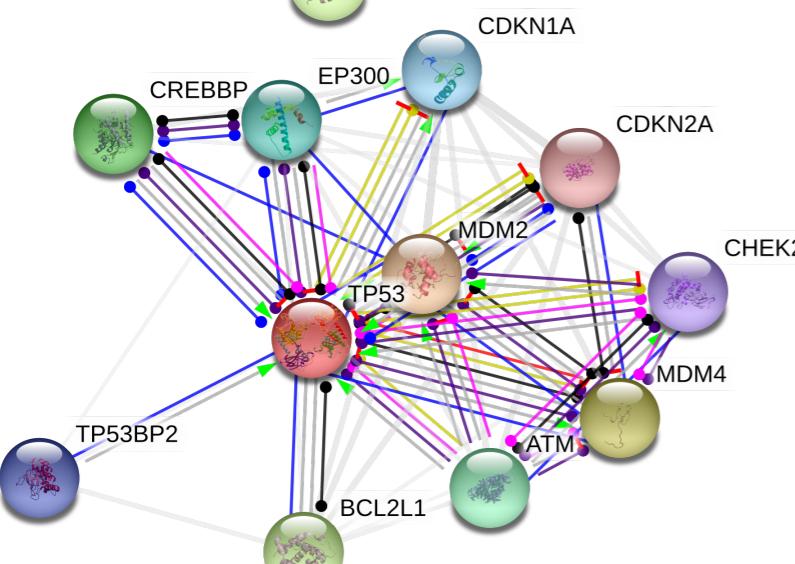
# STRING-db.org: TP53



Multi-edged



Weighted multi-edged



Multi-edged directed



# Bipartite graphs

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A graph

$$G=(V,E)$$

may be partitioned into two sets of nodes ( $V_1, V_2$ ) such that

$$u \in V_1 \text{ and } v \in V_2$$

or

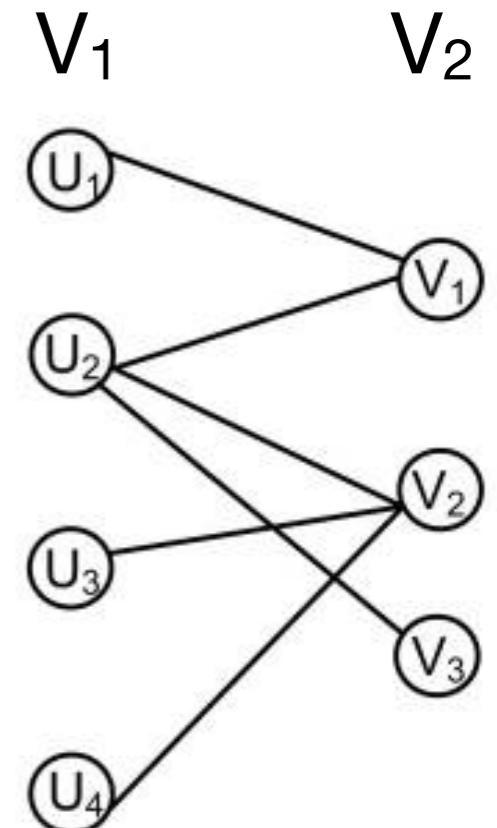
$$u \in V_2 \text{ and } v \in V_1$$

All  $e_i$  has end-nodes in  $V_1, V_2$

A **subgraph** of  $G$  will thus be given by

$$G_1 = (V_1, E_1)$$

Finding associations in  $V_1$



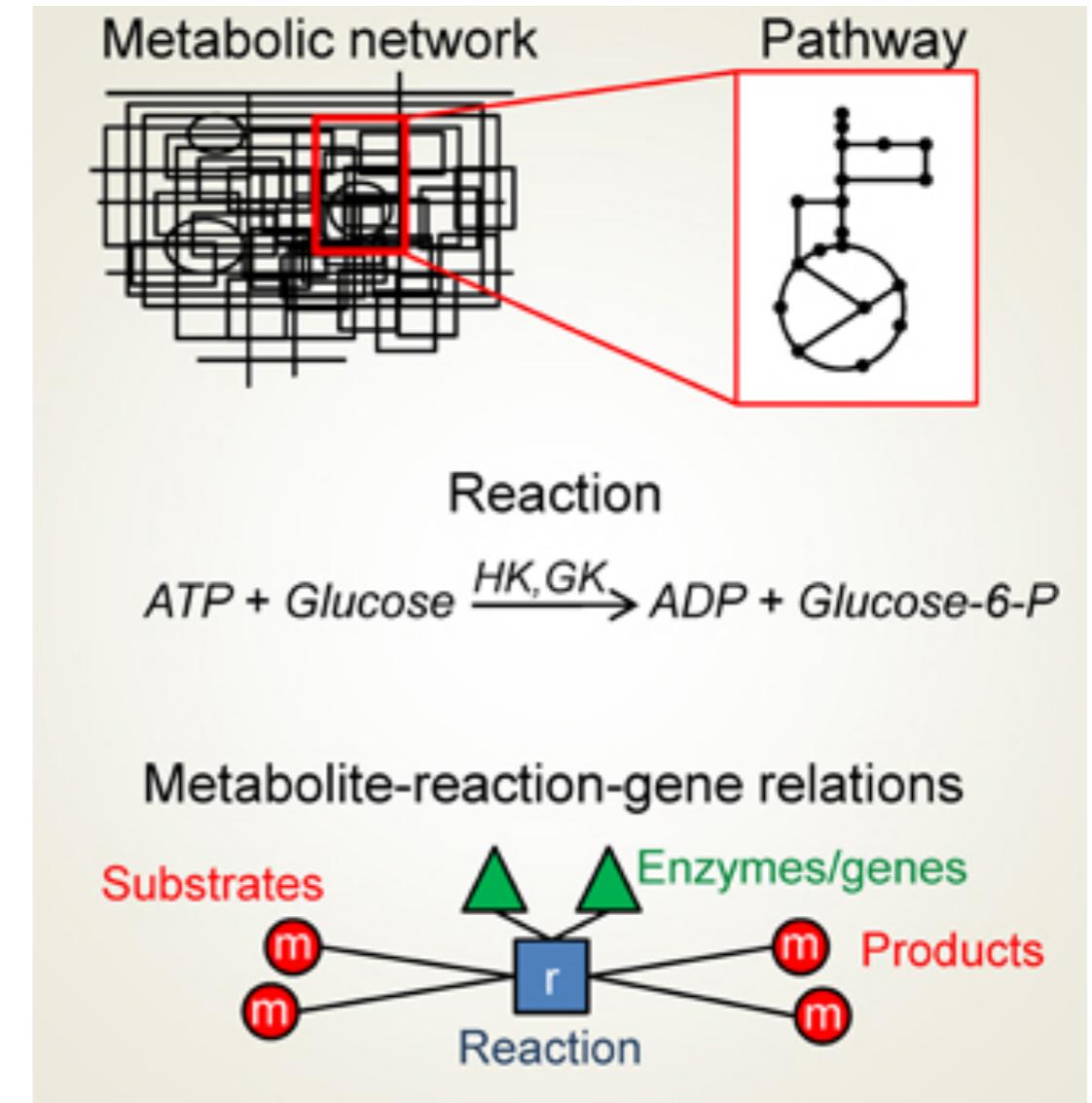
# Bipartite and $k$ -partite graphs

Example of bipartite graph:

Enzyme - Reaction

Metabolite - reaction - enzyme

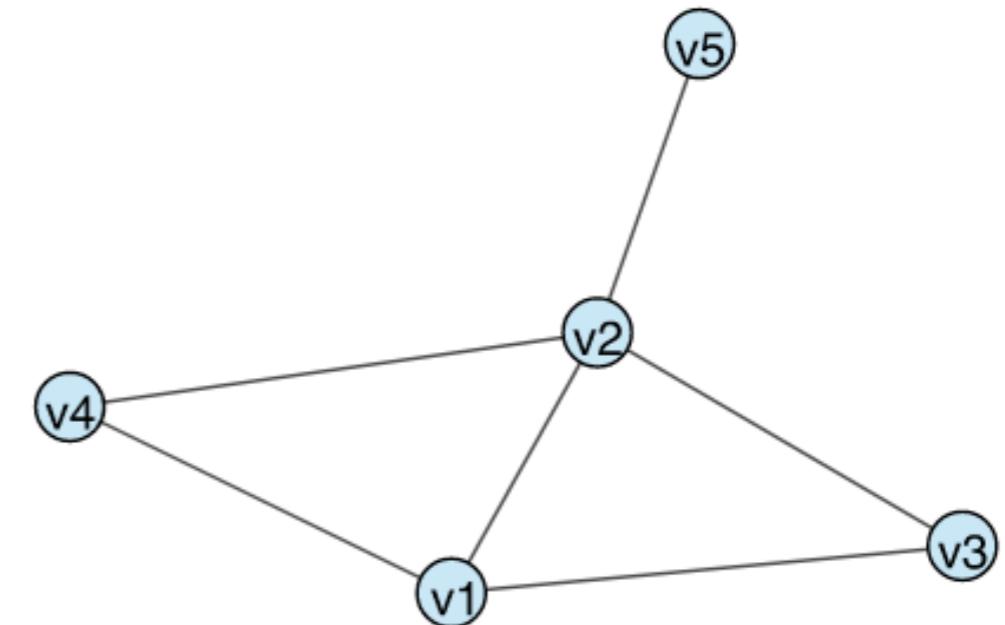
$k$ -partite graphs display  $k$ -types of nodes



# Adjacency matrix (undirected graphs)

**Vertex association  
(undirected network)**

n1	n2
v1	v2
v1	v4
v2	v4
v2	v3
v2	v5
v1	v3



**Adjacency matrix is symmetric**

	v1	v2	v3	v4	v5
v1	0	1	1	1	0
v2	1	0	1	1	1
v3	1	1	0	0	0
v4	1	1	0	0	0
v5	0	1	0	0	0

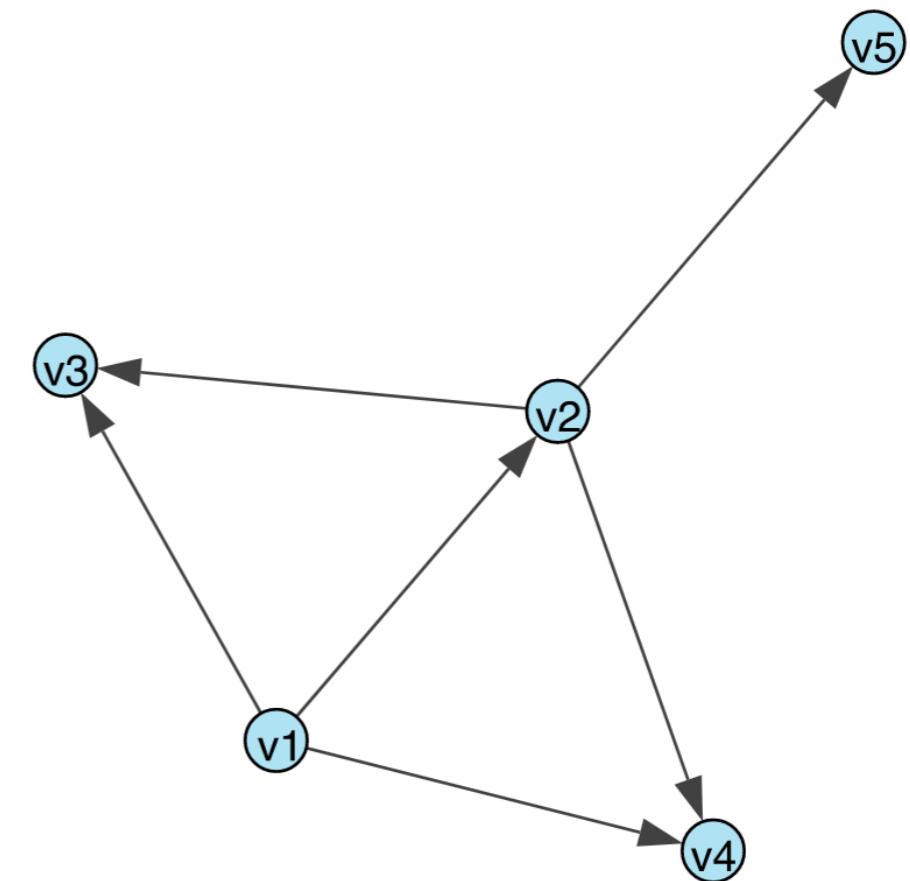
**Upper triangular**

**Lower triangular**

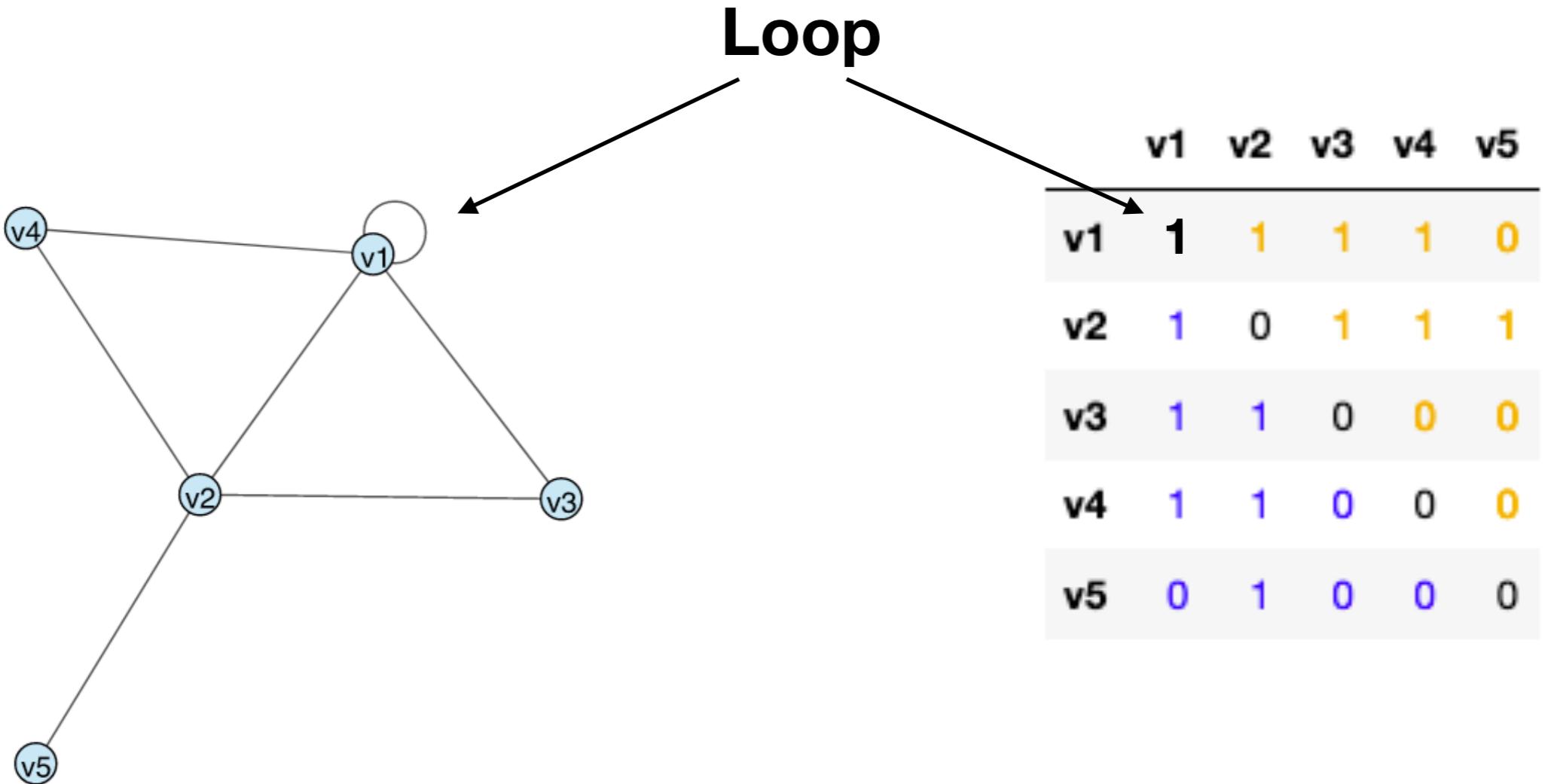
**Diagonal**

# Adjacency matrix (directed graphs)

		Target				
		v1	v2	v3	v4	v5
Source		v1	v2	v3	v4	v5
v1	0	1	1	1	0	
v2	0	0	1	1	1	
v3	0	0	0	0	0	
v4	0	0	0	0	0	
v5	0	0	0	0	0	



# Graphs may contain self-loops



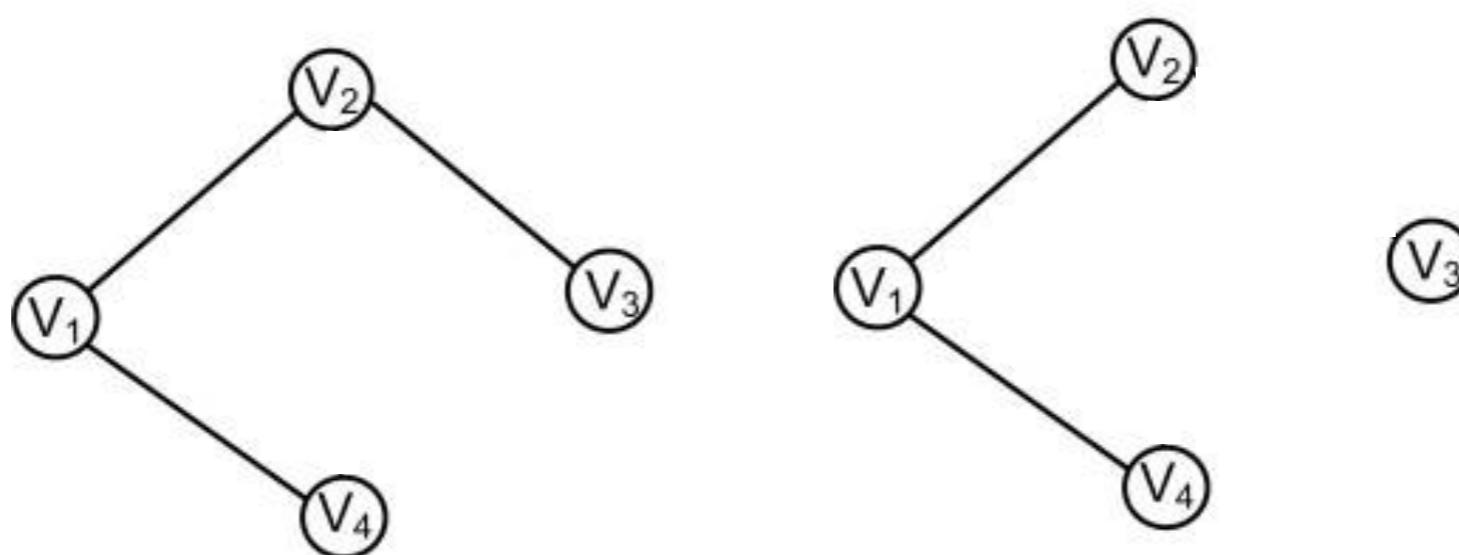
Examples of **self-loops** are auto-regulatory mechanisms in Transcription Factor regulatory networks

# Connected vs disconnected networks

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**Connected network:** there is at least 1 path connecting all nodes in a network

**Disconnected network:** some of the nodes are unreachable

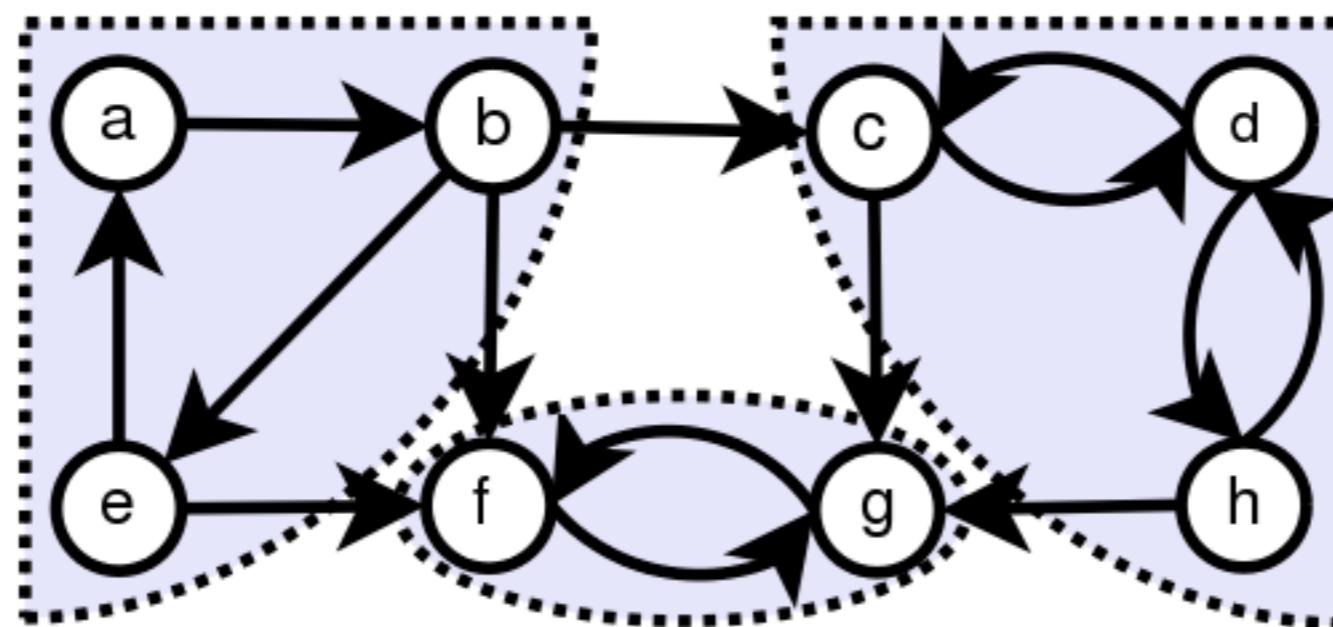


# Connected components

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**Connected components** are those where all nodes of each subgraph are connected.

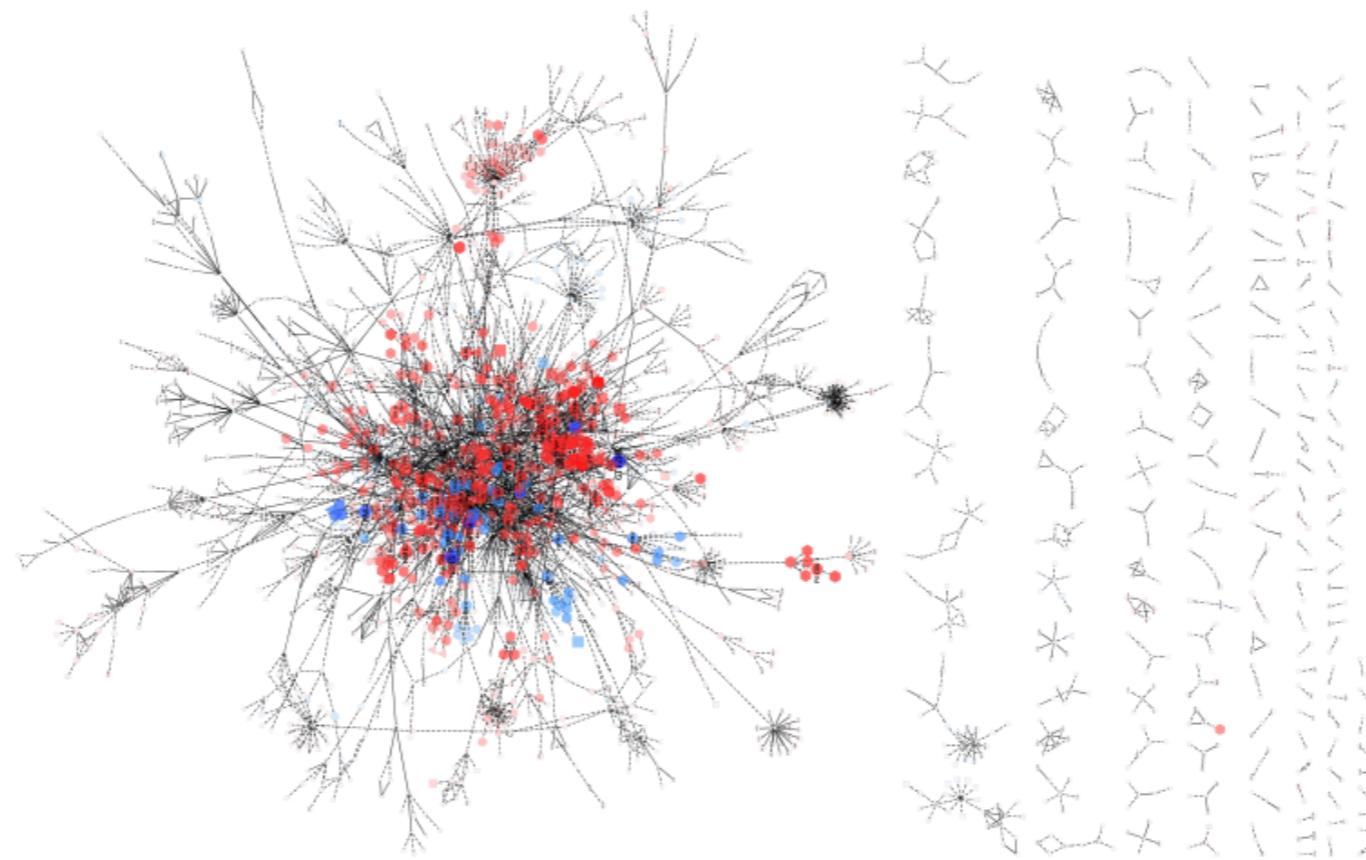
## Weak vs strong components



# Connected components

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In biological networks, often the most insightful properties come from the **largest connected component**

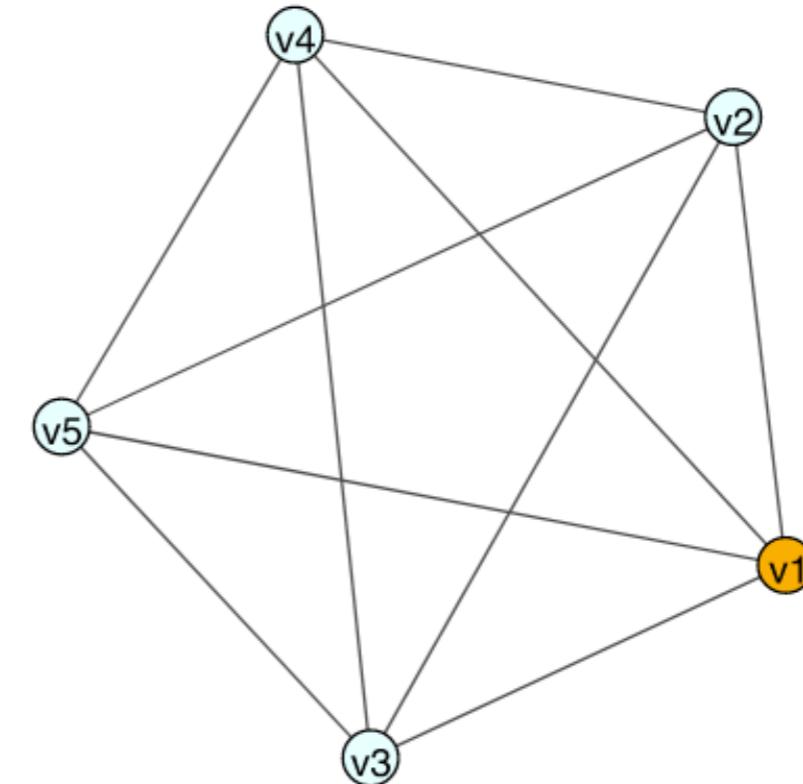
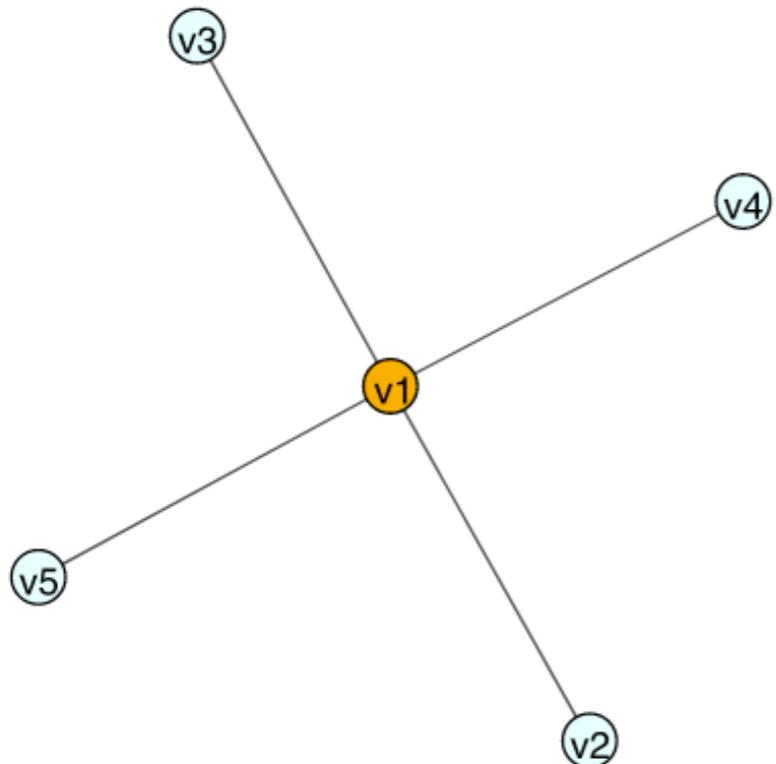


# Stars vs cliques

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A star forms a **complete bipartite subgraph**

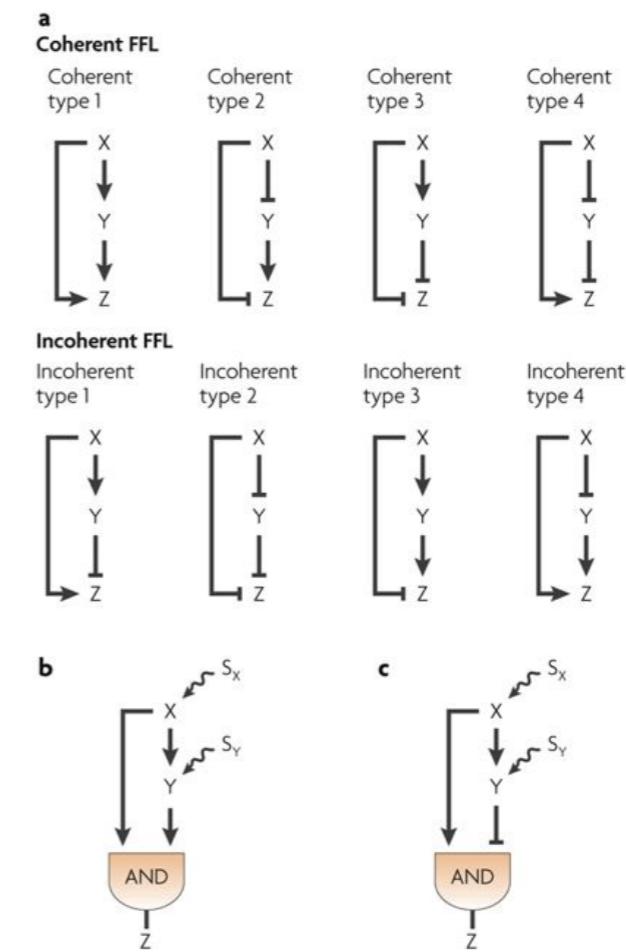
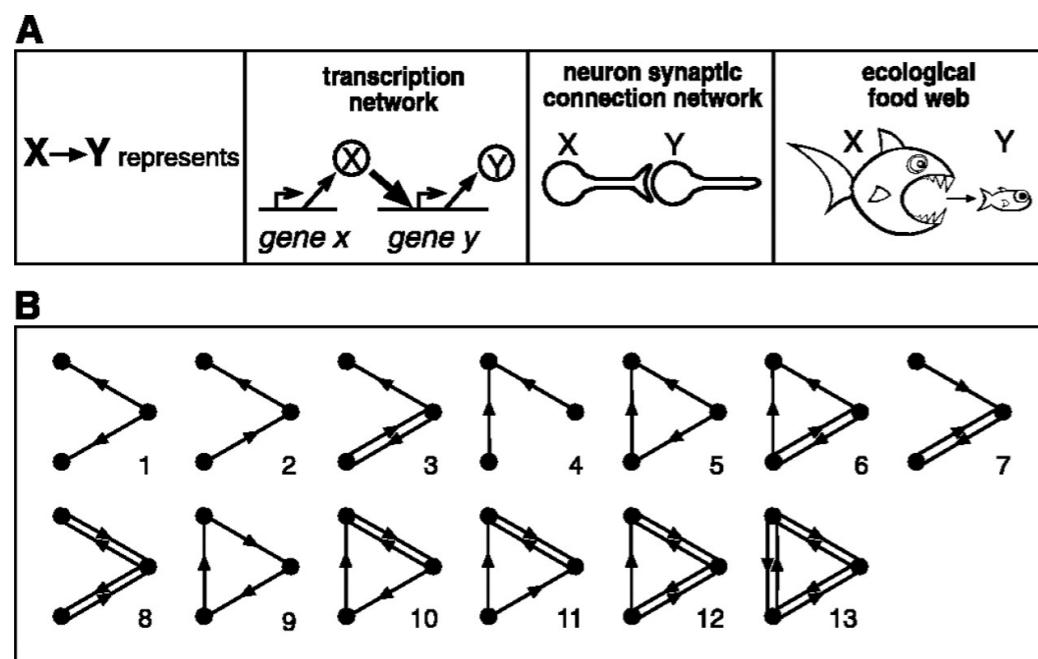
A clique is a subgraph where all nodes are adjacent (i.e. **complete graph**)



# Motifs

Subgraphs are characterised by different motifs

Exploring prevalent motifs may allow us to understand the evolutionary advantage of a given architecture



Milo 2002  
Alon 2007

# Additional reading

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- [Network Science](#) - A fascinating textbook on graph theory and network analysis.
- [Communication dynamics in complex brain networks](#) - Interesting discussion about whether and how network topology may be applied to study the brain networks.
- [A Systematic Evaluation of Methods for Tailoring Genome-Scale Metabolic Models](#) - General review and discussion on methods to use in genome-scale metabolic models.
- [Analysis of Biological Networks](#) - General introduction into biological networks, network notation, and analysis, including graph theory.
- [Multi-omics approaches to disease](#) - Introduction to how integrative approaches may be applied in disease

Additional references displayed as hyperlinks in each slide.