

# Graph-level Tasks

Prof. O-Joun Lee

Dept. of Artificial Intelligence,  
The Catholic University of Korea  
*ojlee@catholic.ac.kr*



네트워크 과학 연구실  
NETWORK SCIENCE LAB



가톨릭대학교  
THE CATHOLIC UNIVERSITY OF KOREA

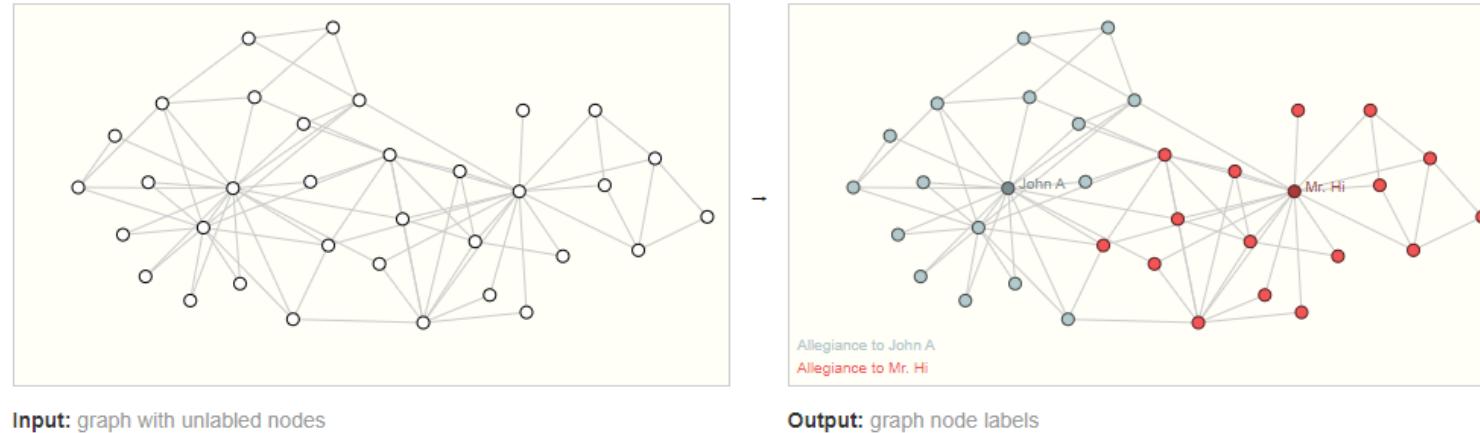


# Contents

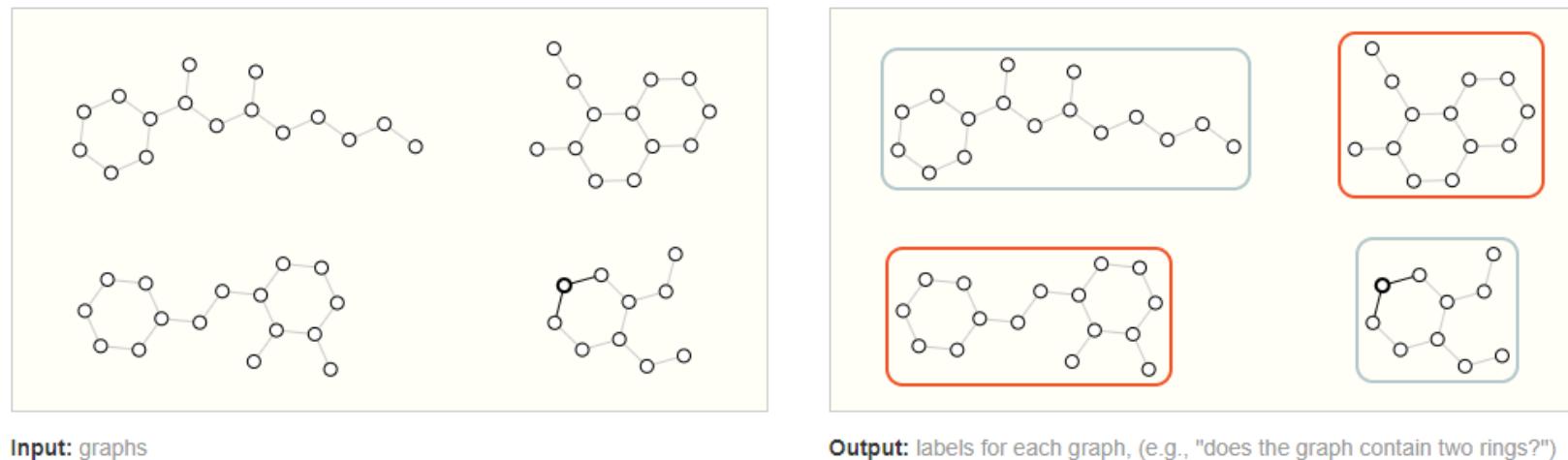


- Graph-level Overview.
- Feature Extraction Methods.
  - Local Features: graph size, density, connectivity, average degree, centrality measurement, diameter, average clustering coefficient, average shortest path length.
  - Global features: motif counts, subgraph, kernel-based, graph spectrum, Community structure.
- Graph-level Tasks:
  - Graph regression, classification, generation, clustering, similarity, and embedding.
- Applications of Graph-level representation learning.

- **Node classification:** given a graph with labels on some nodes, provide a high-quality labeling for the rest of the nodes.

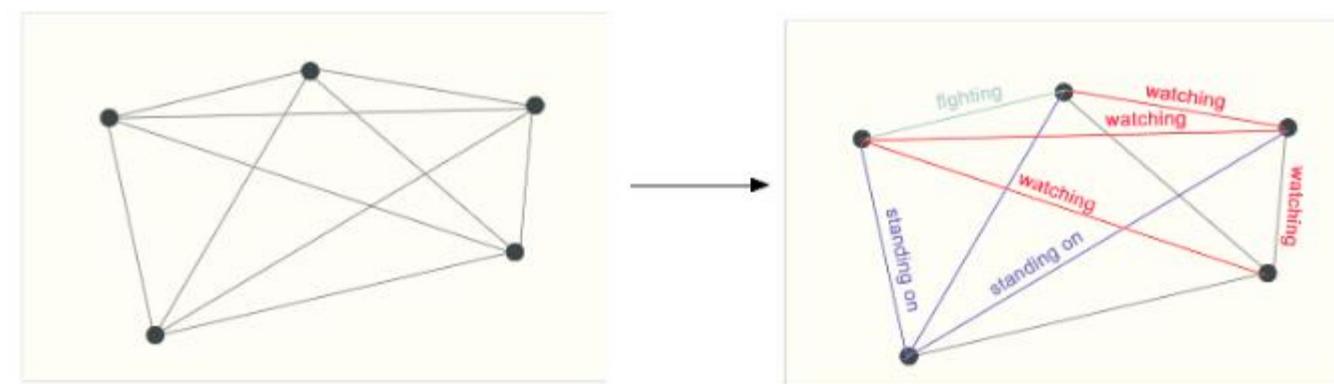
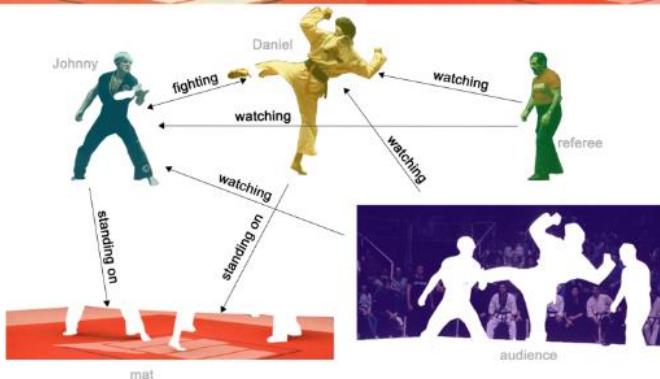


- **Graph classification:** given a set of graphs with known class labels for some of them, decide to which class the rest of the graphs belong.



# Machine Learning Tasks on Graphs

- Edge/Link prediction: given a pair of vertices, predict if they should be linked with an edge.



**Input:** fully connected graph, unlabeled edges

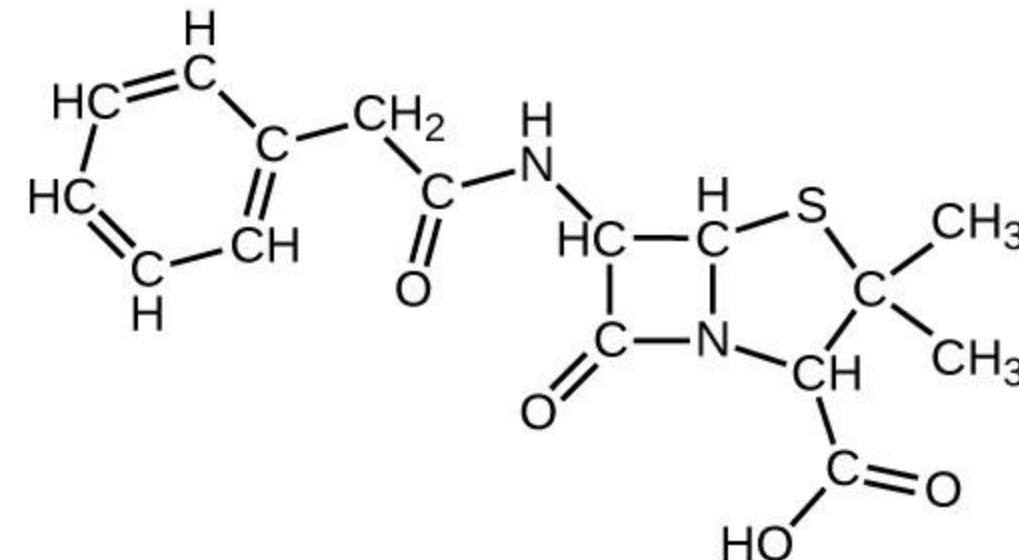
**Output:** labels for edges

## ➤ Intuition:

- Node-level tasks involve making predictions or performing computations at the level of individual nodes within a graph.
  - Each node in the graph is treated as a separate entity, and the task focuses on understanding or predicting properties or behaviors specific to each node.
- Graph-level tasks involve making predictions or performing computations based on the entire graph structure.
  - The entire graph structure is considered as a whole, and the task typically involves understanding or predicting global properties or behaviors of the entire graph.

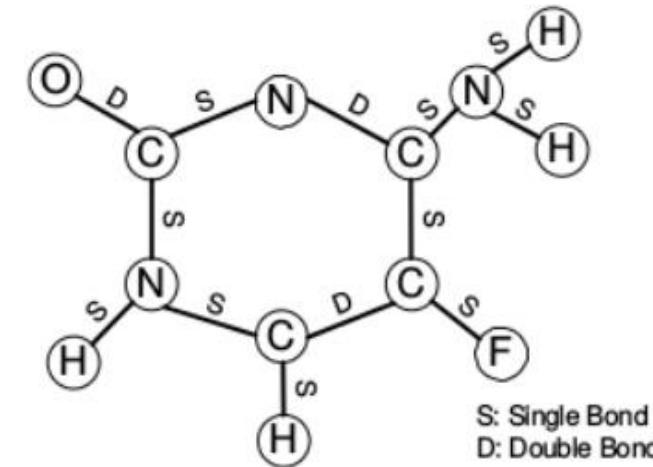
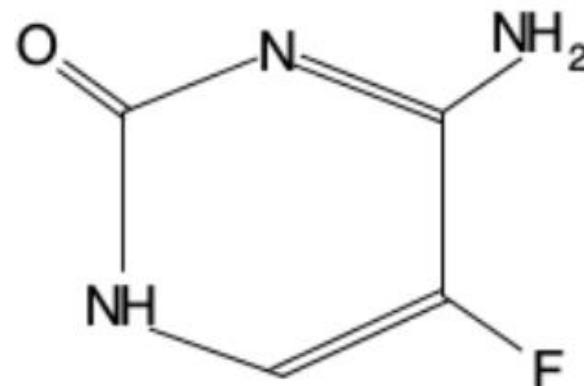
- For each protein, create a graph that contains information about its:

- Structure
- Sequence
- Chemical properties



- Use graph **features** to:
  - measure structural similarity between proteins/molecules
  - predict the function of proteins/molecules

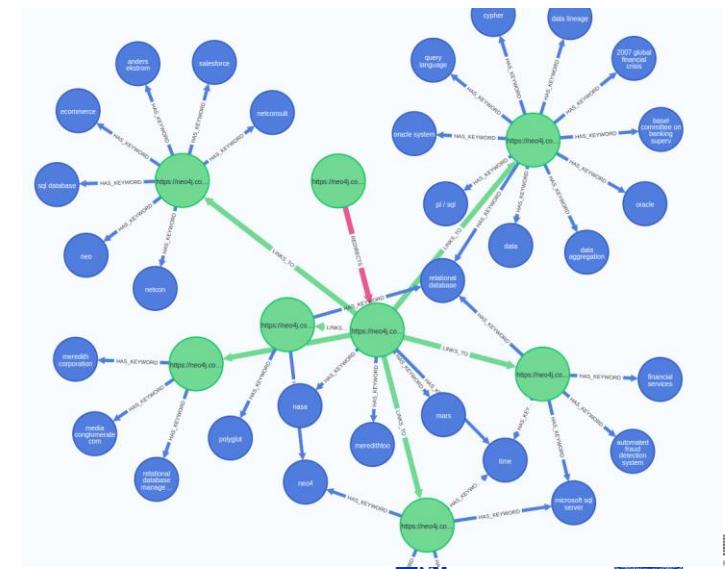
- Represent each chemical compound as a graph



- Use a **frequent subgraph** discovery algorithm to discover the substructures that occur above a certain support constraint.
- Perform feature selection.
- Use the remaining substructures as features for classification.

# Motivation – Anomaly Detection for the Web Graph

- Search engines create snapshots of the web → **Web graphs**.
- These are necessary for
  - monitoring the evolution of the web.
  - Computing global properties such as PageRank.
- Identify anomalies in a single snapshot by comparing it with previous snapshots.
- Employed similarity measures:
  - Node/edge overlap.
  - Node ranking.
  - Node/edge vector similarity.
  - etc.



# Motivation – Malware Detection

- Given a computer program, create its control flow graph:

```

    processed_pages.append(processed_page)
    visited += 1
    links = extract_links(html_code)
    for link in links:
        if link not in visited_links:
            links_to_visit.append(link)

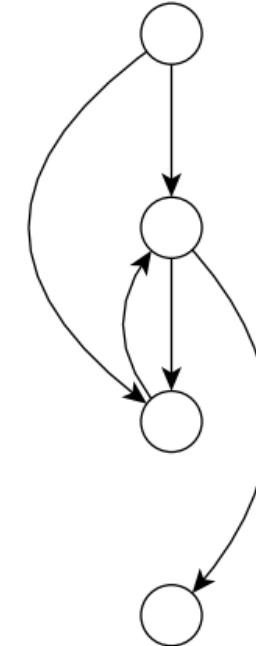
    return create_vocabulary(processed_pages)

def parse_page(html_code):
    punct = re.compile(r'([^\w\.\-\_])')
    soup = BeautifulSoup(html_code, 'html.parser')
    text = soup.get_text()
    processed_text = punct.sub(" ", text)
    tokens = processed_text.split()
    tokens = [token.lower() for token in tokens]
    return tokens

def create_vocabulary(processed_pages):
    vocabulary = {}
    for processed_page in processed_pages:
        for token in processed_page:
            if token in vocabulary:
                vocabulary[token] += 1
            else:
                vocabulary[token] = 1

    return vocabulary

```

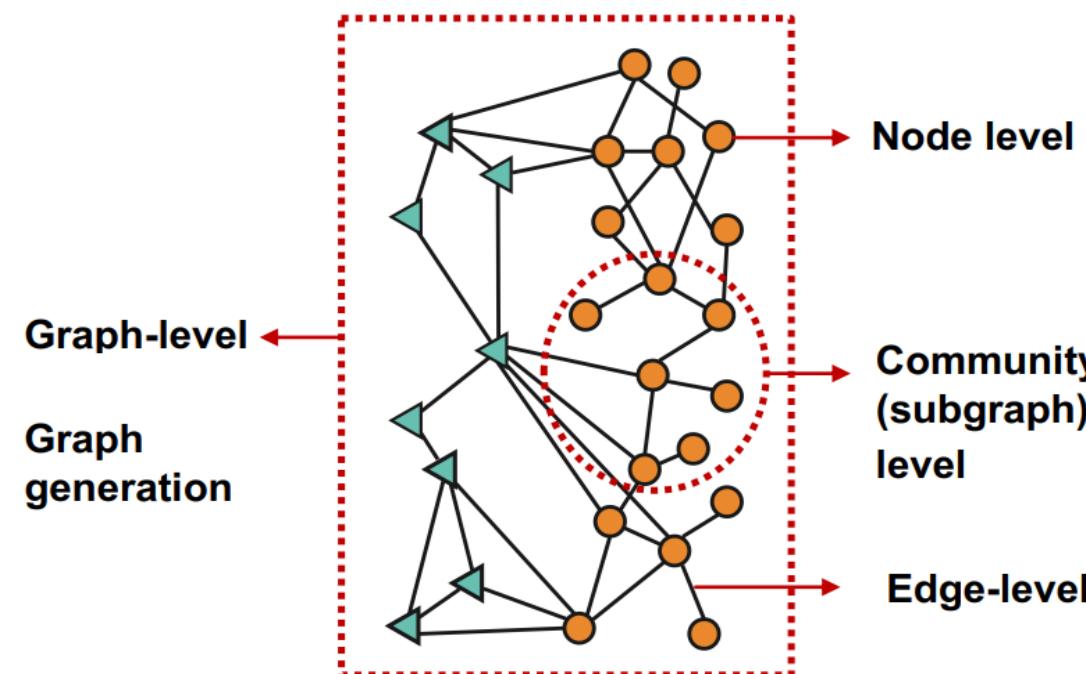


- Compare the control flow graph of the problem against the set of control flow graphs of known malware.
- If it contains a subgraph isomorphic to these graphs → malicious code inside the program

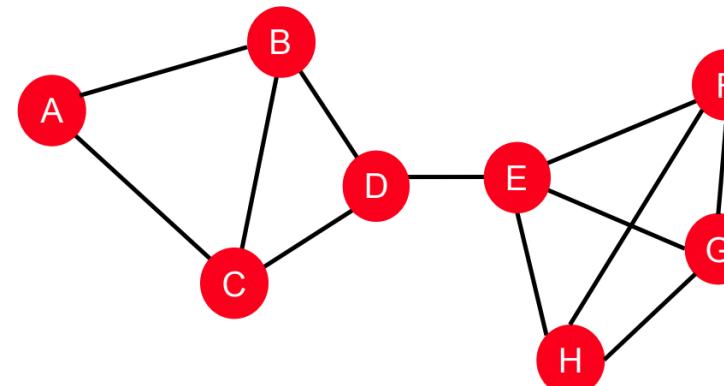
# Feature Extraction Approaches

➤ Three main types of graph components:

1. Node-level features (Previous week).
2. Edge-level features (Previous week).
3. Graph-level features (**This week**).

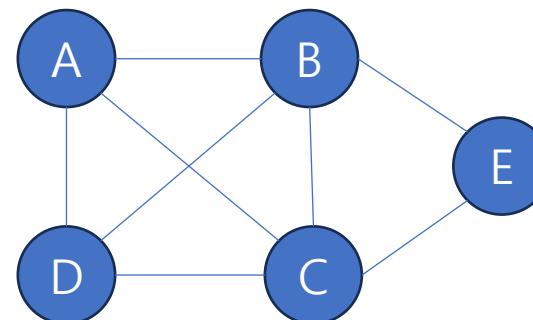


- **Goal:** We want features that characterize the structure of an entire graph.
  - Similar graphs has similar features.
- **Idea:** extract structural information within graphs as graph features.
- **Methods:**
  - Local features: graph size, density, connectivity, degree, centrality, average clustering coefficient, diameter, average shortest path length.
  - Global features: motif/subgraph, kernel, spectral, community.

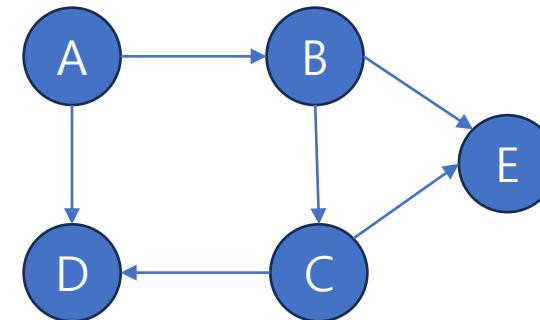


$f(\text{graph}) = ?$

- Graph size provide fundamental information about the graph's scale and complexity:
  - Order of a graph is the number of vertices in the graph
    - denotes as  $|V|$ .
  - Size of a graph is the number of edges in the graph
    - denotes as  $|E|$ .



- $|V| = 5, |E| = 8$



- $|V| = 5, |E| = 6$

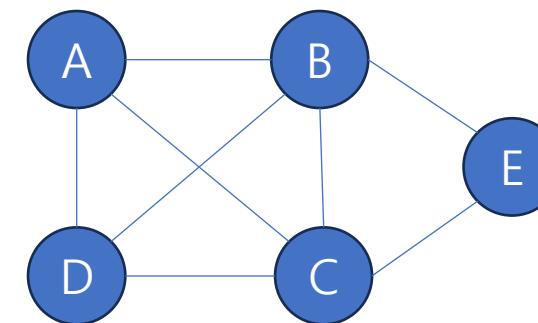
- Graph Density represents the ratio between the edges present in a graph and the maximum number of edges that the graph can contain.

- edge connectivity is key to find dense.

- In undirected graph:

- calculate the maximum number of edges:

$$Max_{EG} = \frac{|V|(|V| - 1)}{2}$$



$$Den_G = \frac{2 * 8}{5(5 - 1)} = 0.8$$

- the edges are divided by the maximum number of edges that the graph can contain. Density graph is defined

$$Den_G = \frac{\frac{|E|}{2}}{\frac{|V|(|V| - 1)}{2}} = \frac{2|E|}{|V|(|V| - 1)}$$

Where  $|V|$  is number of nodes.

$|E|$  is number of edges.

# Local Features: Graph Density

- Similarly, in directed graph: replace each undirected edge with two bidirectional edges in a directed graph
- the maximum number of edges:

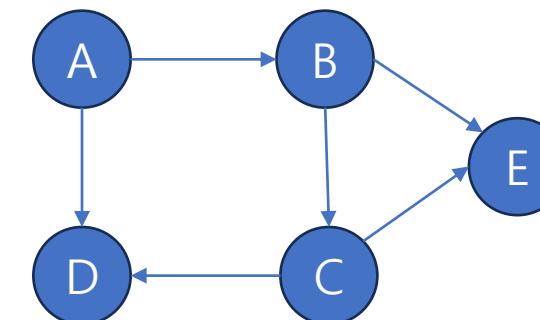
$$Max_{EG} = |V|(|V| - 1)$$

- the edges are divided by the maximum number of edges that the graph can contain.  
Density graph is defined

$$Den_G = \frac{|E|}{|V|(|V| - 1)}$$

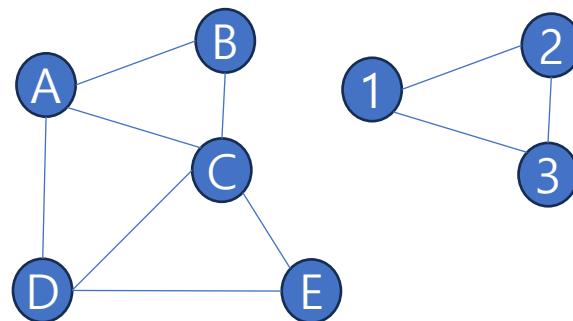
Where  $|V|$  is number of nodes.

$|E|$  is number of edges.

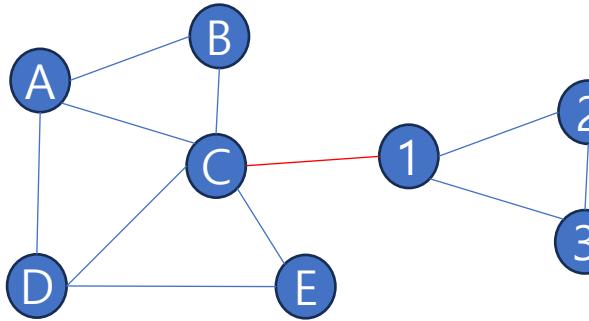


$$Den_{DG} = \frac{6}{5(5 - 1)} = 0.3$$

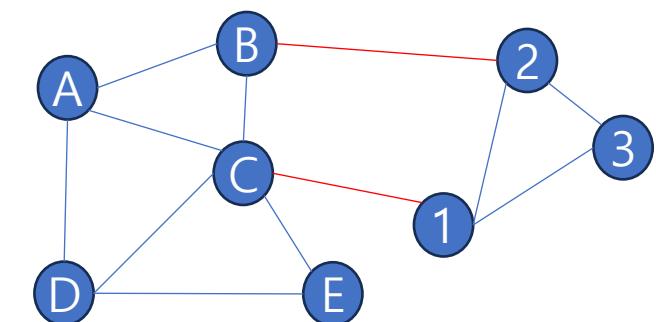
- Graph Connectivity: the minimum number of elements (**nodes or edges**) that need to be **removed** to separate the remaining nodes into two or more isolated subgraphs.



Unconnected graph

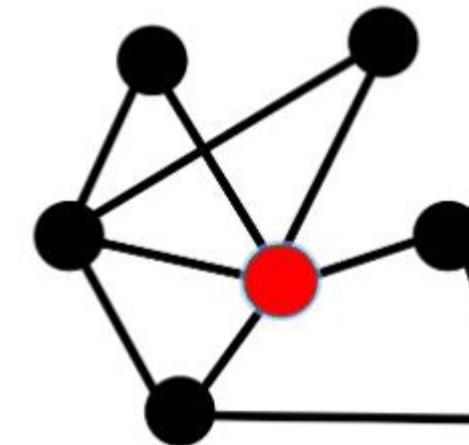


1- connected graph



2- connected graph

- Node degree counts the neighbouring nodes without capturing their importance.
- Node centrality takes the node importance in a graph into account.
- Different ways to evaluate importance:
  - Eigenvector centrality
  - Betweenness centrality
  - Closeness centrality
  - and many others....

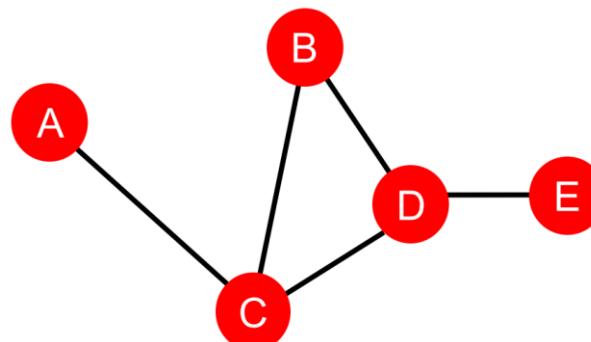


➤ Betweenness Centrality

- A node is important if it **lies on many shortest paths** between other nodes.

$$c_v = \sum_{s \neq v \neq t} \frac{\#(\text{shortest paths between } s \text{ and } t \text{ that contain } v)}{\#(\text{shortest paths between } s \text{ and } t)}$$

- A graph betweenness centrality is **average** of all the nodes' betweenness centrality.
- For example:



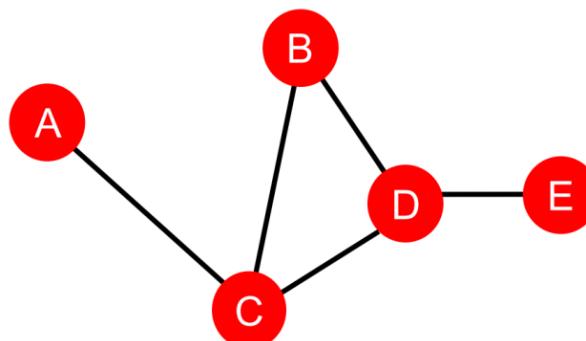
- $C_A = C_B = C_E = 0$
- $C_C = 3$  (A-C-B, A-C-D, A-C-D-E)
- $C_D = 3$  (A-C-D-E, B-D-E, C-D-E)
- $C_G = \frac{0+0+3+3+0}{5} = 1.2$

➤ Closeness Centrality

- A node is important if it has **small shortest path lengths** to all other nodes.

$$c_v = \frac{1}{\sum_{u \neq v} \text{shortest path length between } u \text{ and } v}$$

- A graph closeness centrality is **average** of all the nodes' closeness centrality.
- For example:



- $C_A = 1/(2 + 1 + 2 + 3) = 1/8$   
(A-C-B, A-C, A-C-D, A-C-D-E)
- $C_D = 1/(2 + 1 + 1 + 1) = 1/5$   
(D-C-A, D-B, D-C, D-E)
- $C_G = (\frac{1}{8} + \frac{1}{5} + \frac{1}{6} + \frac{1}{5} + \frac{1}{8})/5 \approx 0.1633$

## ➤ Eigenvector Centrality

- A node  $v$  is important if surrounded by important neighboring nodes  $u \in N(v)$ .
- We model the centrality of node  $v$  as the sum of the centrality of neighboring nodes recursively:

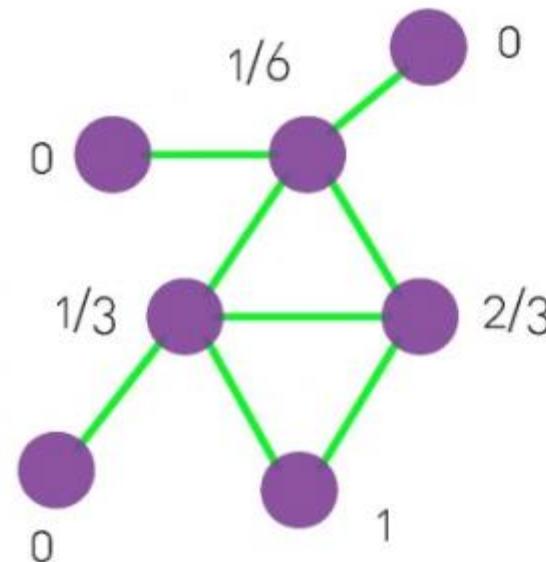
$$c_v = \frac{1}{\lambda} \sum_{u \in N(v)} c_u \quad \longleftrightarrow \quad \lambda c = Ac$$

- $A$ : Adjacency matrix
- $A_{uv} = 1$  if  $u \in N(v)$
- $c$ : Centrality vector
- $\lambda$ : Eigenvalue

- We can obtain the graph-level feature by **averaging** of all the nodes' eigenvector centrality.

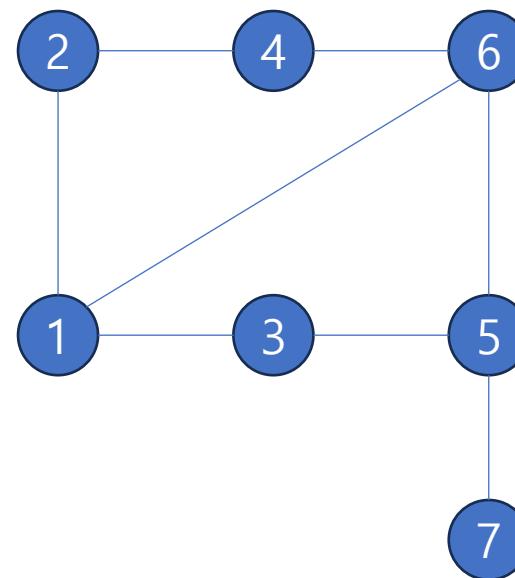
- The degree of clustering of a whole network is captured by the average clustering coefficient, namely  $\langle C \rangle$ , representing the average of all the local clustering coefficient  $C_i$  over all nodes  $i = 1, \dots, N$ .

$$\langle C \rangle = \frac{1}{N} \sum_{i=0}^N C_i$$



$$\langle C \rangle = \frac{1}{7} * \left( 0 + \frac{1}{6} + \frac{1}{3} + \frac{2}{3} + 1 + 0 + 0 \right) = 0.333$$

- The diameter of a graph is the length of the shortest path between the most distanced nodes.
- $d$  measures the extent of a graph and the topological length between two nodes.



Diameter of this graph is 4

- The average number of steps along the shortest paths for all possible pairs of network nodes.
- A measure of the efficiency of information in a graph.
  - i.e. the average number of clicks which will lead you from one website to another,
  - or the number of people you will have to communicate through, on an average, to contact a complete stranger.

$$a = \sum_{\substack{s,t \in V \\ s \neq t}} \frac{d(s,t)}{n(n-1)}$$

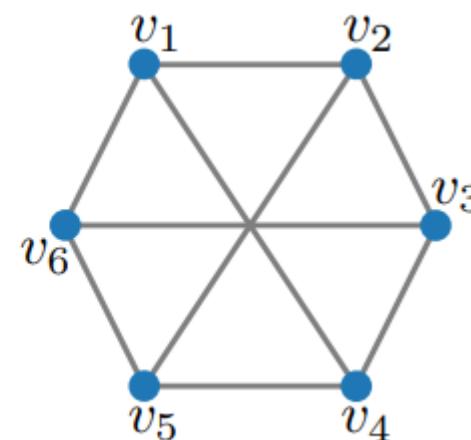
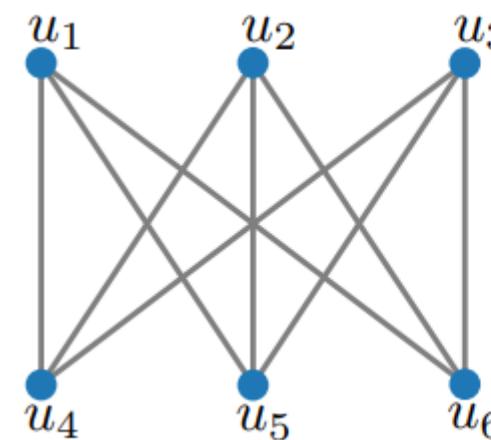
Where  $V$  is the set of nodes in  $G$ ,  $d(s, t)$  is the shortest path from  $s$  to  $t$ , and  $n$  is the number of nodes in  $G$

- For graphs  $G = (V^G, E^G)$  and  $G' = (V^{G'}, E^{G'})$ , if we can define a bijection  $\psi: V^G \rightarrow V^{G'}$ , such that:

$$\forall v_i^G, v_j^G \in V^G, (v_i^G, v_j^G) \in E^G \text{ iff } (\psi(v_i^G), \psi(v_j^G)) \in E^{G'}$$

- The graphs  $G$  and  $G'$  are said to be isomorphic and denoted as

$$G \simeq G'$$



$V^G$	$V^{G'}$
$v_1 \rightarrow u_1$	
$v_2 \rightarrow u_4$	
$v_3 \rightarrow u_2$	
$v_4 \rightarrow u_5$	
$v_5 \rightarrow u_3$	
$v_6 \rightarrow u_6$	

$\psi :$

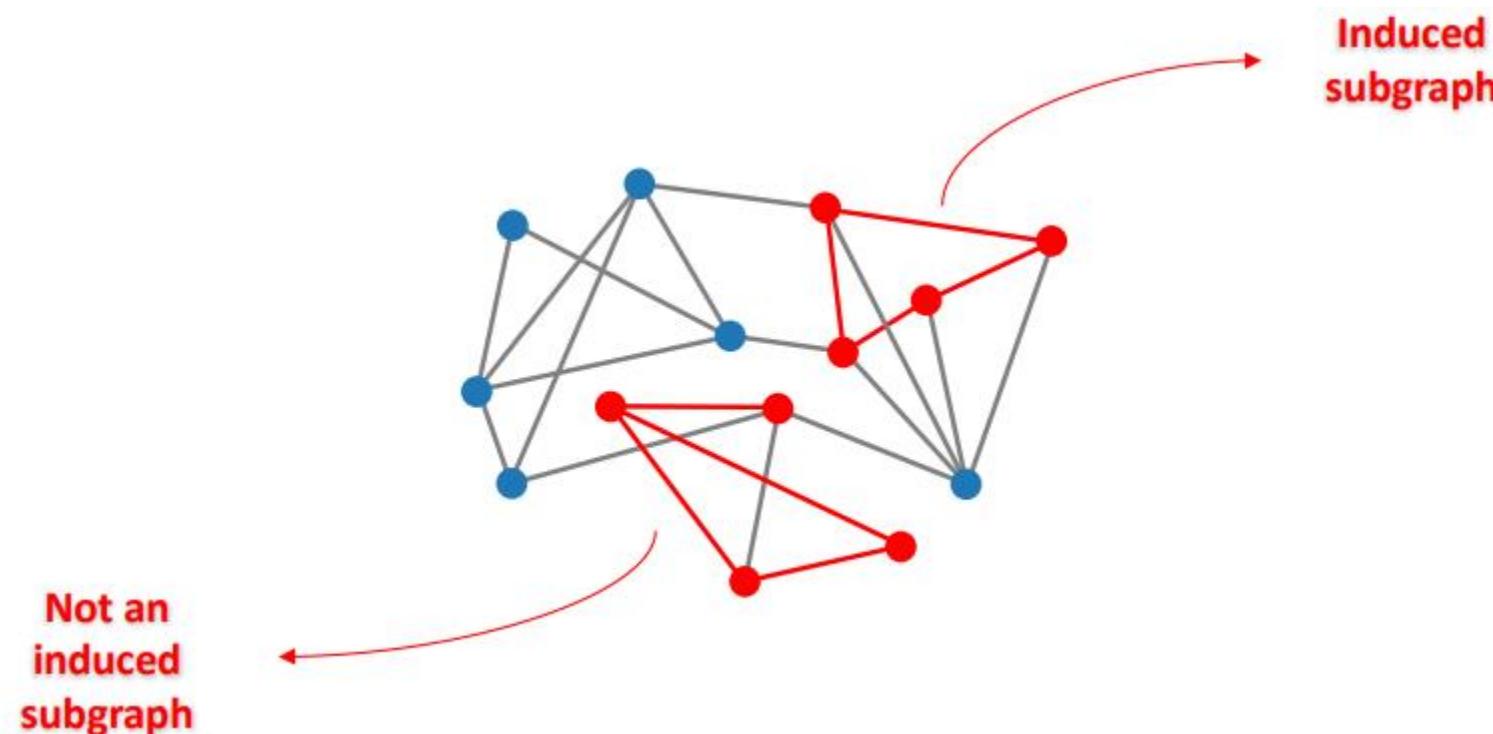
- An induced subgraph is a subgraph  $G' = (V', E')$  consist of a subset of the nodes in the graph  $G = (V, E)$  and all edges that connect them

$$E' = \{(v_i, v_j) \mid v_i, v_j \in V', (v_i, v_j) \in E\}$$



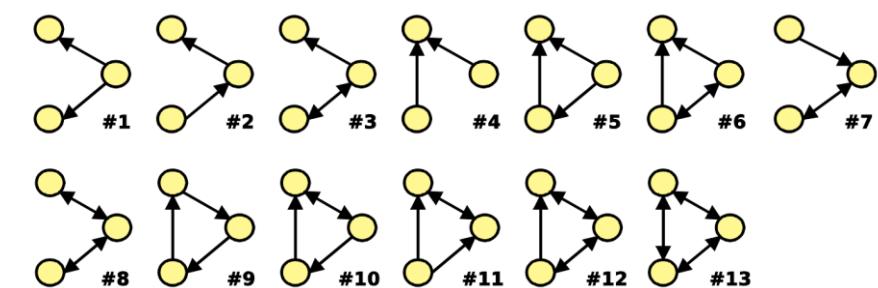
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$$E' = \{(v_i, v_j) \mid v_i, v_j \in V', (v_i, v_j) \in E\}$$



- A measure of similarity for finding graph similarity.

- Given a network, most of the time, some subgraphs are “overrepresented”.
- A connected graph that has many occurrences in a network is called a **motif** of the network.
- Assume set of occurrences  $G'$  in  $G$  is  $occ_G(H)$ .
  - cardinality of  $occ_G(H)$  in  $G$  is **frequent**.
  - How to know if  $G'$  is **frequent** in  $G$ ?



- Compute the probability that  $occ_N(G') \geq occ_G(G')$  for a random network  $N$ .  
 $G'$  is said to be frequent in  $G$  if this probability is small enough.  
To compute this probability, we need to have a distribution over networks.

- Subgraph Isomorphism:

- Input: Two graphs  $G'$  and  $G$
- Question: Does  $G'$  has at least one occurrence in  $G$ ?
- Determining if a graph contains a clique of size k is already NP-complete.

- Occurrences counting:

- Input: Two graphs  $G'$  and  $G$
- Question: Determine occurrence  $occ_G(H)$ .
- This problem is #P-complete.



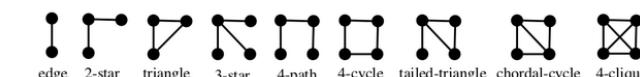
(a) Initial graph



(b) Weighted 4-clique graph



(c) Weighted 4-path graph



(d) Various graph motifs

➤ A quick introduction to Kernels:

- Kernel  $K(G, G') \in \mathbb{R}$  measures similarity between two graphs (data)
- There exists a feature representation  $\phi(\cdot)$  such that:

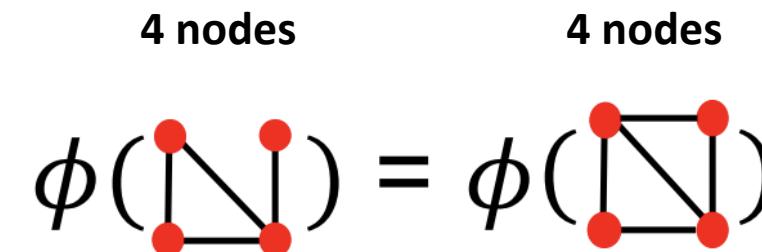
$$K(G, G') = \phi(G)^T \phi(G')$$

- Kernel enables vectors to be operated in higher dimension
- Once the kernel is defined, off-the-shelf ML model, such as kernel SVM, can be used to make predictions.

$$K = ( \quad \begin{array}{c} \text{graph 1} \\ \text{(4 nodes, 3 edges)} \end{array}, \quad \begin{array}{c} \text{graph 2} \\ \text{(4 nodes, 4 edges)} \end{array} ) \rightarrow \varphi ( \quad \begin{array}{c} \text{graph 2} \\ \text{(4 nodes, 4 edges)} \end{array} )$$

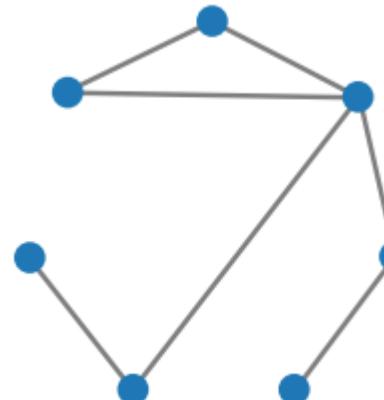
- **Goal:** Design graph kernel  $\phi(G)$
- **Key Idea:** Bag-of-Words (BoW) for a graph
  - In NLP, BoW counts the word's frequency in a document as feature
  - Simplest way on graph: **Regard nodes as words.**
  - For example: in both graph have 4 nodes, we found the features of 2 graphs are same.

4 nodes                  4 nodes

$$\phi\left(\begin{array}{c} \bullet \\ | \\ \bullet \\ | \\ \bullet \end{array}\right) = \phi\left(\begin{array}{c} \bullet \\ | \\ \bullet \\ | \\ \bullet \end{array}\right)$$


- Problem: Bag of node counts doesn't work well...
- What if we use **Bag of Node Degrees?**
  - Characterizes a graph  $G$  based on frequency of different degree values in that graph.
  - For bag of degrees, the set of nodes  $\sigma_n$  is defined as

$$\sigma_n(G) = \{v_i | v_i \in V^G, d_i = n\}$$



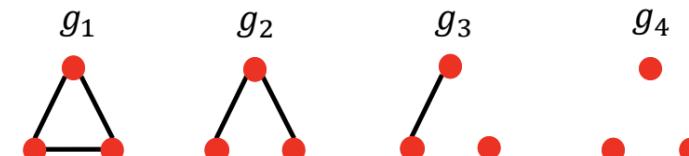
$d = 1$	$d = 2$	$d = 3$	$d = 4$
2	4	0	1

$$\phi_{BN}(G) = (2, 4, 0, 1)$$

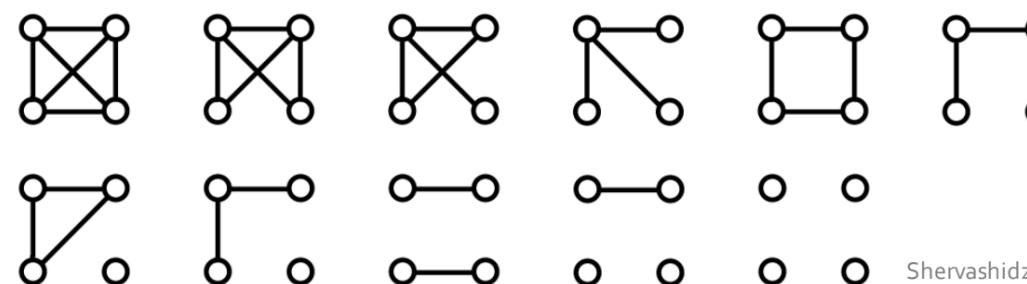
- Does not reflect the global structure of the graph.

- **Key Idea:** Count the number of different graphlets in a graph.
- **Graphlet Differences:**
  - Nodes do not need to be connected.
  - Graphlets are not rooted.
- Let  $G_k = (g_1, g_2, g_3, g_4)$  be a list of graphlet size k.

- For  $k = 3$ , there are 4 graphlets.

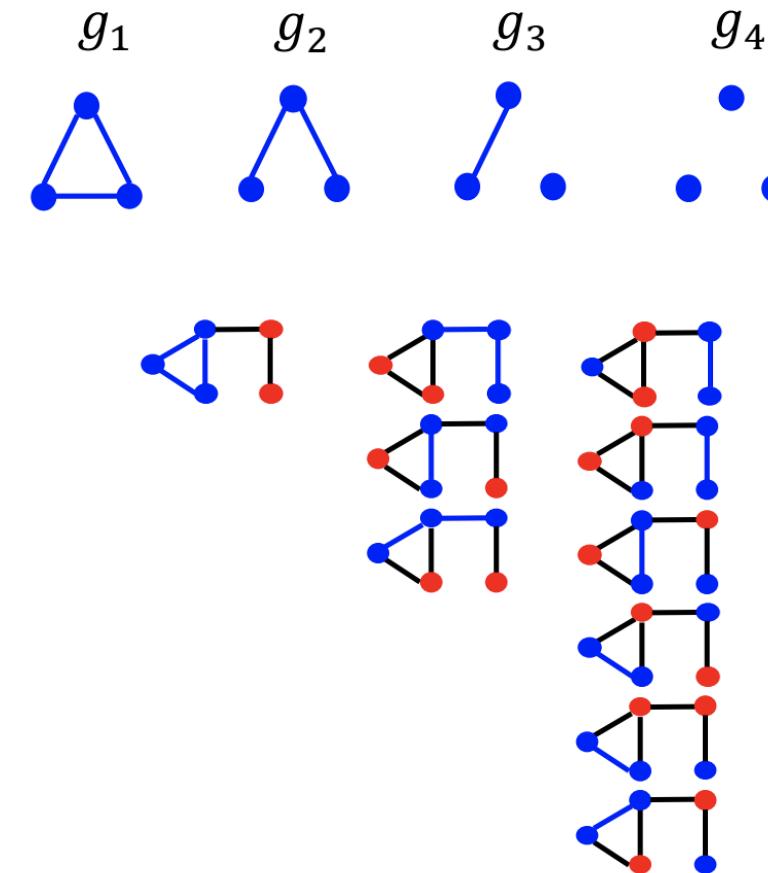
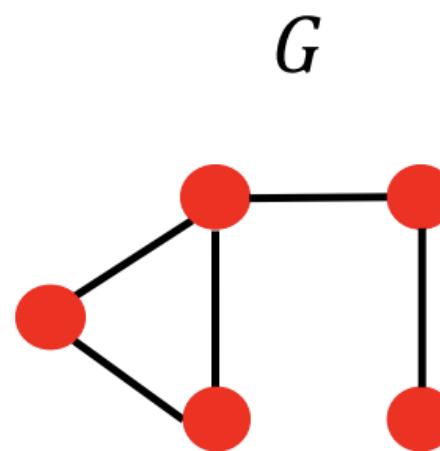


- For  $k = 4$ , there are 11 graphlets.



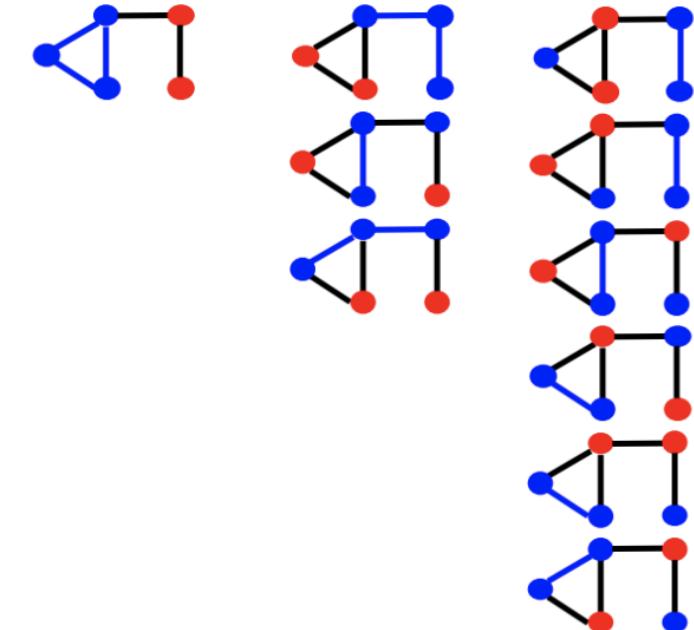
Shervashidze et al., AISTATS 2011

➤ Example for  $k = 3$ :



$$\mathbf{f}_G = (1, 3, 6, 0)^T$$

- Counting graphlets is expensive!
  - Counting size  $k$  graphlets for graph with  $n$  nodes by enumeration takes  $n^k$  time.
  - If our graph changes with time, we must recalculate the features again.
  - Worst-case scenario: unavoidable since subgraph isomorphism test (judging whether a graph is a subgraph of another graph) is **NP-hard**.
  - If a graph's node degree is bounded by  $d$ , an  $O(nd^{k-1})$  algorithm exists to count all the graphlets of size  $k$ .
- **Can we design a more efficient graph kernel?**



- **Goal:** Design an efficient graph feature descriptor  $\phi(G)$ .
- **Key Idea:**
  - Iteratively use neighborhood structure to describe node's neighboring topology.
  - Generalized version of **Bag of node degrees** (node degree only contains one-hop neighborhood information).

→ **Color Refinement Algorithm**

- For a graph  $G$  with nodes  $V$ :
- Assign initial color  $c^{(0)}(v)$  to each node  $v$
- Iteratively refine node colors by:

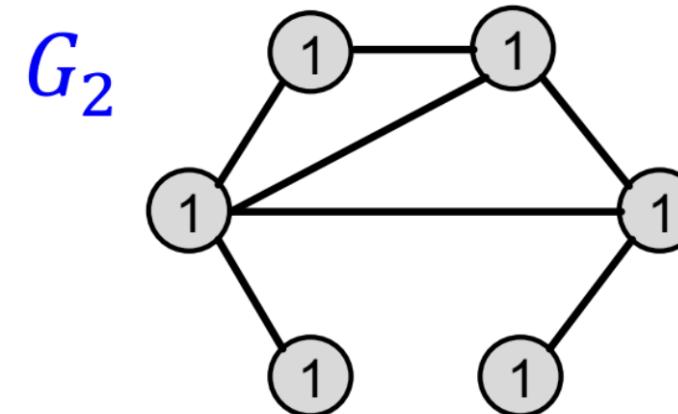
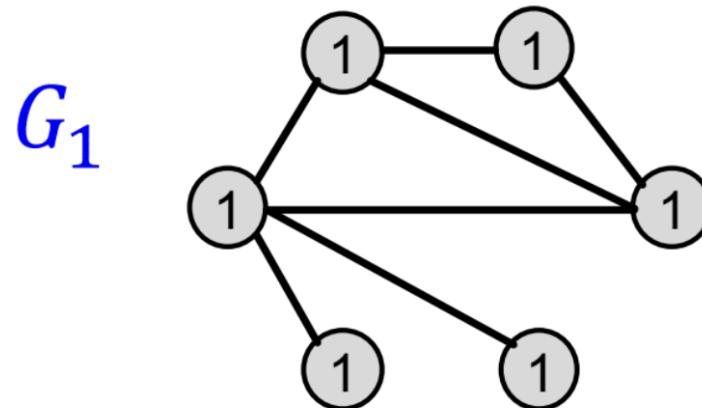
$$c^{(k+1)}(v) = \text{HASH} \left( \left\{ c^{(k)}(v), \left\{ c^{(k)}(u) \right\}_{u \in N(v)} \right\} \right)$$

where HASH maps different inputs to different colors.

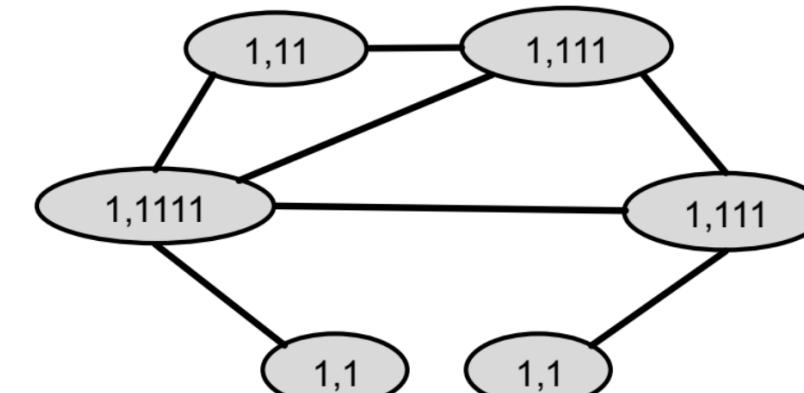
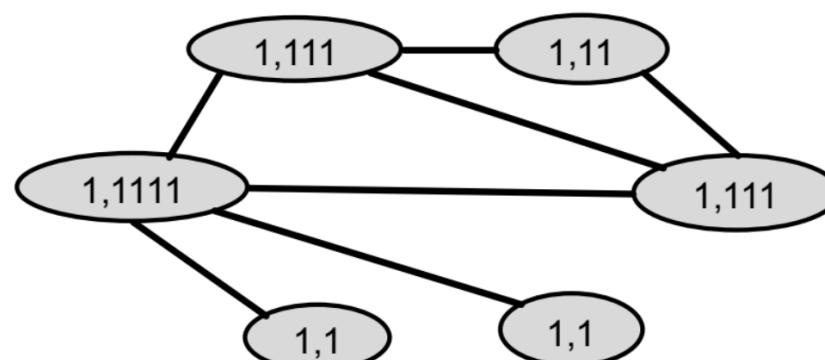
- After  $K$  steps of iteration,  $c^{(K)}(v)$  represents the structure of the  $K$ -hop neighborhood.

- Example with two graphs:

- Assign initial color:

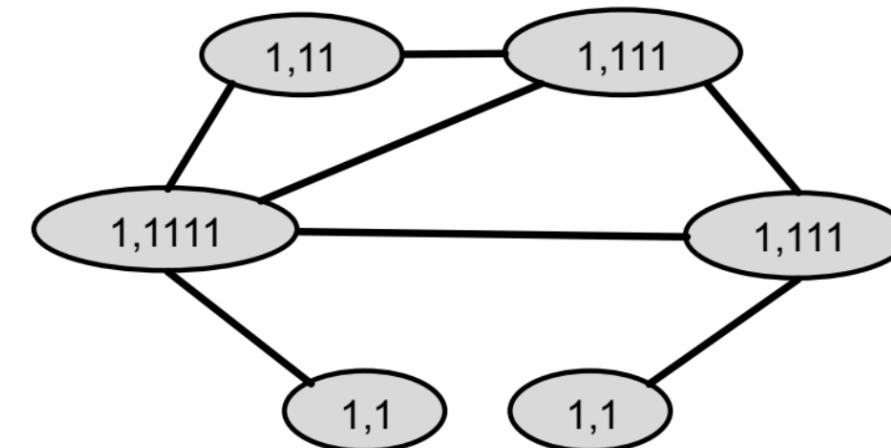
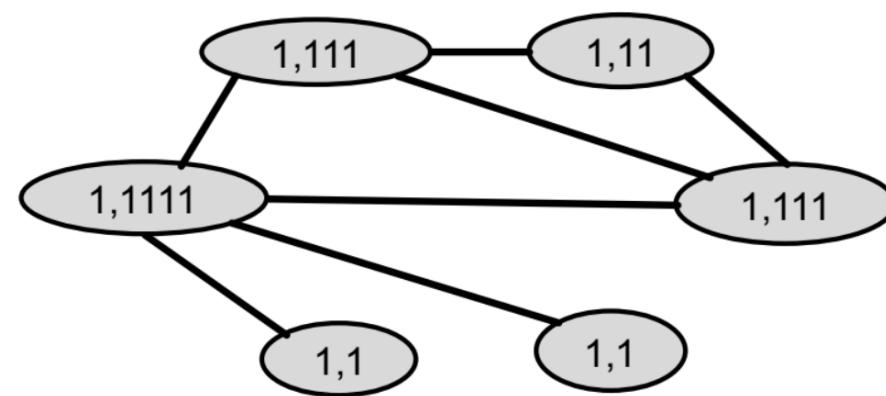


- Aggregate neighboring colors:

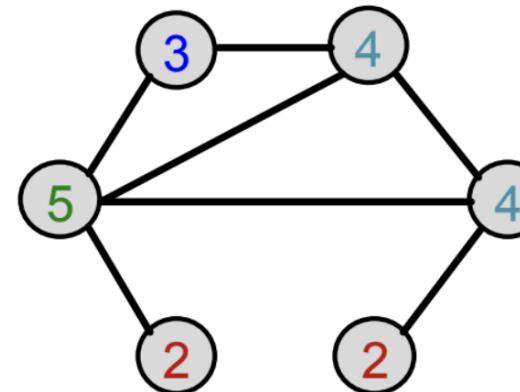
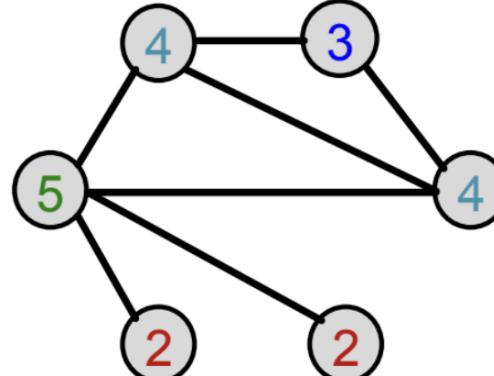


- Example with two graphs:

- Aggregated colors:



- Hash aggregated colors:

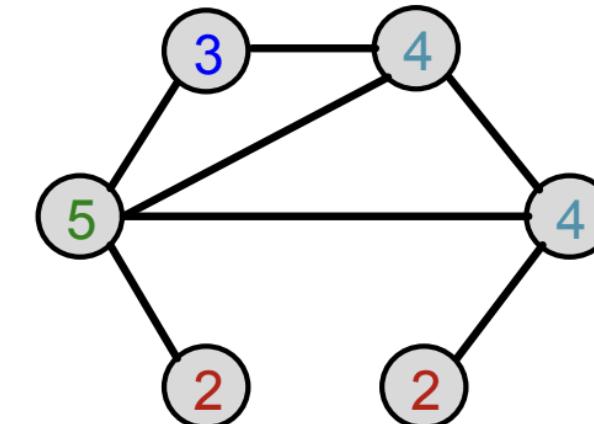
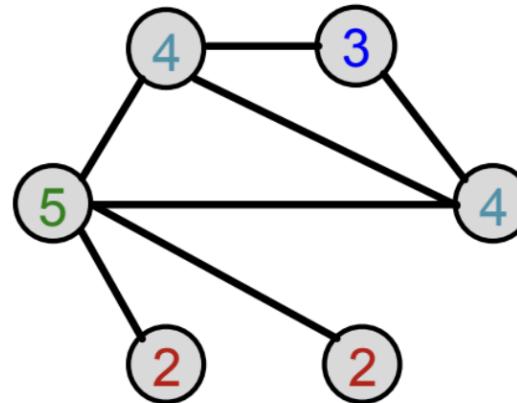


Hash table

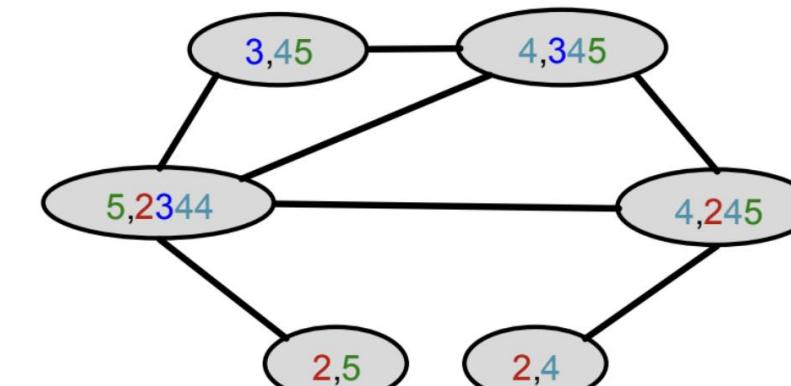
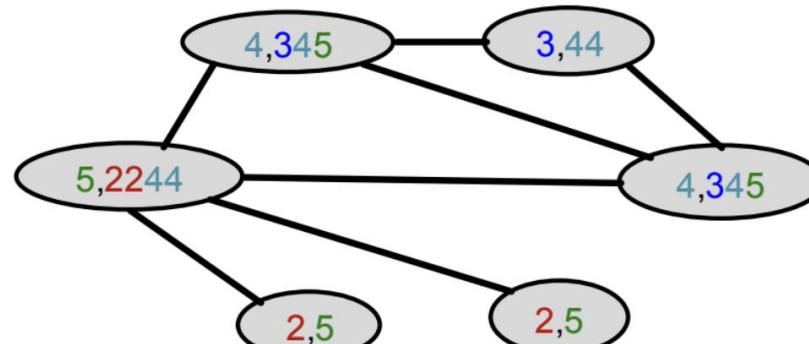
1,1	-->	2
1,11	-->	3
1,111	-->	4
1,1111	-->	5

- Example with two graphs:

- Aggregated colors:

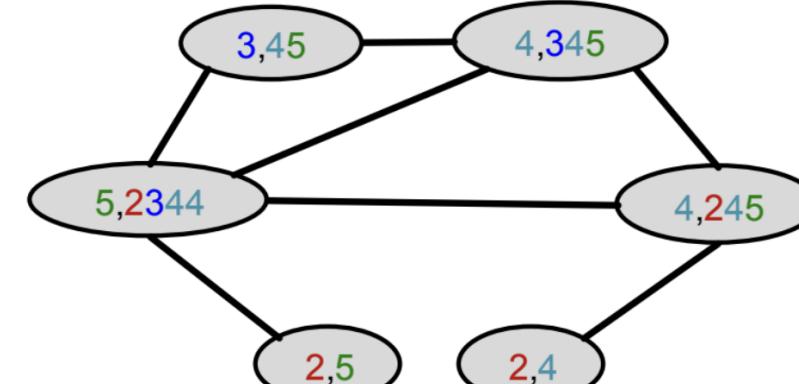
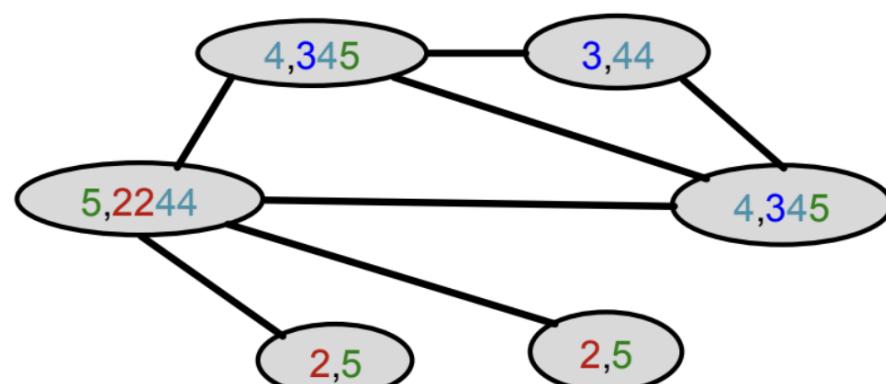


- Hash aggregated colors:

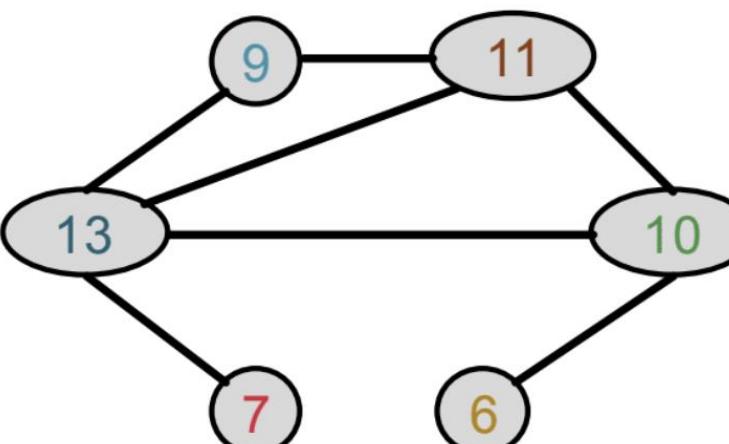
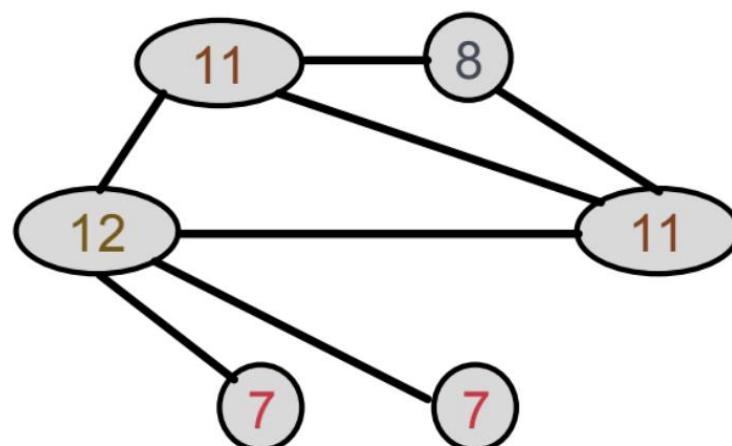


- Example with two graphs:

- Aggregated colors:



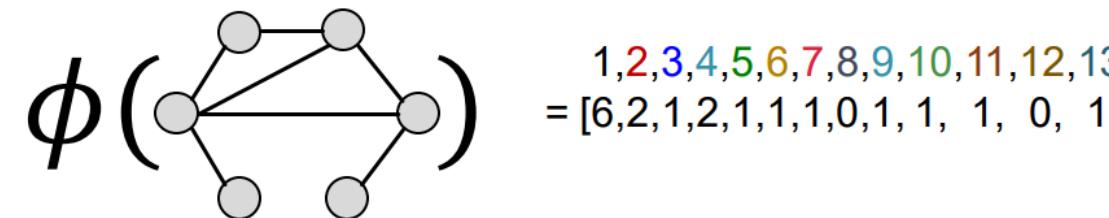
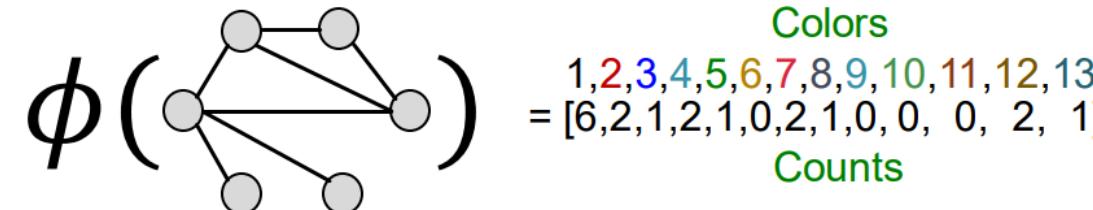
- Hash aggregated colors:



Hash table

2,4	-->	6
2,5	-->	7
3,44	-->	8
3,45	-->	9
4,245	-->	10
4,345	-->	11
5,2244	-->	12
5,2344	-->	13

- After color refinement, WL Kernel counts # of nodes within given colors:



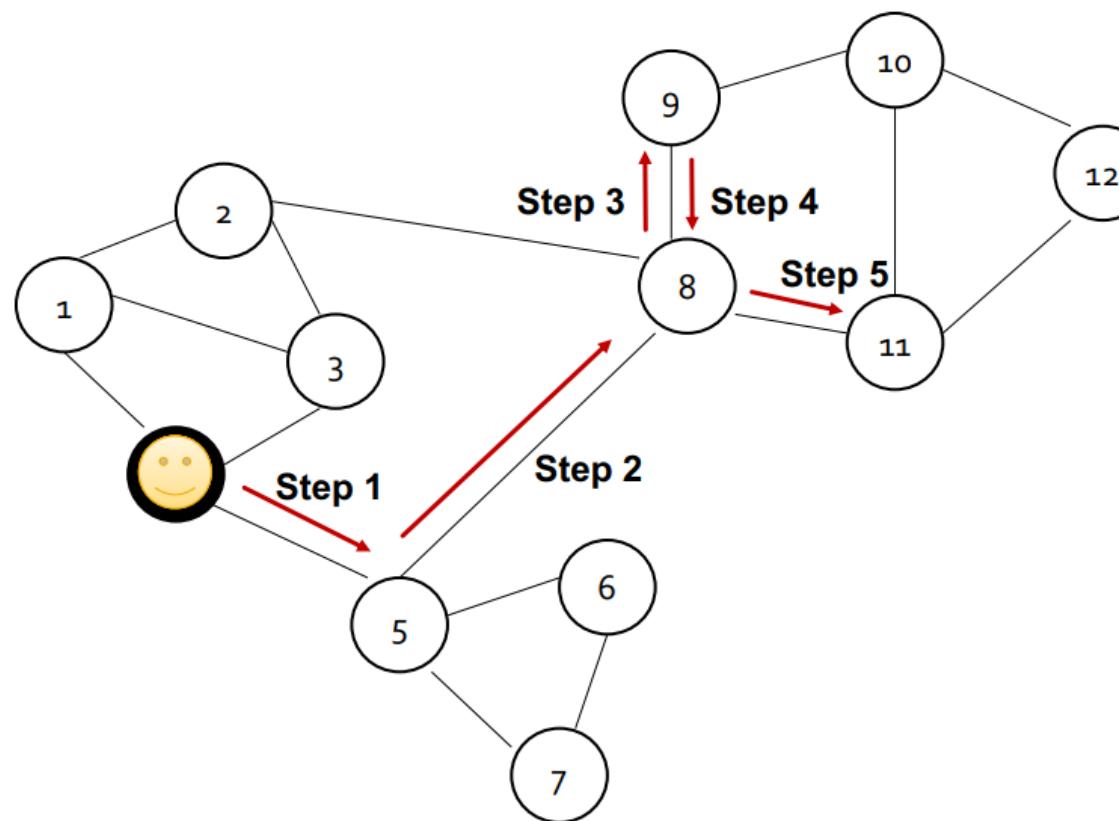
- The WL kernel value is computed by the inner product of the color count vectors:

$$\begin{aligned} K\left(\begin{array}{c} \text{graph 1} \end{array}, \begin{array}{c} \text{graph 2} \end{array}\right) &= \phi\left(\begin{array}{c} \text{graph 1} \end{array}\right)^T \phi\left(\begin{array}{c} \text{graph 2} \end{array}\right) \\ &= 49 \end{aligned}$$

## ➤ WL kernel benefits:

- Computationally efficient (color refinement need #(edges) steps).
- #(colors) depends on total number of nodes - only colors appeared in the two graphs need to be tracked.
- Time complexity is linear in #(edges).
- Can be used to check graph isomorphism.

- For a graph and a starting point, select a neighbor of it at random, and move to this neighbor.
- Select a neighbor of this point at random, and move to it, etc.
- The (random) sequence of points visited this way is a random walk on the graph.



- Compute all-pairs-shortest-paths for  $G$  and  $G'$  via Floyd-Warshall.
- Define a kernel by comparing all pairs of shortest path lengths from  $G$  and  $G'$ :

$$k(G, G') = \sum_{v_i, v_j \in G} \sum_{v'_k, v'_l \in G'} k_{length}(d(v_i, v_j), d(v'_k, v'_l))$$

where  $d(v_i, v_j)$  is the length of the shortest path between node  $v_i$  and  $v_j$ .

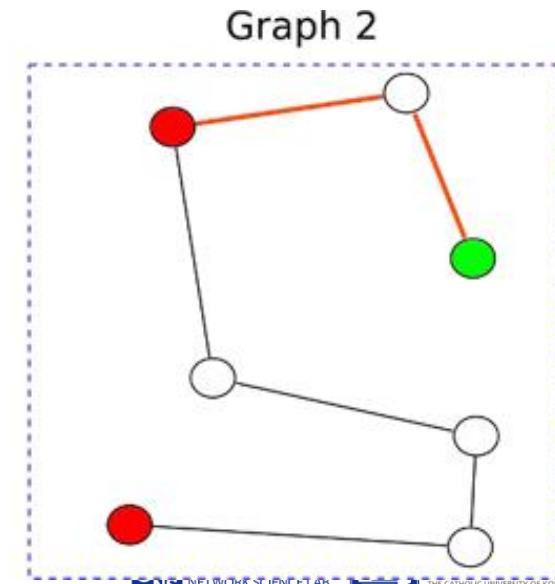
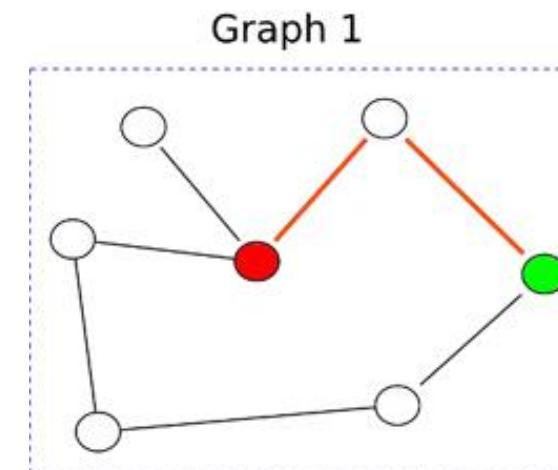
- $k_{length}$  is a kernel that compares the lengths of two shortest paths:

- a linear kernel

$$k(d(v_i, v_j), d(v'_k, v'_l)) = d(v_i, v_j) * d(v'_k, v'_l)$$

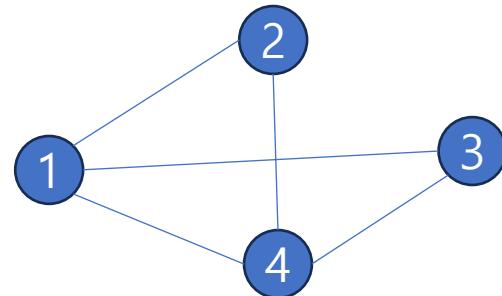
- a delta kernel

$$k(d(v_i, v_j), d(v'_k, v'_l)) = \begin{cases} 1, & \text{if } d(v_i, v_j) = d(v'_k, v'_l) \\ 0, & \text{otherwise} \end{cases}$$



- RWR [Kashima+ '03, Gaertner+ '03, Vishwanathan '10]
- Shortest path kernels [Borgwardt & Kriegel '05]
- Cyclic path kernels [Horvath+ '04]
- Depth-first search kernels [Swamidass+ '05]
- Subtree kernels [Shervashidze+ '09 NIPS, JMLR'11 , Ralaivola+'05]
- Graphlet / Subgraph kernels [Shervashidze+ '09, Thoma+ '10]
- All-paths kernels [Airola+ '08]
- ...

➤ Graph and Associated Matrices



$$G = (V, E)$$

$$|V| = 4$$

$$|E| = 5$$

➤ Laplacian matrix

$$\begin{aligned} L_G &= D_G - A_G \\ &= B_G B_G^T \end{aligned}$$

➤ Adjacency matrix

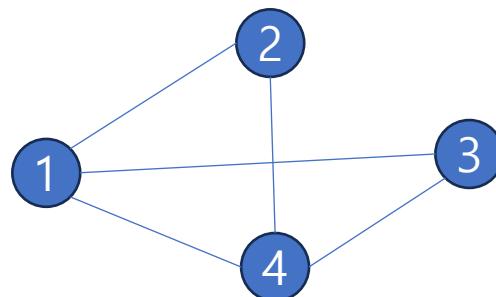
$$A_G = \begin{bmatrix} 0 & 1 & 1 & 1 \\ 1 & 0 & 0 & 1 \\ 1 & 0 & 0 & 1 \\ 1 & 1 & 1 & 0 \end{bmatrix}$$

➤ Degree matrix

$$D_G = \begin{bmatrix} 3 & 0 & 0 & 0 \\ 0 & 2 & 0 & 0 \\ 0 & 0 & 2 & 0 \\ 0 & 0 & 0 & 3 \end{bmatrix}$$

➤ Incidence matrix

$$B_G = \begin{bmatrix} 1 & 1 & 1 & 0 & 0 \\ -1 & 0 & 0 & 1 & 0 \\ 0 & -1 & 0 & 0 & 1 \\ 0 & 0 & -1 & -1 & -1 \end{bmatrix}$$



$$L_G = \begin{bmatrix} 3 & -1 & -1 & -1 \\ -1 & 2 & 0 & -1 \\ -1 & 0 & 2 & -1 \\ -1 & -1 & -1 & 3 \end{bmatrix}$$

Eigenvalue

Eigenvector

$$\lambda = \{0, 2, 4, 4\}$$

$$\begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} \quad \begin{bmatrix} 0 \\ -1 \\ 1 \\ 0 \end{bmatrix} \quad \begin{bmatrix} -1 \\ -1 \\ -1 \\ 3 \end{bmatrix} \quad \begin{bmatrix} -2 \\ 1 \\ 1 \\ 0 \end{bmatrix}$$

- Symmetric  $\rightarrow$  real eigenvalues; eigenvectors are mutually orthogonal.
- Orthogonally diagonalizable  $\rightarrow$  an eigenvalue with multiplicity  $k$  has  $k$ -dimensional eigenvectors.

- For entries  $x = (x_1, x_2, \dots, x_n) \in \mathbb{R}^n$

$$x^T L_G x = x^T B_G B_G^T x = (x^T B_G)(B_G^T x) = \sum_{(i,j) \in E} (x_i - x_j)^2 \geq 0$$

- Meaning that: positive semidefinite  $\rightarrow$  eigenvalues in Laplacian is non-negative.
- Row sum = 0  $\rightarrow$  singular
  - At least one eigenvalue = 0, unity eigenvector (since row sum = 1).
- Orthogonal eigenvector  $u$  = eigenvector of non-zero eigenvalue.

$$\sum_{i=1}^n u_i = 0$$

$$\lambda = \{0, 2, 4, 4\}$$

$$\begin{bmatrix} 1 \\ 1 \\ 1 \\ 1 \end{bmatrix} \quad \begin{bmatrix} 0 \\ -1 \\ 1 \\ 0 \end{bmatrix} \quad \begin{bmatrix} -1 \\ -1 \\ -1 \\ 3 \end{bmatrix} \quad \begin{bmatrix} -2 \\ 1 \\ 1 \\ 0 \end{bmatrix}$$

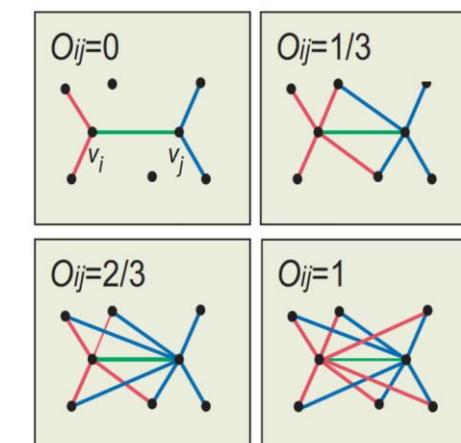
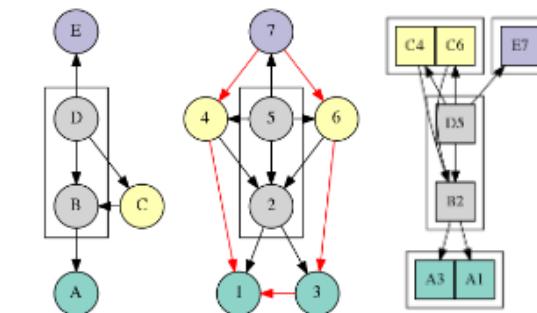
➤ Which graphs are determined by their spectrum?

- Complete Graphs.
- Graphs with one edge.
- Graphs missing 1 edge.
- Regular graphs with degree 2.
- Regular graphs of degree  $n - 3$ .

	Eigenvalues
Complete	$\{0, n^{n-1}\}$
Line	$2 - 2 \cos\left(\frac{\pi k}{n}\right), k = 1, \dots, n$
Ring	$2 - 2 \cos\left(\frac{2\pi k}{n}\right), k = 1, \dots, \frac{n}{2}$
Star	$\{0, 1^{n-2}, 2\}$

- Reminder: Communities in networks is defined with respect to the whole graph.
  - identifying sets of nodes that are densely connected with each other.
- A graph has a community structure if it is different from a random graph.
- Common methods:
  - Structural equivalence: share the same neighbors and are not adjacent
  - Edge Overlap between the number of neighbor  $N(i)$  and  $N(j)$  of node  $i$  and  $j$

$$O_{ij} = \frac{|(N(i) \cap N(j)) \setminus \{i, j\}|}{|(N(i) \cup N(j)) \setminus \{i, j\}|}$$



## ➤ Local:

- Fundamental: Graph size, density, connectivity, Node degree.
- Graph Centrality: Betweenness, Closeness, Eigenvector.
- Average Clustering Coefficient.
- Diameter: the length of the shortest path between the most distanced nodes.
- Average Shortest Path Length: average number of steps along the shortest paths for all possible pairs of nodes.

## ➤ Global:

- Subgraph/Motif counts.
- Kernel-based: Graphlet, Weisfeiler-Lehman, Random Walk, Shortest Path, etc.
- Spectral: Laplacian matrix.
- Community Structure.

➤ There are many graph-level tasks:

- Graph regression.
- Graph classification.
- Graph generation.
- Graph clustering.
- Graph similarity.
- Graph embeddings.

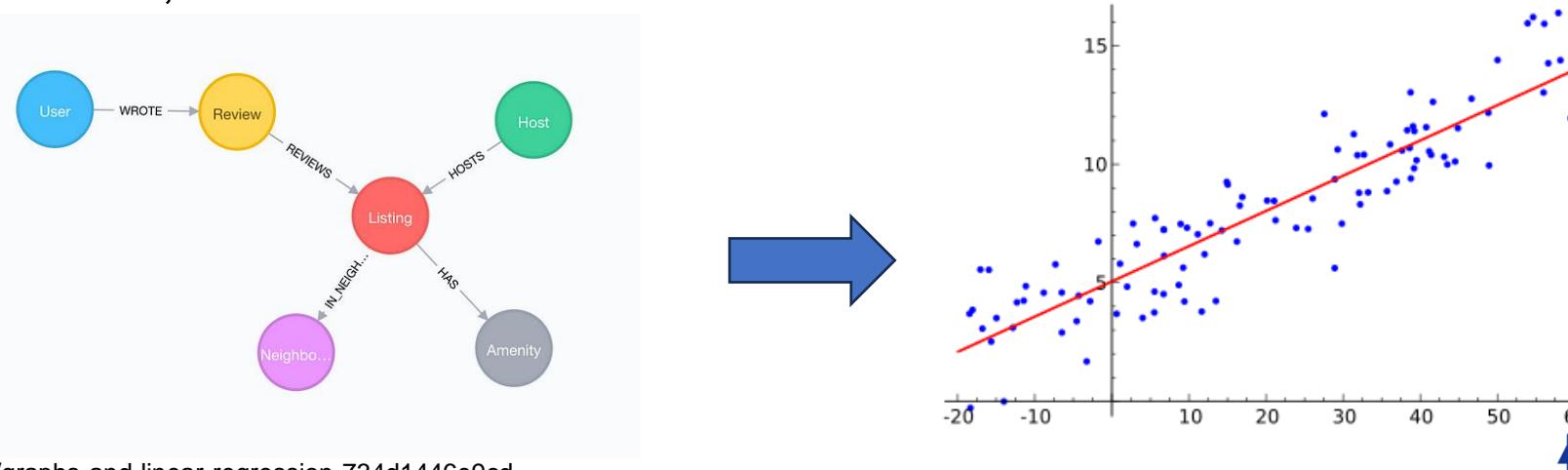
## ➤ Graph regression:

- Given a set of graphs  $G = \{G_1, G_2, \dots, G_n\}$  and their associated target value  $y = \{y_1, y_2, \dots, y_n\}$ .
- The goal is to learn a function  $f$  that map each graph  $G_i$  to a continuous target value  $\hat{y}_i = f(G_i)$  such that the predicted values  $\hat{y}_i$  are close to the true values.

$$\hat{y}_i = f(G_i) + \epsilon_i$$

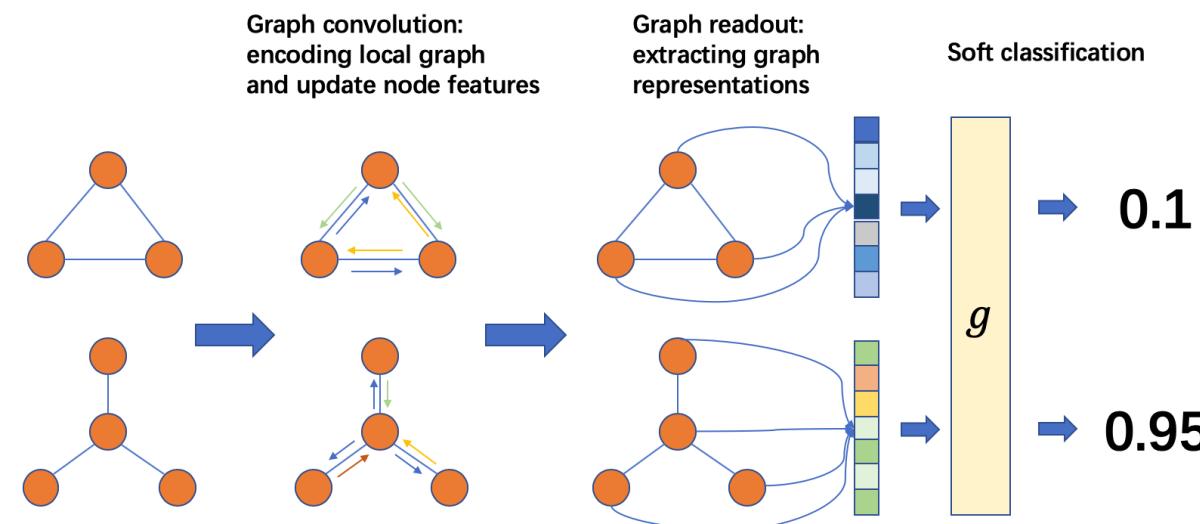
Where  $\epsilon_i$  represents the error or residual between the predicted and true values

- Conventional methods.
  - Kernel method: Subgraph matching, Weisfeiler-Lehman Subtree Kernel, Shortest path, Random walk, etc.



## ➤ Graph classification:

- Given a set of attributed graphs  $D = \{(G_1, l_1), (G_2, l_2), \dots, (G_n, l_n)\}$ , the goal is to learn a function  $f : G \rightarrow L$ , where  $G$  is the input space of graphs and  $L$  is the set of graph labels.
- Each graph  $G_i = (A_{G_i}, D_{G_i})$  is comprised of an adjacency matrix  $A_{G_i}$ , an attribute matrix  $D_{G_i}$  and corresponding label  $l_i$ .
- Conventional methods.
  - Kernel method: Subgraph matching, Weisfeiler-Lehman Subtree Kernel, Shortest path, Random walk, etc.



- Counts the number of matchings between subgraphs of bounded size in two graphs.
- Given two graphs  $G = (V, E)$  and  $G' = (V', E')$ :
  - $B(G, G')$  denote the set of all bijections between sets  $S \subseteq V$  and  $S' \subseteq V'$
  - $\lambda: B(G, G') \rightarrow \mathbb{R}^+$  be a weight function.
  - The subgraph matching kernel is defined as

$$k(G, G') = \sum_{\phi \in B(G, G')} \lambda(\phi) \prod_{v \in S} \kappa_V(v, \phi(v)) \prod_{e \in S \times S'} \kappa_E(e, \psi(e))$$

Where  $S = \text{dom}(\phi)$  and  $\kappa_V, \kappa_E$  are kernel functions defined on vertices and edges.

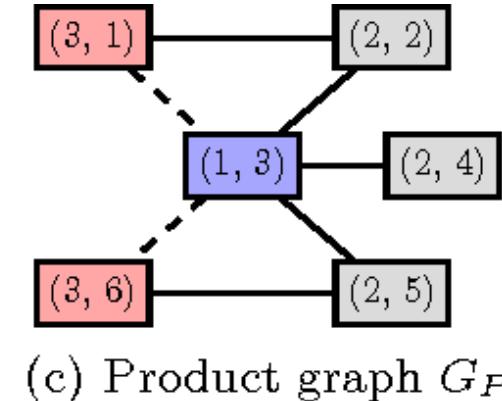
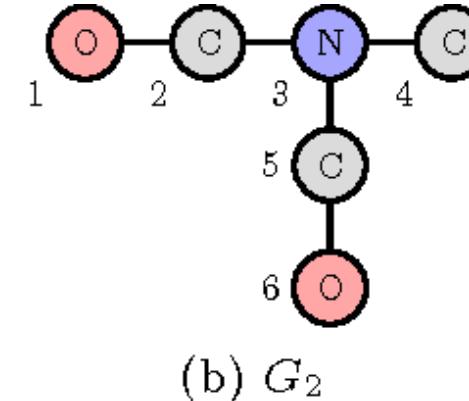
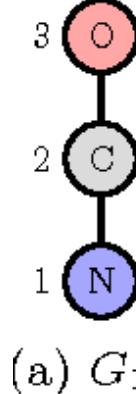
- The instance of the subgraph matching kernel that is obtained if we set the  $\kappa_V, \kappa_E$  functions as follows.

$$\kappa_V(v, v') = \begin{cases} 1, & \text{if } \ell(v) \equiv \ell(v'), \\ 0, & \text{otherwise and} \end{cases}$$

$$\kappa_E(e, e') = \begin{cases} 1, & \text{if } e \in E \wedge e' \in E' \wedge \ell(e) \equiv \ell(e') \text{ or } e \notin E \wedge e' \notin E', \\ 0, & \text{otherwise.} \end{cases}$$

is known as the common subgraph isomorphism kernel.

- This kernel counts the number of isomorphic subgraphs contained in two graphs.



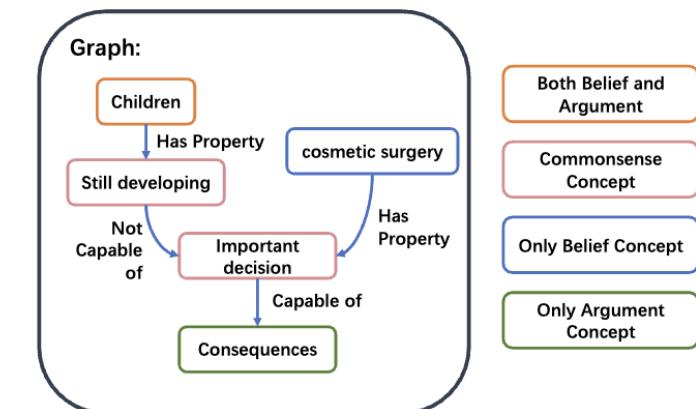
## ➤ Graph generation:

- A quadruplet graph  $G = (V, E, X, E)$ , where  $V$  is the vertex set,  $E \subseteq V \times V$  is the edge set,  $X \in \mathbb{R}^{N \times D}$  is the node feature matrix,  $\mathbf{E} \in \mathbb{R}^{N \times N \times F}$  is the edge attributes, and  $D, F$  are the feature dimensionality.
- Given a set of  $M$  observed graphs  $\mathcal{G} = \{G_i\}_{i=1}^M$ , graph generation learns the distribution of these graphs  $p(G)$ , from which new graphs can be sampled  $G_{new} \sim p(\mathcal{G})$ .
- Conventional methods
  - Preferential Attachment

Belief : Children should be able to consent to cosmetic surgery.  
 Argument : Children do not have the mental capacity to understand the Consequences of medical decisions.  
 Stance: Counter

$$PA = |N(x)| \cdot |N(y)| = d_x \cdot d_y$$

Where  $N(x), N(y)$  are number of neighbors of node  $x$  and  $y$ .



## ➤ Graph clustering:

- Given a set of graphs, partitioning a set of graphs into different groups that share some form of similarity.
- Conventional methods:
  - Hierarchical clustering, K-means clustering, spectral clustering.
  - Modularity: To qualify the graph partitions.
  - Louvian Algorithm: to find partition of a given network with high modularity score

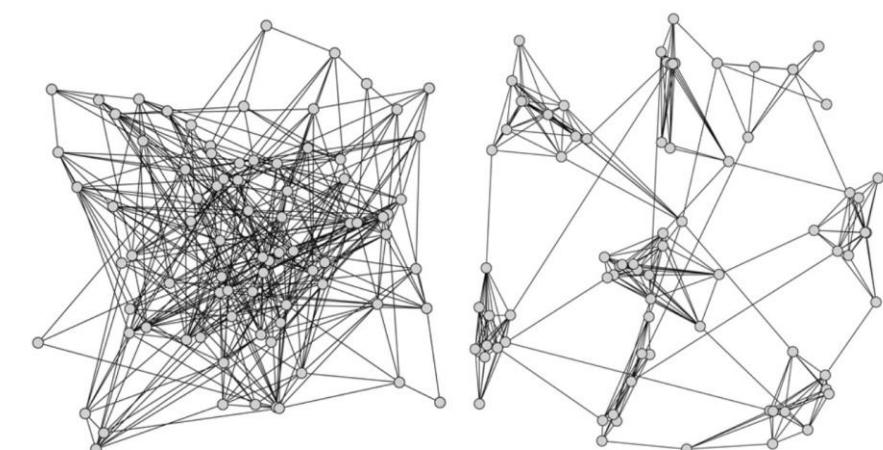
normalization

adjacency matrix

probability a random edge would go between i and j

$$Q = \frac{1}{4m} \sum_{i,j} \left( A_{ij} - \frac{k_i k_j}{2m} \right)$$

$m = \# \text{ edges in graph}$   
 $k_i = \text{degree}(i)$

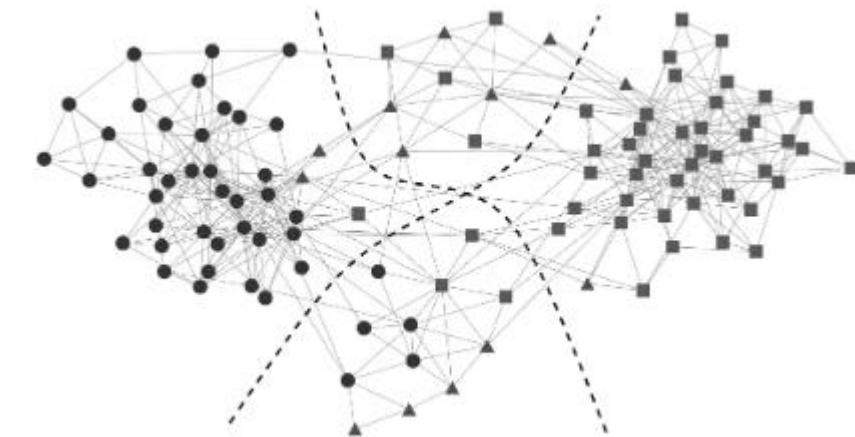


- Normally, modularity only consider to qualify into two graph partition.
- To divide network into more than two communities:

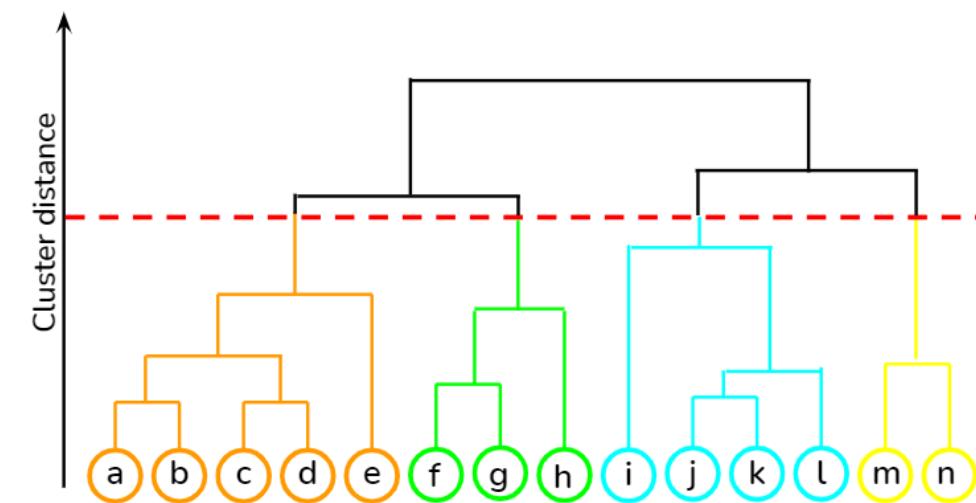
$$\begin{aligned}
 \Delta Q &= \frac{1}{2m} \left[ \frac{1}{2} \sum_{i,j \in g} B_{ij}(s_i s_j + 1) - \sum_{i,j \in g} B_{ij} \right] \\
 &= \frac{1}{4m} \left[ \sum_{i,j \in g} B_{ij} s_i s_j - \sum_{i,j \in g} B_{ij} \right] \\
 &= \frac{1}{4m} \sum_{i,j \in g} \left[ B_{ij} - \delta_{ij} \sum_{k \in g} B_{ik} \right] s_i s_j \\
 &= \frac{1}{4m} \mathbf{s}^T \mathbf{B}^{(g)} \mathbf{s},
 \end{aligned}$$

Where  $\delta_{ij}$  is the Kronecker delta-symbol,  $s_i^2 = 1$  and  $B^{(g)}$  is the  $n_g \times n_g$  matrix with elements indexed by the labels  $i, j$  of nodes within group  $g$  and having values

$$B_{ij}^{(g)} = B_{ij} - \delta_{ij} \sum_{k \in g} B_{ik}.$$

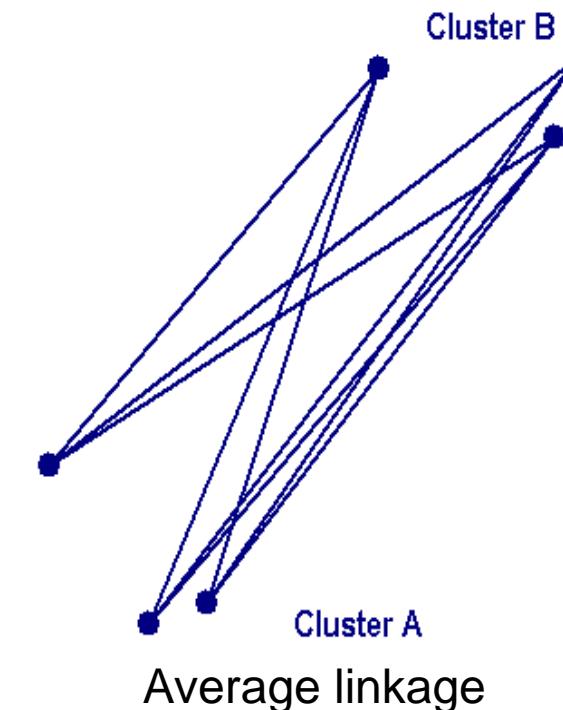
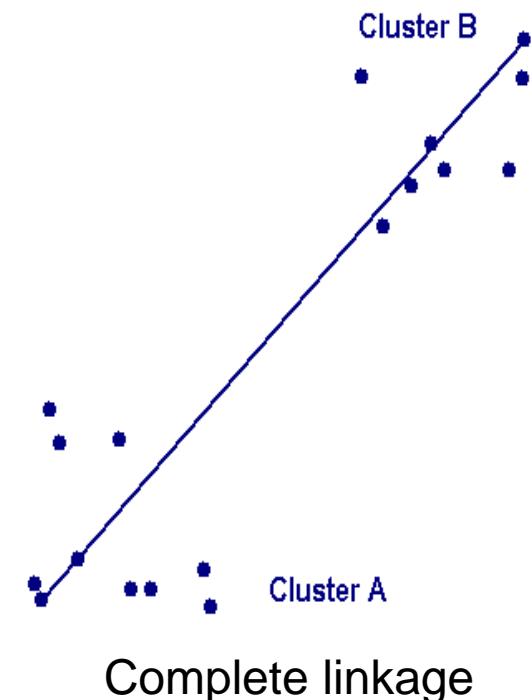
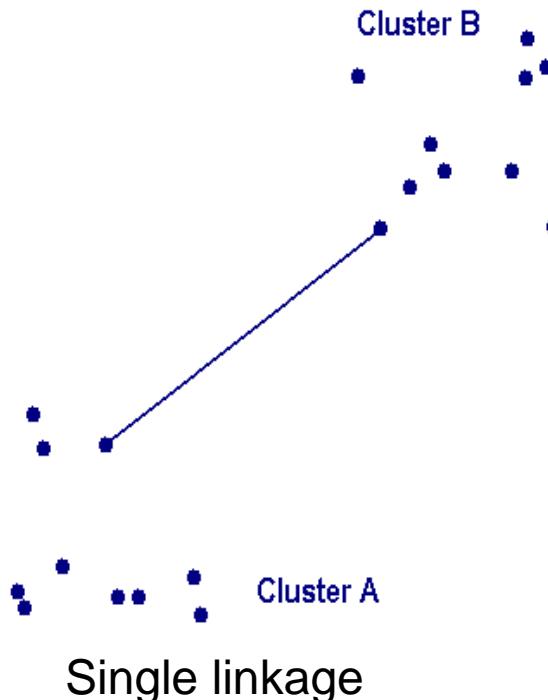


- Hierarchical clustering is a method of cluster analysis which seeks to build a hierarchy of clusters. Two approaches:
  - **Agglomerative** ("bottom up"): each point starts in its own cluster, and pairs of clusters are merged as one moves up the hierarchy – **popular one**.
  - **Divisive** ("top down"): all points start in one cluster, and splits are performed recursively as one moves down the hierarchy:
- Agglomerative clustering algorithm:
  - Maintain a set of clusters.
  - Initially, each instance in its own cluster.
  - Repeat:
    - Pick the two **closest** clusters.
    - Merge them into a new cluster.
    - Stop when there's only one cluster left.



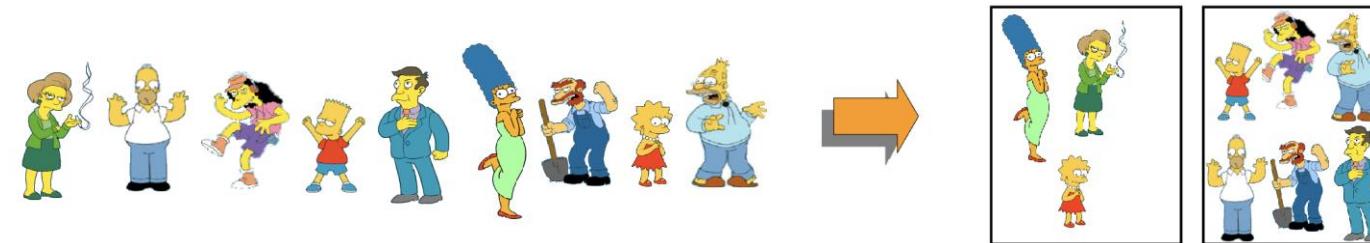
➤ Three Different Distance Measures to define **closest** cluster:

- Minimum distance / Closest distance (single linkage).
- Maximum distance / Farthest distance (complete linkage).
- Group Average (average linkage).



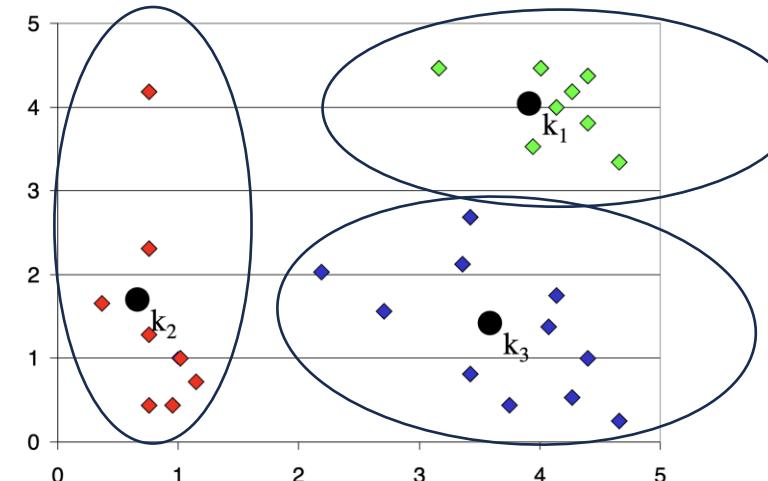
## ➤ Partition clustering:

- Nonhierarchical, each instance is placed in exactly one of K non-overlapping clusters.
- Since the output is only one set of clusters the user has to specify the desired number of clusters K.



## ➤ K-mean clustering algorithm:

- Re-assign and move centers, until ...no objects changed membership.

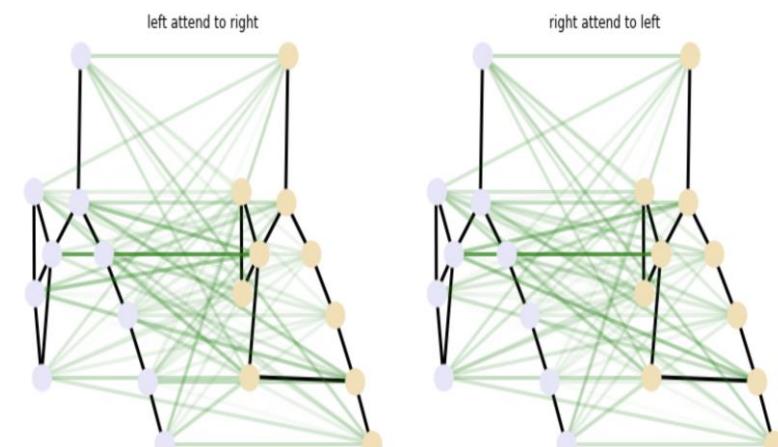


## ➤ Graph similarity:

- Given two graphs  $G_1$  and  $G_2$ , a graph similarity model can be written as a function  $f(G_1, G_2)$  that computes a scalar similarity value.
- Output: find the similarity score between graphs (from 0 to 1).
- Conventional methods:
  - Graph matching, isomorphism testing, etc.
  - Graph edit distances.

$$GED(g_1, g_2) = \min_{(e_1, \dots, e_k) \in P(g_1, g_2)} \sum_{i=1}^k c(e_i)$$

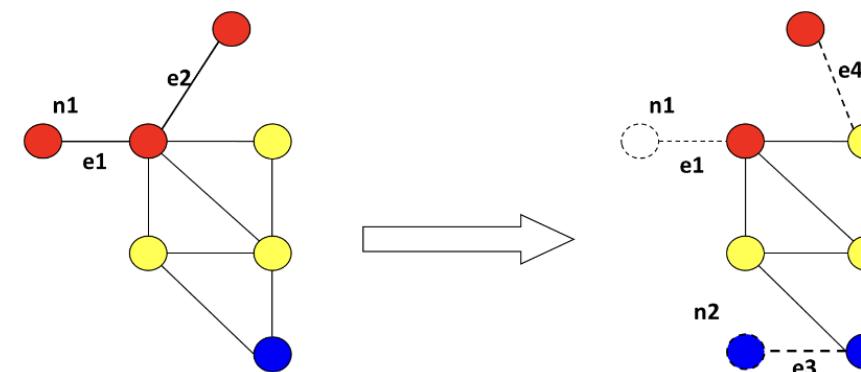
Where  $P(g_1, g_2)$  denotes the set of edit paths transforming  $g_1$  into  $g_2$  and  $c(e) \geq 0$  is the cost of each graph edit operation  $e$ .



- Compute the minimum cost to transform  $g_1$  into  $g_2$ .
- assign cost for operations, e.g.,
  - vertex or edge insertion
  - vertex or edge deletion
  - vertex or edge substitution.

$$GED(g_1, g_2) = \min_{(e_1, \dots, e_k) \in \mathcal{P}(g_1, g_2)} \sum_{i=1}^k c(e_i)$$

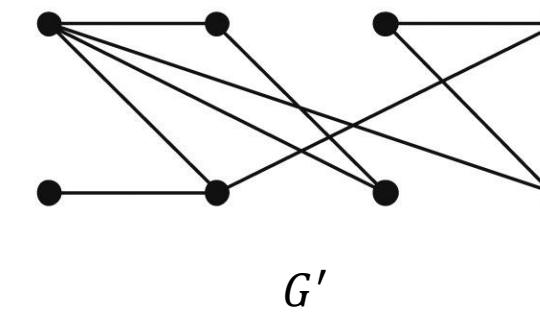
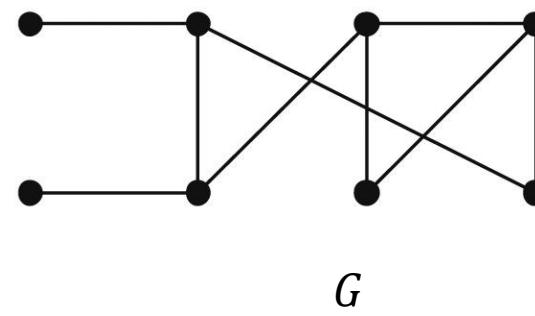
Where  $\mathcal{P}(g_1, g_2)$  denotes the set of edit paths transforming  $g_1$  into  $g_2$  and  $c(e) \geq 0$  is the cost of each graph edit operation  $e$ .



- Given graph  $G$  and  $G'$  of size  $n$  with adjacency spectra  $\lambda^A$  and  $\lambda^{A'}$ .
- Adjacency spectral distance between the two graphs is defined:

$$d_A(G, G') \stackrel{\text{def}}{=} \sqrt{\sum_{i=1}^n (\lambda_i^A - \lambda_i^{A'})^2},$$

- Smaller distance means that two graph are similarity.
- Spectral distances do not require node correspondence.



- Given two graphs,  $G$  and  $G'$ , graphlet kernel is computed as

$$K(G, G') = \mathbf{f}_G^T \mathbf{f}_{G'}$$

- Problem:** if  $G$  and  $G'$  have different sizes, that will greatly skew the value.
- Solution:** normalize each feature vector:

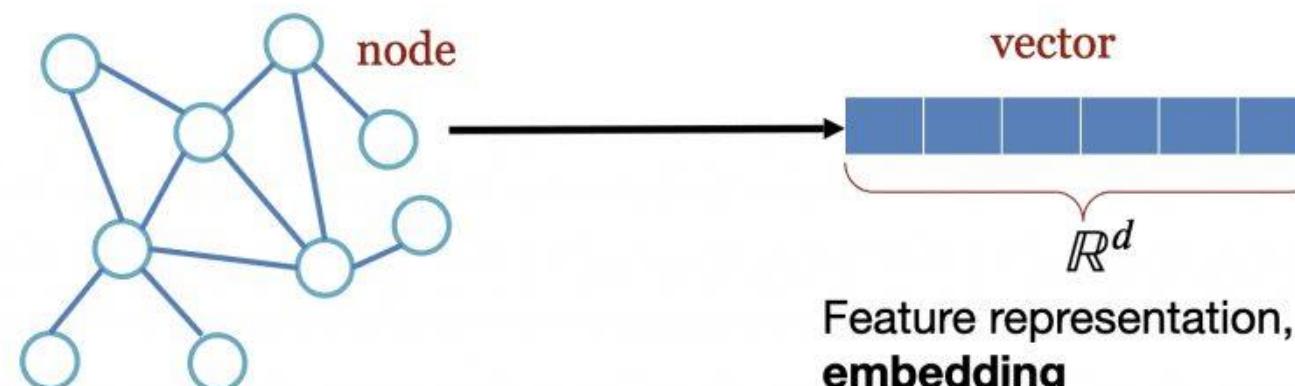
$$\mathbf{h}_G = \frac{\mathbf{f}_G}{\text{Sum}(\mathbf{f}_G)} \quad K(G, G') = \mathbf{h}_G^T \mathbf{h}_{G'}$$

## ➤ Graph Embedding:

- Given a graph  $G = (N, E)$ , where  $V$  is the vertex set,  $E \subseteq V \times V$  is the edge set. Graph embedding aims to learn a low-dimensional vector representation  $x_i$  for each node  $v_i$  from embedding function  $\Phi$  maps:  $x_i = \Phi(v_i) \in \mathbb{R}^d$ .

where  $d$  is the dimensionality of the embedding space.

- Goal: to learn embeddings that preserve important structural properties of the graph, such as node proximity or graph topology, in the low-dimensional space.



Representation Learning on Networks, snap.stanford.edu/proj/embeddings-www, WWW 2018

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## ➤ Graph Embedding:

- Conventional methods
  - Euclidean distance and Cosine similarity.

$$\cos(A, B) = \frac{A \cdot B}{\|A\| \cdot \|B\|} = \frac{\sum_i A_i B_i}{\sqrt{\sum_i A_i^2} \sqrt{\sum_i B_i^2}}$$

Where  $A, B$  denotes two vectors of two graphs.

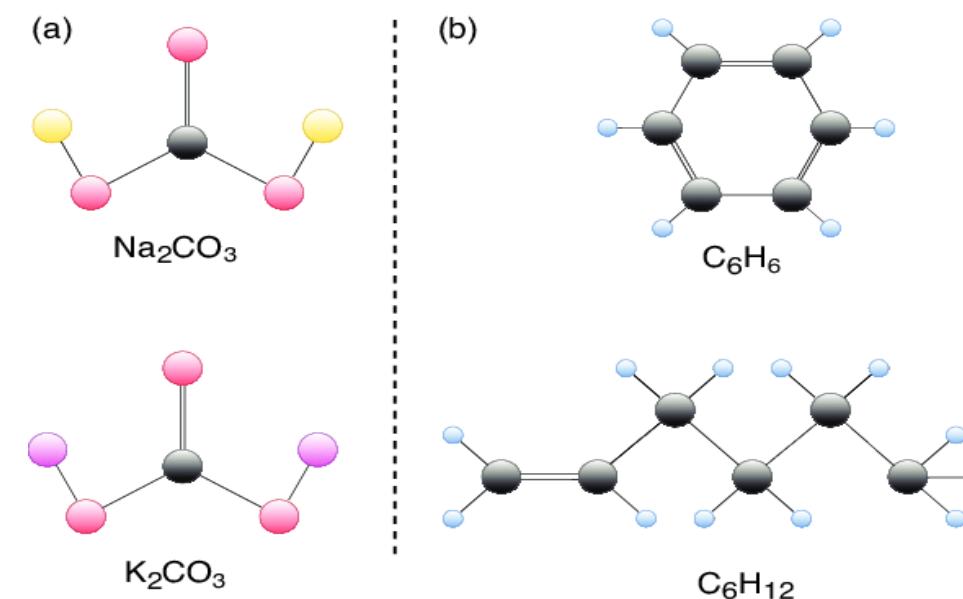
- Laplacian matrix factorization: singular value decomposition, nonnegative matrix factorization.
  - Singular value decomposition:

$$A = UDV^T$$

Where  $A$  denotes adjacency matrix.  $U, V$  are orthonormal and the matrix  $D$  is diagonal with positive real entries.

## ➤ Drug Discovery:

- Classifying a graph itself into different categories.
- Inputs: A collection of graphs.
- For example, determining if a chemical compound is toxic or non-toxic by looking at its graph structure.



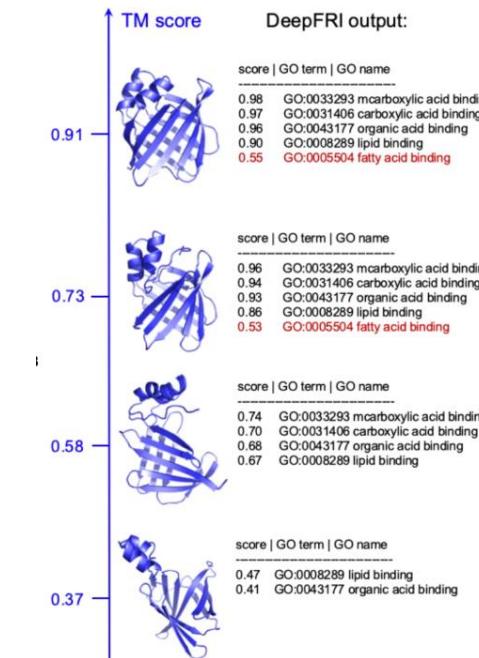
- Programming code recommendation: graph classification tasks

- Program-derived graphs
  - Contains bugs or not.

```
function clearEmployeeListOnLinkClick() {
  document.querySelector("a").addEventListener("click",
    function(event){
      document.querySelector("ul").innerHTML = "";
    }
  );
}

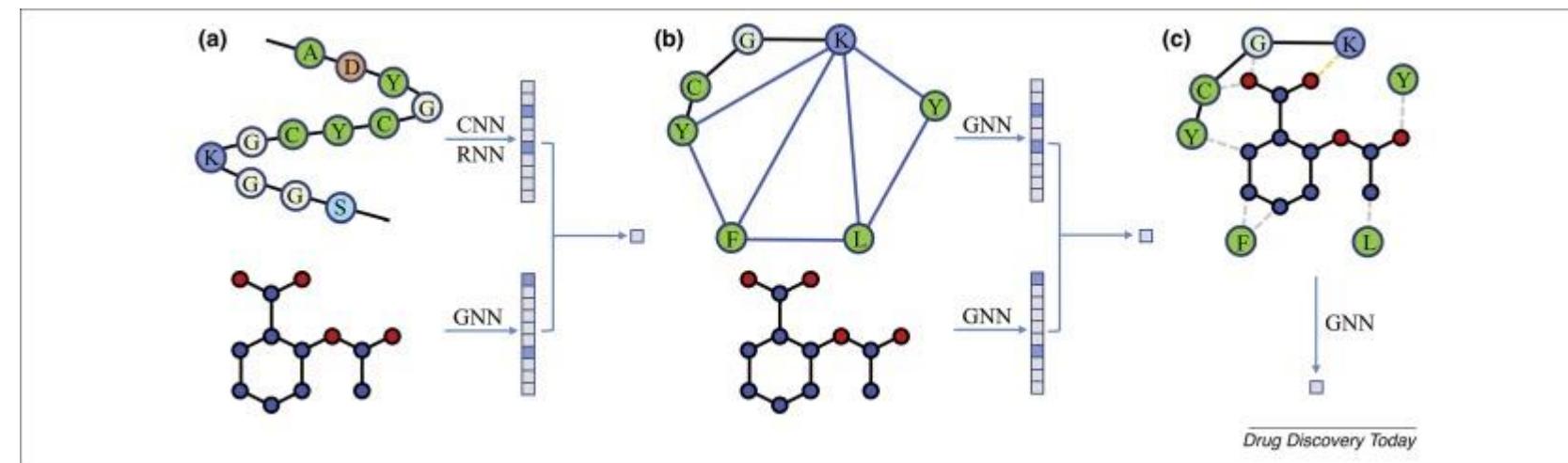
if (matches) {
  return {
    episode: Number(matches.groups.episode),
    hosts: matches.groups.hosts.split(/\[(\w|&)+|\sand\s|\s\]/).map(el => S(el).trim().s)
  };
}
```

- Drug Discovery: graph regression tasks
  - Proteins.
    - Predict protein function from molecular.

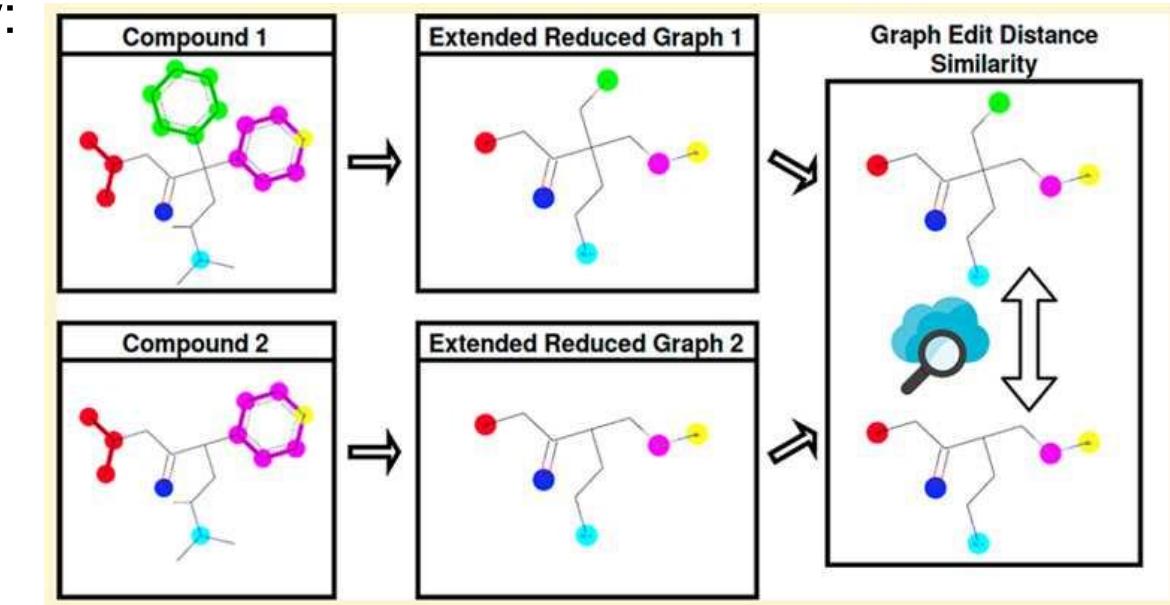


## ➤ Drug-Discovery:

- Molecular-design for drug-discovery using **graph generation**:
  - Generate syntactically valid molecules.
  - Generated molecule should possess certain properties.



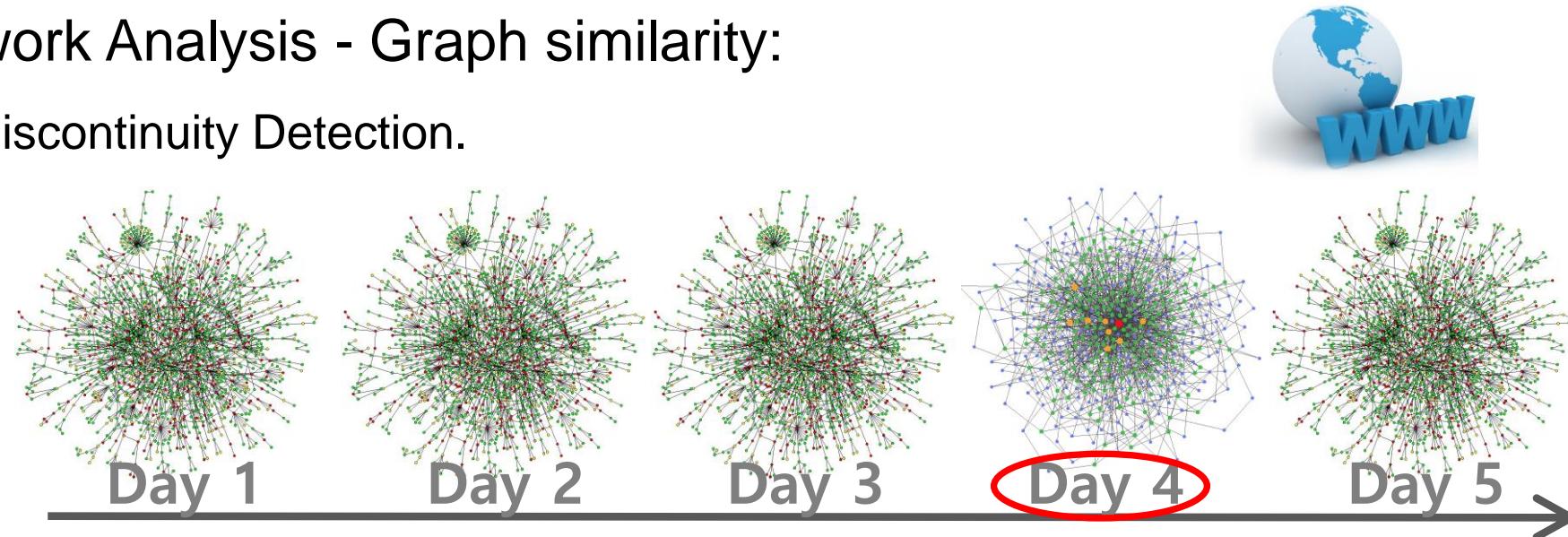
- Drug database:
  - Drug similarity search using **graph similarity**:



- Program database:
  - Code recommendation using graph similarity.

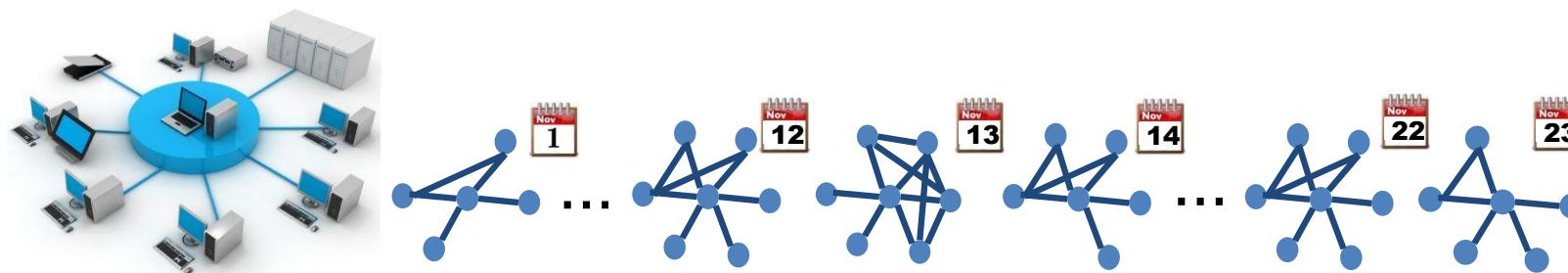
- Network Analysis - Graph similarity:

- Discontinuity Detection.



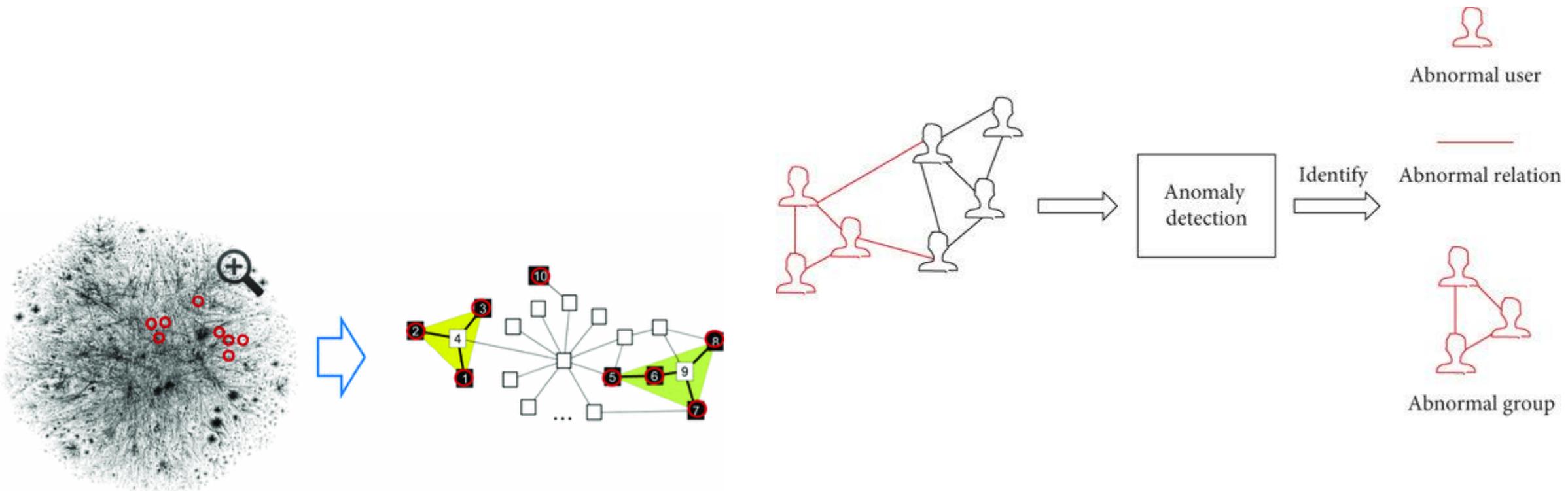
- Intrusion detection:

- Network intrusion.



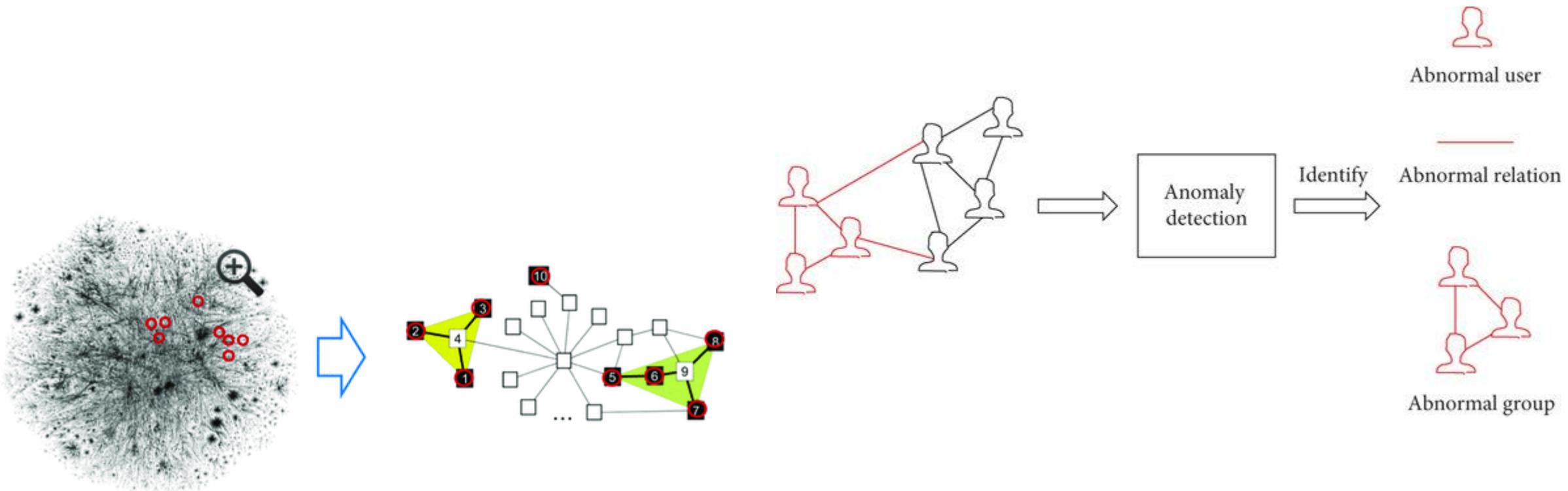
➤ Anomaly detection:

- Abnormal group vs normal group in social network using graph similarity:



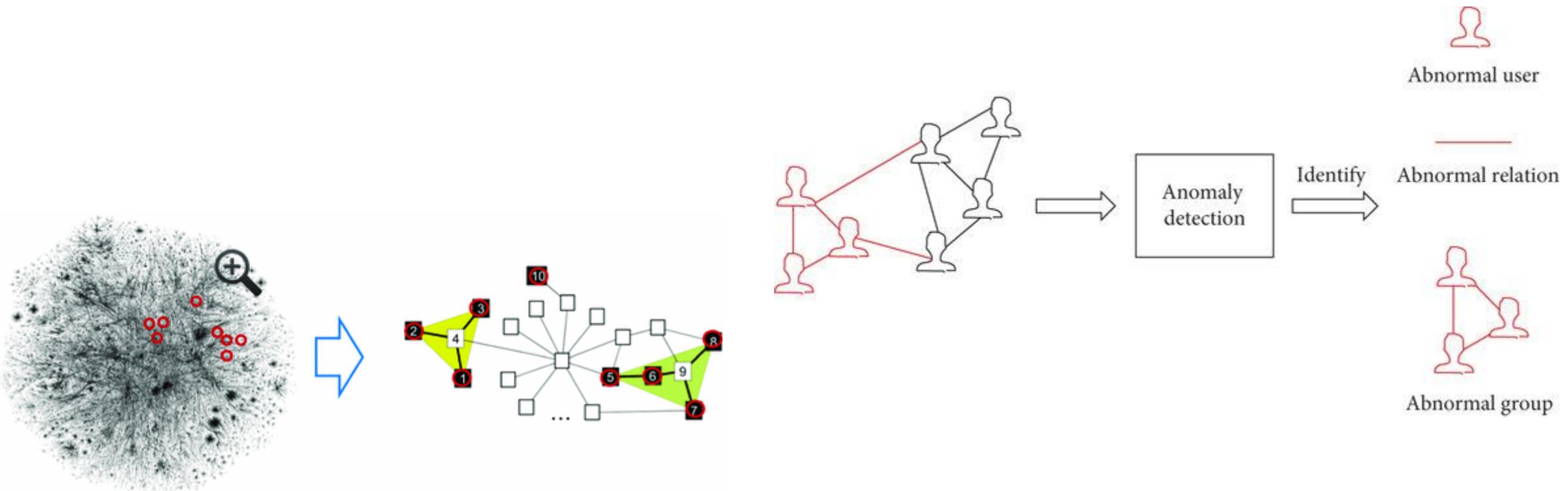
➤ Anomaly detection:

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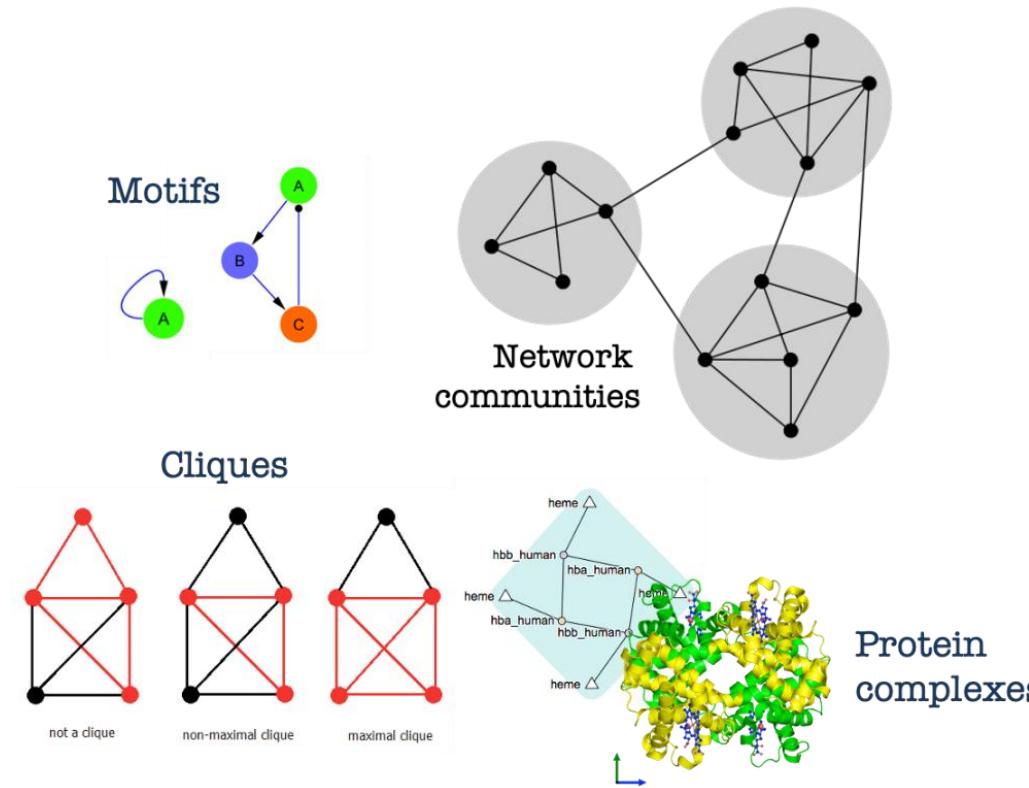
➤ Anomaly detection:

- Abnormal group vs normal group in social network using graph similarity:

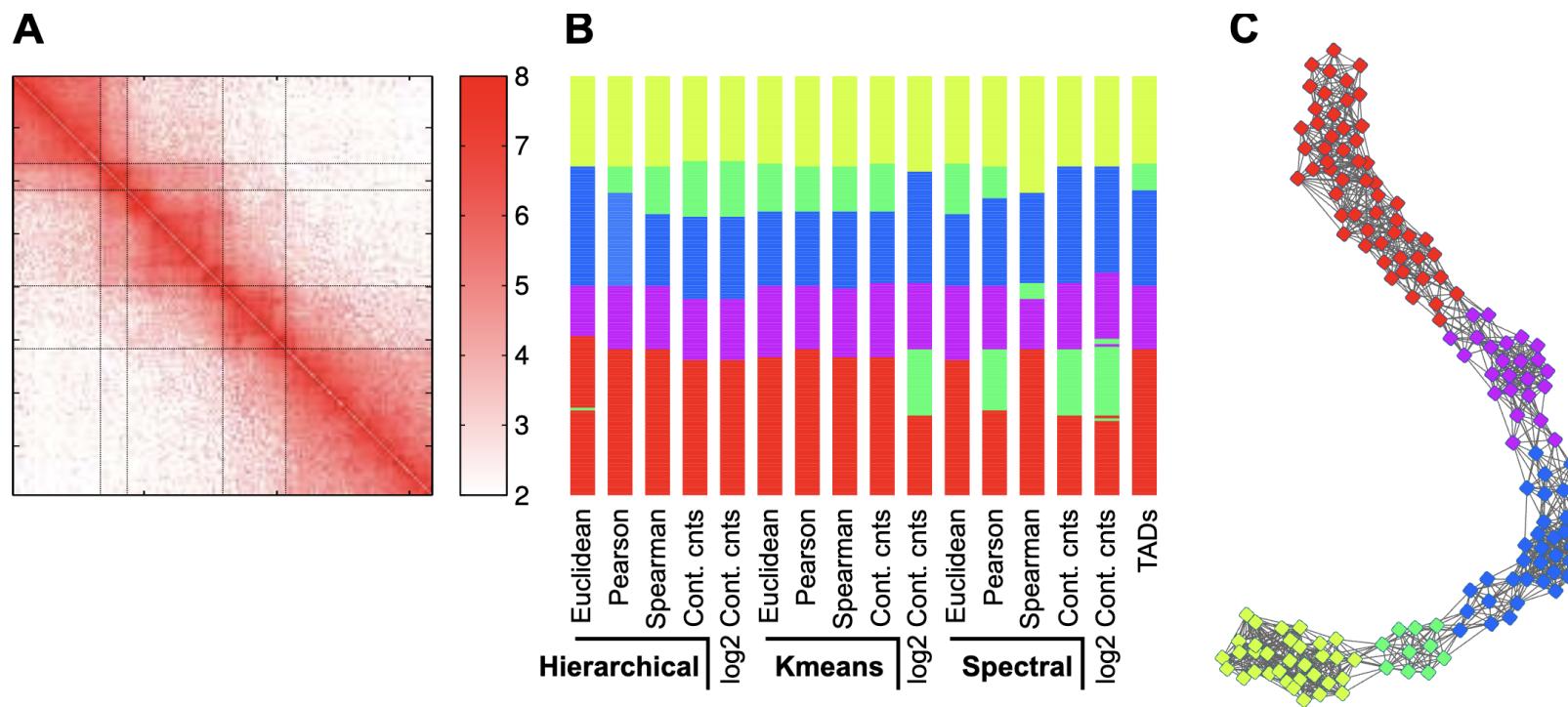


## ➤ Biological network analysis:

- Identifying functional modules in Protein-protein interaction networks using graph clustering.



- Genome analysis in Bioinformatics:
  - Finding higher-order Topologically Associated Domain using graph clustering.





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NETWORK SCIENCE LAB



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