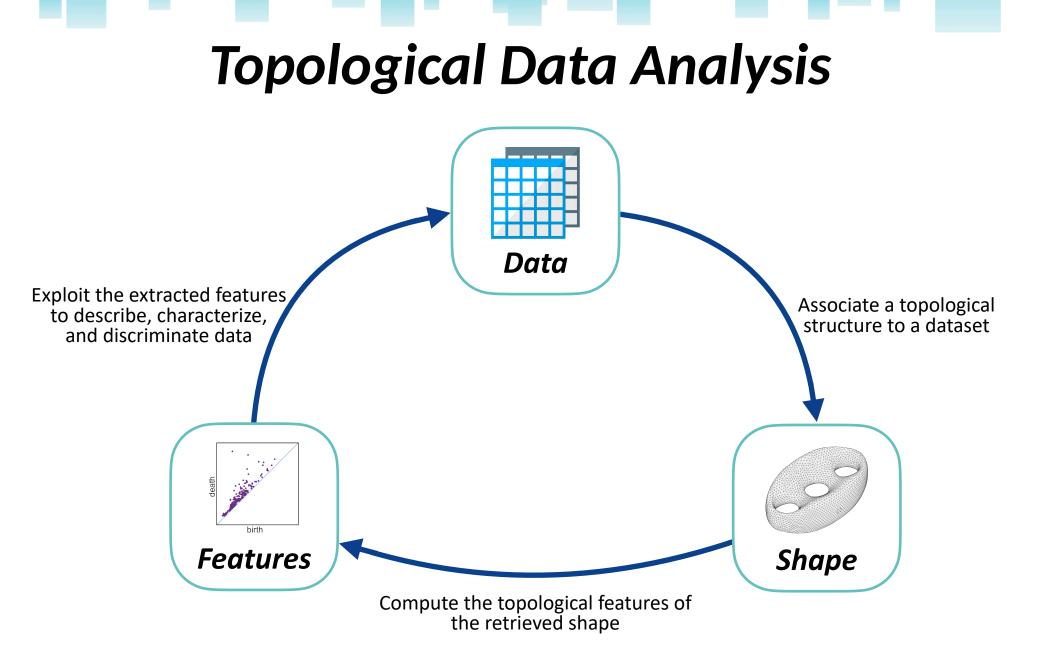
Topological Data Analysis

## Persistence & Networks

**Ulderico Fugacci** 

**CNR - IMATI** 





### A Primer on Complex Networks

- Homological Scaffolds
- Clique Community Persistence

### A Primer on Complex Networks

Homological Scaffolds

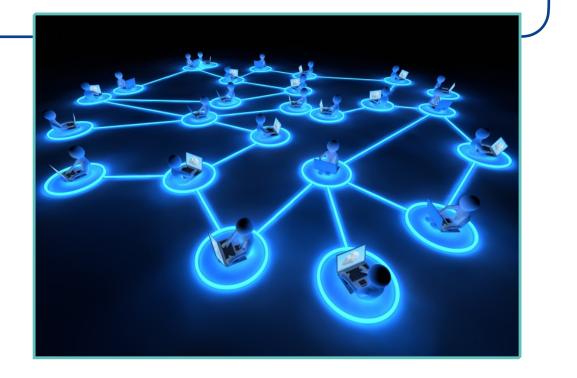
Clique Community Persistence

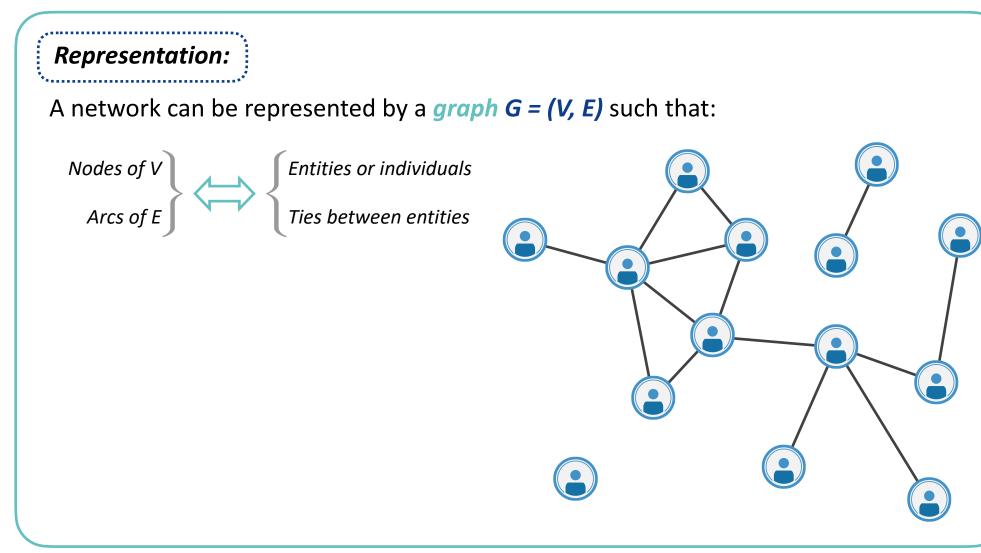
#### Networks:

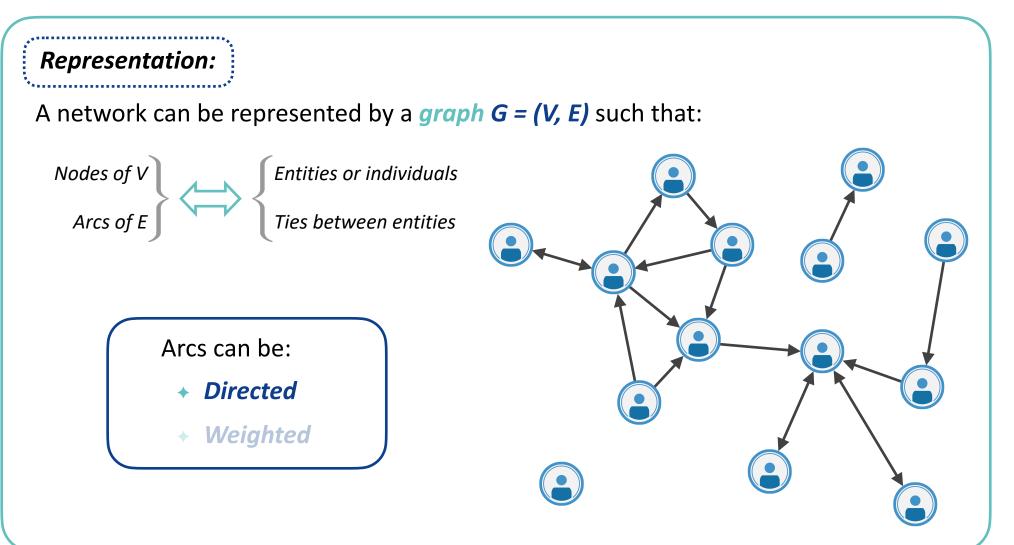
A *network* is a complex system consisting of *individuals or entities connected by specific ties* such as friendship, common interest, and shared knowledge

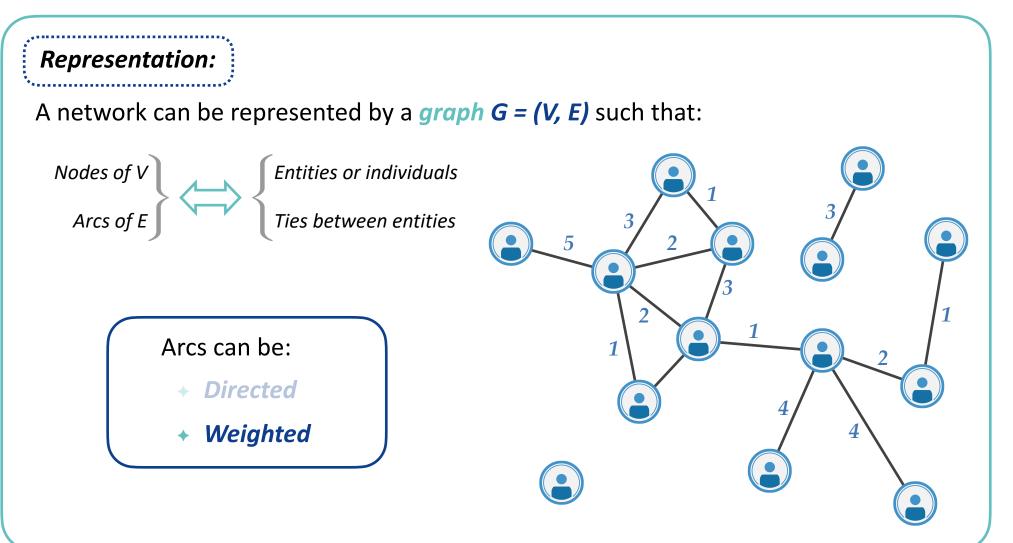
### E.g.

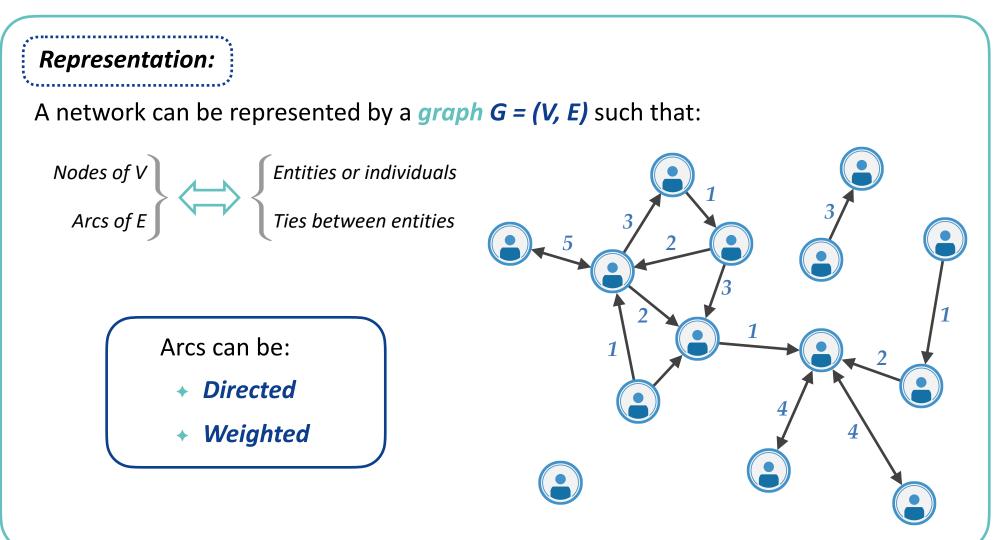
- Social Networks
- Sensor Networks
- + Biological Networks
- Collaborative Networks

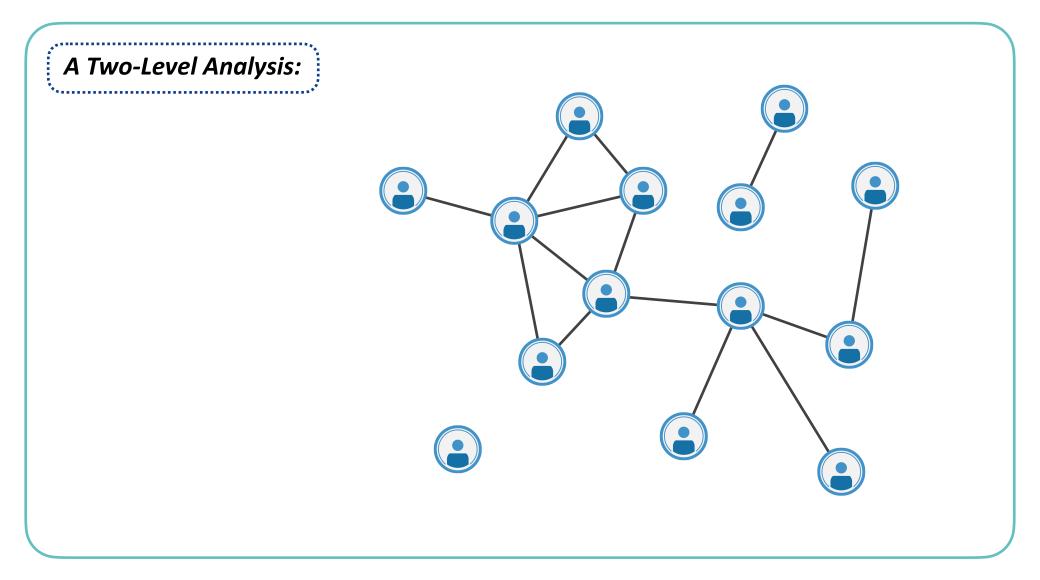


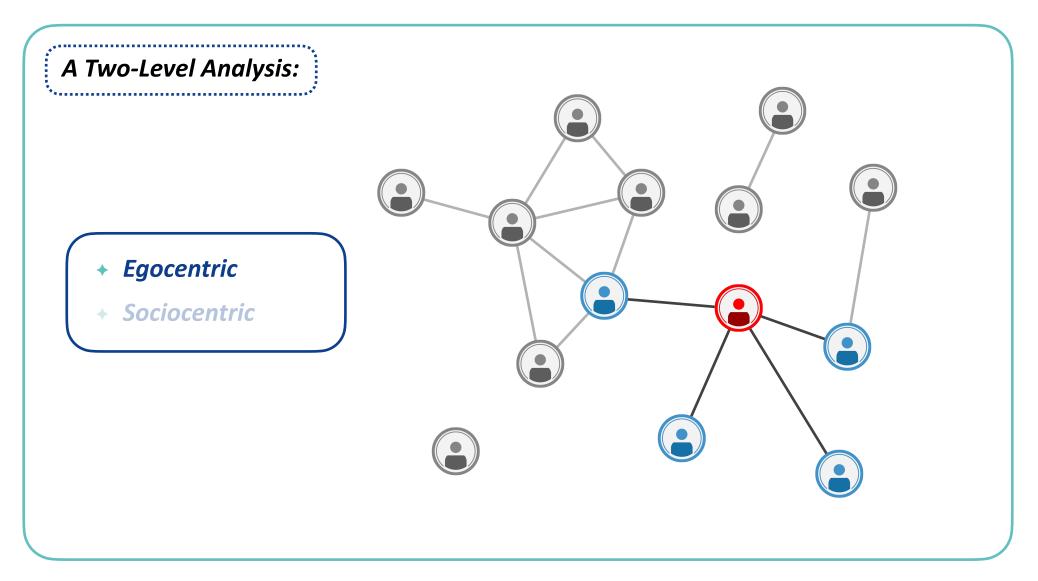


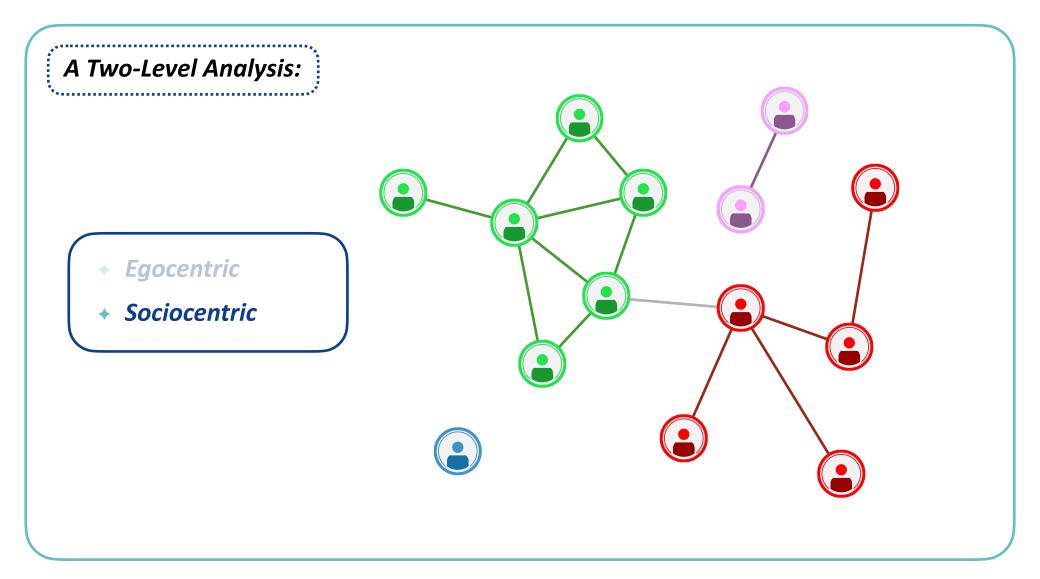




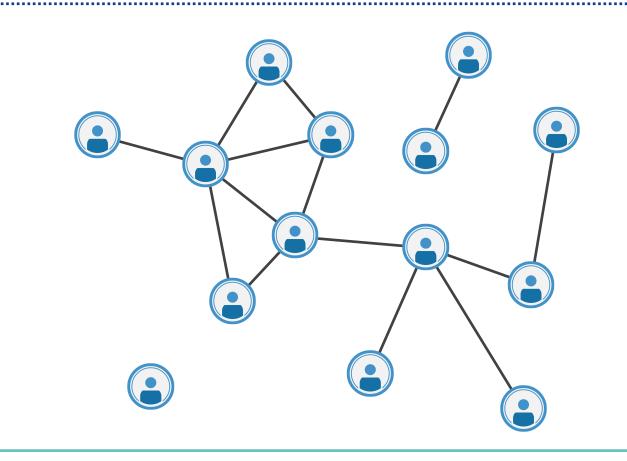




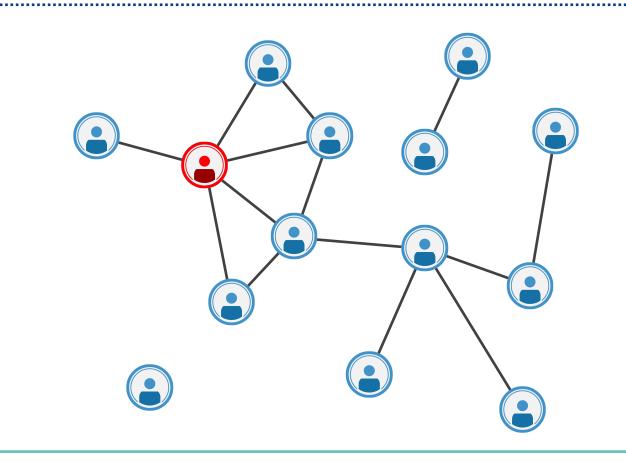




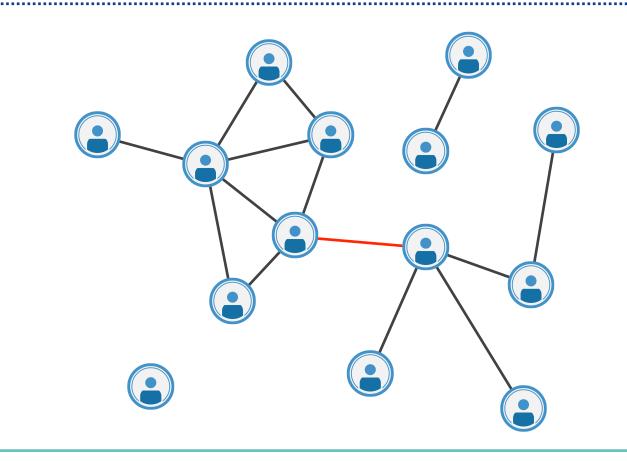
## **Persistence and Complex Networks**



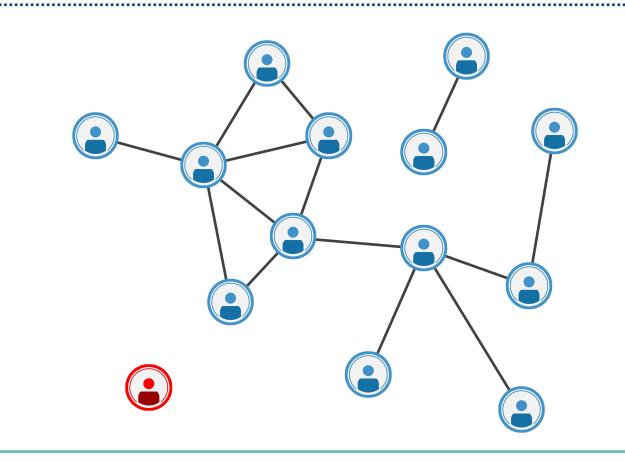
## **Persistence and Complex Networks**

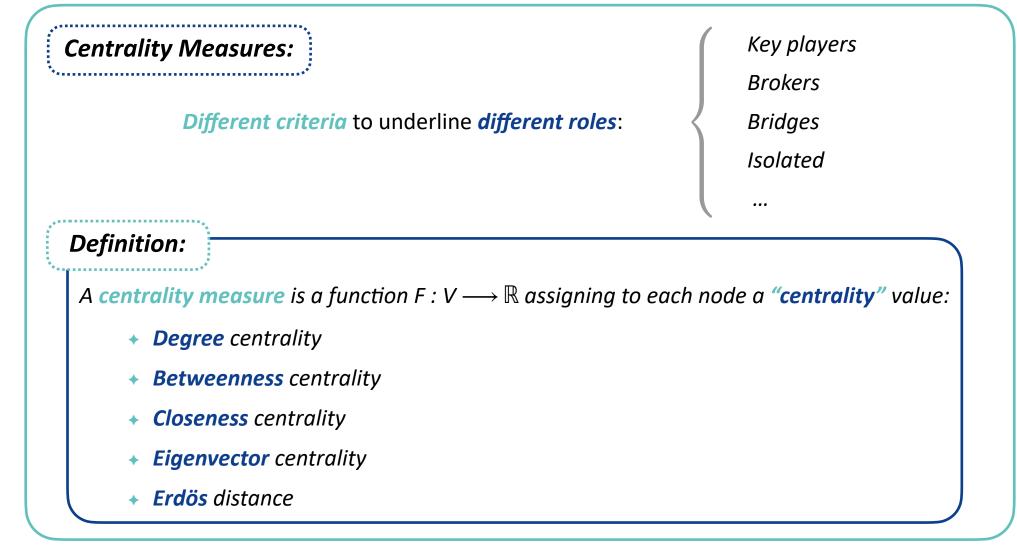


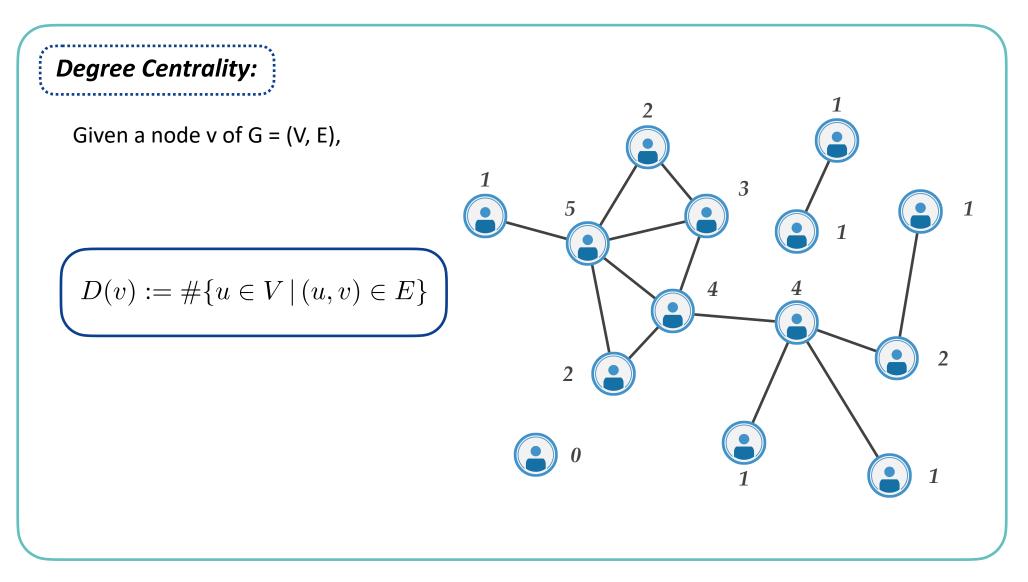
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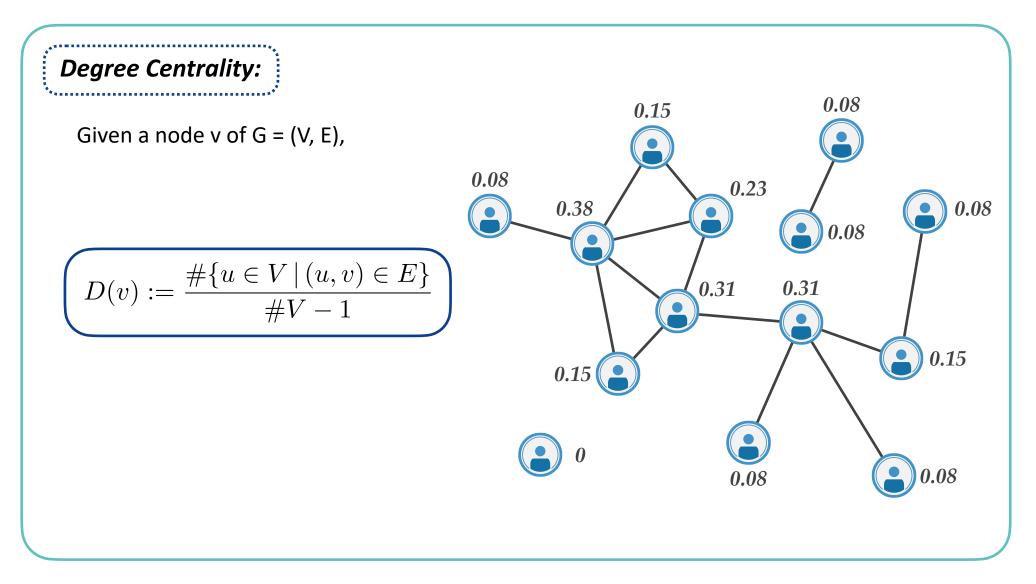


## **Persistence and Complex Networks**









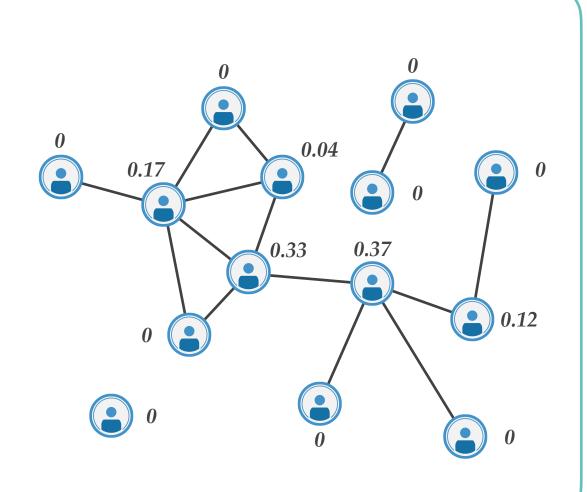
#### Betweenness Centrality:

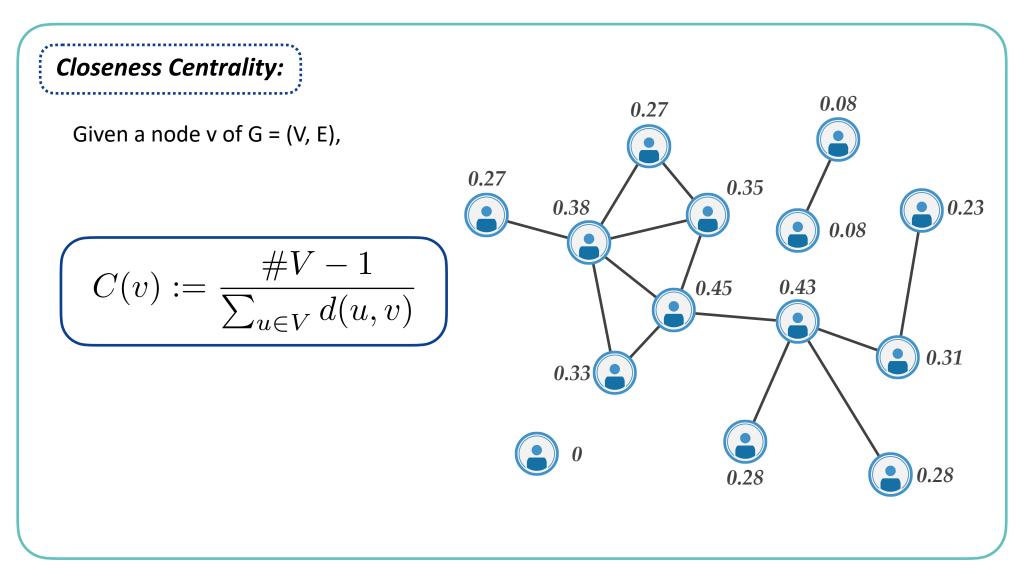
Given a node v of G = (V, E),

$$B(v) := \sum_{s \neq v \neq t} \frac{\sigma_{st}(v)}{\sigma_{st}}$$

where:

- σ<sub>st</sub> is the number of shortest
   paths from s to t
- *σ<sub>st</sub>(v)* is the number of those paths *passing through v*





### Eigenvector Centrality:

Given a node v of G = (V, E),

$$x_v := \frac{1}{\lambda} \sum_{u \in V} A_{uv} \, x_u$$

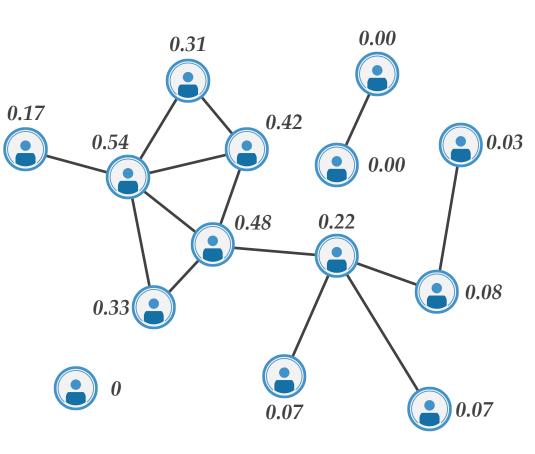
where  $\boldsymbol{\lambda}$  is constant and

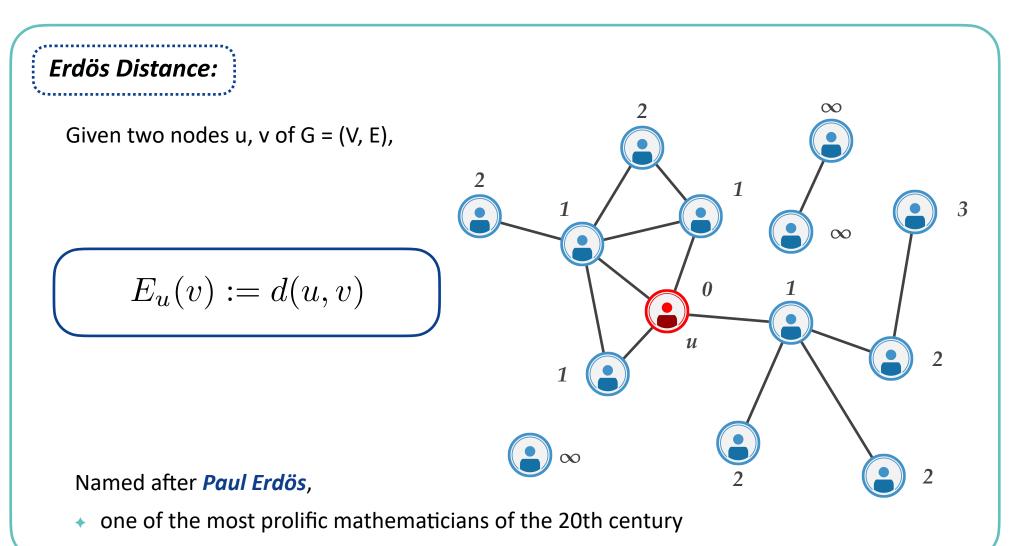
$$A_{uv} := \begin{cases} 1 & if(u,v) \in E\\ 0 & otherwise \end{cases}$$

I.e. the  $v^{\text{th}}$  entry of the eigenvector of

 $A x = \lambda x$ 







Centrality Measures:

A centrality measure for any query!

Degree	How many individuals can v reach directly?
Betweenness	How likely is v to be the most direct route between two individuals?
Closeness	How fast can v reach everyone in the network?
Eigenvector	How well is v connected to other well-connected individuals?
Erdös	How far is v from a specific individual?

### Sociocentric Networks:

#### Structural Metrics:

- \* Average of a Centrality Measure
- \* Diameter
- \* Density
- \* Transitivity
- \* ...

#### • Community Decompositions:

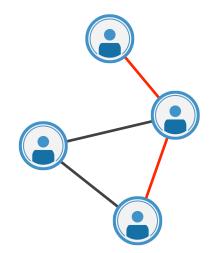
- \* Atomic Communities
- Clustering Techniques

### Structural Metrics:

#### How far are two individuals at most?

#### Diameter:

The longest shortest path between any two nodes



Diameter(G) = 2

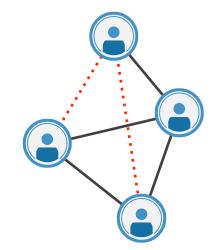
### Structural Metrics:

How close is G to being an "everyone knows everyone" network?

**Density**:

Number of edges of G

Number of all possible edges



Density(G) = 4/6 = 0.67

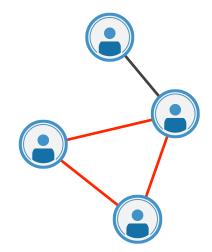
### Structural Metrics:

How likely are two individuals connected to an individual v connected to each other?

#### Transitivity:

Number of closed triplets of nodes

Number of connected triplets

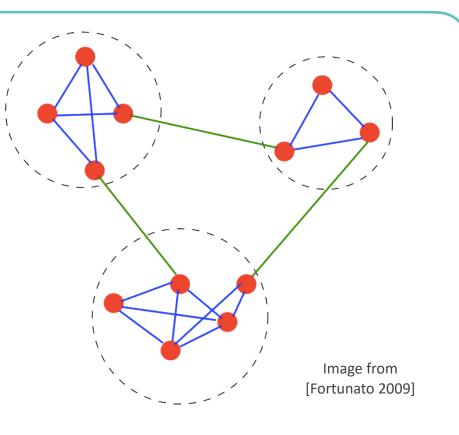


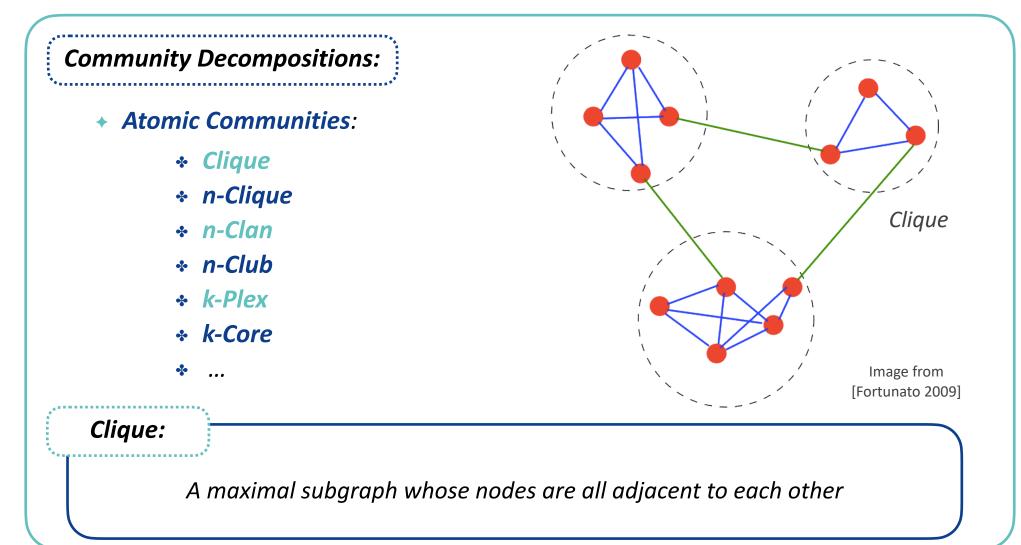
*Transitivity*(*G*) = 1/3 = 0.33

### **Persistence and Complex Networks**

### Community Decompositions:

- Atomic Communities:
  - \* Clique
  - \* n-Clique
  - ✤ n-Clan
  - \* n-Club
  - \* k-Plex
  - \* k-Core
  - \* ...



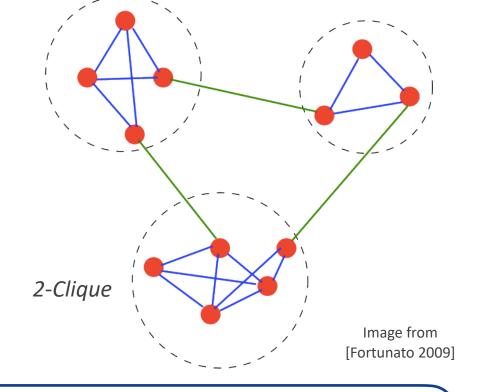


### **Persistence and Complex Networks**

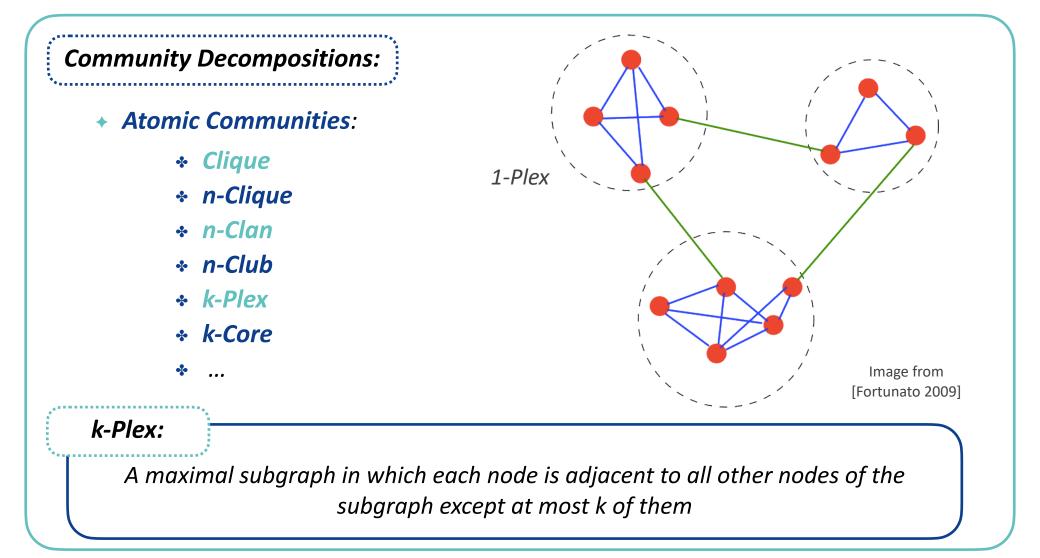
### Community Decompositions:

- + Atomic Communities:
  - \* Clique
  - \* n-Clique
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  - \* n-Club
  - \* k-Plex
  - \* k-Core

*n-Clique:* 



A maximal subgraph such that the distance of each pair of its nodes is not greater than n



### Clustering Techniques:

Agglomerative (bottom-up)

Divisive (top-down)

approach based on

**Centrality Measures** 

**Atomic Communities** 

**Quality Functions** 

### Clustering Techniques:

Agglomerative (bottom-up)

Divisive (top-down)

#### Girvan-Newman Algorithm:

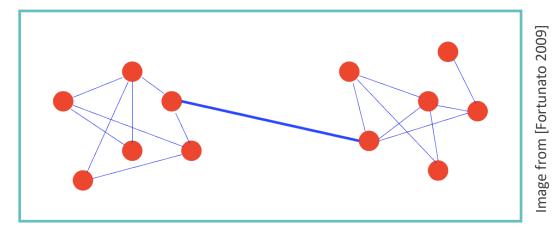
approach based on

#### **Centrality Measures**

Atomic Communities

Quality Functions

*Iterated removal* of the edge with largest *betweenness centrality* 



approach based on

# **Persistence and Complex Networks**

### Clustering Techniques:

Agglomerative (bottom-up)

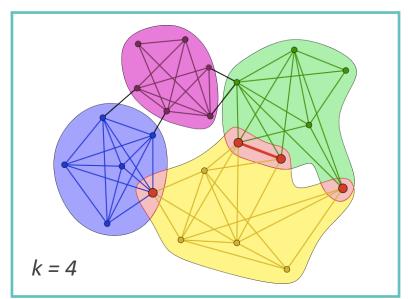
Divisive (top-down)

### Clique Percolation:

*k-adjacency*: two cliques of size *k* are *k*-adjacent if they share *k*-1 nodes

*k-clique community*: maximal union of cliques of size *k* pairwise connected by a sequence of *k*adjacent cliques

**Decomposition** in k-clique communities



Centrality Measures

#### **Atomic Communities**

Quality Functions

approach based on

## **Persistence and Complex Networks**

### Clustering Techniques:

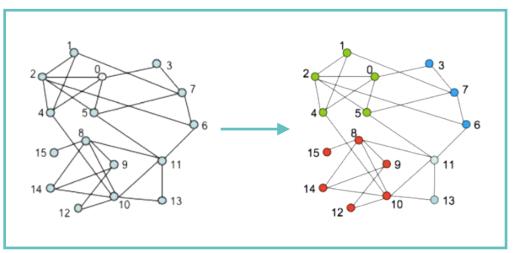
Agglomerative (bottom-up)

Divisive (top-down)

### Modularity-based Algorithm:

*Modularity*: measure for clustering quality

Iterated aggregation of communities of nodes whose merging increases modularity

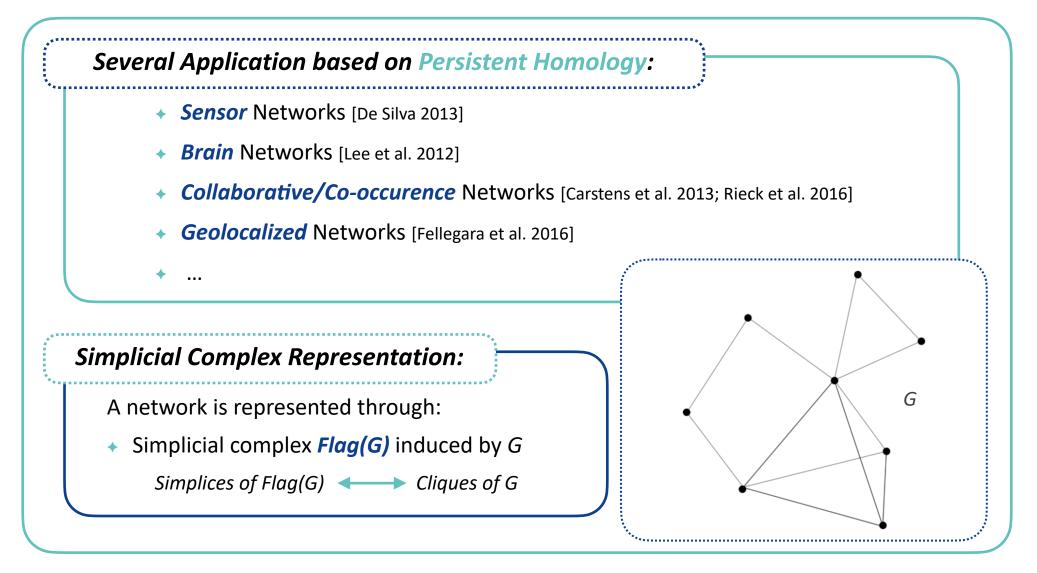


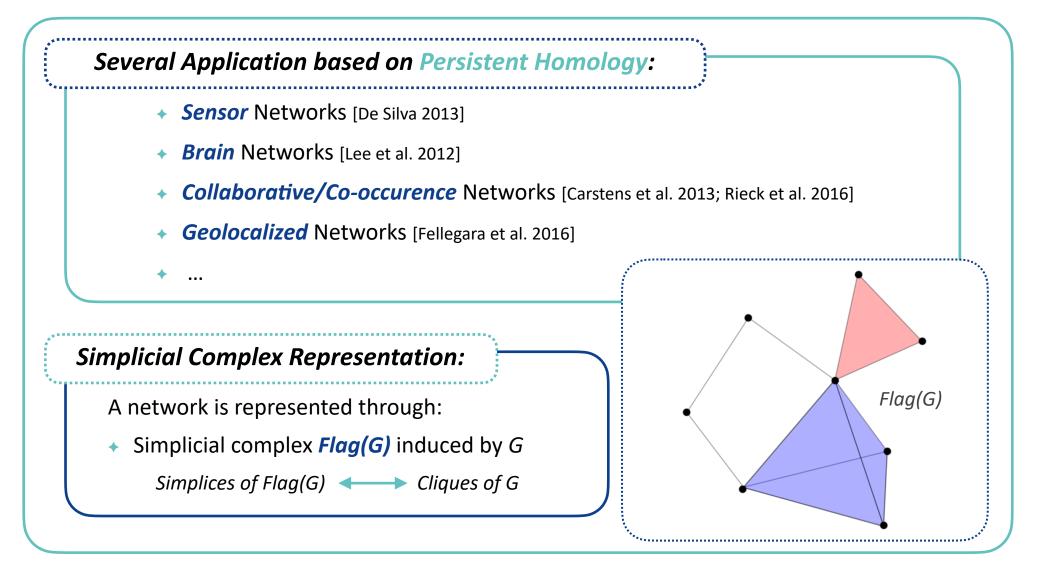
### **Centrality Measures**

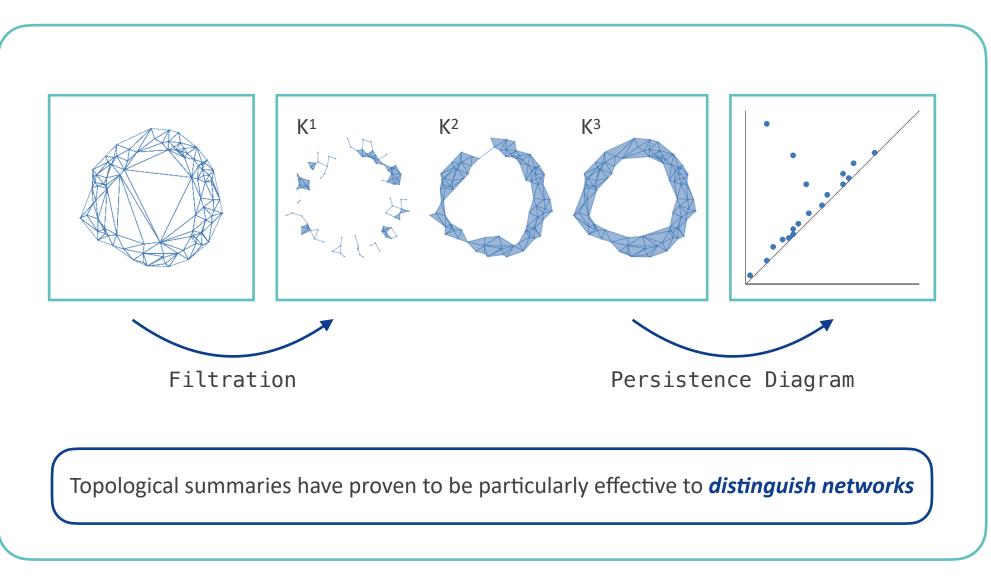
#### Atomic Communities

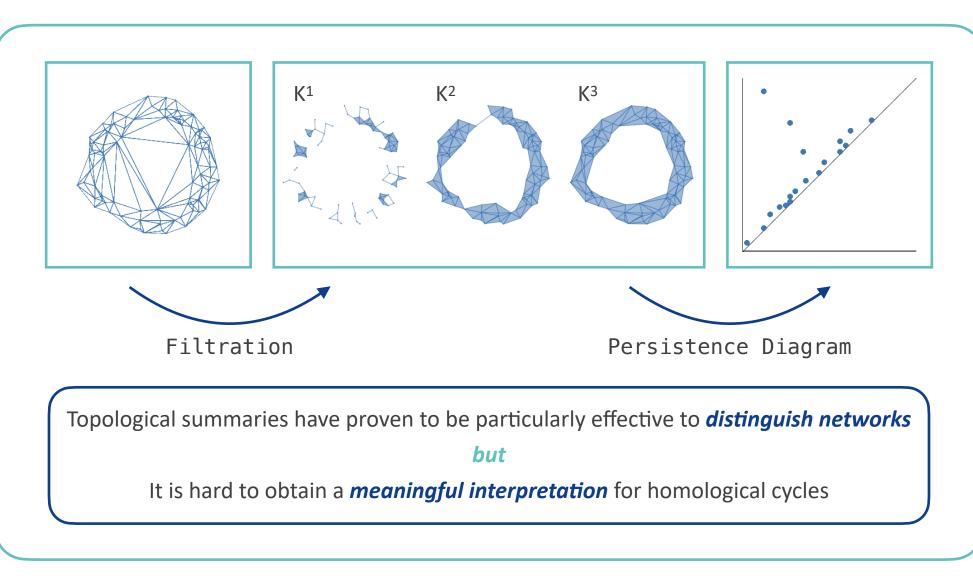
**Quality Functions** 

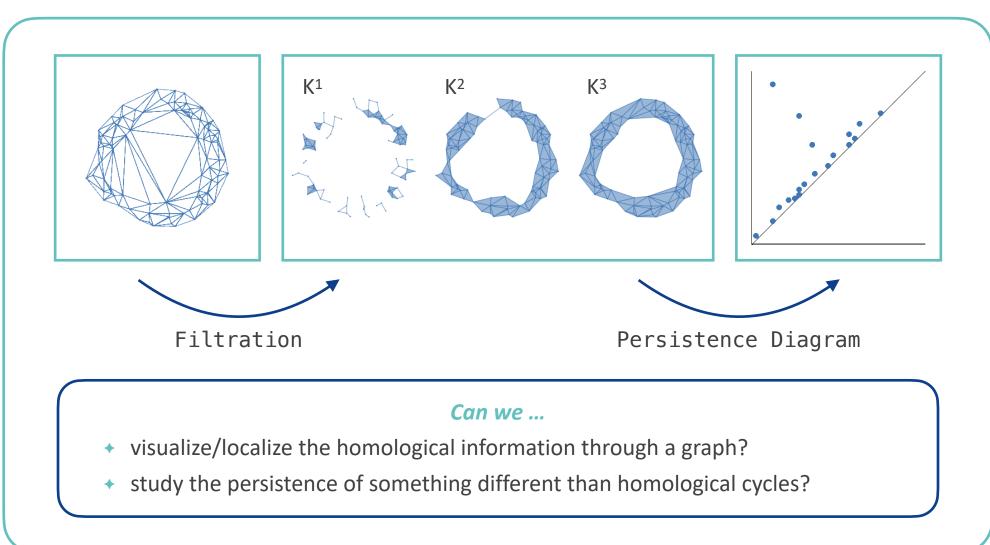
mage from [Blondel et al. 2008]











#### A Primer on Complex Networks

#### Homological Scaffolds

Clique Community Persistence

#### Dataset:

Goal:

A collection of **30** weighted graphs derived from **fMRI** (functional magnetic resonance imaging) obtained by scanning 15 different subjects For each graph,

 Nodes
 169 (Sub)Cortical Brain Regions

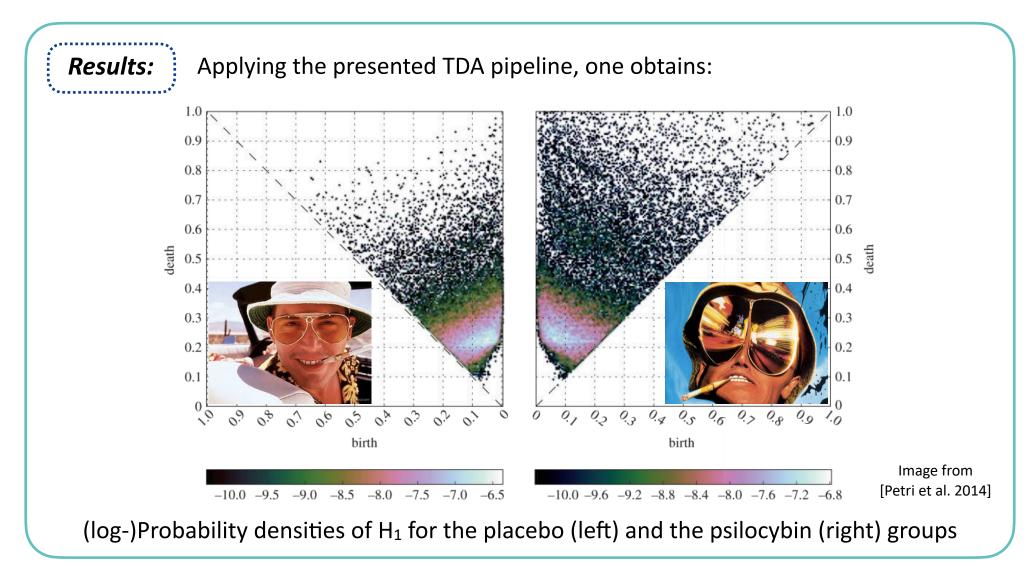
 Arcs Weights
 (Inverse of) Partial Correlations



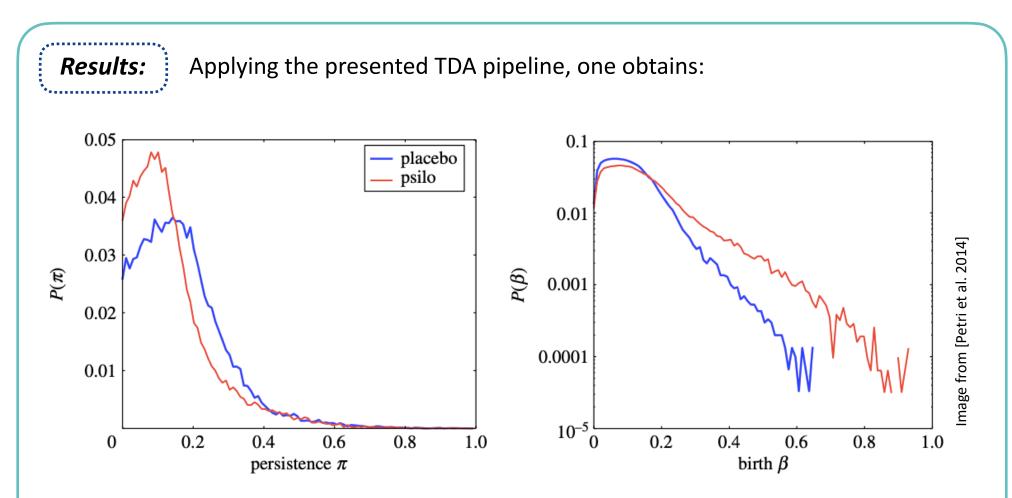
For each subject, 2 graphs obtained on 2 separate occasions, 14 days apart:

- Placebo (10 ml saline, intravenous injection) in one case
- Psilocybin (2 mg dissolved in 10 ml saline) in the other one

Spot the differences between the two situations



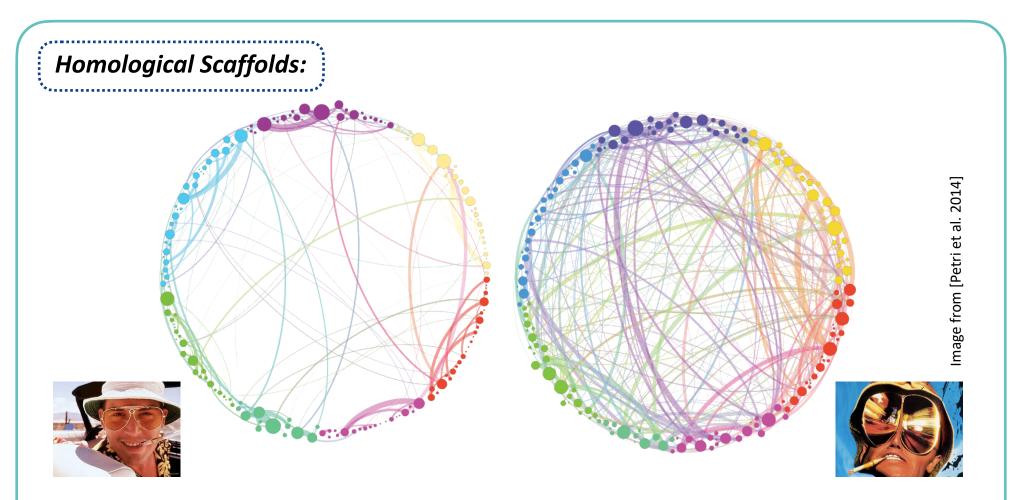
#### **Persistence and Complex Networks**



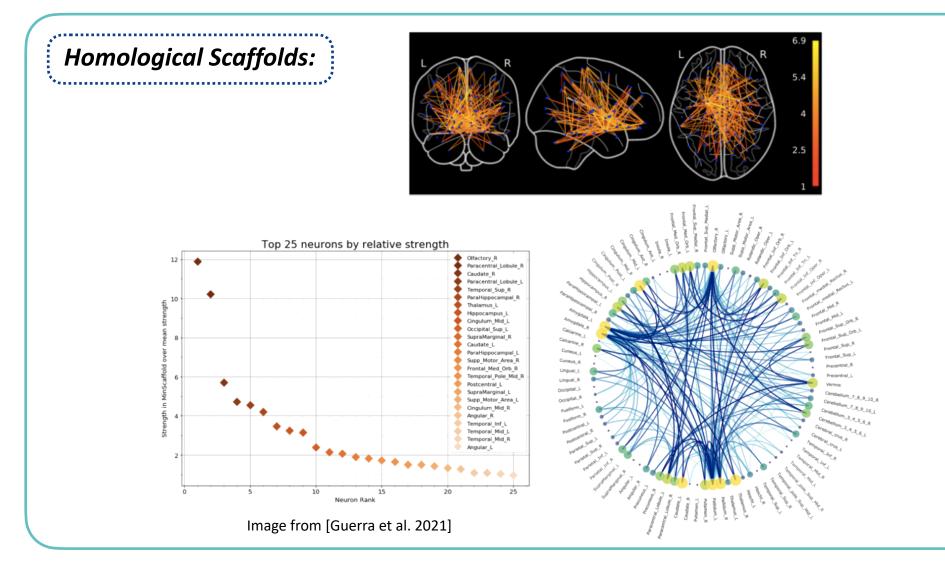
Persistence and birth distributions of H<sub>1</sub> for the placebo (blue) and the psilocybin (red) groups

Homological Scaffolds: How to visualize/localize the homological information? Let  $g_1, g_2, ..., g_m$  be the representative cycles of  $H_1$  occurring along the filtration of a weighted graph G = (V, E, w:  $E \rightarrow \mathbb{R}$ ), the *frequency homological scaffold* is the graph  $H^{f}_{G} = (V, E, w^{f}: E \rightarrow \mathbb{R})$ defined by mage from [Lord et al. 2016]  $w^{f}(e) = \#\{i \mid e \in g_i\}$ а 3

Homological Scaffolds: How to visualize/localize the homological information? Let  $g_1, g_2, ..., g_m$  be the representative cycles of  $H_1$  occurring along the filtration of a weighted graph G = (V, E, w:  $E \rightarrow \mathbb{R}$ ), the *persistence homological scaffold* is the graph  $H^{p}_{G} = (V, E, w^{p}: E \longrightarrow \mathbb{R})$ 1) defined by mage from [Lord et al. 2016] d e ) 0.2 0.2  $w^p(e) = \sum \pi_{g_i}$ 0.2 0.3 0.5  $i \mid e \in q_i$ 0.3a 0.3 2 3



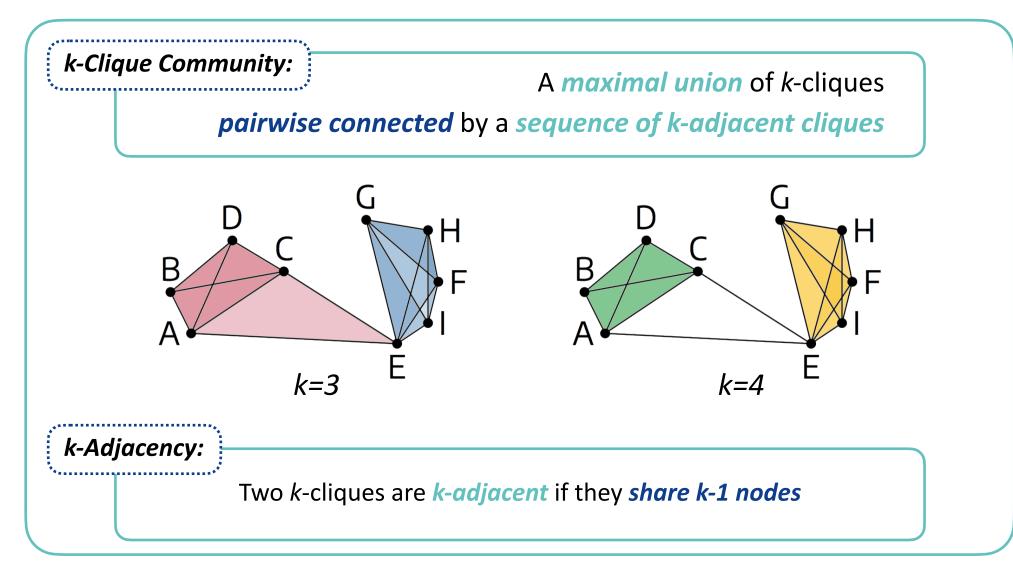
Persistence homological scaffolds for the placebo (left) and the psilocybin (right) groups



#### A Primer on Complex Networks

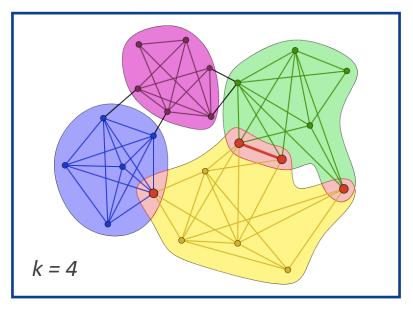
Homological Scaffolds

Clique Community Persistence



#### **Persistence and Complex Networks**

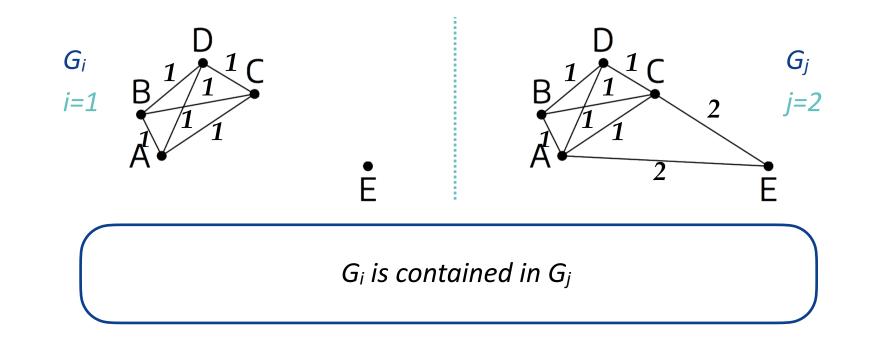
#### k-Clique Community Decomposition:



- Reveal *highly connected* communities
- Allow overlaps
- + Have a *hierarchical structure*

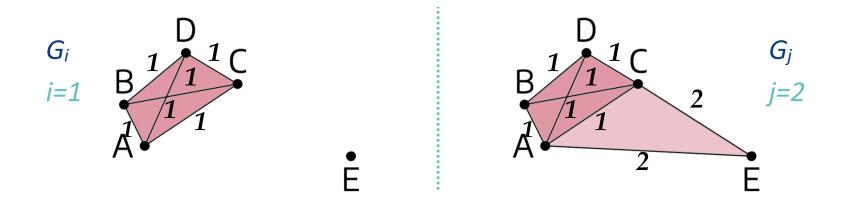
Clique Communities and Weighted Networks:

Given a weighted network **G** and two threshold values **i** < **j**,



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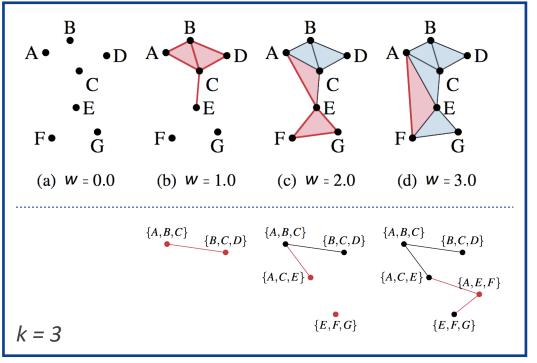
Each *k*-clique community of *G<sub>i</sub>* is *contained* in *exactly one k*-clique community of *G<sub>j</sub>* 

#### Clique Community Persistence:

Fixing a value for k and varying the edge-weight threshold, the **persistence** of **k-clique communities** of G can be tracked by:

- Building a sequence of k-dual graphs:
  - · vertices  $\leftrightarrow$  k-cliques
  - edges ↔ adjacent k-cliques

 Tracking the *connected components* of the sequence of *k*-dual graphs



Clique Community Persistence:

The presented approach allows for designing tools for:

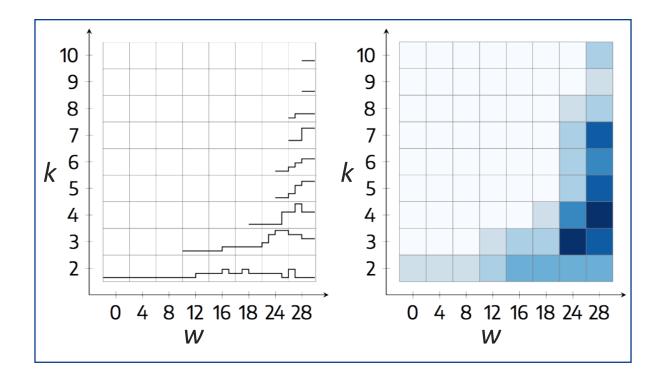
- Network Comparison
  - Comparison Measures
    - Persistence Indicator Function (PIF)
    - PIF-based distance
  - Clique Community *Centrality Measure*
- Single Network Analysis
  - Interactive Visualization Tool based on Nested Graphs

Persistence Indicator Function:

Defined as the function  $f_k : \mathbb{R} \longrightarrow \mathbb{N}$ 

assigning:

#### *w* → *# k-cliques communities "alive" at threshold w*



Appanion 1

Appamion 2

Appa@tion 3

Witch Witch 3

Witch 1

Memeith

Porter

Macduf

Youngiward

Malcolm

ROSS

Lennox

Banquo Duncan

Lady Macbeth

Macbeth

Donabain

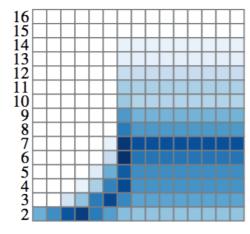


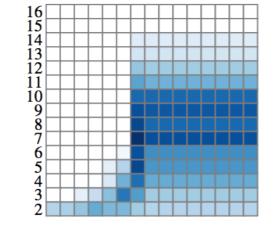
- Co-occurrence networks of Shakespearean plays
  - 37 plays considered

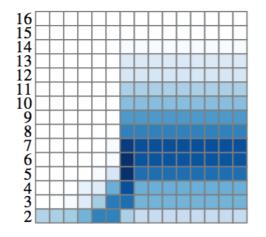
- In each network:
  - $\cdot$  **nodes**  $\leftrightarrow$  **characters** of the play
  - $\cdot$  edges  $\leftrightarrow$  characters appearing in the same scene
  - edge weight ↔ inverse of the number of interactions

Persistence Indicator Function:

PIF enables a comparison of structural differences between groups of plays







Comedies





PIF-Based Distance:

Given two persistence indicator functions f and g,

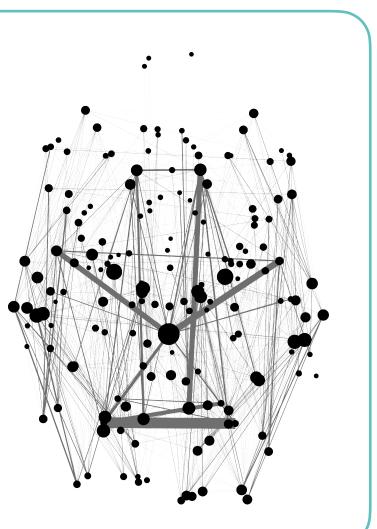
**PIF-based distance** is defined to be the L<sup>p</sup> distance between f and g:

$$dist(f,g) = \left(\int_{\mathbb{R}} |f(x) - g(x)|^p \, dx\right)^{\frac{1}{p}}$$

- Quantifies dissimilarities between PIFs
- Easier to be computed than Wasserstein and bottleneck distances
- Highly correlated to Wasserstein distance

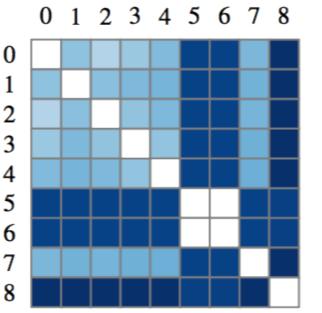
- PIF-Based Distance:
- Biological networks representing variants of human brain connectivity
  - 9 instances considered

- In each network:
  - $\cdot$  nodes  $\leftrightarrow$  brain areas
  - $\cdot$  edges  $\leftrightarrow$  fibers connecting different areas



#### PIF-Based Distance:

Variant	Density	Diam. (weighted)	Avg. degree (weighted)
0	0.125	4 (60.0)	21.21 (2300.3)
1	0.124	4 (60.0)	21.06 (2296.0)
2	0.124	4 (60.0)	21.13 (2295.2)
3	0.124	4 (60.0)	21.16 (2282.0)
4	0.124	4 (60.0)	21.15 (2279.3)
5	0.125	4 (60.0)	21.19 (2264.0)
6	0.125	4 (60.0)	21.19 (2264.0)
7	0.124	4 (60.0)	21.16 (2279.6)
8	0.125	4 (60.0)	21.20 (2257.5)



PIF-based distance reveals differences between networks that common graph measures are incapable of detecting

Clique Community Centrality:

*Clique community centrality* of a node *v* is defined as

$$centrality(v) = \sum_{C \ni v} pers(C)$$

where:

- C is any clique community containing v
- pers(C) is the "lifespan" of C

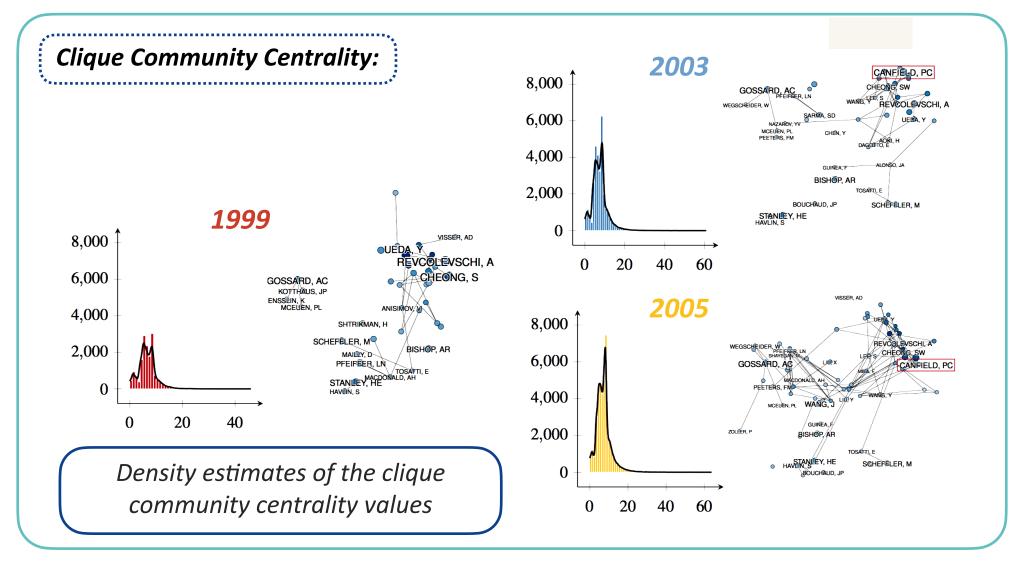
Nodes belonging to high-persistence communities are identified as relevant

#### Clique Community Centrality:

- Collaborative networks describing scientist co-authorship of the "Condensed Matter" arXiv category
  - *3* snapshots in time considered (1999, 2003, 2005)
- Network sizes:
  - 16K 40K nodes
  - 47K 175K edges

Clique community centrality allows for

- evaluating the evolution of network connectivity
- filtering away the less relevant nodes



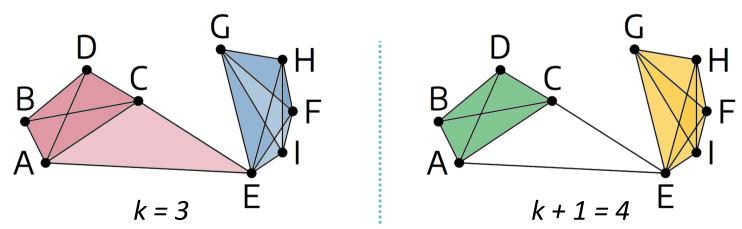
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Clique Communities and Multiple k-Values:

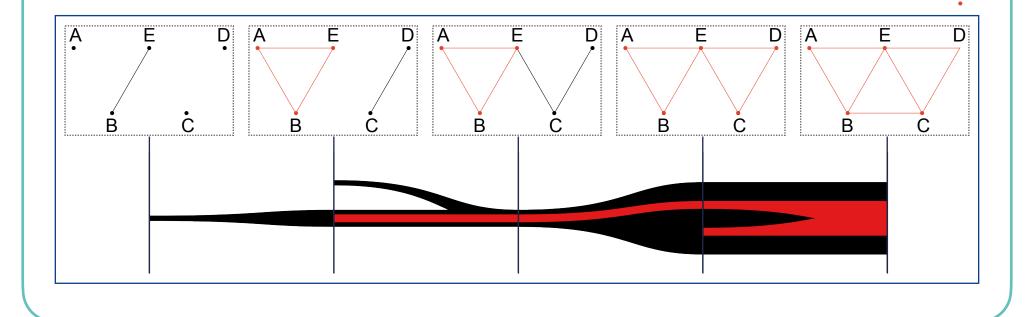
Given a weighted network **G** and any threshold value **i**,

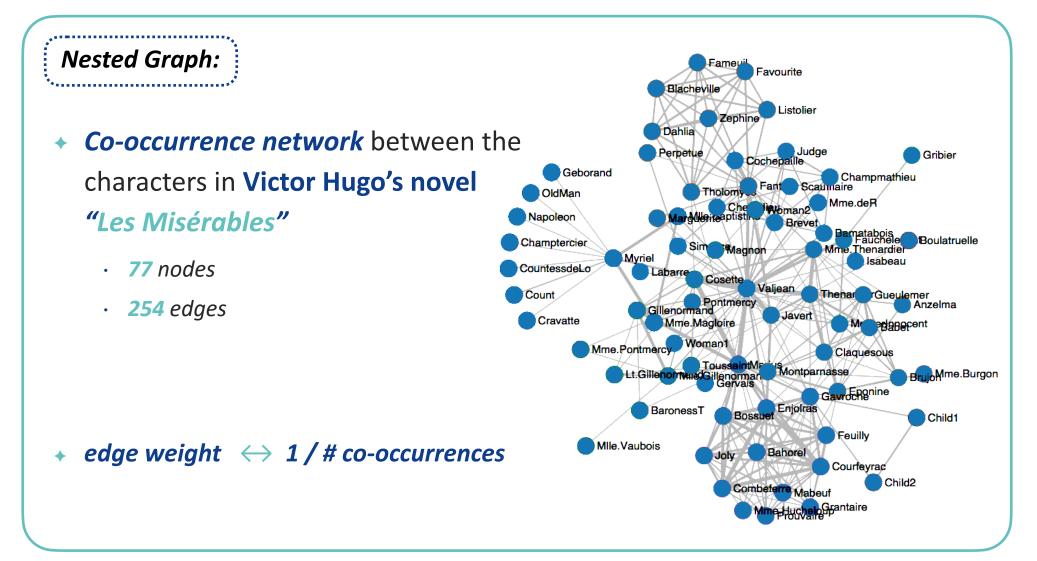


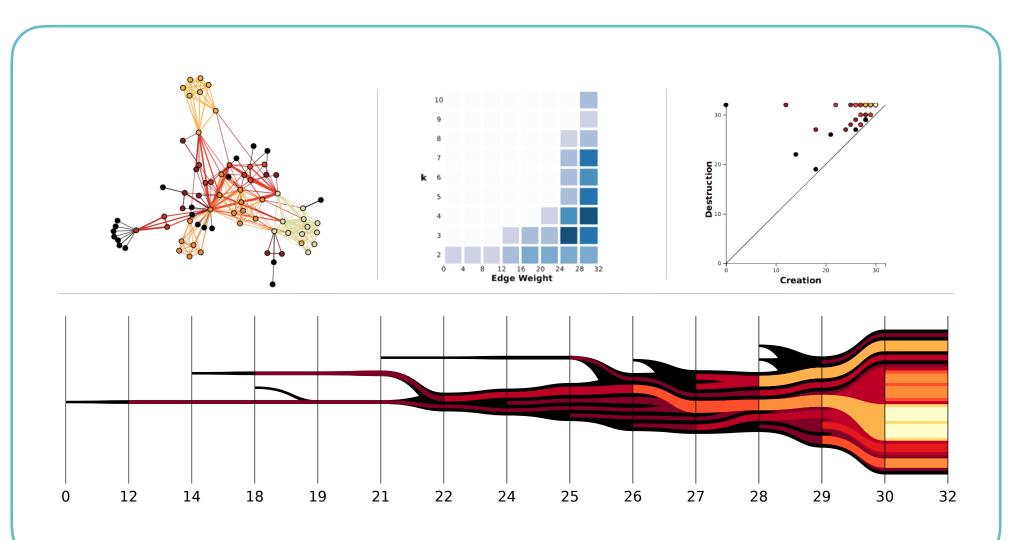
Each (*k*+1)-clique community of *G<sub>i</sub>* is **contained** in *exactly one k*-clique community of *G<sub>i</sub>* 

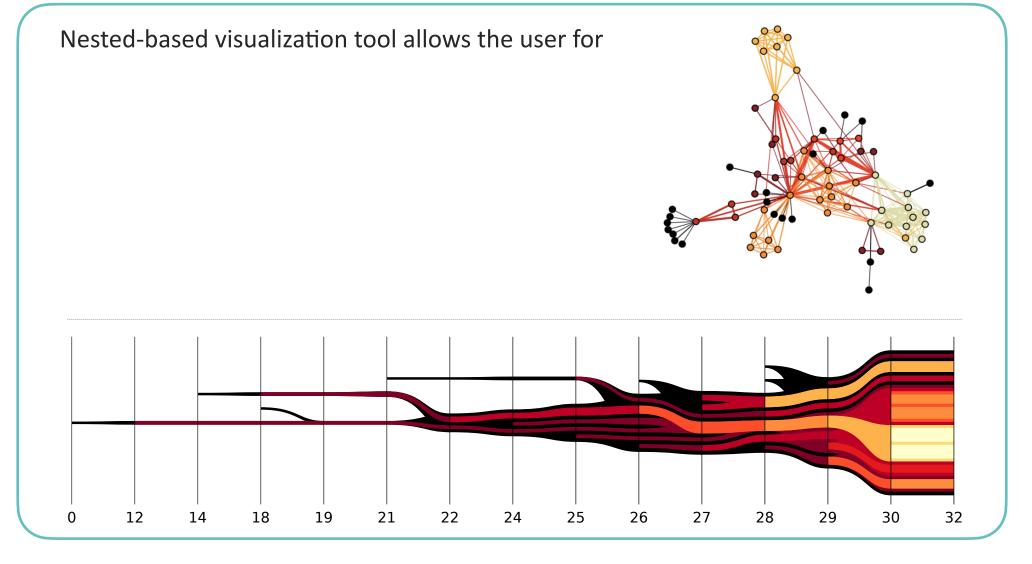
#### Nested Graph:

- Originally defined for connected components in scalar fields [Lukasczyk et al. 2017]
- Illustrates evolutions across two parameters



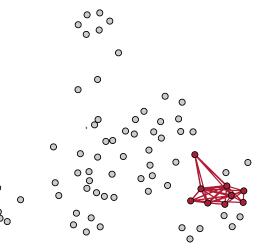




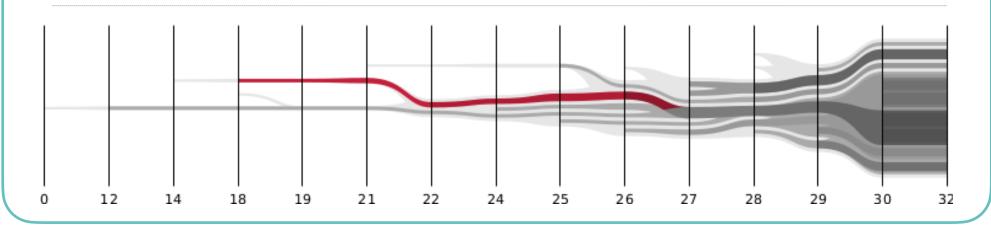


Nested-based visualization tool allows the user for

- focusing on the evolution of a specific clique community
- selecting and interactivity exploring different
   edge weights and clique degrees

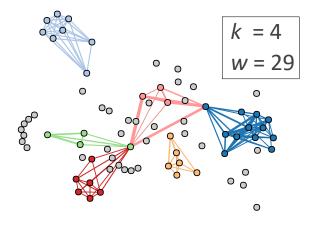


while the force-directed graph layout and the nested graph *change accordingly* •

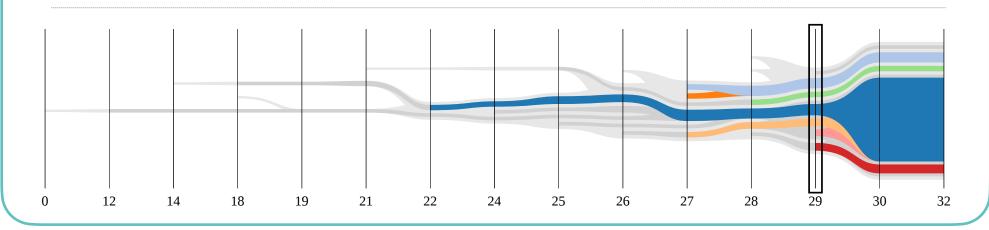


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- focusing on the evolution of a specific clique community
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Nested-based visualization tool allows the user for

- + **focusing on** the evolution of a **specific clique community**
- selecting and interactivity exploring different edge weights and clique degrees

while the force-directed graph layout and the nested graph *change accordingly* 

#### Intuitively:

edge-weight variation↔reveal the core part of a communityclique-degree variation↔analyze community according to<br/>different granularities

# Bibliography

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#### Today's References:

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