

# Detecting Communities in Complex Networks using a Hybrid Immunological Algorithm

ROCCO ALESSANDRO SCOLLO

Complex Intelligent System  
Department of Mathematics and Computer Science  
University of Catania, Italy

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# Complex Networks

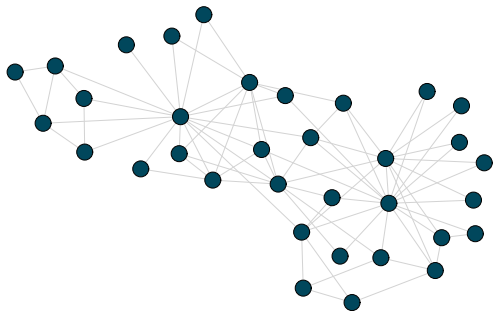
**Real networks** have complex and non-trivial topological features:

- social science
- biology
- computer science
- ...

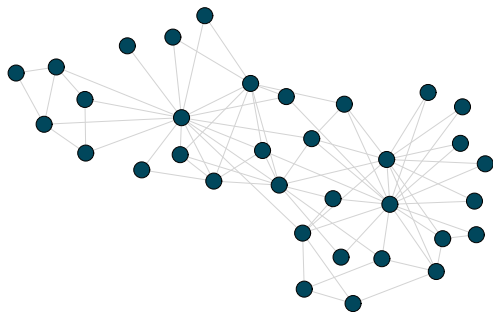
Nowadays, with Internet, these networks have reached millions or billions of vertices and interactions (e.g. Facebook, Twitter, ...).

**Graphs** are useful tools for representing and analysing real networks.

# Complex Networks



# Complex Networks



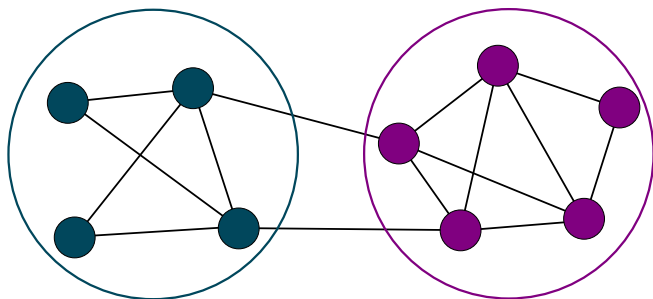
## Community structure

High number of edges within groups of vertices and low number between these groups.

# Community Structure

**Communities** are groups of vertices with similar properties and/or role.

Many real networks exhibit a community structure.



# Community Detection: Applications

- **Classification** of individuals that belong to the same communities.
- **Clustering** the clients of an e-commerce with similar interests of from the same country.
- **Identifying** groups of proteins with the same function in biological networks to understand the physiology of a cell.

# Community Detection: Problem

The aim of **community detection** is to identifying **clusters** of nodes and their hierarchical organization.

The concept of community or cluster is not well-defined.

A graph with a community structure is different from a **random graph**, that usually does not have a community structure.



# Modularity

The **modularity** is the most popular evaluation function for the community detection, proposed by *Newman* and *Girvan* in 2004 [7].

Uses a randomized version of the original graph, called **null model**, with edges rewired at random and with the same expected degree for each vertices.

$$Q = \frac{1}{2m} \left[ \sum_{i=1}^N \sum_{j=1}^N \left( A_{ij} - P_{ij} \right) \delta(i, j) \right]$$

where  $P_{ij}$  is the expected number of edges between vertices  $i$  and  $j$  in the null model.

# Modularity

Using a null model with the **same degree distribution** of the original graph,  $P_{ij}$  is:

$$P_{ij} = \frac{k_i k_j}{2m}$$

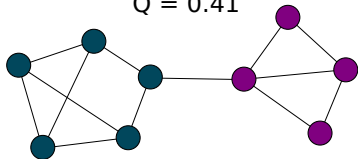
Only pairs of vertices belonging to the same cluster contribute to the sum:

$$Q(C) = \sum_{c \in C} \left[ \frac{\ell_c}{m} - \left( \frac{d_c}{2m} \right)^2 \right]$$

# Modularity

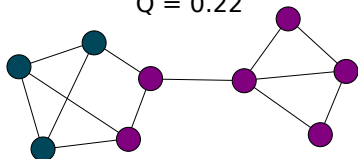
OPTIMAL PARTITION

$Q = 0.41$



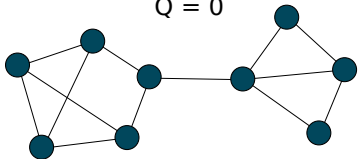
SUBOPTIMAL PARTITION

$Q = 0.22$



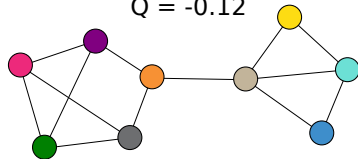
SINGLE COMMUNITY

$Q = 0$



NEGATIVE MODULARITY

$Q = -0.12$



# Hybrid-IA

HYBRID-IA is an **immunological algorithm** inspired by the clonal selection principle of the immune system.

It is a population-based **metaheuristic** that uses a local search procedure to improve the search.

It is based on three main **immune operators**:

- cloning
- hypermutation
- aging

# Hybrid-IA

The **cloning operator** create a population copying the current set of solutions:

- static cloning
- dynamic cloning

The **aging operator** removes old solutions for maintaining diversity within the population.

# Hybrid-IA

The **hypermutation operator** modifies the cloned solutions in order to explore their neighbourhood.

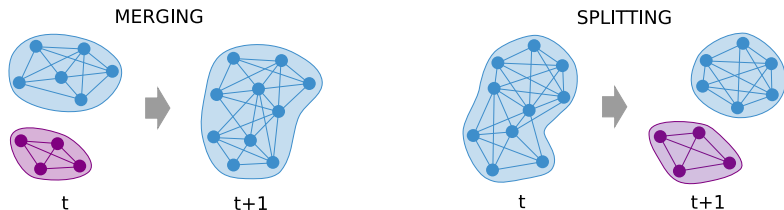
The **mutation rate** (number of mutations) can be

- static:  $M = k$
- dynamic:  $M = \lfloor (\alpha \times \ell) + 1 \rfloor$ , with  $\alpha = e^{-\rho \hat{f}(\vec{x})}$

# Hybrid-IA

For the community detection problem,  $\alpha$  is the **probability** to move a node from a community to another one.

The operator chooses two communities  $C_i$  and  $C_j$ , with  $C_i \neq C_j$ , and moves all vertices from  $C_i$  to  $C_j$  with a probability of  $\alpha$ .



# Hybrid-IA: Local Search

The **local search operator** trying to improve the modularity value of the selected solutions moving a node from its community to nearby community.

It is based on the **move vertex** operator of *Kernighan* and *Lin* [5] for the clustering problem.



# Hybrid-IA: Local Search

The **move gain** is defined as the variation in modularity when moving the node  $u$  from the community  $C_i$  to the community  $C_j$ :

$$\Delta Q_u(C_i, C_j) = \frac{l_{C_j}(u) - l_{C_i}(u)}{m} + d_V(u) \left[ \frac{d_{C_i} - d_V(u) - d_{C_j}}{2m^2} \right]$$

where  $C_j$  is a community in the neighbourhood of node  $u$ .

# Hybrid-IA: Local Search

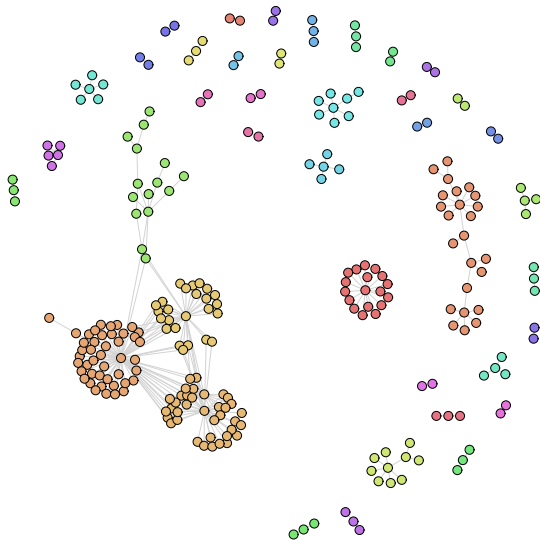
The local search tries to repair **not well-formed** communities, i.e. communities with a low ratio between internal links and sum of degrees.

Then the move operator is applied to nodes that **lies on the boundaries** of the communities and share links with other modules.

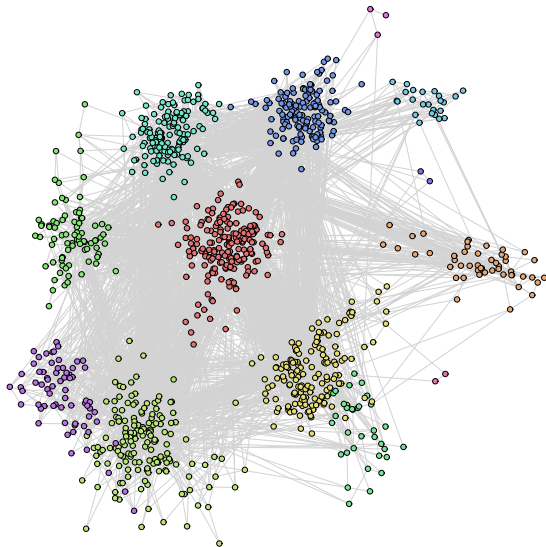
# Hybrid-IA: Results

<i>Networks</i>		HYBRID-IA	LOUVAIN [1]	HDSA	BADE	SSGA	BB-BC	BA	GSA
Cattle PPI	$Q$	<b>0.7195</b>	<b>0.7195</b>	<b>0.7195</b>	0.7183	0.7118	0.7095	0.7143	0.7053
	$N_C$	40	40	40	41	40	48	42	43
E.coli TRN	$Q$	0.7785	0.7793	<b>0.7822</b>	0.7680	0.7507	0.7520	0.7629	0.7416
	$N_C$	43	41	47	58	61	71	56	61
C.elegans MRN	$Q$	<b>0.4506</b>	0.4490	0.4185	0.3473	0.3336	0.3374	0.3514	0.3063
	$N_C$	10	10	13	25	22	21	22	24
Yeast TRN	$Q$	0.7668	<b>0.7683</b>	-	-	-	-	-	-
	$N_C$	33	26	-	-	-	-	-	-
Helicobacter pylori PPI	$Q$	0.5359	<b>0.5462</b>	0.5086	0.4926	0.4726	0.4681	0.4900	0.4600
	$N_C$	51	24	52	69	70	75	62	77
E.coli MRN	$Q$	<b>0.3817</b>	0.3734	-	-	-	-	-	-
	$N_C$	13	8	-	-	-	-	-	-
Yeast PPI (2)	$Q$	0.5796	<b>0.5961</b>	-	-	-	-	-	-
	$N_C$	159	46	-	-	-	-	-	-
Yeast PPI (1)	$Q$	0.7002	<b>0.7648</b>	-	-	-	-	-	-
	$N_C$	353	213	-	-	-	-	-	-

# Hybrid-IA: Community Structure



# Hybrid-IA: Community Structure



# Benchmarks

Modularity is a good evaluation function but does not reflect *true* partition.

**LFR Benchmarks** [6] generates weighted undirected and directed synthetic networks, with simple or overlapping communities.

# Normalized Mutual Information

**Normalized Mutual Information** [3] measures the similarity between two partitions using the **information theory**:

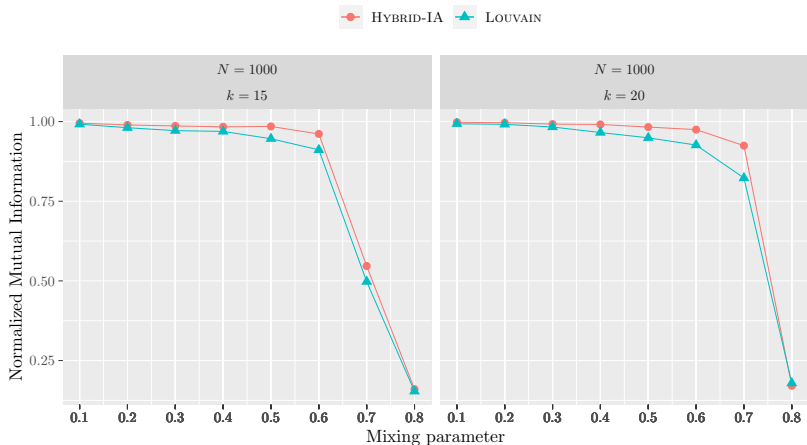
$$NMI(X, Y) = \frac{2(H(X) - H(X|Y))}{H(X) + H(Y)}$$

where

$$H(X) = - \sum_x P(x) \log P(x)$$

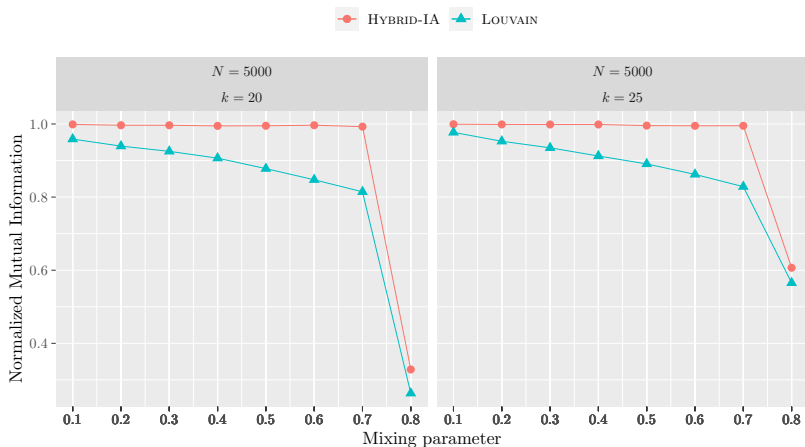
$$H(X|Y) = - \sum_{x,y} P(x, y) \log P(x|y)$$

# Normalized Mutual Information





# Normalized Mutual Information



# Local Search

A study to investigate on how the position of the **local search operator** can influence HYBRID-IA.

Three different positions within the evolutionary cycle:

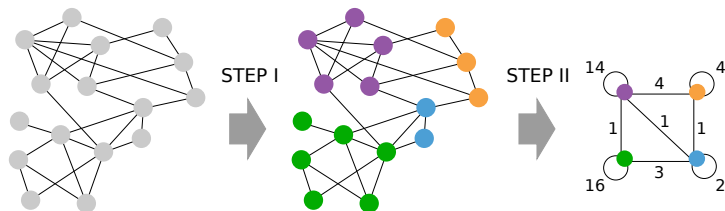
- A) after the selection operator
- B) after the hypermutation operator replacing mutated individuals
- C) after the hypermutation operator producing new individuals

# Local Search: Results

Instance	<i>A</i>			<i>B</i>			<i>C</i>		
	$N_C$	$Q$	Time	$N_C$	$Q$	Time	$N_C$	$Q$	Time
(300, 15, 0.5)	11.6	<b>0.392061</b>	8.3	11.6	<b>0.392061</b>	14.5	11.6	<b>0.392061</b>	15.5
(300, 20, 0.5)	11.2	<b>0.386560</b>	9.4	11.2	<b>0.386560</b>	16.9	11.2	<b>0.386560</b>	17.9
(500, 15, 0.5)	17.6	0.436989	13.7	16.8	<b>0.437168</b>	24.6	16.8	<b>0.437168</b>	26.1
(500, 20, 0.5)	17.0	<b>0.430526</b>	16.3	17.0	<b>0.430526</b>	29.7	17.0	<b>0.430526</b>	31.3
(1000, 15, 0.5)	34.4	0.467073	28.0	30.0	0.468122	51.2	30.4	<b>0.468205</b>	53.9
(1000, 20, 0.5)	37.0	0.468532	33.8	33.0	<b>0.469451</b>	62.6	32.2	0.469442	65.2
(5000, 20, 0.5)	196.4	0.493532	182.4	190.2	0.493985	346.0	189.4	<b>0.493994</b>	353.5
(5000, 25, 0.5)	193.0	0.493379	228.8	185.4	<b>0.493741</b>	438.1	184.6	0.493740	427.1

# Future Works

Adapt HYBRID-IA with a **multi level** approach for very large networks.



Use **Data Mining** techniques, like frequent pattern, or probability learning to gather useful information to guide the search.

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Thanks for your attention!