Community Detection, With Lower Time Complexity, Using Coupled Kuramoto Oscillators

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ABSTRACT

For about two decades, the research topic of Complex Networks has been presented ubiquitously. As a simple and effective framework to express agents and their relationships, several fields of study, from Physics to Sociology, have taken advantage of the powerful representation provided by complex networks. A particular feature inherited by almost any real world network is the presence of densely connected groups of vertices, named modules, clusters or communities. The majority of the proposed techniques does not take advantage of specific features commonly encountered on real networks, such as the power law distribution of vertices' degree (presence of hubs) and its dynamic nature, i.e. vertices, edges and communities normally does not persist invariant regarding to time. Aiming to take into account these two important features, an another ubiquitous phenomenon is applied on detecting communities: synchronization, expressed by coupled Kuramoto oscillators. Here, we extend the Kuramoto's model by introducing a negative coupling between hubs in the network. Moreover, two adjacency lists are used to represent, efficiently, the network structure. Tests have been performed in real network benchmarks, with consistent results achieved.

Categories and Subject Descriptors

E.1 [**Data Structures**]: Graphs and Networks; E.2 [**Data**]: Data Storage and Representations—*linked representation*

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Keywords

Community Detection, Kuramoto Model, Time Complexity, Real Networks

1. INTRODUCTION

Since 1736, when the Swiss scientist and mathematician Leonhard Euler published his studies on the Königsberg bridges [7], pioneering Graph Theory, much has been developed under the framework of this discrete mathematical structure.

The scientifical community would have to wait until the $5th$ decade of the $20th$ century to appreciate a change on researchers' mindset about the developing direction of Graph Theory. Paul Erdős and Alfréd Rényi (ER) [6], let back the common practice of cataloging graphs and its properties (mainly regular ones) by starting to ask about the formation mechanism of real world graph structures, to which they named networks, based on their belief that such graphs' topology were originated by random linkage among vertices and, as consequence, each vertex had almost the same degree, in a Poissonian-like distribution [6].

Although an elegant, simple and powerful mathematical theory on network [1] formation, randomly linked vertices would result in a world where any person would have, approximately, the same number of friends or atoms would link to the same amount of other atoms, not forming specific molecules [3]. This almost all-to-all network topology is not encountered regularly in nature, which demanded further research to better understand their formation mechanism [3].

In 1998, Duncan Watts and Steven Strogatz [22], ressurecting the small-world property originated by a Stanley Milgram's experiment [15], realized that from a regular lattice, just changing some of its edges would produce another network with small-world property. This approach emerges the

[1]From now on, the words graph and network will be used interchangeably.

presence of clusters, which was much more aligned with the topologies normally presented in nature [3].

One year later, Albert-László Barabási, Hawoong Jeong and Réka Albert [1], studying the topology of the *world wide web* (the virtual network of the Internet), concluded that apart from the property of having clusters, another feature was recurrent in such networks: the presence of hubs (vertices with above average degree). During the dynamical formation of a network, new vertices tend to follow a preferential attachment when taking part of it. This produces network topologies where the distribution of vertices' degree obeys a power law, with a small number of nodes having higher degrees, while the majority of them has few edges incident [1].

At providing a technique for detecting communities in complex networks, which absorbs the dynamic nature of network formation (the property of growth [1]), we apply the dynamic phenomenon of synchronization, expressed by the Kuramoto Model [11]. In [24] Wu et al introduce a negative coupling applied only betweeen unconnected vertices, which as consequence provide, at the stable state, synchrony within communities. In this work, aiming to have a lower time complexity for the dynamics, we modified the Kuramoto Model proposed in [24], by introducing a negative coupling only between hubs, since these vertices, by the formation rule, are few in number and the most influent ones. With this modification, we avoid the global repulsion interaction, which is the most time-consuming part of Wu et al's model.

This paper is structured as follows. In Section 2, the model description is given, besides the modification by Wu et al. Also in this section, a discussion about time complexity is presented, which will be the motivation for changing the data structure representing the network. In Section 3, the computer simulations are detailed, how the data structures are applied and which networks are used. The paper is concluded with the synthesis of the results achieved and imminent future works to be developed further.

2. MODEL DESCRIPTION

Complex Networks is a ubiquitous research topic, from Physics to Sociology [18],[3],[16],[9] researchers have taken advantage of their powerful representation to better understand a variety of phenomena concerning their fields of study.

An important common feature in a wide number of networks is the presence of sets or groups of highly dense connected vertices, named modules, clusters or communities [8],[17],[14],[9]. Detecting these modules can reveal the network domain and how a specific kind of relationship among vertices affects its topology [5].

In [8], Santo Fortunato has compiled a variety of community detection techniques, showing their advantages and drawbacks. Almost every model shown in this *survey* is able to deal only with static networks.

Real world networks are dynamic, i.e. their formation is not invariant regarding to time [3],[1],[10],[20]. Aiming to absorb this feature, in this paper, a dynamic phenomenon is used for detecting communities: synchronization.

2.1 Kuramoto Model

In 1975, the Japanese physicist Yoshiki Kuramoto [11], intrigued by the works of the American biologist Arthur Winfree, on modeling biological phenomena [23], worked on a simple yet complete mathematical model which could express the essential aspects of synchronization, which is shown as follows:

$$\frac{d\theta_i}{dt} = \omega_i + \frac{K}{N}\sum_{j=1}^{N} a_{ij} sin(\theta_j - \theta_i), \qquad i = 1, \ldots, N \quad (1)$$

where θ_i is the phase variable and ω_i is the intrinsic frequency of the i^{th} oscillator (vertex i), N is the total number of oscillators in the system, K is the coupling parameter (coupling strength) which carry the oscillators to a common phase value at the dynamic equilibrium and, finally, a_{ij} is the cell element at the row i and column j of the adjacency matrix $[a_{ij}]$ related to the input complex network.

In its standard form, the Kuramoto model, at the dynamical stability, will not realize communities, since the coupling parameter will make every node in the network evolve to a same phase value (it is called phase locking in the synchronization jargon [19]). In [2], Arenas et al shown that when applying the Kuramoto model in clustered networks, they will, at first synchronize locally and then, globally, reaching a collective stable state.

In a way to highlight the local synchronization when the system reaches stability, [24], inspired by [12] proposed a modified Kuramoto model as follows:

$$\begin{aligned}\frac{d\theta_i}{dt} = \omega_i &+ \frac{K_p}{N}\sum_{j=1}^{N} a_{ij} sin(\theta_j - \theta_i) \\ &+ \frac{K_n}{N}\sum_{j=1}^{N}(1 - a_{ij}) sin(\theta_j - \theta_i) \qquad (2)\end{aligned}$$

$$i = 1, \ldots, N \qquad K_p > 0, K_n \leqslant 0$$

in this new form, phases of connected oscillators ($a_{ij} = 1$) are under the original rule, having their phases evolving together but, unconnected oscillators will have the tendency to reach far different phases due to the negative coupling strength.

In the next subsection, a discussion about time complexity is given and also its importance concerning the results achieved in this paper.

2.2 Time Complexity

When storing a graph on a computer, its primitive elements (vertices and edges) have to be placed in memory for fully represent it. By this storage, an adjacency matrix can be generated highlighting which pair of vertices produces an edge, or not.

Networks with community structure are sparse [8], therefore the number of edges participating in the positive coupling are much less than the number of fictitious edges for the negative one.

Using the Big O notation for a graph with n vertices, necessarily applying the positive coupling to the network and the negative coupling to its complementary, the dynamics will demand a computational complexity of $O(n^2)$.

Considering that real networks, e.g. social networks (*Twitter*, *Facebook*), normally are large, with millions of nodes and that their topologies have, most of the time, the presence of community structure and hubs, thus they are indeed sparse, i.e. the number of $1's$ is less than of $0's$ in the adjacency

matrix.

To make a better use of the computational process, we will represent the network with two adjacency lists [2], one for hubs only (pseudo adjacency list), and the other as traditional. Figures 2 and 3 present the schemes of the data structures used to represent the network, based on this approach, the dynamics equation expressed in (2) can be rewritten as follows:

$$\frac{d\theta_i}{dt} = \omega_i + \frac{K_p}{N}\sum_{j\in L(i)}\sin(\theta_j - \theta_i) + \frac{K_n}{N}\sum_{j\in P(i)}\sin(\theta_j - \theta_i) \tag{3}$$

where $L(i)$ represents the adjacency list of vertex i and, whether i is considered a hub, $P(i)$ represents the hub's pseudo-adjacency list of vertex i, otherwise $P(i)$ is empty and the second summation of Equation (3) is ignored. The parameters K_p and K_n are the same as in Equation (2).

By Equation (3), suppose, for a network with n vertices, that each vertex has degree 1, using adjacency list as the data structure, then for the positive coupling, the time complexity will be $O(n\langle k\rangle)$, where $\langle k\rangle$ is the average degree of the vertices in the network, in this particular case, $\langle k\rangle = 1$, therefore $O(n)$. For the negative coupling, the complexity reached will be $O(n(n - \langle k\rangle))$, which yields $O(n^2)$. Nevertheless, applying the dynamics as in Equation (3) leads to a lower time complexity, since hubs are not very frequent in real networks, as will be shown in section 3.

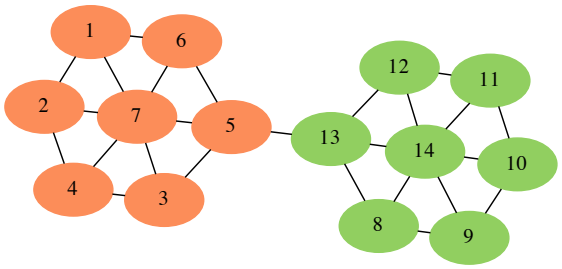

Figure 1: A simple network, with 14 vertices and 2 communities. Vertices 7 and 14 were the only considered hubs.

To clarify the idea behind our strategy. the sample network in Figure 1 will be used. Setting as rule of centrality that for a vertex being considered a hub, it should have an above average degree ($\langle k\rangle + 1$), only vertices 7 and 14 will deal with the negative coupling (see Figure 3). Generalizing for whatever h ($h \geqslant 0$), the time complexity for the pseudo-adjacency list will have an upper bound of $O(h^2)$. Using the model by [24], the number of computational steps for the dynamics will be 196 ($K_p = 30.0$ and $K_n = -10.0$) and with our approach it yields $50 + 2 = 52$ ($K_p = 5.0$ and $K_n = -50.0$) steps, which is a sensible computational processing economy to complete one iteration. Figure 4 shows the stable state reached at the $500th$ iteration using Wu et al's model, depicting two well defined clusters, classified using a threshold of 0.2 radians [3]. Figure 5 shows the sta-

[2]We had preserved the name adjacency list, although one is for actual links and the other, referred to as pseudo-adjacency list, is for hubs only, either connected or not.

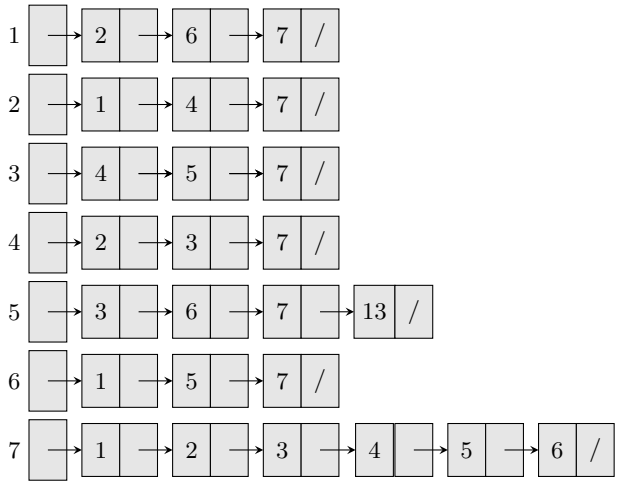

Figure 2: Adjacency list for the vertices belonging to the orange community in Figure 1. Links between hubs are not presented (see Figure 3).

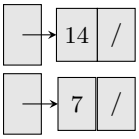

Figure 3: Pseudo-adjacency list for hubs. Respectively from top to down, vertices 7 and 14 of the network in Figure 1.

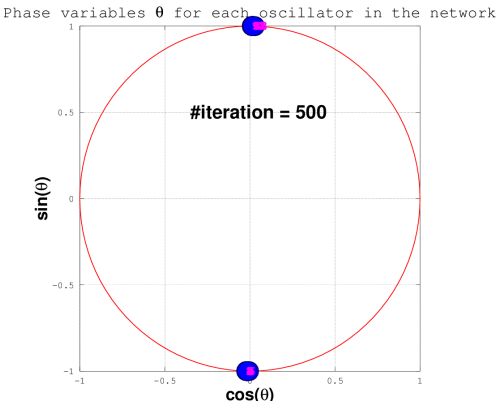

Figure 4: The scenario encountered after 500 iterations, applying the negative coupling between each and every unconnected vertices in the network. 2 communities has been detected, using a threshold of 0.2 radians. $K_p = 30.0$ and $K_n = -10.0$

[3]The phase values in the unit cycle are classified respecting the cycling nature of the space values e.g., supposing a phase

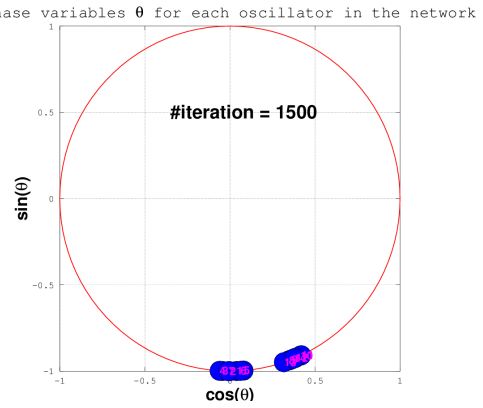

Figure 5: The scenario encountered after 1500 iterations, applying the negative coupling only between hubs (vertices 7 and 14). 2 communities has been detected, using a threshold of 0.2 radians. $K_p = 5.0$ and $K_n = -50.0$

ble state reached at the $1500th$ iteration, but applying the negative coupling only between hubs. Since in this sample network, the two hubs don't have much higher degree if compared with the non-hubs vertices, the number of iterations needed for phase lock within clusters is considerably greater if compared to the all-to-all approach. Even in this disadvantageous case, the two clusters could be well detected for a threshold of 0.2 radians and, also considering the number of iterations, this new approach is yet preferable concerning computational cost (A decrease of total steps from 98000 to 78000). As will be shown in section 3, for the real networks under study, the numerical difference on the number of iterations to reach dynamical stability between these two approaches will be at most 200.

The next section we will present the computer simulations on real network benchmarks, comparing the results achieved with those gotten by the original model [24].

3. COMPUTER SIMULATIONS

Once applying the lower complexity algorithm in a sample artificial network, in this section, following the methodology in [24], the same real networks will be used for comparison: The Zachary Karate Club Network [26], The Lusseau's Bottlenose Dolphins Network [13] and The Protein Interaction Network [21].

For comparing the outcomes in [24] with those achieved by our approach, phase values will be represented by tables not by plots as in Figures 4 and 5, since highlighting numerically which are these values will be very important. The only exception is for the Lusseau's Bottlenose Dolphins Networks, since a table representation would demand too much space.

Table 1 shows, for the Zachary's Karate Club Network the phase values reached for each vertex both, in the all-to-all approach and ours with hubs. The colors in the table matches with those in Figure 6, except for the ones in gray which denotes overlapping nodes (vertices in the limits of the modules). Nodes without phase values (marked with a dash −) are core-peripheral vertices, they are part of the network but with only one connection with it, then placed at the periphery of the graph, as in [24] they will automatically be classified as members of the same community of the node they are attached to.

Although the table shows only one instance of the outcome, an interesting aspect has to be highlighted. Running about 200 instances of the dynamics for each network, when reaching the stable state (considering the same values for K_p and K_n), a fixed relative disposition of the oscillators is repeated for each and every instance (like a signature of the network), the only difference is the absolute position of the ensemble at a particular iteration. Therefore, although the phase values could be different, the community classification will always be the same, supposing an unchanged threshold.

3.1 Zachary's Karate Club Network [26]

As previously said, Table 1 depicts the scenario for the Zachary's Karate Club Network. For the all-to-all approach the values for K_p and K_n are, respectively, 30.0 and −10.0, when applying the negative coupling only between hubs the values used are 100.0 and −300.0, the threshold for phase classification is 0.2 in both cases. For higher values of K_p the network easily reaches global synchronization (the same happens for lower values of K_n) and for higher values of K_n the network does not synchronize at all (the same happens for lower values of K_p).

Applying the same rule for classifying a vertex as hub as in the toy sample ($k_h \geqslant \langle k \rangle + 1$) [4,5]. For this network, the vertices classified as hubs are 1, 2, 3, 4, 32, 33 and 34, i.e. 20.5% of the nodes.

Comparing the all-to-all model as in [24] with our approach, the following can be said:

The community in orange is merged with the community in red, since there are no hubs in the orange module and that the limitrophe nodes 7, 6 and 5 are all connected to 1, which is a red hub.

Vertices 9 and 10 were kept as overlapping nodes, the other ones (3, 14, 29 and 31) although not in gray, their community membership is in accordance with their placement in the network.

Finally, the total number of steps, for each iteration, with the all-to-all model is 1156 (stable at the $300th$ iteration) and with our approach, given that $\langle k \rangle$ is roughly 5, results in $170 + 49 = 219$ steps as upper bound (stable at the $500th$ iteration), which lowers in 81% the amount of computation for the dynamics and also provides a consistent coarse-grained community detection.

3.2 Protein Attraction Network [21]

Figure 7 shows a protein interaction network first presented in [21] and also analyzed by [24].

The results for community detection, following the same methodology as for the Karate Club Network, are presented in Table 2. It is worth noting that, in this case, although not having any hubs, the community in red could be detected by the approach with hubs due to the shielding given by the overlapping nodes 5 and 12. By the way, this overlapping nodes could not be detected, being classified as members of

value of r radians and a threshold of k. It will be considered as of belonging to a same community, any oscillator with phase value in the range $[r - k, r + k]$.

[4] k_h is the degree of the hub h.

[5] This rule will be kept for the other experiments.

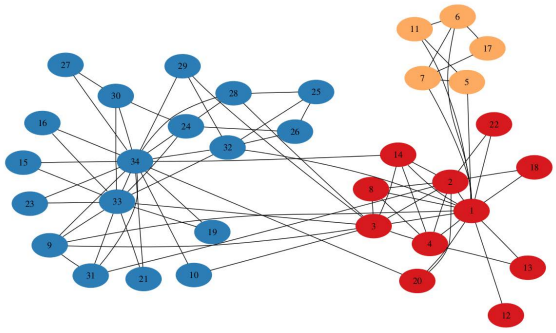

Figure 6: Zachary's Karate Club Network.

Table 1: ***Comparison between [24] model with the Hubs lower cost approach for the Zachary's Karate Club Network. At iteration*** 300 ***and*** 500***, respectively.***

Zachary's Karate Club Network		
n	**All-to-all**	**With Hubs**
1	**1.295**	**4.031**
2	**1.498**	**4.019**
3	**2.256**	**3.872**
4	**1.452**	**3.989**
5	**0.976**	**4.118**
6	**0.943**	**4.161**
7	**0.947**	**4.146**
8	**1.480**	**3.983**
9	**3.311**	**1.417**
10	**2.860**	**6.074**
11	**0.977**	**4.116**
12	**-**	**-**
13	**1.173**	**4.040**
14	**1.589**	**3.941**
15	**4.519**	**0.942**
16	**4.522**	**0.961**
17	**0.940**	**4.228**
18	**1.198**	**4.035**
19	**4.512**	**0.961**
20	**1.242**	**4.682**
21	**4.504**	**0.983**
22	**1.199**	**4.058**
23	**4.511**	**0.959**
24	**4.585**	**0.968**
25	**4.611**	**0.966**
26	**4.659**	**0.962**
27	**4.697**	**0.940**
28	**4.517**	**1.041**
29	**4.052**	**0.986**
30	**4.589**	**0.969**
31	**3.637**	**1.184**
32	**4.587**	**0.983**
33	**4.588**	**1.037**
34	**4.562**	**0.928**

the community in orange, which is in accordance with their position in the graph.

For this network, the average degree is roughly 4 and the vertices considered hubs are 11, 16, 17, 18, 25, 28, 29, 30, 32, 33, 36 and 37, i.e. 31% of the network.

Fixing the threshold for phase classification in 0.2 radians, for the all-to-all model ($K_p = 30.0$, $K_n = -10.0$ and stable at the $500th$ iteration), the amount of steps is 1444 and with the hubs approach ($K_p = 150.0$, $K_n = -300.0$ and stable at the $700th$ iteration) it yields $152 + 144 = 296$ steps as upper bound, an economy of 79.5% of computational cost for each iteration, while detecting the communities satisfactorily.

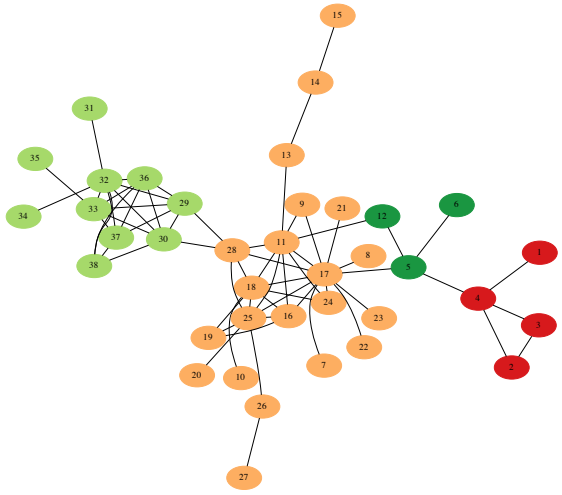

Figure 7: Protein Interaction Network.

3.3 Lusseau's Bottlenose Dolphins Network [13]

For this particular network, the table representation is not used, since it would demand much space, being difficult for the reader to analyze node by node. In Figure 8 it is shown the communities disposition as in [24] and in Figure 9 the disposition acquired with our approach.

Note that again a smaller community is merged with a larger one (since there is no shielding as in the Protein Network). Once nodes of the module in yellow are more densely connected with nodes of the community in green, if compared to those in orange, the merging has resulting in yellows becoming greens.

Vertices 19, 20, 21 and 22 are corrected identified as overlapping nodes (see Figure 9).

For this network, nodes 3, 8, 9, 13, 15, 18, 27, 31, 35, 36, 40, 43, 45, 48, 53, 54 and 60 had been classified as hubs, i.e. 28% of the vertices. The average degree is roughly 5.

Fixing the threshold for phase classification in 0.3 radians, in an all-to-all technique, the positive coupling used is 50.0 and the negative is -10.0 (the stability is certainly reached at the $500th$ iteration), for this the amount of steps will be 3844 and with our approach ($K_p = 150.0$, $K_n = -300.0$ and reaching stability at the $700th$ iteration) it leads to $310 + 289 = 599$ steps as upper bound, which results in an economy of 85% in computational cost per iteration, while providing a reasonable community detection outcome.

3.4 The Algorithm

Algorithm 1 synthesizes the process in a form of a pseudo-code and, in the sequence, the next section presents the

Table 2: ***Comparison between [24] model with the Hubs lower cost approach for the Protein Interaction Network. At iteration*** 500 ***and*** 700***, respectively.***

Protein Interaction Network		
n	**All-to-all**	**With Hubs**
1	**5.239**	**5.316**
2	**5.235**	**5.310**
3	**5.235**	**5.284**
4	**5.408**	**5.294**
5	**6.252**	**1.888**
6	**-**	**-**
7	**1.480**	**2.032**
8	**1.485**	**2.017**
9	**1.671**	**1.950**
10	**-**	**-**
11	**1.778**	**1.867**
12	**0.548**	**1.912**
13	**-**	**-**
14	**-**	**-**
15	**-**	**-**
16	**1.707**	**1.950**
17	**1.574**	**1.977**
18	**1.787**	**1.934**
19	**1.725**	**1.960**
20	**1.644**	**1.999**
21	**1.486**	**2.023**
22	**1.478**	**2.036**
23	**1.483**	**2.014**
24	**1.717**	**1.939**
25	**1.668**	**1.962**
26	**-**	**-**
27	**-**	**-**
28	**2.247**	**2.045**
29	**4.218**	**2.248**
30	**4.218**	**2.248**
31	**4.535**	**2.232**
32	**4.403**	**2.292**
33	**4.384**	**2.288**
34	**4.534**	**2.326**
35	**4.519**	**2.340**
36	**4.367**	**2.283**
37	**4.390**	**2.289**
38	**4.392**	**2.289**

conclusions for the results achieved. Additionally, imminent future works are also discussed.

4. CONCLUSIONS

In this paper, we had applied a modified Kuramoto model for community detection in a toy sample network and three real world ones. Based on the results achieved, we believe to have highlighted an important feature of real world networks, the presence of highly connected nodes, named hubs. Taking advantage of them we were able to reduce the time complexity of the algorithm, from the standard $O(n^2)$ to $O(n\langle k\rangle) + O(h(h-1))$ [6] , where $\langle k\rangle$ is the average degree of the vertices and h is number of hubs in the network. Although the outcome of community classification is under the dependence of how the hubs are positioned in the network, applying it on real networks has proved to be a fast consistent coarse-grained method for detecting communities. It is an important contribution for achieving scalability while detecting the clusters with synchronization.

[6] $O(n\langle k\rangle)+O(h^2)$ is an upper bound, as used for comparison in the *Computer Simulations* section.

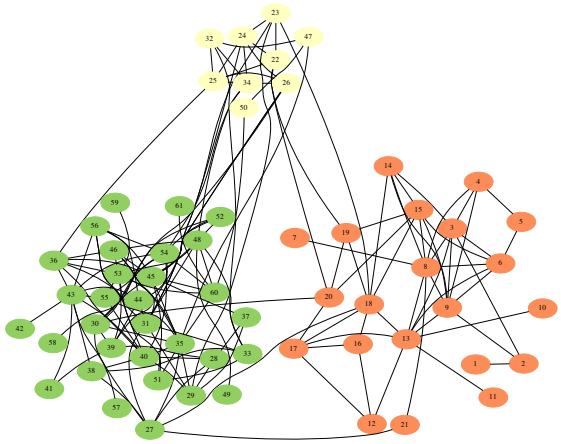

Figure 8: Lusseau's Bottlenose Dolphins Network, with the communities disposition as in [24].

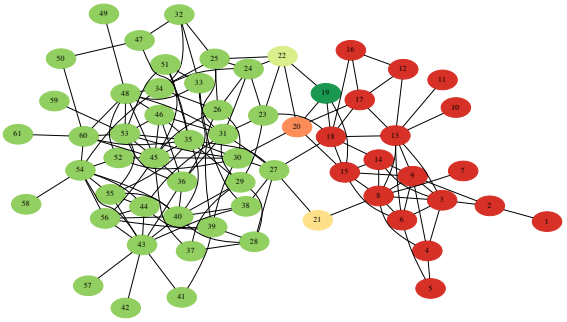

Figure 9: Lusseau's Bottlenose Dolphins Network, disposition acquired with our approach.

For future work, at first, two things are imminent:

(1) The unit cycle lacks expressiveness, i.e., depending on the threshold value used, the number of communities possible to be realized is reduced. It is an obstacle not only concerning the number of communities but also when hierarchical communities are present, since the phase values will be too close to indicate any difference by a threshold. Very recently [25] have proposed a way to overcome this limitation, by analyzing the frequencies of phases, when oscillators are coincident in the cycle, their phase frequencies are in tune only inside the modules. Our approach has not yet been tested taking into account this new technique.

(2) A deeper study on the intervenient parameters and how good choices could be made depending on the input network.

We believe this paper has discussed an interesting intersection point between Computer Science and Physics.

Data: The network G
initialization;
Express G as a standard adjacency list L;
Calculate each vertex degree k_i;
for *Every vertex i in G* **do**
  if $k_i \geqslant \langle k \rangle + 1$ **then**
    i is a hub;
  end
end
Construct the pseudo-adjacency list P with the hubs;
while *Not in stable state* **do**
  for *Every node in L* **do**
    Apply the positive coupling as in *Eq.*3;
  end
  for *Every node in P* **do**
    Apply the negative coupling as in *Eq.*3;
  end
end

Algorithm 1: Synchronization Dynamics

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