MULTI-SCALE COMMUNITY DETECTION USING STABILITY AS OPTIMISATION CRITERION IN A GREEDY ALGORITHM

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Abstract: Whether biological, social or technical, many real systems are represented as networks whose structure can be very informative regarding the original system's organisation. In this respect the field of *community detection* has received a lot of attention in the past decade. Most of the approaches rely on the notion of *modularity* to assess the quality of a partition and use this measure as an optimisation criterion. Recently *stability* was introduced as a new partition quality measure encompassing former partition quality measures such as modularity. The work presented here assesses stability as an optimisation criterion in a greedy approach similar to modularity optimisation techniques and enables multi-scale analysis using Markov time as resolution parameter. The method is validated and compared with other popular approaches against synthetic and various real data networks and the results show that the method enables accurate multi-scale network analysis.

1 INTRODUCTION

In biology, sociology, engineering and beyond, many systems are represented and studied as graphs, or networks (e.g. protein networks, social networks, web). In the past decade the field of community detection attracted a lot of interest considering community structures as important features of real-world networks (Fortunato, 2010). Given a network of any kind, looking for communities refers to finding groups of nodes that are more densely connected internally than with the rest of the network. The concept considers the inhomogeneity within the connections between nodes to derive a partitioning of the network. As opposed to clustering methods which commonly involve a given number of clusters, communities are usually unknown, can be of unequal size and density and often have hierarchies (Fortunato, 2010). Finding such partitioning can provide information about the underlying structure of a network and its functioning. It can also be used as a more compact representation of the network, for instance for visualisations.

Detecting community structure in networks can be split into two subtasks: how to partition a graph, and how to measure the quality of a partition. The latter is commonly done using *modularity* (Newman and Girvan, 2004). Partitioning graphs is an NP-hard task (Fortunato, 2010) and heuristics based algorithms have thus been devised to reduce the complexity while still providing acceptable solutions. Considering the size of some real-world networks much effort is put into finding efficient algorithms able to deal with larger and larger networks such as modularity optimisation methods. However it has been shown that networks often have several levels of organisation (Simon, 1962), leading to different partitions for each level which modularity optimisation alone cannot handle (Fortunato, 2010). Methods have been provided to adapt modularity optimisation to multi-scale (multi-resolution) analysis using a tuning parameter (Reichardt and Bornholdt, 2006; Arenas et al., 2008). Yet the search for a partition quality function that acknowledges the multi-resolution nature of networks with appropriate theoretical foundations has received less attention. Recently, *stability* (Delvenne et al., 2010) was introduced as a new quality measure for community partitions. Here we investigate its use as an optimisation criterion for multi-scale analysis. We show how stability can be used in place of modularity in modularity optimisation methods and present a new greedy agglomerative algorithm using stability as optimisation function and enabling multi-scale analysis using Markov time as a resolution parameter.

The next section reviews related work. Then our method is presented followed by experiments assessing its potential, discussion and conclusion.

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2 BACKGROUND

While several community partition quality measures have been used (Fortunato, 2010), the most commonly found in the literature is modularity (Newman and Girvan, 2004). Given a partition into c communities let e be the community matrix of size $c \times c$ where each e_{ij} gives the fraction of links going from a community i to a community j and $a_i = \sum_j e_{ij}$ the fraction of links connected to i. (If the graph is undirected, each e_{ij} not on the diagonal should be given half of the edges connecting communities i and j so that the number of edges connecting the communities is given by $e_{ij} + e_{ji}$ (Newman and Girvan, 2004).) Modularity Q_M is the sum of the difference between the fraction of links within a partition linking to this very partition minus the expected value of the fraction of links doing so if edges were randomly placed:

$$Q_M = \sum_{i=1}^{c} (e_{ii} - a_i^2) \tag{1}$$

One advantage of modularity is to impose no constraint on the shape of communities as opposed for instance to the clique percolation method (Palla et al., 2005) that defines communities as adjacent k-cliques thus imposing that each node in a community is part of a k-clique.

Modularity was initially introduced to evaluate partitions. However its use has broadened from partition quality measure to optimisation function and modularity optimisation is now a very common approach to community detection (Newman, 2004; Clauset et al., 2004; Newman, 2006; Blondel et al., 2008). (Recent reviews and comparisons of community detection methods including modularity optimisation methods can be found in (Fortunato, 2010; Lancichinetti and Fortunato, 2009).) Modularity optimisation methods commonly start with each node placed in a different community and then successively merge the communities that maximise modularity at each step. Modularity is thus locally optimised at each step based on the assumption that a local peak should indicate a particularly good partition. The first algorithm of this kind was *Newman's fast algorithm* (Newman, 2004). Here, for each candidate partition the variation in modularity ΔQ_M that merging two communities i and j would yield is computed as

$$\Delta Q_{M_{ij}} = 2(e_{ij} - a_i a_j) \tag{2}$$

where i and j are the communities merged in the new candidate partition. Computing only ΔQ_M minimises the computations required to evaluate modularity and leads to the fast greedy algorithm given in Algorithm 1. This algorithm enables the incremental building of a hierarchy where each new partition is the local optima maximising Q_M at each step. It was shown to provide good solutions with respect to the original Girvan-Newman algorithm that performs accurately but is computationally highly demanding and is thus not suitable for large networks (Newman and Girvan, 2004). (Note that accuracy refers in this context to a high modularity value. Other measures, such as stability, might rank partitions differently.) Since then other methods have been devised such as (Clauset et al., 2004) optimising the former method, another approach based on the eigenvectors of matrices (Newman, 2006) or the Louvain method (Blondel et al., 2008). The last method has shown to outperform in speed previous greedy modularity optimisation methods by reducing the number of intermediate steps for aggregating all the nodes.

Algorithm 1: Greedy algorithm sketch for modularity optimisation.

1. Divide in as many clusters as there are nodes.
2. Measure modularity variation ΔQ_M for each candidate partition where a pair of clusters are merged.
3. Select the network with the highest ΔQ_M.
4. Go back to step 2.

These methods all rely on modularity optimisation. Yet modularity optimisation suffers from several issues. One issue is known as the resolution limit meaning that modularity optimisation methods can fail to detect small communities or over-partition networks (Fortunato and Barthélemy, 2007) thus missing the most natural partitioning of the network. Another issue is that the modularity landscape admits a large number of structurally different high-modularity value solutions and lacks a clear global maximum value (Good et al., 2010). It has also been shown that random-graphs can have a high modularity value (Guimerà et al., 2004).

Some biases have been introduced to alter the behaviour of the method towards communities of various sizes (Danon et al., 2006; Reichardt and Bornholdt, 2006; Arenas et al., 2008). In (Danon et al., 2006), the authors observed that large communities are favoured at the expense of smaller ones biasing the partitioning towards a structure with a few large clusters which may not be an accurate representation of the network. They provided a normalised measure of ΔQ_M defined as

$$\Delta Q'_{M_{ij}} = max\left(\frac{\Delta Q_{M_{ij}}}{a_i}, \frac{\Delta Q_{M_{ij}}}{a_j}\right) \tag{3}$$

which aims at treating communities of different sizes equally. In (Reichardt and Bornholdt, 2006), modularity optimisation is modified by using a scalar parameter γ in front of the null term (the fraction of edges connecting vertices of a same community in a random graph) turning equation (1) into

$$Q_{M_\gamma} = \sum_i (e_{ii} - \gamma a_i^2) \quad (4)$$

where γ can be varied to alter the importance given to the null term (modularity optimisation is found for $\gamma = 1$). In (Arenas et al., 2008), modularity optimisation is performed on a network where each node's strength has been reinforced with self loops. Considering the adjacency matrix A, modularity optimisation is performed on $A + rI$ where I is the identity matrix and r is a scalar. Varying the value of r enables the detection of communities at various coarseness levels (modularity optimisation is found for $r = 0$). With their resolution parameter, the two latter methods enable a multi-scale network analysis.

Significant attention has been given to modularity but little attention has been given to new partition quality measures. Recently, stability was introduced in (Delvenne et al., 2010) as a new partition quality measure unifying some known clustering heuristics including modularity and using Markov time as an inner resolution parameter. The stability of a graph considers the graph as a Markov chain where each node represents a state and each edge a possible state transition. Let n be the number of nodes, m the number of edges, A the $n \times n$ adjacency matrix containing the weights of all edges (the graph can be weighted or not), d a size n vector giving for each node its degree (or strength for a weighted network) and $D = diag(d)$ the corresponding diagonal matrix. The stability of a graph considers the graph as a Markov chain where each node represents a state and each edge a possible state transition. The chain distribution is given by the stationary distribution $\pi = \frac{d}{2m}$. Let also Π be the corresponding diagonal matrix $\Pi = diag(\pi)$. The transition between states is given by the $n \times n$ stochastic matrix $M = D^{-1}A$. Assuming a community partition, let H be the indicator matrix of size $n \times c$ giving for each node its community. The clustered auto-covariance matrix at Markov time t is defined as:

$$R_t = H^T(\Pi M^t - \pi^T \pi)H \quad (5)$$

Stability at time t noted Q_{S_t} is given by the trace of R_t and the global stability measure Q_S considers the minimum value of the Q_{S_t} over time from time *0* to a given upper bound τ:

$$Q_S = \min_{0 \leq t \leq \tau} trace(R_t) \quad (6)$$

This model can be extended to deal with real values of t by using the linear interpolation:

$$R_t = (c(t) - t) \cdot R(f(t)) + (t - f(t)) \cdot R(c(t)) \quad (7)$$

where $c(t)$ returns the smallest integer greater than t and $f(t)$ returns the greatest integer smaller than t. This is useful to investigate for instance time values between 0 and 1. It was indeed shown in (Delvenne et al., 2010) that the use of Markov time with values between 0 and 1 enables detecting finer partitions than those detected at time 1 and above.

Also, this model can be turned into a continuous time Markov process by using the expression $e^{(M-I)t}$ in place of M^t (where e is the exponential function) (Delvenne et al., 2010).

Stability has been introduced as a measure to evaluate the quality of a partition hierarchy and has been used to assess the results of various modularity optimisation algorithms. Further mathematical foundations have been presented in (Lambiotte et al., 2008; Lambiotte, 2010). The work presented here investigates stability as an optimisation function with various practical test cases. It presents and assesses a greedy algorithm that optimises stability similarly to modularity optimisation methods and uses stability's inner Markov time as a resolution parameter. While related approaches such as Arenas et al's and Reichardt et al's methods also offer a multi-scale analysis with their respective parameters, these methods offer a tuneable version of modularity optimisation by modifying the importance of the null factor or by adding self-loops to nodes. Such analysis remains based on a one step random walk analysis of the network with modifications of its structure. Stability optimisation enables on the contrary random walks of variable length defined by the Markov time thus exploiting thoroughly the actual topology of the network. As communities reflect the organisation of a network, and hence its connectivity, this approach seems to be more suitable. The next section presents the method followed by experiments assessing it and comparing it to other relevant approaches.

3 METHOD

As discussed in (Delvenne et al., 2010) the measure of stability and the investigation of stability of a partition along the Markov time (stability curve) for a partition can help addressing the partition scale issue and the optimal community identification. The results from the authors indeed show with the stability curve that the clustering varies depending on the time window during which the Markov time is considered. From there, our work uses the Markov time as a resolution parameter in an optimisation context where stability is used as the optimisation criterion.

Considering the Markov chain model, it has been shown in (Delvenne et al., 2010) that stability at time 1 is modularity. From equation (5) it can also be derived that stability at time t is the modularity of a graph whose adjacency matrix is $A_t = DM^t$ (or $A_t = De^{(M-I)t}$ for the continuous time model).

Considering stability at time t as the modularity of a graph given by the adjacency matrix A_t allows us to apply the work done on modularity optimisation to stability. Stability optimisation then becomes a broader measure where modularity is the special case $t = 1$ in the Markov chain. Using the modularity notation from equation (1), stability at time t can be defined as:

$$Q_{S_t} = \sum_i (e_{t_{ii}} - a_i^2) \tag{8}$$

where e_t is the community matrix for Markov time t computed from A_t.

Modularity optimisation is based on computing the change in modularity between an initial partition and a new partition where two clusters have been merged. The change in modularity when merging communities i and j is given by equation (2) and similarly the change in stability at time t is

$$\Delta Q_{S_{t_{ij}}} = 2(e_{t_{ij}} - a_i a_j) \tag{9}$$

Following equation (6) the new Q_S value Q'_S is:

$$Q'_S = \min_{0 \le t \le \tau} (Q_{S_t} + \Delta Q_{S_t}) \tag{10}$$

At each clustering step, the partition with the best Q'_S value is kept and Q_S is then updated as $Q_S = Q'_S$. For computational reasons the time needs to be sampled between 0 and τ. Markov time can be sampled linearly or following a log scale. The latter is usually more efficient for large time intervals.

The matrices e_t are computed in the initialisation step of the algorithm and then updated by successively merging the lines and columns corresponding to the merged communities. This leads to the greedy stability optimisation (GSO) algorithm given in Algorithm 2, based on the principle of Algorithm 1.

Depending on the Markov time boundaries the partitions will vary as the larger the time window, the longer a partition must keep a high stability value to get a high overall stability value, as defined in equation (6). The Markov time thus acts as a resolution parameter.

Compared to Newman's fast algorithm the additional cost of stability computation and memory requirement is proportional to the number of times considered in the Markov time window. For each time t considered in the computation, a matrix e_t must be computed and kept in memory. Let n be the number of nodes in a network, m the number of edges and s the number of time steps required for stability computation. The number of merge operations needed to terminate are $n-1$. Each merging operation requires to iterate through all edges, hence m times, and for each edge to compute the stability variation s times. The computation of each ΔQ can be performed in constant time. In a non optimised implementation the merging of communities i and j can be performed in n steps, hence the complexity of the algorithm would be $O(n(m.s+n))$. However the merging of communities i and j really consists in adding the edges of community j to i and then deleting j. To do so there is one operation per edge. The size of a cluster at iteration i is given by $cs(i) = \frac{n}{n-i}$. and therefore the average cluster size over all iterations is

$$\bar{cs} = \frac{1}{n} \cdot \sum_{i=1}^{n} cs(i) = \sum_{i=1}^{n} \frac{1}{i} \approx ln(n) + \gamma \tag{11}$$

with γ the Euler-Mascheroni constant. As the number of edges is bounded by the number of nodes squared, the algorithm can be implemented with the complexity $O(n(m.s + ln^2(n)))$ provided the appropriate data structures are used to exploit this, as discussed in (Clauset et al., 2004). Considering that s should be low, the complexity is $O(n(m + ln^2(n)))$.

Also a large time window does not imply many time values. The speed-accuracy trade-off comes from the number of steps s within the boundaries, whatever the boundaries. While the full mathematical definition of stability considers all Markov times in a given interval, all Markov times may not be crucial to a good (or even exact) approximation of stability. The fastest way to approximate stability is to compute it with only one time value. As stability tends to decrease as the Markov time increases, we are seeking when the following approximation can be made:

$$Q_S = \min_{0 \le t \le \tau} trace(R_t) \approx trace(R_\tau) \tag{12}$$

The need for considering consecutive time values in the computation of stability addresses an issue encountered within random walks. Considering for instance a graph with three nodes a, b and c with an edge between nodes a and b and between nodes b and c. Using a Markov time of 2 only (i.e. a random walk of 2 steps with no consideration of the first step) starting from a there would be no transition between a and b as after one step from a the random walker would be in b and then it could only go back to a or walk to c. However, the more densely connected the clusters, the less likely this situation is to happen as many paths can be borrowed to reach each node. This time optimisation is assessed with the rest of the method in the next section.

4 EXPERIMENTS & RESULTS

To assess our method we use various known networks made of real or synthetic data that have been used in related work and are publicly available. For comparison, other relevant methods are tested along with our method: Newman's fast algorithm (Newman, 2004), Danon et al's method (Danon et al., 2006), the Louvain method (Blondel et al., 2008), Reichardt et al's method (Reichardt and Bornholdt, 2006), and Arenas et al's method (Arenas et al., 2008). Both Reichardt et al's and Arenas et al's methods use a resolution parameter that enables multi-scale community detection based on this parameter. The Louvain method also returns a succession of partition (not tuneable). The other two methods are not multi-scale and hence only return one partition.

The community detection algorithms were implemented in Matlab[1] except for the code of the Louvain method downloaded from the authors website[2] (we used their hybrid C++ Matlab implementation). All experiments were run using Matlab R2010b under MacOS X on an iMac 3.06GHz Intel Core i3.

4.1 Networks

The networks considered are two synthetic and four real-world data networks [3] that have been used as benchmarks in the literature to assess community detection algorithms. The networks have been chosen for their respective properties (e.g. multi-scale, scale-free) and popularity that enable an assessment of our method and comparisons with other approaches. While selecting very large networks can demonstrate speed efficiency, the results are commonly ranked using modularity which as previously discussed is not suitable for this work. We therefore deemed appropriate to use here networks of smaller size with some knowledge of their structure or content used for the evaluation of the results, similarly to what has been done in related work (Reichardt and Bornholdt, 2006; Arenas et al., 2008).

[1]The code developed for this work is available on request. More also at http://www.elemartelot.org.

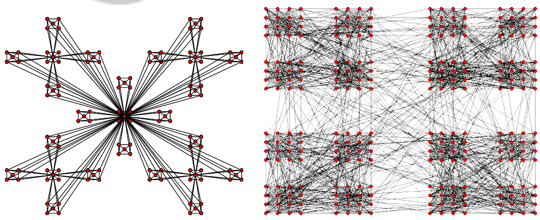
[2]http://sites.google.com/site/findcommunities/

[3]Available from http://www-personal.umich.edu/ mejn/netdata/

4.1.1 Synthetic Datasets

Ravasz et al's Scale-free Hierarchical Network. This network was presented in (Ravasz and Barabási, 2003) and defines a hierarchical network of 125 nodes as shown in Figure 1(a). The network is built iteratively from a small cluster of 5 densely linked nodes. A node at the centre of a square is connected to 4 others at the corners of the square themselves also connected to their neighbours. Then 4 replicas of this cluster are generated and placed around the first one, producing a 25 nodes network. The centre of the central cluster is linked to the corner nodes of the other clusters. This process is repeated again to produce the 125 nodes network. The structure can be seen as 25 clusters of 5 nodes or 5 clusters of 25 nodes.

Arenas et al's Homogeneous in Degree Network. This network taken from (Arenas et al., 2006) and named H13-4 is a two hierarchy levels network of 256 nodes organised as follow. 13 edges are distributed between the nodes of each of the 16 communities of the first level (internal community) formed of 16 nodes each. 4 edges are distributed between nodes of each of the 4 communities of the second level (external community) formed of 64 nodes each. 1 edge per node links it with any community of the rest of the network. The network is presented in Figure 1(b).



(a) Ravasz 125 nodes. (b) H13-4.

Figure 1: (a) Hierarchical scale free network generated in 3 steps producing 125 nodes at step 3 (Ravasz and Barabási, 2003). (b) Network presented in (Arenas et al., 2006) made of 256 nodes organised in two hierarchical levels with 16 communities of 16 nodes for the first level and 4 communities of 64 nodes for the second level.

4.1.2 Real-world Datasets

Zachary's Karate Club. This network is a social network of friendships between 34 members of a karate club at a US university in 1970 (Zachary, 1977). Following a dispute the network was divided into 2 groups between the club's administrator and the club's instructor. The dispute ended in the instructor creating his own club and taking about half of the initial club with him. The network can hence be divided into 2 main communities. A division into 4 communities has also been acknowledged (Medus et al., 2005).

Algorithm 2: Greedy stability optimisation (GSO) algorithm taking in input an adjacency matrix and a Markov time window, and returning a partition and its stability value.

```
Divide in as many communities as there are nodes
Set this partition as current partition C_cur and as best known partition C
Set its stability value as best known stability Q
Set its stability vector (stability values at each Markov time) as current stability vector QV
Compute initial community matrix e
Compute initial community matrices at Markov times e_t
while 2 communities at least are left in current partition: length(e) > 1 do
    Initialise best loop stability Q_loop ← −∞
    for all pair of communities with edges linking them: e_ij > 0 do
        for all times t in time window do
            Compute dQV(t) ← ΔQ_{S_t}
        end for
        Compute partition stability vector: QV_tmp ← QV + dQV
        Compute partition stability value by taking its minimum value: Q_tmp ← min(QV_tmp)
        if current stability is the best of the loop: Q_tmp > Q_loop then
            Q_loop ← Q_tmp
            QV_loop ← QV_tmp
            Keep in memory best pair of communities (i, j)
        end if
    end for
    Compute C_cur by merging the communities i and j
    Update all community matrices e and e_t by merging rows i and j and columns i and j
    Set current stability vector to best loop stability vector: QV ← QV_loop
    if best loop stability higher than best known stability: Q_loop > Q then
        Q ← Q_loop
        C ← C_cur
    end if
end while
return best found partition C and its stability Q
```


Lusseau et al's Dolphins Social Network. This network is an undirected social network resulting from observations of a community of 62 bottle-nose dolphins over a period of 7 years (Lusseau et al., 2003). Nodes represent dolphins and edges represent frequent associations between dolphin pairs occurring more often than expected by chance. Analysis of the data revealed 2 main groups and a further division can be made into 4 groups (Lusseau and Newman, 2004).

American College Football Dataset. This dataset contains the network of American football games (Girvan and Newman, 2002). The 115 nodes represent teams and the edges represent games between 2 teams. The teams are divided into 12 groups containing around 8-12 teams each and games are more frequent between members of the same group. Also teams that are geographically close but belong to different groups are more likely to play one another than teams separated by a large distance. Therefore in this dataset the groups can be considered as known communities.

Les Misérables. This dataset taken from (Knuth, 1993) represents the co-appearance of 77 characters in Victor Hugo's novel *Les Misérables*. Two nodes share an edge if the corresponding characters appear in a same chapter of the book. The values on the edges are the number of such co-appearances.

4.2 Results

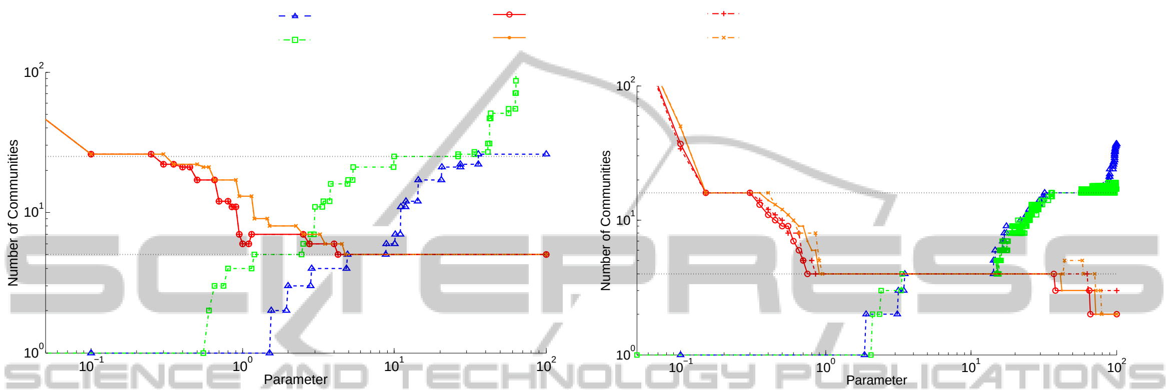
The networks are analysed by the 5 aforementioned community detection methods and our stability optimisation algorithm for which both discrete and continuous Markov time versions are used. Also two time window setups are considered to investigate the approximation from equation (12): one that considers a time window $[0,\tau]$ and another that considers only τ.

Table 1 provides the results of the community detection methods that have no resolution parameter. The results show that these methods do not necessarily find the most meaningful partitions and that different methods can identify different partitions. Yet this does not imply that an unexpected result is meaningless. For example in Ravasz et al's network, the central node of the central community has many more connections than the other nodes and more connections outside its community than inside. Therefore this node can be seen as a community on its own.

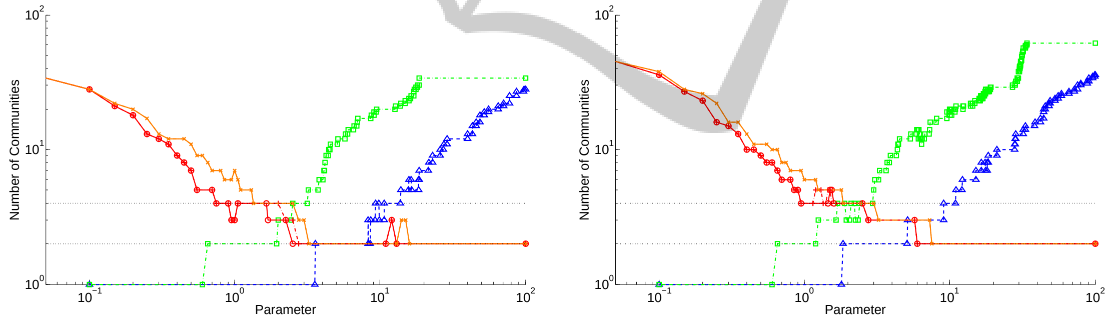
Figure 2 plots the results of the tuneable meth-

Table 1: Number of detected communities by fast Newman, Louvain and Danon et al's methods on the presented networks. The identified division(s) known for these networks are also indicated ('-' indicates that there is no clear a priori knowledge). The Louvain method returns a hierarchy of partitions, given in order.

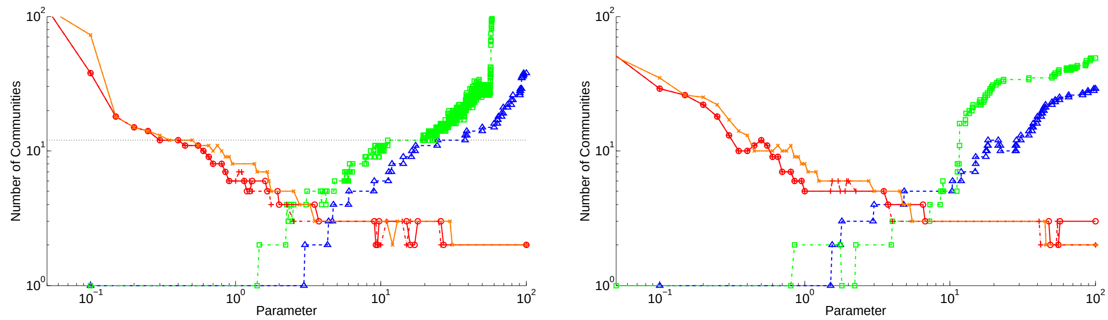
Algorithm	Ravasz	H13-4	Karate	Dolphins	Football	Miserables
Fast Newman	6	4	3	4	6	5
Danon	6	4	4	4	6	6
Louvain	30, 10, 6	12, 4	6, 4	10, 5	12, 10	9, 6
Identified	5, 25	4, 16	2, 4	2, 4	12	-



(a) Ravasz et al's network. (b) Hierarchical 13-4 network.



(c) Karate club network. (d) Dolphins social network.



(e) American football network. (f) Les Misérables characters network.

Figure 2: Number of partitions returned by Reichardt et al's, Arenas et al's and our stability optimisation methods. The x-axis represents 10γ for Reichardt et al's method, $r - r_0$ for Arenas et al's and t for ours. The setup using a time window is noted $[0,t]$ while the setup using only one time value is noted t. The time discrete Markov model (Markov chain) is noted (Dis) and the time continuous Markov model is noted (Con). The dotted horizontal lines indicate known partitions size: (a) 5 and 25, (b) 4 and 16, (c) 2 and 4, (d) 2 and 4, (e) 12.

ods along their respective parameter values. For Reichardt et al's algorithm, the x-axis represents 10γ. For Arenas et al's the x-axis represents $r - r_0$ where $r_0 = -\frac{m}{n}$ with m the number of edges and n the number of nodes. (See (Arenas et al., 2008) for details. The authors use the lower bound $r_{asymp} = -\frac{2m}{n}$ but here we found that values of r below r_0 were irrelevant.) The value of r_0 is calculated for each network. For our algorithm, the x-axis represents the Markov time t. For the time window setup the sampling is done from time 0 to 100 with a step of 0.05 between within $[0,2]$, a step of 0.25 within $[2,10]$ and a step of 1 afterwards. The steps between successive values of the parameter are 0.05 for Arenas and $\frac{0.05}{10} = 0.005$ for Reichardt et al's (as the x-axis represents 10γ).

Considering only stability optimisation we can observe that the two Markov processes behave in a very similar way. We can also observe that the difference between the runs considering the time window and those considering only its upper bound is minimal. The curves are similar or overlapping thus suggesting that the approximation from equation (12) holds.

From Figure 2 it can be observed that the behaviour of our method is opposite to those of the two other tuneable methods. At low values of t partitions are small (at $t = 0$ our method finds as many partitions as there are nodes). Then as t increases, partitions tend to become larger. Conversely, the two other methods start by partitioning in large clusters when their parameter is minimal. Then they find finer partitions as their parameter increases. As the discrete and continuous time versions of our algorithm have a very similar behaviour, and as the time optimised setups almost overlap with the full time interval setups, we will only comment on the discrete time version.

Considering Figure 2(a) for instance, after $t = 4$, the result of our algorithm remains stable on 5 clusters that represent the most *stable* partition. A partition in 6 elements can also be found and corresponds to the 5 large communities with the centre of the central community in a separate community. Also, when $t \in [0.1, 0.2]$ the algorithm finds a partition in 26 communities (25 small communities plus central node on its own). Arenas et al's method detects the 5 communities around about $r - r_0 \in [1.5, 2.5]$. Then it grows to stabilise on 25 communities around $r - r_0 \in [9, 25]$ and then goes up to 26 communities and more. Reichardt et al's stabilises around 5 communities around $\gamma = [0.5, 0.9]$ and around 26 communities around $\gamma = 3.6$ and onwards. Looking at the stability optimisation and Reichardt et al's method compared to Arenas et al's method, the two former tend to stabilise at intermediate partitions of a size 1 larger than those detected by the latter. By using the resistance parameter r, Arenas et al's method alters the impact of edge weights across the network. In this instance this blends the central node into the small central community. However when considering the partition in 25 communities, this central node has 4 connections with all communities, including its own. By adding it to any community, this community would gain 4 edges pointing inside and 80 pointing outside. Therefore it is ambiguous whether this node should belong to the small central community or any of the others. This is handled in our method by keeping this node in a separate community until it is clear that it belongs to the central community of the 5 communities partition (it then shares 20 edges inside its own community and 16 edges with each of the 4 others).

On Figure 2(b), the intended partitions in 16 and then 4 communities are clearly detected. As expected the most stable partition is the partition in 4 communities, as indicated by the stability optimisation methods with the long stretch of time settling on this partition compared to the shorter plateau for 16 communities.

Considering Figure 2(c), our algorithm quickly settles on the 2 expected partitions, found by Arenas et al's for about $r - r_0 \in [0.7, 2]$ and by Reichardt et al's for about $\gamma \in [0.4, 0.8]$. It also consistently settles beforehand on the partition in 4 communities, revealing the relevance of this partition, as suggested by other analysis (Medus et al., 2005).

Regarding Figure 2(d), our algorithm settles on 2 partitions, as expected from the results (Lusseau and Newman, 2004) that analysed the dataset using modularity. Arenas et al's solution for $r - r_0 \in [0.7, 1.2]$ and Reichardt et al's solution for $\gamma \in [0.2, 0.5]$ corresponds to the partition of (Lusseau and Newman, 2004). Our algorithm also stops over on 4 partitions for $t \in [0.5, 3[\setminus 1.5$ which is another relevant division size of the network (Lusseau and Newman, 2004).

On Figure 2(e) we can observe several scales of relevance. Based on the knowledge of the teams distribution, a community of size 12 is expected. Such partition is detected at an early time ($t = 0.3$) with our method and is the first plateau. A normalised mutual information value of 0.919 compared with the 12 known groups can be found by our method on this plateau. Most of the nodes are therefore placed into the right communities. Regarding the remaining nodes, (Khadivi et al., 2011) explains that some nodes do not fit in the expected classification. Therefore other divisions can also be of relevance. While stability settles on a few plateaus the two other methods tend to detect shortly many intermediate partitions. As the time grows communities also grow bigger and get more stable. A partition into 3 communities is consistently identified followed by a partition with 2 communities. Analysing the former we find that it reflects the geographical locations of the teams, reflecting the fact that teams located geographically closer are more likely to play one another. This partition separates the country roughly into West, South-east and North-east. Then the partition with 2 communities divides the country into West and East. Therefore the successive stable partitions reflect the organisation of the teams, first locally with the 12 communities partition and then nationally with the partitions in 3 and 2 communities (other partitions in between may also reflect smaller geographical divisions). Another analysis could consider the large and stable communities (e.g. of size 2 or 3) and sub-partition them to analyse the games distribution at a smaller geographical scale.

Analysing the network of the characters from *Les Misérables* several divisions appear. Considering stability optimisation 2 main partitions appear, as shown on Figure 2(f), while the other methods detect more partitions on short intervals. The first one consistently identified by our method contains 5 communities and the second one contains 3 communities. In the partition into 5 communities the first is a central community containing most of the main plot characters such as Valjean, Javert, Cosette, Marius or the Thenardier. The second community relates to the story of Fantine, the third one relates to Mgr Myriel, the fourth one relates to Valjean's story as a prisoner and contains other convicts. The fifth one relates to Gavroche, another main character. Considering the partition in 3 communities, the central community is merged with the fourth community (convicts, judge, etc) and the third community. The community mainly represents characters connected to Valjean at a moment of his story. The second community remains as well as the fifth one with Marius now part of it.

These results highlight the fact that different methods provide different approaches and solutions to the problem of community partitions. Consistent or *stable* partitions are used to identify relevant divisions in a network. Considering the three tuneable methods the results show that stability optimisation tends to stabilise on fewer partitions and often more consistently than the other two methods. This is useful to identify most relevant partitions and hence inform about networks structure in the absence of a priori knowledge. To better detect stable partitions the normalised mutual information (NMI) (Fred and Jain, 2003) between successive partitions (e.g. found at times t and $t+dt$) was also sometimes used. A persistent high NMI value confirms that successive partitions of same size are indeed the same or similar, thus ruling out the possibility of having different partitions that happen to have the same number of communities.

5 CONCLUSIONS

This work investigated stability as an optimisation criterion for a greedy approach similar to the one used in (Newman, 2004; Danon et al., 2006; Reichardt and Bornholdt, 2006; Arenas et al., 2008). The results showed that our method enables accurate multi-scale analysis and tackles the problem differently than other methods by finding *stable* partitions over a Markov time which is part of the definition of stability. The method was tested against various networks and compared to five relevant community detection algorithms. Stability optimisation can be seen as an extension of modularity optimisation that does not alter the graph (like Arenas et al's) or the importance of the null factor (like Reichardt et al's) but instead exploits the graph by interpreting it as a Markov process. By analysing it over different time scales it explores the graph thoroughly by considering paths of various lengths between nodes where each considered Markov time defines a path length. This analysis can be performed without complexity increase compared to modularity optimisation methods such as fast Newman's algorithm. Two Markov processes have been tested for our method, one based on a Markov chain model of a network and the other one extending this model to a continuous time Markov process. Experiments showed that both models behave similarly considering the cases studied in this work. They also showed that stability can be optimised with almost no loss of accuracy by only using the upper bound of a Markov time interval, as opposed to the whole interval suggested by the mathematical definition of stability. This heuristic provides a significant gain in speed.

The results showed that multiple levels of organisations are clearly identified when optimising stability over time. Stability optimisation tends to settle for longer on fewer partitions than other related approaches considered here, thus highlighting better partitions of relevance. Stability optimisation also converges towards large and *stable* clusters. This behaviour also differs from those of other approaches and in the absence of a priori knowledge our method has therefore the advantage of leading to stable and relevant communities from where a deeper analysis could be performed in each community subgraph.

The complexity of our method with the time-optimised heuristic is in $O(n(m+ln^2(n)))$ which compares to similar approaches using modularity and scaling to large networks. Therefore our method should scale up very well to large networks.

Further work will consider a randomised algorithm similarly to the randomised modularity optimisation algorithm presented in (Ovelgönne et al., 2010) that would reduce the complexity to $O(n \cdot ln^2(n))$. Another possible optimisation is a multi-step approach as presented in (Schuetz and Caflisch, 2008) for modularity optimisation. This work can also be applied to detecting overlapping communities by using the line graph of the initial graph as in (Pereira-Leal et al., 2004), thus working on link communities (Ahn et al., 2010). Further work could also consider a self-tuneable algorithm that returns the most stable partition(s). Another algorithm could then provide a stable hierarchy by repeatedly subdividing the stable partitions found at each hierarchical level.

REFERENCES

Ahn, Y.-Y., Bagrow, J. P., and Lehmann, S. (2010). Link communities reveal multiscale complexity in networks. *Nature*, 466:761–764.

Arenas, A., Díaz-Guilera, A., and Pérez-Vicente, C. J. (2006). Synchronization reveals topological scales in complex networks. *Physical Review Letters*.

Arenas, A., Fernandez, A., and Gomez, S. (2008). Analysis of the structure of complex networks at different resolution levels. *New Journal of Physics*, 10:053039.

Blondel, V. D., Guillaume, J.-L., Lambiotte, R., and Lefebvre, E. (2008). Fast unfolding of communities in large networks. *Journal of Statistical Mechanics: Theory and Experiment*, 10:1742–5468.

Clauset, A., Newman, M. E. J., and Moore, C. (2004). Finding community structure in very large networks. *Physical Review E*, 70:066111.

Danon, L., Díaz-Guilera, A., and Arenas, A. (2006). The effect of size heterogeneity on community identification in complex networks. *Journal of Statistical Mechanics: Theory and Experiment*, 2006(11):P11010.

Delvenne, J.-C., Yaliraki, S. N., and Barahona, M. (2010). Stability of graph communities across time scales. *PNAS*, 107(29):12755–12760.

Fortunato, S. (2010). Community detection in graphs. *Physics Reports*, 486(3-5):75–174.

Fortunato, S. and Barthélemy, M. (2007). Resolution limit in community detection. *PNAS*, 104(1):36–41.

Fred, A. L. N. and Jain, A. K. (2003). Robust data clustering. *IEEE Computer Society Conference on Computer Vision and Pattern Recognition*, 2:128–133.

Girvan, M. and Newman, M. E. J. (2002). Community structure in social and biological networks. *PNAS*, 99:7821–7826.

Good, B. H., de Montjoye, Y.-A., and Clauset, A. (2010). Performance of modularity maximization in practical contexts. *Physical Review E*, 81(4):046106.

Guimerà, R., Sales-Pardo, M., and Amaral, L. A. N. (2004). Modularity from fluctuations in random graphs and complex networks. *Physical Review E*, 70(2):025101.

Khadivi, A., Ajdari Rad, A., and Hasler, M. (2011). Network community-detection enhancement by proper weighting. *Physical Review E*, 83(4):046104.

Knuth, D. E. (1993). *The Stanford GraphBase. A Platform for Combinatorial Computing*. Addison-Wesley.

Lambiotte, R. (2010). Multi-scale Modularity in Complex Networks. *ArXiv e-prints*.

Lambiotte, R., Delvenne, J.-C., and Barahona, M. (2008). Laplacian Dynamics and Multiscale Modular Structure in Networks. *ArXiv e-prints*.

Lancichinetti, A. and Fortunato, S. (2009). Community detection algorithms: A comparative analysis. *Physical Review E*, 80(5):056117.

Lusseau, D. and Newman, M. E. J. (2004). Identifying the role that individual animals play in their social network. *Proceedings of the Royal Society London B*, 271:S477–S481.

Lusseau, D., Schneider, K., Boisseau, O. J., Haase, P., Slooten, E., and Dawson, S. M. (2003). The bottlenose dolphin community of doubtful sound features a large proportion of long-lasting associations. can geographic isolation explain this unique trait? *Behavioral Ecology and Sociobiology*, 54(4):396–405.

Medus, A., Acuna, G., and Dorso, C. (2005). Detection of community structures in networks via global optimization. *Physica A: Statistical Mechanics and its Applications*, 358(2-4):593–604.

Newman, M. E. J. (2004). Fast algorithm for detecting community structure in networks. *Physical Review E*, 69(6):066133.

Newman, M. E. J. (2006). Finding community structure in networks using the eigenvectors of matrices. *Physical Review E*, 74:036104.

Newman, M. E. J. and Girvan, M. (2004). Finding and evaluating community structure in networks. *Phisical Review E*, 69:026113.

Ovelgönne, M., Geyer-Schulz, A., and Stein, M. (2010). Randomized greedy modularity optimization for group detection in huge social networks. In *Proceedings of the 4th SNA-KDD Workshop '10 (SNA-KDD'10)*, pages 1–9, Washington, DC, USA.

Palla, G., Derenyi, I., Farkas, I., and Vicsek, T. (2005). Uncovering the overlapping community structure of complex networks in nature and society. *Nature*, 435(7043):814–818.

Pereira-Leal, J. B., Enright, A. J., and Ouzounis, C. A. (2004). Detection of functional modules from protein interaction networks. *Proteins*, 54:49–57.

Ravasz, E. and Barabási, A. L. (2003). Hierarchical organization in complex networks. *Physical Review E*, 67(2):026112.

Reichardt, J. and Bornholdt, S. (2006). Statistical mechanics of community detection. *Phys Rev E*, 74(1 Pt 2):016110.

Schuetz, P. and Caflisch, A. (2008). Efficient modularity optimization by multistep greedy algorithm and vertex mover refinement. *Physical Review E*, 77(4):046112.

Simon, H. A. (1962). The architecture of complexity. In *Proceedings of the American Philosophical Society*, pages 467–482.

Zachary, W. W. (1977). An information flow model for conflict and fission in small groups. *Journal of Anthropological Research*, 33(4):452–473.