A new method for community identification is proposed which is founded on the analysis of successive neighborhoods, reached through hierarchical growth from a starting vertex, and on the definition of communities as a subgraph whose number of inner connections is larger than outer connections. In order to determine the precision and speed of the method, it is compared with one of the most popular community identification approaches, namely Girvan and Newman’s algorithm. Although the hierarchical growth method is not as precise as Girvan and Newman’s method, it is potentially faster than most community finding algorithms.

I. INTRODUCTION

Lying at the intersection between graph theory and statistical mechanics, complex networks exhibit great generality, which has allowed applications to many areas such as modeling of biological systems, social interactions, and information networks, to cite just a few. An important problem which has been subject of great interest recently concerns the identification of modules of densely connected vertices in networks, the so-called communities. These structures result from interactions between the network components, defining structural connecting patterns in social networks, metabolic networks, as well as the worldwide air transportation network.

Despite the intense efforts dedicated to community finding, no consensus has been reached on how to define communities. Radichi et al. suggested the two following definitions. In a strong sense, a subgraph is a community if all of its vertices are more intensely connected one another than with the rest of the network. In a weak sense, a subgraph corresponds to a community whenever the number of edges inside the subgraph is larger than the number of connections established with the remainder of the network.

Along the last few years, many methods have been proposed for community identification based on a variety of distinct approaches such as: (i) link removal, as used by Girvan and Newman and Radicchi et al.; (ii) spectral graph partitioning; (iii) agglomerative methods, including hierarchical clustering; (iv) maximization of the modularity, as in Newman and Duch and Arenas; and (v) consideration of successive neighborhoods through hierarchical growth emanating from hubs. A good survey of community identification methods has been provided by Newman and Danon et al. This subject has also been partially addressed in the surveys by Costa et al. and Boccaletti et al.

Arguably, the most popular method for community identification is that proposed by Girvan and Newman. This approach considers that the edges interconnecting communities correspond to bottlenecks between the communities, so that the removal of such edges tend to partition the network into communities. The bottleneck edges are identified in terms of a measurement called edge betweenness, which is given by the number of shortest paths between pairs of vertices that run along the edge. This algorithm has been proven to be effective for obtaining communities in several types of networks. However, its effectiveness implies a computational cost of order $O(n^2m)$ in a network with $m$ edges and $n$ vertices.

An alternative algorithm to calculate betweenness centrality, based on random walks, has been proposed which, although conceptually interesting, is also computationally demanding.

The method described in the present article overcomes runs faster than the Girvan-Newman’s algorithm while offering reasonable, though smaller, precision for identification of communities. It is based on the consideration of successive neighborhoods of a set of seeds, implemented through hierarchical growth. Starting from a vertex (seed), the links of its successive neighborhood are analyzed in order to verify if they belong to the same community than the seed. This process starts from each vertex in the network and, at each step, inter-community edges are removed splitting the network into communities.

A related approach was previously proposed by Costa, who developed a method based on the flooding the network with wavefronts of labels emanating simultaneously from hubs. The expanding region of each label was implemented in terms of hierarchical growth from the starting hubs and the communities are found when the wavefronts of labels touch each one. Competitions along the propagating neighborhoods are decided by considering an additional criterion involving the moda of the labels at the border of the neighborhood and the number of emanating connections. The possibility to detect communities by using expanding neighborhoods has also been addressed by Bagrow and Bollt.
who proposed an algorithm based on the growth of an \textit{l-shell} starting from a vertex $v_0$, with the process stopping whenever the rate of expansion is found to fall below an arbitrary threshold. The \textit{l-shell} is composed by a set of vertices placed at distance $l$ from the vertex $v_0$, which is analogous to the concept of \textit{ring} defined by Costa \cite{27, 28} in order to introduce hierarchical measurements. At each expansion, the total emerging degree of a shell of depth $l$ is calculated as corresponding to the sum of the emerging degree of each vertex at distance $l$ from $v_0$, i.e. the degree of $i$ minus the number of links that connect $i$ with vertices inside the shell (analogous to the concept of hierarchical degree introduced by Costa \cite{27, 28}). When the rate between the total emerging degree at distance $l$ and $l-1$ is shorter than a given threshold, the set of vertices inside the \textit{l-shell} is classified as a community. Despite its simplicity, the determination of the local community is accurate just when the vertex $v_0$ is equidistant from all parts of its enclosing community \cite{24}. In order to overcome this limitation, Bragrow and Bollt suggested starting from each vertex and then find a consensus partitioning of the network using a membership matrix. Such an approach makes the algorithm more precise. On the other hand, it is slow because it requires sorting the membership matrix, which is of order $O(n^3)$.

The method reported in the present article also involves the consideration of expanding neighborhoods and completion of growth in terms of rate of expansion. However, it differs from the method of Bagrow and Boltt because it analyzes the connections of each vertex at the border of the community individually instead of all vertices at same time. Besides, it considers not only the first neighborhood of the community, but the second one too. At each expansion from an starting vertices, edges can be removed considering two trials based on the first and second neighborhood of the enclosing community. Another difference is that our method uses a threshold just at the second neighborhood, whose value is determined so as to obtain the best value of the modularity, i.e. the value of this threshold varies from 0 to a maximum value and at each variation it is computed the modularity. The procedure is to that used by Girvan-Newman, as the modularity is calculated at each edge removal.

The next sections describe the suggested method as well as its application to community detection in real and in computer generated networks. A comparison with the Girvan-Newman method in terms of precision and execution time is also presented and discussed.

\section{Hierarchical Growth Method}

A community is formed by a set of densely connected vertices which is sparsely connected with the remainder of the network. The proposed hierarchical growth method finds communities by considering two expanding neighborhoods. The first neighborhood of a given vertex is composed by those vertices at a distance of one edge from that vertex. Similarly, the set of vertices at distance of two edges from that given vertex constitutes its second neighborhood. Following this definition, two steps are performed in order to determine if a given vertex $i$ located in the first neighborhood of a known community belongs to this community, i.e.

\begin{enumerate}
  \item \[ \frac{k_{in}(i)}{k_{out}(i)} \geq 1, \] \hfill (1)
  \begin{itemize}
    \item where $k_{in}(i)$ is the number of links of the vertex $i$ with vertices belonging to community and with vertices in the first neighborhood, and $k_{out}(i)$ is the number of links between the vertex $i$ and vertices in the remainder of the network.
  \end{itemize}
  \item \[ \frac{k_{in2}(i)}{k_{out2}(i)} > \alpha, \] \hfill (2)
  \begin{itemize}
    \item where $k_{in2}(i)$ is the number of links of the neighbors of $i$ located in the second community neighborhood with vertices belonging to the first neighborhood, and $k_{out2}(i)$ is the number of links between the neighbors of $i$ and vertices in the remainder of the network. The parameter $\alpha$ varies from 1 to a threshold value which is determined according to the higher value of the modularity.
  \end{itemize}
\end{enumerate}

The first condition is sufficient to determine if a vertex belongs to the community, but it is not necessary. The coefficient $\alpha$ acts as a threshold ranging from one to a maximum value. The extension of the current method for weighted network is straightforward.

The hierarchical growth starts from each vertex of the network at each step, with the vertices with highest clustering coefficient \cite{8} selected first because they are more likely to be inside communities. So, the first and/or the second conditions are analyzed at each step, while the ring between the starting vertex grows, adding vertices to the community or removing edges. Nodes satisfying the first and/or the second conditions (equations 1 and 2) are added to the community. Otherwise, their links with the known community are removed. Figure 1 illustrates a simple application example of the method. In order to determine the best division of the network the threshold $\alpha$ is varied from 0 to a maximum value and at each variation, the modularity $Q$ is computed. The modularity is a measure of the quality of a particular division of networks \cite{24}. If a particular network is to be split in $c$ communities, $Q$ is computed defining a symmetric $c \times c$ matrix $E$ whose elements of diagonal, $e_{ii}$, give the connections between vertices in the same community and the remainder elements, $e_{ij}$, give the number of connections between the communities $i$ and $j$.

\[ Q = \sum_i [e_{ii} - (\sum_j e_{ij})^2] = Tr(E) - ||E^2||, \] \hfill (3)
In this section we illustrate applications of the hierarchical growth to particular problems while analyzing its accuracy and the performance. In the first case, its accuracy is determined by comparing the obtained results with expected divisions of different networks. With the purpose of determining the performance, we compared the hierarchical growth method with Girvan-Newman’s algorithm, whose implementation is based on the algorithm developed by Brandes [29] for computing of vertex betweenness centrality.

In order to split the network into communities the Girvan-Newman algorithm proceeds as follows:

1. Calculate the betweenness score for each of the edges.
2. Remove the edge with the highest score.
3. Compute the modularity for the network.
4. Go back to step 1 until all edges of the networks are removed, resulting in N non-connected nodes.

The best division is achieved when the highest modularity value is obtained. In this way, the Girvan-Newman method runs in two steps: (i) first all edges are removed from the network and the modularity value is computed at each removal, (ii) next, the highest value of modularity is determined and the corresponding edges removed.

### A. Computer generated networks

A typical procedure to quantify how well a community identification method performs adopts networks with known community structure, called computer generated networks, which are constructed by using two different probabilities [20]. Initially, a set of $n$ vertices are classified into $c$ communities. At each subsequent step, two vertices are selected and linked with probability $p_{in}$ if they are in the same community, or $p_{out}$ if not. The values of $p_{in}$ and $p_{out}$ can be selected so as to control the sharpness of the separation between the communities. When $p_{in} \ll p_{out}$, the communities can easily be visualized. On the other hand, when $p_{in} \rightarrow p_{out}$, it is difficult to distinguish the communities and the methods used for community identification lose precision in the correct classification of the vertices into communities.

We generated networks with 128 vertices, divided into four communities of 32 vertices each. The total average vertex degree $k_{in} + k_{out}$ of the network was kept constant and equal to 16. In this way, as the value of $k_{out}$ is varied from 0 to 8, the more difficult the network communities recognition becomes. The proposed community finding algorithm was applied to each network configuration, and the fraction of vertices classified correctly was calculated. In Figure 4 it is shown the sensitivity of the hierarchical growth method.

![Figure 1: Application example of the hierarchical growth. The process is started at vertex 0. Its neighborhood, indicated by black vertices, are analyzed next, and the vertices 1, 2, 4 and 5 are added to community following the first condition (equation 1). The vertex 3 is added to community following the second condition (equation 2 with $\alpha = 1$). The current community neighborhood (gray vertices) is then checked, and the vertices 6, 7 and 8 are added because of the first condition. Next, the links between the community and the vertices 9 and 10 are removed, splitting the network into two communities.](image)

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Algorithm 1: The general algorithm for the hierarchical growth method.

```plaintext
for each vertex of the network do
    put the next vertex with highest clustering coefficient value in C
while C does not stop growing do
    put the neighbors of C in R
    for each vertex $i$ in R do
        compute $k_{in}(i)$ and $k_{out}(i)$
        if $k_{in}(i) \geq k_{out}(i)$ then
            insert the vertex $i$ in C
        else
            select the neighbors of $R$ and put in R1
            compute $k_{in}(i)$ and $k_{out}(i)$
            if $k_{in}(i) > \alpha k_{out}(i)$ then
                insert the vertex $i$ in C
            else
                remove the links between the vertex $i$ and the vertices in C
        end if
    end if
end for
Clean C, R and R1
```

where $Tr(E)$ is the trace of matrix $E$ and $\|E\|$ indicates the sum of the elements of the matrix $E$.

Thus, the splitting of the network considers the value of $\alpha$ that provides the highest value of the modularity. The pseudocode which describes the hierarchical growth method is given in Algorithm 1.
growth method compared with the results obtained by using Girvan-Newman’s method.

As Figure 2 shows, the algorithm performs near full accuracy when $k_{out} \leq 5$, classifying more than 90% of vertices correctly. For higher values, this fraction falls off as the connections between communities gets denser. When $k_{out} > 5$, the Girvan-Newman’s method gives a better result, so it tends to be more suitable for this kind of networks.

The execution times of both methods were compared considering the computer generated cases for which the hierarchical growth method provides exact results (i.e. we used $k_{out} = 2, 3$ and $4$). We considered the network size varying from $N = 128$ until $N = 1,024$ and kept the average degree $k_{in} + k_{out} = 16$. The hierarchical growth method resulted faster than the Girvan-Newman’s method, as shown in Figure 3. While the time of processing of the Girvan-Newman’s method scales as $N^{3.0\pm0.1}$, the time of hierarchical growth method scales as $N^{1.6\pm0.1}$. Each data point is an average over 10 graphs.

### B. Zachary karate club network

In order to apply the hierarchical growth method to a real network, we used the popular Zachary karate club network [30], which is considered as a simple benchmark for community finding methodologies [22, 23, 25]. This network was constructed with the data collected observing 34 members of a karate club over a period of 2 years and considering friendship between members. The two obtained communities are shown in Figure 4. This partitioning of the network corresponds almost perfectly to the actual division of the club members, while only one vertex, i.e. vertex 3, has been misclassified. This result is analogous to that obtained by using the Girvan-Newman algorithm based on measuring of betweenness centrality [18].

### C. Image segmentation

A third application of our method is related to the important problem of image segmentation, i.e. the partition of image elements (i.e pixels) into meaningful areas corresponding to existing objects. As described by Costa [31], an image can be modeled as a network and methods applied to networks characterization can be used to identify image properties. The application of a community finding algorithm to image segmentation was proposed in that same work [23]. Since digital images are normally represented in terms of matrices, where each element corresponds to a pixel, it is possible to associate each pixel to a node using network image representation. The edge weight between every pair of pixels can be determined by...
FIG. 4: The friendship Zachary karate club network divided into two communities, represented by circles and squares. The division obtained by the hierarchical growth is the same as the one provided by the Girvan-Newman’s method.

FIG. 5: The real image and its respective segmentation. The image is transformed into a network and a threshold $T = 0.25$ is used to eliminate weak links.

the Euclidean distance between feature vectors composed by visual properties (e.g. gray-level, color or texture) at or around each pixel. Thus, considering the distance between every feature vector of pair of pixels in the image, this approach results in a fully-connected network, where closer pixels are linked by edges with higher weights. To eliminate weak links, a threshold can be adopted over the weighted network, resulting in a simplified adjacency matrix. The connections whose distance is shorter than the threshold are assigned to zero, otherwise, to one.

The mapping between a pixel in the image to a node in the network and the reverse operation, is defined by

$$i = y + (x - 1)M,$$  
$$x = \lfloor (i - 1)/M \rfloor + 1,$$  
$$y = \text{mod}(i - 1, M) + 1,$$

where $M$ is the size of the square image, and $1 \leq x, y \leq M$ are the pixel positions in the image. In this way, the resulting weighted network has $N = M^2$ nodes and $n = N(N - 1)/2$ edges.

Figure 4 shows the initial image and its respective segmentation. The results obtained by the hierarchical growth method and by using the Girvan-Newman’s method are similar. Since the network obtained typically for images can be substantially large ($N = M^2$), a faster method to community identification is necessary for practical applications, a demand potentially met by hierarchical growth method.

IV. CONCLUSIONS

In this paper we have proposed a new method to identify communities in networks. The method is based on a hierarchical growth from a starting node while its neighborhood is analyzed, and edges removed according to two rules based on the first and/or second neighborhoods of the growing community. We have applied this method to computer generated networks in order to determine its precision and performance comparing it with the popular method based on edge betweenness centrality proposed by Girvan and Newman [18]. Despite resulting not so precise as the Girvan-Newman’s method, the proposed algorithm is promisingly fast for determining communities. We have also applied the hierarchical growth method to the Zachary karate club network and image segmentation. In both cases, the resulting networks are similar to those obtained by the Girvan-Newman’s algorithm.

As discussed by Danon et al. [16], the most accurate methods tend to be computationally more expensive. The method presented in this article can not provide as good precision as most of the methods, but it yields competing velocity. As a matter of fact, performance and accuracy need to be considered when choosing a method for practical purposes. Particularly in the case of image segmentation, the suggested method is particularly suitable given the large size of the typical networks (increasing with the square of the image size, $N = M^2$) and the sharpened modular structure often found in images.

As a future work, the algorithm proposed here can be improved considering other conditions to include nodes in the growing community as, for example, higher levels of community neighborhood. Besides, consideration of local modularity can be also considered in order to obtain a more precise partition of the network.

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