Communities recognition in the Chesapeake Bay ecosystem by dynamical clustering algorithms based on different oscillators systems

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Abstract. We have recently introduced [1, 2] an efficient method for the detection and identification of modules in complex networks, based on the de-synchronization properties (dynamical clustering) of phase oscillators. In this paper we apply the dynamical clustering technique to the identification of communities of marine organisms living in the Chesapeake Bay food web. We show that our algorithm is able to perform a very reliable classification of the real communities existing in this ecosystem by using different kinds of dynamical oscillators. We compare also our results with those of other methods for the detection of community structures in complex networks.

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1 Introduction

Complexity theory and associated methodologies are transforming ecological research, providing new perspectives on old questions as well as raising many new ones. Patterns and processes resulting from interactions between individuals, populations, species and communities in landscapes are the core topic of ecology. These interactions form complex networks, which are the subject of intense research in complexity theory, informatics and statistical mechanics. This research has shown that complex natural networks often share common structures such as loops, trees and clusters, which contribute to widespread processes including feedback, non-linear dynamics, criticality and self-organization.

In ecosystems, and in particular in food webs, these structures have strong implications for their stability and dynamics. Actually, a food web constitutes a special description of a biological community with focus on trophic interactions between consumers and resources [3]. Food webs are deeply interrelated with ecosystem processes and functioning since the trophic interactions represent the transfer rates of energy and matter within the ecosystem. In particular it is known that trophic webs are not randomly assembled, but are the result of the interaction of different cohesive subgroups (modules or community structures). Therefore, identifying the tightly connected groups within these networks is an important tool for understanding the main energy flows of the networks itself, as well as for defining a hierarchy of nodes and connections within a complex structure.

For practical purposes, modules can be defined as subsets of network nodes within which the network connections (links) are dense, but between which they are sparse (see Fig.1). In the last years many efficient heuristic methods have been proposed to investigate the presence of these structures in complex networks, and their performances have been tested on both real and computer generated networks with a
known subdivision in different communities \[4, 5\]. We have recently presented a dynamical clustering (DC) algorithm for modules identification based on the de-synchronization properties of a given dynamical system associated to the network \[1, 2\]. It combines topological and dynamical information in order to recognize modular structures with a precision and a computational cost \(O(N^2)\) on a sparse graph competitive with the majority of the other techniques. In this paper we apply the DC algorithm to a well-known food web of marine organisms living in the Chesapeake Bay, situated on the Atlantic coast of the United States (see Fig. 2). We implement our algorithm by using several dynamical systems and we compare the results of the simulations among them and also with those obtained with other methods.

2 Dynamics of weighted networks of coupled oscillators

The DC algorithm is based upon the well-known phenomenon of synchronization of coupled phase oscillators \[6\], each one associated to a node of a given network, and interacting through the edges or links of the graph. In Ref.\[7\] it has been shown that an enhancement in the capability of synchronization can be achieved by using the information contained in the overall topology of the network. This can be realized in practice through a weighting procedure which associates a load to each link of the network. The load \(l_{ij}\) of the link connecting nodes \(i\) and \(j\) can be quantified by the so called edge betweenness, i.e. the fraction of shortest paths that are making use of that link. Within this assumption, the dynamics of a network of \(N\) coupled oscillators \(\{x_i\}_{i=1,...,N}\) is described by the following set of first order differential equations:

\[
\dot{x}_i = F(x_i) - \frac{\sigma}{\sum_{j \in K_i} l_{ij}^a} \sum_{j \in K_i} l_{ij}^a H[x_i - x_j],
\]

where \(F = F(x)\) governs the dynamics of each individual oscillator, \(H = H(x)\) is the coupling function, \(\sigma\) is the overall coupling strength and \(K_i\) is the set of neighbors of node \(i\). Notice that the loads \(l_{ij}\) have been raised to a power \(\alpha\), where \(\alpha\) is a real tunable parameter which regulates the dynamical clustering process.

In Ref.\[1\] we showed that, for a given dynamical system \(F(x_i)\) and for a given value of the coupling strength \(\sigma\), if the system starts in a perfectly synchronized state at \(\alpha = 0\) and \(\alpha\) is let to slowly decrease in time from 0 to \(-\infty\), the links with the higher load will be weighted less and less with respect to the other links, thus inducing a progressive desynchronization (dynamical clustering) of the system in a hierarchy of clusters of oscillators corresponding to different configurations of modules for the network considered. In order to select which one of these configurations is the best one as a function of \(\alpha(t)\), we decided to look to local or global maxima of the modularity \(Q\). The latter simply compares the fraction of edges within \(n_c\) arbitrary communities (intra-community links) of a given network with the expected fraction of such edges in a random network, which does not exhibits community structures \[8\]. Actually, it is possible to define a \(n_c \times n_c\) size matrix \(e\) where the elements \(e_{ij}\) represent the fraction of total links starting at a node in partition \(i\) and ending at a node in partition \(j\). Then, the sum of any row (or column) of \(e\), \(a_i = \sum_j e_{ij}\) corresponds to the fraction of links connected to \(i\). If the communities were allocated without any regard to the underlying structure, the expected number of intra-community links would be just \(a_i \times a_i\). On the other hand, we know that the fraction of links exclusively within a partition is \(e_{ii}\). So, we can compare the two directly and sum over all the partitions in the graph:

\[
Q = \sum_i (e_{ii} - a_i^2)
\]

Fig. 2. Geographic position of the Chesapeake Bay ecosystem, situated on the Atlantic coast of the United States.

Obviously it makes sense to look for high values of \(Q\). In fact, if we take the whole network as a single community, we get \(Q = 0\), while values approaching \(Q = 1\) indicate strong community structure; on the other hand, for a random network we get again \(Q = 0\). It is important to notice that the expression \(Q\) is not normalized, so that \(Q\) cannot reach in practice the value 1. For networks with an appreciable subdivision in classes, \(Q\) usually falls in the range from about 0.2 to 0.7.

In Refs.\[1, 2\] we applied the DC algorithm to several real and trial networks, using as dynamical systems the Opinion Changing Rate and the Rössler ones and adopting modularity \(Q\) to choose the best subdivision for a given network. In the next sections, by using those and other dynamical systems - like the Kuramoto’s one -, we will adopt again the modularity approach in order to explore the complex modular structure of the trophic relationships among organisms living in the Chesapeake Bay.
3.1 Dynamical clustering with a system of Rössler oscillators

The dynamics of a system of $N$ identical (three-dimensional) chaotic Rössler oscillators, defined over the nodes of a given network, is ruled by Eq. (1), with $\mathbf{x}_i = (x_i, y_i, z_i)$, $\mathbf{F}(\mathbf{x}_i) = [-\omega y_i - z_i, \omega x_i + 0.165y_i, 0.2 + z_i(x_i-10)]$, and $\mathbf{H}(\mathbf{x}) = [x, 0, 0]$ (thus the coupling acts only on the $x$ variable). In other words we have the following equations of motion [2]:

$$\dot{x}_i = -\omega y_i - z_i - \frac{\sigma}{\sum_{j \in K_i} l_{ij}} \sum_{j \in K_i} l_{ij}^1 (x_i - x_j)$$

$$\dot{y}_i = \omega x_i + 0.165y_i$$

$$\dot{z}_i = 0.2 + z_i(x_i-10) \quad i = 1, \ldots, N.$$
the edge betweennesses) is calculated once forever for the chosen network (in this case the CB food web). In order to evaluate the degree of synchronization of the Rössler system \( (3.1) \) one has to calculate the order parameter \( \Psi = \left\langle \frac{1}{N} \sum_{i=1}^{N} e^{j \Phi_i(t)} \right\rangle_t \), where \( \Phi_i(t) = \arctan \left( \frac{y_i(t)}{x_i(t)} \right) \) indicates the instantaneous phase of the \( i \)-th oscillator and \( \langle ... \rangle_t \) stays for a time average. If all the oscillators rotate independently, no clusters exist and we have \( \Psi \sim \frac{1}{\sqrt{N}} \). On the contrary, if their motions are synchronized in phase, only one cluster exists and we obtain \( \Psi \sim 1 \). Once a network is fixed, the first task is to find the value of the coupling parameter \( \sigma \) providing a fully synchronized starting state for the Rössler oscillators at \( \alpha = 0 \) (i.e. at \( t = 0 \)). Then, one can let \( \alpha \) to decrease in time and study the dynamical clustering process acting on the instantaneous phases \( \Phi_i(t) \)'s of the oscillators. We call "cluster" a group of contiguous phases in the \( \Phi \)'s interval (usually \([-3,3]\]) separated by a distance of more than 0.02 units. For each value of \( \alpha \) a different configuration of clusters (corresponding to a given network subdivision) will appear and one has to calculate the corresponding modularity and select the configuration with the best modularity score.

In Fig.4 we show the result of a typical event of the Rössler DC algorithm for a value of the interaction strength \( \sigma = 1 \) (such that the system would lie in its synchronized phase for \( \alpha = 0 \)). The clusters evolution (top panel) and the corresponding modularity \( Q(t) \) (bottom panel) are plotted as a function of \( \alpha(t) \) (note that, in the top panel, the average instantaneous phase of the system has been subtracted from the instantaneous phases of the oscillators in order to have a symmetric plot). The system starts in a fully synchronized state \( (x_i(0) = y_i(0) = z_i(0) = 0 \ \forall i) \) at \( \alpha_{\text{start}} = 0 \) and evolves through decreasing values of \( \alpha(t) \) (with a decrement \( \delta \alpha = 0.0008 \), up to the value \( \alpha_{\text{end}} = -2 \). Even if the system strongly oscillates during the desynchronization process, clusters' configurations (i.e. community structures of the underlying network) with large values of modularity appear. The detailed configuration with the highest modularity peak (see the arrow in the bottom panel) is reported in Table 1. It consists of 6 clusters with a \( Q_{\text{best}} = 0.43 \), obtained for \( \alpha_{\text{best}} = -1.62 \), and it is quite consistent with the distinction between pelagic organisms (clusters n.1,2 and 4) and benthic organisms (clusters n.3,5 and 6). Furthermore, if compared with the reference configuration, where \( Q_{\text{ref}} = 0.337 \), the configuration we found here seems evidently (having a higher modularity) to better reflect the underlying structure emerging from the global information stored in the edge betweennesses of the food web.

**3.2 Dynamical clustering with the Kuramoto model**

The Kuramoto model describes a population of \( N \) periodic oscillators having natural frequencies \( \omega_i \) and coupled through the sine of their phase differences \( \Omega_i \). It is simple enough to be analytically solvable, still retaining the basic principles to produce a rich variety of dynamical regimes and synchronization patterns \( 13, 14 \).
The dynamics of the model is given by

\[ \dot{\theta}_i(t) = \omega_i + \frac{K}{N} \sum_{j=1}^{N} \sin(\theta_j - \theta_i) \quad i = 1, \ldots, N \tag{4} \]

where \( \theta_i(t) \) is the phase (angle) of the \( i \)th oscillator at time \( t \), while \( \omega_i \) is its intrinsic frequency randomly drawn from a symmetric, unimodal distribution \( g(\omega) \) with a first moment \( \omega_0 \) (typically a Gaussian distribution or a uniform one). These natural frequencies \( \omega_i \) are constant and time-independent. The sum in the above equation is running over all the oscillators so that this is an example of a globally coupled system. The most interesting feature of the model is that, despite the difference in the natural frequencies of the oscillators, it exhibits a spontaneous transition from incoherence to collective synchronization beyond a certain threshold \( K_c \) of the coupling strength \( K \) \cite{13}. For small (positive) values of \( K \), each oscillator tends to run independently with its own frequency, while for large values of \( K \), the coupling tends to synchronize (in phase and frequency) the oscillator with all the others. In the Kuramoto model, it is possible to define a complex mean field order parameter as

\[ r e^{i\Psi} = \frac{1}{N} \sum_{j=1}^{N} e^{i\theta_j}, \tag{5} \]

where the magnitude \( 0 \leq r(t) \leq 1 \) is a measure of the coherence of the population and \( \Psi(t) \) is the average phase. In other words, as \( N \) approaches infinity, the magnitude \( r_\infty \) the average instantaneous phase of the system has been subtracted from the instantaneous phases of the oscillators in order to have a symmetric plot) of the complex mean field after a transient time should be zero in the incoherent state with \( K \leq K_c \) and different from zero in the coherent state with \( K > K_c \). Actually, as \( K \) increases beyond \( K_c \), more and more oscillators will be recruited toward the mean phase \( \Psi(t) \) and \( r_\infty \) is expected to continuously increase from zero to one.

In order to use Kuramoto model as dynamical system in the context of our dynamical clustering algorithm, we immediately note that, at variance with the Rössler system, Eqs.\( \ref{eq:rossler} \) are already very similar to Eqs.\( \ref{eq:rossler} \) providing that one considers \( x_i = \theta_i, \ F(x_i) = \omega_i, \sigma = K, \ l_{ij} = 1 \) and \( H(x) = \sin(\theta_j - \theta_i) \). In other words Kuramoto equations already have a coupling term, containing a nonlinear function that becomes approximatively linear in the synchronization manifold (where \( \theta_j \sim \theta_i \)). This makes Kuramoto model particularly suitable for our purpose. In fact in this case, after having chosen a given network and having associated an oscillator to each node, we can directly apply the weighting procedure of section 2 (see Eq.\( \ref{eq:weights} \) to Eqs.\( \ref{eq:rossler} \)) without adding further coupling terms, thus simply obtaining:

\[ \dot{\theta}_i(t) = \omega_i + \frac{K}{\sum_{j \in K_i} l_{ij}} \sum_{j \in K_i} l_{ij} \sin(\theta_j - \theta_i) \quad i = 1, \ldots, N \tag{6} \]

where as usual, \( l_{ij} \) is the load of the link connecting nodes \( i \) and \( j \) in the chosen network, \( K_i \) the set of neighbors of node \( i \)th and \( \alpha \) is a real tunable parameter.

As in the previous section, our task is now to test the sensitivity of the Kuramoto dynamical clustering algorithm on the CB food network. First of all, we have to fix the coupling parameter \( K \) of Eq.\( \ref{eq:rossler} \) in order to obtain a fully synchronized state of the system for \( \alpha \sim 0 \). We found that for \( K > 5 \) such a state is guaranteed, thus we will reasonably set \( K = 10 \). In our simulations of the Kuramoto system we will always use as initial conditions uniform distributions for both the \( \theta_i \)'s (in the interval \([−\pi, \pi]\)) and \( \omega_i \)'s (in the interval \([−2, 2]\)). We remind that the latter are constant in time. At variance with the Rössler case, we are now interested to the instantaneous frequencies \( \dot{\theta}_i(t) \) of the oscillators (which at \( t = 0 \) coincide with the natural frequencies \( \omega_i \)). Again, the average instantaneous frequency of the system will be subtracted from the instantaneous frequencies of the oscillators in order to have a symmetric plot.

In Fig.\( \ref{fig:kuramoto} \) we show a typical run of the Kuramoto DC algorithm for the CB food network. As before, the simulation starts from \( \alpha_{\text{start}} = 0 \) then \( \alpha \) decreases in time with a given step (\( \delta \alpha = 0.0008 \)): one sees that in a few steps the system suddenly synchronizes (due to the high value of \( K \)) then slowly relaxes producing a progressive desynchronization that is, again, very oscillating in time; for each value of \( \alpha(t) \) the instantaneous clusters’ configuration of frequencies is identified (being the definition of ‘cluster’ the same than in the previous section), and the correspondent modularity calculated. The detailed configuration with the highest modularity peak (see the arrow in the bottom panel) is reported in Table\( \ref{table:modularity} \). It consists of 6 clusters with a \( Q_{\text{best}} = 0.404 \), obtained for \( \alpha_{\text{best}} = -3.50 \); even if this value of modularity is less than in the Rössler case, on the other hand it is greater than \( Q_{\text{ref}} = 0.337 \) and in any case is again quite consistent with the distinction between pelagic organisms and the benthic ones.

### 3.3 Dynamical clustering with the Opinion Changing Rate model

As a last example of application of the dynamical clustering algorithm to the Chesapeake Bay food web, let us consider as dynamical system the so called Opinion Changing Rate (OCR) model \[14\]. It was originally introduced in Ref.\[15\] as a modification of the Kuramoto
model, in order to study how the personal inclination to change, randomly distributed in a group of individuals, can affect the opinion dynamics of the group itself. The dynamics of a system of $N$ fully coupled individuals (oscillators) is governed by the following set of differential equations:

$$\dot{x}_i(t) = \omega_i + \frac{\sigma}{N} \sum_j \beta \sin(x_j - x_i)e^{-\beta|x_j - x_i|} \quad i = 1, \ldots, N$$  

(7)

where $x_i(t)$ is the opinion of the $i$th agent at time $t$. Here the opinions have a very general meaning and can be usefully represented by means of unlimited real numbers $x_i \in (-\infty, +\infty), \quad \forall i = 1, \ldots, N$. Opinions interact by means of the coupling term, where $\sigma$ is the coupling strength and the exponential factor, tuned by the parameter $\beta$, ensures that opinions will not influence each other any longer when the reciprocal distance exceeds a certain threshold. This is perhaps the most remarkable feature of the OCR model, since it allows the system to reach an asymptotic stationary state where the configuration of opinions does not vary any longer. The parameter $\beta$ appears also as a factor of the sine in the coupling term and simply rescales the range of the coupling strength. We typically adopted the value $\beta=3$, which ensures a consistent behavior of the exponential decay. Finally, the $\omega_i$'s - corresponding to the natural frequencies of the oscillators in the Kuramoto model - represent here the so-called natural opinion changing rates, i.e. the intrinsic inclinations of the agents to change their opinions. For this reason we called this model the Opinion Changing Rate (OCR) model [15]. The values $\omega_i$'s, which do not depend on time, are uniformly distributed in the range $[-0.5, 0.5]$ and represent also the initial conditions for the instantaneous frequencies $\dot{x}_i(t)$'s.

Many numerical simulations were performed in Ref. [15] starting from a uniform distributions of the initial opinions $x_i(t = 0)$ in the range $[-1, 1]$. As a function of the coupling strength $\sigma$, a transition was observed from an incoherent phase ($\sigma < \sigma_c$), in which people tend to preserve different opinions and different frequencies according to their natural changing rates $\omega_i$, to a partially synchronized phase, where people share a small number of opinions, and, finally, to a fully synchronized one ($\sigma > \sigma_c$) in which all the people share the same opinion changing with the same rate. In order to measure the degree of synchronization of the system, it can be adopted an order parameter related to the standard deviation of the instantaneous frequencies and defined as $R(t) = 1 - \sqrt{\frac{1}{N} \sum_{j=1}^{N} (\dot{x}_j(t) - \bar{X}(t))^2}$, where $\bar{X}(t)$ is the average over all individuals of $\dot{x}_j(t)$. From such a definition it follows that $R = 1$ in the fully synchronized phase and $R < 1$ in the incoherent or partially synchronized phase.

3.3.1 Standard Opinion Changing Rate model

In order to utilize the OCR model as dynamical system for recovering community structures in the CB food network we put together Eq.4 and Eq.7, thus obtaining

$$\dot{x}_i(t) = \omega_i + \frac{\sigma}{\sum_{j \in K_i} l_{ij}^2} \sum_{j \in K_i} \beta l_{ij}^2 \sin(x_j - x_i)e^{-\beta|x_j - x_i|},$$  

(8)

where $i = 1, \ldots, N$, $\alpha$ is the usual real tunable parameter and $K_i$ is the set of neighbors of node $i$th. As in the case of Kuramoto model, we do not need any further coupling term in Eqs. 5 since such a term is already present in the OCR model. We will follow now the time evolution of the instantaneous frequencies $\dot{x}_i(t)$ starting, as usual, from a completely synchronized state at $\alpha \sim 0$: more precisely, as in the Kuramoto case, the initial frequency distribution is uniform inside the interval $[-0.5, 0.5]$ (since it coincides with the $\omega_i$'s distribution) but we chose $\sigma = 5.0$, a coupling that ensures a rapid synchronization for $t > 0$. Then we let $\alpha$ to decrease in time with a step $\delta\alpha = 0.01$. We are confident that, at variance with the previous examples, the exponential factor in the coupling term could trigger the aggregation of frequencies in stable clusters corresponding to community configurations of the network.

In Fig.4 we plot the OCR frequencies' time evolution for the Chesapeake Bay food web, together with the respective modularity. One can immediately appreciate the stability of the desynchronization process, which produces...
(due to the exponential factor in the coupling term) a branching sequence of metastable plateaux corresponding to different clusters configurations. The best one is obtained for $-5.9 > \omega_{\text{best}} > -8.3$ with a modularity $Q_{\text{best}} = 0.404$ and corresponds exactly to the same best configuration (six clusters) of the Kuramoto case, see Table 3. But the stability of the synchronized manifold makes useless, in this case, to adopt lower values of $\delta \alpha$, thus making also the simulation less expensive in terms of computational cost.

3.3.2 Opinion Changing Rate model with HK dynamics

In order to further improve the performances of the OCR system, in Ref. [1] we taught to modify the natural opinion changing rates $\omega_i$’s following a suggestion from the Hegselmann and Krause (HK) model of opinion formation. The HK model [16] is based on the concept of bounded confidence, i.e. on the presence of a parameter $\epsilon$, called confidence bound, which expresses the compatibility among the agents in the opinion space. If the opinions of two agents $i$ and $j$ differ by less than $\epsilon$, their positions are close enough to allow for a discussion, which eventually leads to a change in their opinions, otherwise the two agents do not interact with each other. In our case, the opinion space is one-dimensional, being usually $x_i(t) \in [-1, 1]$. Thus we fixed a small value for $\epsilon$ and we let the $\omega_i$’s to change in time (while in the standard OCR version the $\omega_i$’s are time independent) starting from a random uniform distribution in the interval $[-0.5, 0.5]$ and according to the following HK dynamics: at each time step a given agent, with an opinion $x_i$ and a natural frequency $\omega_i$, checks how many of its neighbors (according to the network topology) are compatible, i.e. lie inside the confidence range $[x_i-\epsilon, x_i+\epsilon]$ in the opinion space. Next, the $\omega_i(t)$ of the agent takes the average value of the $\omega$’s of its compatible neighbors at time $t-1$. We will refer to this new system as OCR – HK. In the OCR-HK system the secondary process acting on the $\omega$’s is superimposed to the main dynamical evolution of $\text{Eq}(5)$ and contributes to further stabilize the instantaneous frequencies $\dot{x}_i(t)$ of the agents (oscillators).

In Fig. 7 the new simulation with the OCR-HK system are shown for the Chesapeake Bay food web. This simulation was performed again with $\alpha = 5.0$ and a $\delta \alpha = 0.01$, with a confidence bound $\epsilon = 0.0005$. Again a branching desynchronization process with well defined metastable plateaux occurs. But in this case, as expected, the HK dynamics produces a highest value of modularity $Q_{\text{best}} = 0.42$ (very near to that obtained with the Rössler algorithm), which is reached for $-6.77 > \omega_{\text{best}} > -10.67$, yielding a subdivision of the food web into five communities, whose detailed structure is shown in Table 4. It clearly appears that, besides the greater value of $Q$, the distinction between pelagic and benthic organisms is improved with respect to the standard OCR case too. In any case, both the standard OCR and the OCR-HK algorithm give a best configuration whose modularity is higher than the reference one $Q_{\text{ref}} = 0.337$.

4 Discussion and Conclusions

Summarizing, the dynamical clustering (DC) algorithm, which exploits the synchronization properties of some dynamical system of oscillators associated with the nodes of a given complex network, seems to work very well in identifying the underlying community structure of the Chesapeake Bay food web of trophic relationships. In fact we shown that, whatever the dynamical system we use (Rössler, Kuramoto, OCR or OCR-HK), the DC algorithm discovers community configurations with high values of modularity, in all the cases higher than the reference configuration of Fig. 3 related to the main subdivision of the Chesapeake Bay network in Benthic and Pelagic organisms. This would imply also that, if we consider modularity optimization as a valid method to retrieve the best community structure compatible with the information stored in the topology of a given network, then we should conclude that the rigid subdivision in Benthic and Pelagic organisms is not the optimal one for the Chesapeake Bay food web. Actually, modularity method has been recently questioned by [17], which showed that it is $\alpha - \text{priori}$ impossible to tell whether a module, detected through modularity optimization, is indeed a single module or a cluster of smaller modules, but the problem is still open. In any case it is worthwhile to notice that the DC algorithm produces bet-

![Fig. 7. A typical run of the DC algorithm for the Chesapeake Bay food web: time-evolution of both the OCR-HK’s frequencies (top panel) and the corresponding modularity (bottom panel) as a function of $\alpha(t)$.](image)

| cluster | nodes |
|---------|-------|
| cluster 1 (2 nodes) | 31,32 |
| cluster 2 (11 nodes) | 3,14,15,16,18,19,25,26,27,28,29 |
| cluster 3 (2 nodes) | 4,17 |
| cluster 4 (14 nodes) | 1,2,7,8,9,10,11,12,13,20,21,22,23,24,30,33 |
| cluster 5 (2 nodes) | 5,6 |
ter results also if compared with other methods for detecting community structures using modularity optimization, which in the past were applied to the Chesapeake Bay (CB) food web. For example in Ref.[8], where Girvan and Newman presented their original iterative method, based in finding and removing progressively the edges with the largest betweenness until the network breaks up into its components, the best modularity value for the CB food web was $Q_{GN} = 0.380$; and in Ref.[11], where another method based on the Information Centrality, was proposed and applied to the CB food web, the best score for the modularity was $Q_{IC} = 0.376$.

In conclusion, the DC algorithm, in particular in the version using the OCR-HK system (which produces large modularity configurations with very stable synchronization patterns), seems to be a very efficient method for the study of community structures in ecosystems and food webs, even if in the approximation of non-directed networks. In this direction, a further improvement in the DC algorithm performance probably could come from the use of a recent generalization of the modularity approach which incorporate also the information contained in edge directions [18].

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