

Ecological Networks: From Structural Analysis to Synchronization

N. F. F. Ebecken, G. C. Pereira

Abstract—Ecological systems are exposed and are influenced by various natural and anthropogenic disturbances. They produce various effects and states seeking response symmetry to a state of global phase coherence or stability and balance of their food webs. This research project addresses the development of a computational methodology for modeling plankton food webs. The use of algorithms to establish connections, the generation of representative fuzzy multigraphs and application of technical analysis of complex networks provide a set of tools for defining, analyzing and evaluating community structure of coastal aquatic ecosystems, beyond the estimate of possible external impacts to the networks. Thus, this study aims to develop computational systems and data models to assess how these ecological networks are structurally and functionally organized, to analyze the types and degree of compartmentalization and synchronization between oscillatory and interconnected elements network and the influence of disturbances on the overall pattern of rhythmicity of the system.

Keywords—Ecological networks, plankton food webs, fuzzy multigraphs, dynamic of networks.

I. INTRODUCTION

THE biological world is complex. All living things interact not only with individuals of their own species, but also with hundreds or even thousands of different individuals of other species, forming complex ecological networks [1]. These networks represent the structure of the biological community [2] and exhibit extremely heterogeneous interactions, which are not simply random [3].

The topology of ecological networks (Fig. 1) depends on the nature of the interactions established between the species so that, asymmetries in their number and intensity are important and common in nature. Indeed, different types of mutual movement [4], [5], for example, have asymmetric distribution of key connections between species and general experts. These asymmetries are also found in antagonistic interactions such as herbivory [6], parasitism [7], and predation [8]. These relationships and interactions among species change over time so that the species mutually adapted to each other through co-evolution causing the community structure patterns change constantly due to periodic disturbances ranging from simple events, whose effects are localized, even those catastrophic consequences of creating an ecological succession scenario. While Communities of Ecology is concerned with identifying the richness patterns, abundance, species composition and the mechanisms that

create these patterns of communities in modern evolutionary theory, these mechanisms fall into four broad classes: Speciation, Dispersal, Drift and Niche. In reality there is an extensive feedback interaction between species and evolution [9]. If on one hand the development has the potential to modify interactions between species and community properties, for example, the displacement of characters can facilitate coexistence species, or the appearance (development) in a mutualistic community could drastically affect productivity. Furthermore, interactions of several species have the potential to limit or facilitate the developments of the relevant characteristics for the community's properties, such as interactions with competitors may influence the development of defense mechanisms.

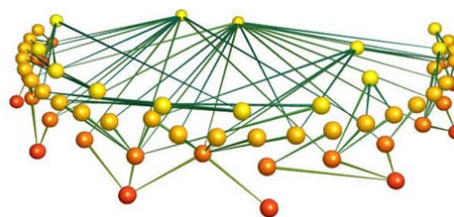


Fig. 1 Example of a topology graph of specie interactions

The investigation of the structure of ecological networks is a major modern ecology issues. Understanding how communities are assembled and evolve will give a deep insight into the organization of natural ecosystems. A major focus of this theory is to understand how (or if) the topological properties of food webs change with system-wide. Thus, a large number of network measurements is introduced in order to describe and compare different network structures of ecological and the number and species abundance of the top, bottom and intermediate and their effects on functioning of the network [10] and others such as [11], which introduces the evolution of the individual level by mutations that may result in different offspring of parents (speciation). Evolution is a very slow but steady process, compared with the way that species come (appear) and go out (disappear) from the communities is for migration, dispersal processes or invasion or extinction. The interaction between the structure of ecological network, the dynamics, and various aspects of its stability, such as persistence, strength, endurance and complexity in real-world networks became one of the greatest current challenges [12], [13].

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II.DYNAMICS

In 1942, [14] proposed the trophic dynamics of the ecosystem referring to a progressive attenuation of energy through trophic levels envisioned in a linear and homogeneous chain of plants, herbivores, primary carnivores, and sometimes secondary carnivores. A trophic level is a group of bodies that acquire their energy from the adjacent closely source. This community theory is known as bottom-up approach based on thermodynamic energy transfer. In contrast, the green world hypothesis (HSS) is primarily a top-down theory with plenty of each level is determined, directly or indirectly, by the top of the consumer chain. Thus suppress carnivores herbivores, leaving the plants grow. The exploitation ecosystem hypothesis - EEH generalizes HSS for more than three trophic levels. Trophic cascades are a crude example of EEH. The conceptual basis of EEH proposed that a strong consumption leads to alternating high and low levels of biomass between successive trophic levels. But proponents of EEH differ about the role of bottom-up effect. The most productive systems support side carnivores, therefore has four trophic levels and low plant biomass. Low productivity systems support only a trophic level - plants (tundra, for example) and more productive environments (forest) three. Thus, interactions between trophic levels influence the connections of the networks for their energy significance.

The omnivorism, in turn, is the concept of contravention of trophic levels; it can provide a large number of food relations (5 to over 100) from other levels. Thus, they diffuse the effect of consumption and productivity by trophic spectrum rather than focusing on a particular trophic level. Furthermore, it may affect the dynamics of competition in an analogous manner. Eating prey "not normal" can increase the size of the population of consumers and consequently promote a top-down control and reduce trapped "normal". On the other hand, predator's intra guild and cannibalism eat trophically similar consumers so that each can significantly alter the dynamics of the prey and the network. Scavengers are considered saprophytes, another common form of omnivorism.

Almost all natural systems are open and spatially heterogeneous so that the trophic links may vary across habitats due to differences of their nutrients, debris, arrested and consumers. The spatial coupling of habitats can be decisive for the dynamics of networks due to the import process, export of materials and migratory movements. Another important factor to be considered in the dynamics of food webs is the life story of omnivorism (life history omnivory) describing changes in diet during development (i.e. during phases of metamorphic species or according to the individual's age), which they are often coupled to ontogenetic changes in habitat. Thus, the life story of omnivorous diet can also prevent the user control or amplify the suppression way of resources similar to spatial subsidies and derived detrital. Thus, the strength of "engagement" (interaction strength) between the consumer and their resources depends on the resource supply (supply resources) for each stage. This "supply resource", in terms of abundance and renewal fees of food resources, establishes the maximum potential size of a

population in a network stage. The interplay of forces that occur on the network are weak or strong but all connections must be "controlled by the recipient" (controlled recipient) meaning, consumers substantially depress the populations of resources ("donors"). If a connection is weak or just "donor" controlled (the consumer does not affect the resource replacement rate), the effect of predation will not cascade (spread from top to bottom - top-down) on the network. As can be seen, ecological systems are extremely dynamic, with parts and changing interactions through time and space because of a slew of factors that influence the various populations and communities structures, causing the networks seem like pulsating.

How can a system react to stimuli with millisecond precision to decades if the responses of the sensors vary significantly to the same stimulus? Synchronization is the answer to these questions.

The tendency to synchronize is one of the most mysterious and universal forces of nature. A number of phenomena that occur synchronously happen spontaneously almost as if nature wanted to order. Spontaneous synchronization phenomena [15] are connected by the same mathematical theme: the spontaneous emergence of order out of chaos.

During the last two decades there has been considerable progress to generalize the concept of synchronization and the resurgence in the analysis of the behavior of complex networks that interact in larger systems. On the one hand, the article [16] on the theory of stability of the synchronized movement coupled oscillating systems and subsequently the article [17] on the synchronization chaotic systems caused a plethora of work in this area. In this way synchronization, synchronization complete call, the state variables of individual systems converge toward each other and is said to be more restrictive than the phase synchronization that has been studied since the 17th century by [18] which may be easier to analyze. More recently, there seems to be agreement and consensus protocols on interconnected autonomous agents has been widely studied in control communities systems.

"Watches" ("clocks") synchronized are of fundamental importance in coordinating the rhythmic behavior of individual elements in a community or a large complex system [19], [20]. In physics and engineering, for example, the Huygens paradigm coupled pendulum clocks have permeated various fields of development since the arrays of lasers [21] and superconducting junctions [22] until GPS [23] to distributed sensor networks [24]. In biology, a wide range of intercellular coupling mechanisms lead governing the synchronized oscillators fundamental physiological processes such as somitogenesis, heart function, respiration, secretion of insulin and circadian rhythms [25]-[27]. For [19], usually synchronization helps stabilize a desired behavior resulting from untrustworthy network elements and which have inherent noise. But sometimes, however, the synchronization oscillations may lead to a serious malfunction of a biological system such as seizures [28], [29].

In ecological systems synchronization it is also a very important phenomenon, widespread [30], [31] and observed at

different levels of organization. Interestingly many animal populations are able to collectively synchronize over huge spatial scales. A classic example [32] is the ten-year cycle of the hare-Canadian lynx, whose populations from different regions were strongly synchronized for hundreds of years. The Great Barrier Reef in Australia, another example, many species of corals synchronize their reproductive cycles so that in a single day each year, just after the full moon of November, collectively release millions of gametes in a large-scale spawning [33], thereby enhancing the survival of the next generation. On a continental scale, [34] reported synchronized fluctuations in the abundance of mussel populations in an entire continent. The authors show that, despite limited larval dispersal (planktonic) between neighboring populations interact with local demographic processes to generate spatial synchrony of characteristic patterns that can "govern" the dynamic distribution of the abundance of mussels by more than 1,800 km of coastline.

Another level of organization, [35] shows the role of sync for the stability of food webs meta-communities. In this, the authors report that in a constant environment, compensatory dynamics between species can maintain the stability of the food web, but factors that synchronize the fluctuation of populations among the between communities are expected to be destabilizing.

III. DATA ACQUISITION, STRUCTURAL ANALYSIS AND SYNCHRONIZATION

Flow cytometry is a method that performs both physical measures such as chemical particles (cells/bodies) in suspension in a sample liquid stream.

In this work we use data from the CytoSence flow cytometry (BV Cytobuoy, The Netherlands) available at the Technology Transfer Center of Federal University of Rio de Janeiro.

The instrument is equipped with a solid blue laser (488 nm), forward scatter side sensors and fluorescence orange/yellow, green/yellow and red allowing the particle analysis of up to 1 mm and volume of water that can reach 4×10^{-3} liters per sample [36]. According to the manufacturer the device can deal with concentrations of 102 to 1010 particles per liter analyzed flows that can reach the 10-5l/s thereby permitting the transfer of 500 data sets, or 500 particles per second.

The CytoSence software, provided by the manufacturer, generates two types of files with the data generated in the form of matrices. The first format basically reflects the optical signature of the particle itself and the second lists format in which each line representing a particle is formed by variables obtained by direct measurement and by the application of mathematical models obtained by the device as the sensors, reaching up to 46 distinct values.

The modeling of the ecological relationships of competition, predation and herbivory, follow the concepts of fuzzy theory [37] and viewing the graph as shown by [38].

The identification of the fuzzy graphs will be made through computational methods as the optimization algorithm by colony [39]. This algorithm has been studied in a number of

applications, among which the detection of communities. The classic mechanism is the formation of a trail of artificial pheromone associated with each edge, as presented by these authors in the simplified solution of the problem of the shortest path in a graph. Variations of the ant colony algorithm, which does not employ the mechanism of pheromone trail, but which preserve good performance in detecting communities and if tested may include those shown by [40]-[42].

Research on synchronization phenomena inevitably focuses on determining the main response mechanisms for the collective synchronous behavior among members of a population or community. To achieve overall consistency activity, a set of oscillating elements which interact is required. The rhythmic activity of each element may be due to internal processes or external sources (external or forcing stimuli). Even if the internal processes responsible for rhythmicity have different physical or biochemical origin and can be very complex, one can understand the essence of synchronization in terms of some basic principles.

Consider three basic elements: a graph in which the nodes i.e. edges (i, j) represent groups of species (patches) and leakage fluxes flowing between the patches; variability describing population dynamics vector $n(i)$ i patch when the patch isolated from other network; the flow rates of each component of the vector population.

Several synchronization forms are possible in ecological networks. The stronger is the complete synchronization that occurs when a synchronous solution $n(i)(t) = n(j)(t)$ for all $i \neq j$ for all existing and stable t . A somewhat weaker synchronization, is called almost-complete synchronization requires that the maximum difference between populations is small. Much weaker forms, but very interesting synchronization is the phase synchronization [43]-[45], out-of-phase synchronization and intermittent synchronization [46].

Reference [47] states that in general when the parameters of a meta community are not far from the values that give rise to full synchronization, that is, when the parameters are in a region called the pre-synchronization, somehow weak synchronization is present, and is revealed by the different spatiotemporal patterns.

The Kuramoto model [48] assumes a specific form of engagement, represented by a non-weighted and globally connected graph, called mean field. Reference [49] analyzed the consequences of the adoption of other different topologies originally proposed, better suited to the representation of real systems. The study of small-world network coupling geometries concluded the need for a small number of long-distance connections. Also noted that critical coupling value K_c , above which there passes the timing, becomes larger as the graph representing the connections becomes less random.

Other work on the timing of small-world network sought to characterize the behavior of the system opposite to variations of the reconnection probability (p) and intensity of the coupling (K) [50]. Simulation results with varying sized networks 100-3200 elements showed that partially emerges timing for any nonzero probability p . Furthermore, it was

found that the level of timing systems with saturating this topology for $p \approx 0.5$. The authors suggested that the adoption of value for building networks would be advantageous from an economic point of view; it would be possible to obtain overall consistency with less expenditure of resources by reducing the number of long-range connections. It was confirmed that the critical value increases with decreasing p , being higher for small-world network than for globally connected networks.

A study to determine the formation of timing patterns in random and scale free networks provided a new perspective on this emerging phenomenon [51]. The analysis focused on global and local aspects of timing. Therefore, the authors proposed a new parameter called r_{link} , to measure the local creation of timing patterns. This new parameter would represent the fraction of all possible links synchronized in the network. Detailed dynamic evolution of the patterns obtained by numerical simulations showed that complex networks may use different mechanisms to achieve global synchronization state. In random networks, a large number of oscillator's synchronized pairs happens in the first place. Subsequently, they are grouped by means of a rapid process of agglutination by increasing the coupling strength. In the case of scale-free networks, oscillators are incorporated into larger agglomerated, substantially one at a time from a core containing a large amount of network vertices. This difference in behavior was attributed to the heterogeneous nature of free networks of scale and the role played by their hubs. The results in this same work showed that even when the values of the order parameter are close to zero, the inconsistency regime between the oscillators, the system organizes itself into the timing. It was also found that the development of microscopic sync pattern is faster on random networks, and such networks more "synchronizable" locally than that observed in scale-free networks.

IV. RESULTS

A sample of data was collected and processed like the first one to assess the developed methodology. The new network created also preserved approximately 95% of the original particles with significant dominance of nanoplankton, but without micro plankton, originally very sparse, as shown in Fig. 2. Among the properties of this network, the amount of connections highlights because it is much larger (971,740) than the previous one, which influences the increase of several other properties. This can be explained by the small difference between the amounts of primary producers and of all consumers, which promotes a network with more connections than before. The clustering coefficient of this network is higher (0.567) and the average number of triangles in relation to its degree continues to show the power law distribution behavior, with the coefficient of determination reaching 0.9284 and $\alpha \sim 2.056$. The ant colony algorithm detected five communities, as shown in Fig. 3, probably due to the higher occurrence of primary and secondary consumers.

With the described methodology the following objectives can be achieved:

- Set as the temporal variability of the different nodes and their ecological networks interaction forces influence its dynamics,
- To establish the degree distribution of the network interaction forces and the subnets and the relationship with species richness;
- To establish the degree of homogeneity and / or heterogeneity among the various ecological networks;
- Understand the pattern of clustering, fragmentation and self-organization of communities and their degree of cohesion;
- Establish mechanisms and degree of synchronization of ecological networks and the implications of such an organization regarding the spread of different disorders.

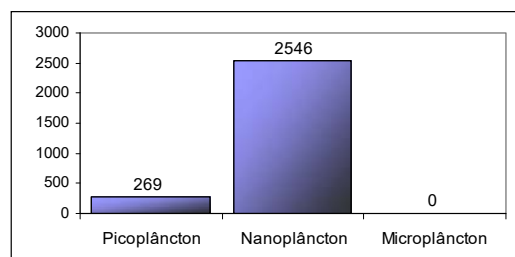


Fig. 2 Amount of individuals by size

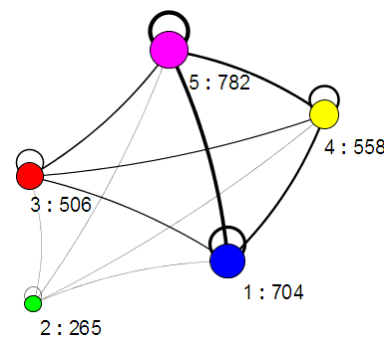


Fig. 3 Communities' graph, the notation $x : y$ indicates that x is the identification number of a community and y is its amount of nodes

V. CONCLUSION

Because of all vulnerability and importance of the environment of the coastal zone, study and development of methodologies to understand the dynamics of its varied ecosystems are timely and integrated, can take paper relevance in the management and preservation of this endangered environment. With the aim of contribute to these efforts, this study explored various resources and implemented tools for analysis of planktonic networks, generating useful information for applications in coastal management.

Finally, it can be considered achieved the objectives of this work, which brought contributions to both the computational area, as for research on plankton marine, efforts in higher instance, will collaborate to the applicability and improvement of coastal management. The results opens up new horizons study and will serve as a basis for work wishing to extend and

deep modeling and analysis of planktonic networks generated from cytometric data flow.

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