



Fuzzy modeling of plankton networks



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ABSTRACT

This work aims to show the trophic structure of a real plankton community from Angra dos Reis estuary using in situ flow cytometry for data acquisition, and how competition, as a non-trophic interaction, is structured amid the trophic interactions – predation and herbivory. As no previous information is given, a great research challenge is how to mathematically represent such relations and their interaction strengths. For this purpose, such data were modeled by a fuzzy complex network through a multigraph view. To reduce its complexity, an ant colony algorithm was employed to detect its sub-structures called communities or compartments. These approaches have allowed the discrimination and the quantification of relevant linkages and process, search into topological characteristics as triangles or loop distribution to the node degrees, and access the number of communities within network. Furthermore, it was considered the distribution of organisms according to their sizes and ecological roles. Comparisons with other network indices and patterns found in the literature and in nature, respectively, indicate that our approach is adequate.

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1. Introduction

Despite of common chaotic changes in population levels, the existing ecological relationships among all organisms were believed to function in a “natural balance”. These relationships form a vast and complex adaptive network (Sayama et al., 2013) of ecological interactions traditionally known as food webs (Hui, 2012; McCann, 2012). They show how biological communities are organized and how ecosystems function. Actually, their structure and dynamics suffer several disturbances while functioning in a permanent state of change between chaos (Hastings and Powell, 1991) and stability (Holling, 1973). This has required huge efforts to understand the adverse impacts on ecosystems and, ultimately, its consequences on human life.

In all aquatic systems, for example, plankton are a key element (Odum and Barret, 2001). As they are a highly dynamic system formed by tiny representative species of all biological kingdoms, they can be used as an environmental quality indicator (Suthers and

Rissik, 2009). However, Worden et al. (2015), show the great complexity of planktonic relationships, while Malkassian et al. (2011) warn that is necessary to obtain accurate information to understand the complex dynamics of plankton and its control parameters. According to DeAngelis et al. (1989), abundance and distribution of plankton depend on factors such as nutrient concentration and physical state of the water column. However, such complexity cannot be fully represented by traditional food web models constituting a great challenge nowadays. In this way, ecological networks have emerged as another approach going beyond food webs (Ings et al., 2009) since they are able to simultaneously represent more relations than the information about who eats whom or what.

With the recent technological developments, flow cytometry has become an attractive tool to monitor plankton due to its ability to perform in situ high frequency measurements at the level of individual particles (Dubelaar and Gerritzen, 2000; Olson et al., 2007). Meanwhile, to cope with the huge amount of data, machine learning methods have been developed (Pereira and Ebecken, 2011). On the other hand, two of the greatest difficulties to evolve planktonic networks from quasi real time data are to establish connections between organisms, due to the great diversity of life strategies as disclosed by Worden et al. (2015), and determining the values of traits such as interaction strength variability under field conditions, which is a challenge for all food web researches (Paine, 1992). Such

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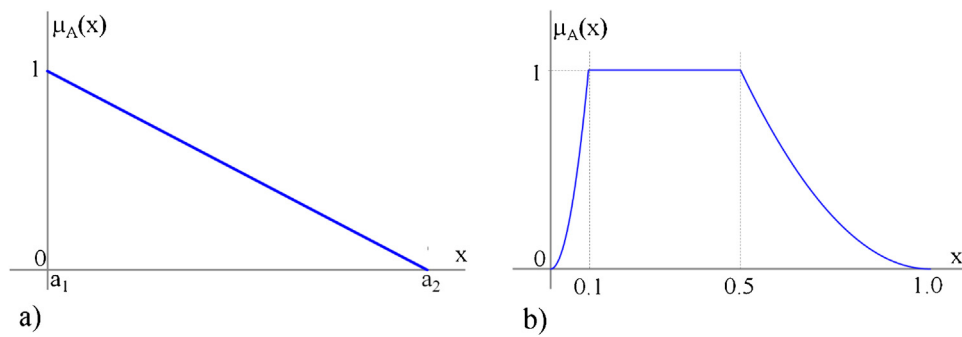


Fig. 1. The membership functions used for (a) competition and for (b) predation and herbivory relationships.

variability always brings some degree of uncertainty and various Monte-Carlo methods exist to calculate uncertainty on parameter estimation (Fedra, 1983). However, according to Reichert and Omlin (1997), these procedures underestimate the uncertainty which favors the use of fuzzy set theory. It has been used to study environmental issues such as the vulnerability (Tran, 2002), impact indication (van der Werf and Zimmer, 1998), assessment of water quality (Wang et al., 2014), chlorophyll production (Pereira et al., 2009), or evolving networks (Ramsey and Veltman, 2005; Pereira et al., 2014, 2016).

Therefore, to deal with the highly dynamic behavior of plankton, the high volume of data acquired and the complexity of planktonic networks, this work presents a methodology to evolve networks from in situ flow cytometry data in which a fuzzy multigraph is used to represent functional differences between linkages. Here, predation and herbivory relations are modeled beyond the competition presented by Pereira et al. (2014). Of course, this will increase network complexity and connectance but allow us for screening different processes. So, the aims of this paper are (i) to present a network approach to show how competition, a non-trophic interaction, is structured, (ii) discriminate and quantify different links (e.g. predation, herbivory, competition) on a multigraph, (iii) explore topological characteristics of the network, such as distribution of triangles by the degree of nodes, (iv) assess the amount of communities detected. In graph theory, a triangle is understood as the complete link between three nodes in a graph and it is equivalent to a loop in ecological studies, which is usually related to interactions strengths and network stability (Neutel et al., 2002). Likewise, communities in complex networks are denser regions within the network which may be interpreted as interconnected subnetworks (Girvan and Newman, 2002). In ecology, such communities should be understood as compartments or subsets of species that interact more frequently among themselves than with other species (Stouffer and Bascompte, 2011). Since flow cytometers detect individual particles, it is noteworthy that network here is not a species-averaged web, but an individual one which represents the highest resolution within a single sea water drop.

2. Methodology

2.1. Flow cytometry data

Cytometry is a process that measures physical and chemical characteristics of particles – cells, organisms or other biological or non-biological elements (Shapiro, 2003) and may be used for macro ecological studies (Li, 2009). Shortly, in flow cytometry, suspended particles on a stream of fluid cross a laser beam which allows a large number of sequential measurements. Alternatively, this information can be obtained by traditional approach of plankton sampling and microscope analysis, which are time consuming activities. Some of the great advantages of flow cytometry process

are the fast and huge data acquisition and the more precise measurements, which is statistically better for a research. In this work, plankton data from the near bottom (1 m above) of Angra dos Reis estuary (Rio de Janeiro, Brazil) were acquired by the submersible CytoSense scanning flow cytometer (CytoBuoy BV, Woerden, The Netherlands). This instrument is the only one which allows in situ high frequency data acquisition and still generates pulse shape profiles (optical signatures) for each particle from its five sensors. The forward scatter sensor is commonly used to estimate the size of the particles; the sideward scatter sensor captures the structural complexity of them; while yellow, orange and red fluorescence sensors discriminate autotrophs (Veldhuis and Kraay, 2000; Dubelaar et al., 2007). Therefore, the CytoClus data analyzing software provided by CytoSense manufacturer was used because it allows great particles discrimination since it is the only one that offers six additional measures (mathematical models) for each of these sensors. They are pulse length, mean amplitude, fill factor, asymmetry, inertia and estimated number of cells in a colony. Although a large amount of data is available for each sample, no direct information about links between particles is given by the equipment.

2.2. Building the ecological network

2.2.1. Fuzzy graphs

Unlike the traditional approach that uses the Lotka-Volterra equations to model predator-prey interactions, this work uses cytometric data set to create fuzzy sets to model competition with a triangular membership function (Fig. 1a) (Pereira et al., 2014), and predation and herbivory with a quadratic function (Fig. 1b).

On the competition modeling, a membership function is defined to each particle, in which the domain is the set of estimated similarities between the particle and the others. As in Pereira et al. (2014), here it is assumed that similar particles compete with more intensity. So, among many possibilities, triangular functions are the simplest way to model this decrescent behavior. This strategy can be described by the following steps:

- (1) Normalize each attribute (variable) in cytometric data by its amplitude;
- (2) Create a matrix of Euclidean distances between the particles;
- (3) For each target particle A , fuzzify all the others by the triangular function:

$$\mu_A(x) = \frac{a_2 - x}{a_2 - a_1}, \quad \forall x \in X$$

in which a_1 and a_2 are the minimum and maximum distance between the particle A and all other particles in the sample data, and X is the set of Euclidean distances in relation to A ;

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