

# Environmental monitoring through functional biodiversity tools



Tonio Di Battista, Francesca Fortuna\*, Fabrizio Maturo

Department of Philosophical, Pedagogical and Quantitative Economic Sciences, University G. D'Annunzio, Chieti–Pescara, Italy

## ARTICLE INFO

### Article history:

Received 8 October 2014

Received in revised form 22 May 2015

Accepted 27 May 2015

### Keywords:

Biodiversity profiles

Functional data analysis

Derivatives

Radius of curvature

Arc length

Environmental monitoring

## ABSTRACT

The foundational concept for our research, which is largely shared by statisticians and ecologists, is that biodiversity is one of the most important indicators for environmental assessment. Because this indicator decreases in relation to ecosystem stressors, its measurement is essential for predicting future biological impacts of environmental damages. Although many indices have been proposed, no universally accepted measure for biodiversity has yet been established. In this context, the use of diversity profiles allows the analyst to display a family of indices in a single graph. However, this approach presents two critical limitations: first, a community composition is not always interpretable; second, the diversity profiles could lead to ranking issues when the curves intersect each other. The aim of this paper is to resolve these limitations by introducing functional biodiversity tools. In particular, three functional measures are proposed: the derivatives, the radius of curvature and the curve length. The analysis of derivatives and of the radius of curvature addresses the first limitation and highlights the characteristics, the differences and the similarities among communities. Arc length addresses the second limitation, providing a scalar measure that leads to a unique communities ranking for a given pattern of richness even if profiles intersect. The proposed functional models are applied to a real data set involving lichen biodiversity in the province of Genoa, Italy. Our approach allowed us to analyze the characteristics of lichen communities and to identify the biodiversity ranking. The combined use of these tools provides a useful method for identifying areas of high environmental risk, with the potential to address the monitoring of environmental policies.

© 2015 Elsevier Ltd. All rights reserved.

## 1. Introduction

The issue of preserving biodiversity is a central aim of current environmental policy (Paoletti, 1999; McCann, 2002; Vackar et al., 2012). In an ecological framework, diversity relies on the variety of living organisms in a delineated study area (Pielou, 1975). Due to increasing human impact and the mismanagement of the environment, the term biodiversity is now inextricably linked to preserving essential ecosystem functions. Generally, a high level of biodiversity is associated with natural conditions in an ecosystem, and vice versa. For this reason, biodiversity plays a fundamental role in determining environmental health (Burger et al., 2013). In this context, biomonitoring represents a useful tool for assessing the effects of human-related stressors on exposed populations (Nash, 1996). This technique is based either on the tendency of some organism to accumulate pollutants in its tissues (bioaccumulation) or on the changes that occur in the composition of animal and plant communities after exposure to pollutants (bioindication). This paper

focuses on the latter; thus, biodiversity assessment of some specific organisms becomes useful for quantifying environmental damage. For example, epiphytic lichens are one of the best-suited organisms for evaluating the effects of atmospheric pollutants (Nimis et al., 1989; Cislighi and Nimis, 1997). Due to their morphological and physiological characteristics, lichens respond rapidly to atmospheric changes, in particular changes caused by anthropogenic factors.

Thus, the resulting imperative is to provide a suitable measure for biodiversity. Despite the enormous number of indices that have been developed to assess the biological health of a community (Gove et al., 1994), a universally accepted measure has not been established (Ricotta, 2005). A diversity index is, in general terms, a mathematical expression that combines species richness and species evenness (Pielou, 1977). However, these two components are confounded when a single index is considered. The problem is that a community with few species and high evenness could have the same diversity measure as another community with many species and low evenness (Pielou, 1977). Therefore different indices could lead to different community ranking (Patil and Taillie, 1982). The choice of an index must be considered with care. In the literature the most frequently used diversity indices

\* Corresponding author. Tel.: +39 3286537741.

are the species richness, Shannon (Shannon, 1948) and Simpson (Simpson, 1949) indices. Species richness is the simplest index, but it does not take into account evenness. The Simpson diversity index is a good measure of dominance, but not a good predictor of species richness, whereas the Shannon index is affected by both the number of species and their evenness (Evangelista et al., 2012). However, the Shannon index is particularly sensitive to the presence of rare species in a community, while the Simpson index is particularly sensitive to changes in the relative abundances of the most dominant species. This highlights how the use of a single indicator greatly reduces the complexity of the ecological systems and hides the multidimensional aspect of biodiversity (Gattone and Di Battista, 2009; Gove et al., 1994; Patil and Taillie, 1979; Di Battista and Gattone, 2003; Fattorini and Marcheselli, 1999).

In the literature, diversity profiles are presented as a possible solution for this limitation (Hill, 1973; Patil and Taillie, 1982; Tóthmérész, 1995; Carranza et al., 2007). A diversity profile is a curve depicting several values of diversity indices simultaneously, including Shannon, Simpson and species richness. Therefore, the diversity profile is a family of measures, that is a family of diversity indices dependent upon a single continuous parameter that is sensitive to both rare and common species. The plot of diversity profiles plays a fundamental role in comparing different communities. Indeed, if the diversity profiles do not intersect, the higher curve corresponds to the community with greater diversity.

The primary limitation of this approach lies in the difficulty of comparing communities with intersecting profiles. To solve this problem, we suggest additional tools to improve the analysis of biodiversity profiles. Because these profiles are presented as curves, the functional data analysis (FDA) approach can be considered (Gattone and Di Battista, 2009; Di Battista and Fortuna, 2013). FDA is a useful tool for a deeper analysis of phenomena varying in a fixed domain (Ramsay and Silverman, 2005; Ferraty and Vieu, 2006). This approach allows for the evaluation of the behaviour of a diversity profile throughout the reference domain. In particular, we propose three functional measures to inspect diversity profile characteristics: the derivatives, the radius of curvature and the length of the diversity profile. The combined use of these indicators allows the analyst to consider the multidimensional aspects of diversity and resolves some limitations of classical methods. The paper is organized as follows: Section 2 introduces the theories and presents a comparison between the previous conventional measures of biodiversity and the new proposed method. Section 3 deals with an application of these theories to a real-world data set. Finally, Section 4 concludes the paper.

## 2. Theory

### 2.1. Functional biodiversity measures

Let us suppose that an ecological population is composed of  $N$  units and is partitioned into  $s$  species ( $i = 1, 2, \dots, s$ ). Let  $\mathbf{N} = (N_1, \dots, N_s)$  be the species abundance vector whose generic element  $N_i$  represents the number of individuals belonging to the  $i$ th species, and let  $\mathbf{p} = (p_1, \dots, p_s)$  be the relative abundance vector with  $p_i = N_i / \sum_{i=1}^s N_i$ , such that  $0 \leq p_i \leq 1$  and  $\sum_{i=1}^s p_i = 1$  (Gattone and Di Battista, 2004).

To evaluate the community biodiversity, we consider the  $\beta$  diversity profile proposed by Patil and Taillie (1979, 1982):

$$\Delta_\beta = \sum_{i=1}^s \frac{(1 - p_i^\beta)}{\beta} p_i \quad \beta \geq -1 \tag{1}$$

where the value of  $\beta$  denotes the relative importance of richness and evenness.  $\Delta_\beta$  is defined for any  $\beta \in \mathbb{R}$ , and the restriction;  $\beta \geq -1$ ; assures certain desirable properties. Calculating and

**Table 1**

Relative abundances for four hypothetical communities composed of five species.

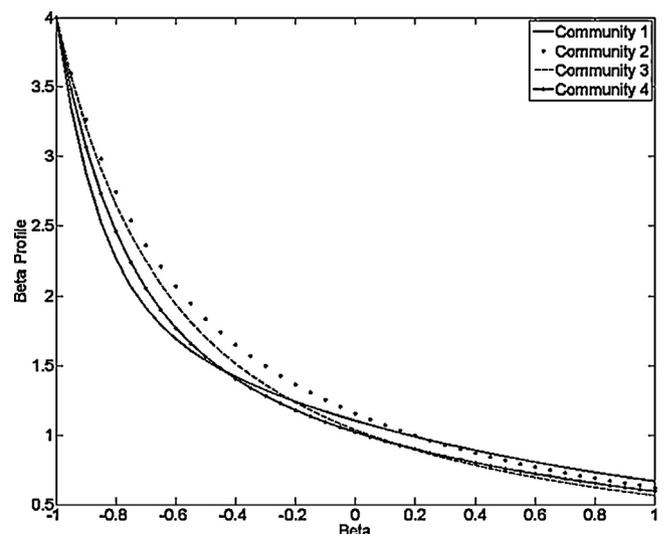
Species	Community 1	Community 2	Community 3	Community 4
Species 1	0.3470	0.5488	0.6066	0.5550
Species 2	0.3470	0.2033	0.2104	0.1925
Species 3	0.3053	0.1789	0.1503	0.2475
Species 4	0.0003	0.0671	0.0301	0.0025
Species 5	0.0003	0.0020	0.0027	0.0025

plotting  $\Delta_\beta$  for  $\beta > 1$  may not be helpful because the profiles tend to converge quickly beyond this point (Patil and Taillie, 1979, 1982).  $\Delta_\beta$ , thus, can be considered as a function of  $\beta$  in a closed domain,  $\beta \in [-1, 1]$ .

The plot of  $\Delta_\beta$  versus  $\beta$  provides the diversity profile. It is a decreasing and concave upward curve showing different values of biodiversity for each value of  $\beta$ . The most frequently used indices of biodiversity are special cases of Eq. (1):  $\beta = -1$  generates the richness index;  $\lim_{\beta \rightarrow 0}$  represents the Shannon diversity index; and  $\beta = 1$  results in the Simpson index.

The diversity profile displays a complete picture of diversity. Its plot allows the analyst to rank different communities. Indeed, the higher curve highlights biological populations with higher diversity and vice versa. Moreover, the plot tends towards a straight line, decreasing from  $-1$  to  $1$ , in the case of maximum equitability with few species, and it becomes more curved with the prevalence of a few species over the others. Difficulties arise if we compare communities with intersecting profiles. In this case, it is impossible to determine which curve is the highest.

The following example of four communities, each composed of five species, serves to clarify this concept. Table 1 shows the relative abundances of the species. The  $\beta$  diversity profiles (Eq. (1)) are plotted in Fig. 1. Because the profiles intersect, a unique ranking among the communities is unattainable. In this typical case, the analysis of the beta profile does not solve the ranking issue. In particular, for  $-1 \leq \beta \leq -0.5$ , the profiles do not intersect, and the diversity of the communities can be sorted in descending order as follows: community 2, 3, 4, 1. For  $-0.5 \leq \beta \leq 0.2$ , two intersections exist: the first between communities 1 and 2, and the second between communities 3 and 4. This situation leads to a different ordering according to the Shannon and the Simpson indices. For  $\beta \geq 0.2$ , there are no intersections, and the communities ranking is: 1, 2, 4 and 3. The first and the second parts of the domain lead to different results, reflecting distinct aspects of biodiversity (the richness and the evenness, respectively).



**Fig. 1.**  $\beta$  profiles ( $\Delta_\beta$ ) for four hypothetical communities composed of five species.

متن کامل مقاله

دریافت فوری ←

**ISI**Articles

مرجع مقالات تخصصی ایران

- ✓ امکان دانلود نسخه تمام متن مقالات انگلیسی
- ✓ امکان دانلود نسخه ترجمه شده مقالات
- ✓ پذیرش سفارش ترجمه تخصصی
- ✓ امکان جستجو در آرشیو جامعی از صدها موضوع و هزاران مقاله
- ✓ امکان دانلود رایگان ۲ صفحه اول هر مقاله
- ✓ امکان پرداخت اینترنتی با کلیه کارت های عضو شتاب
- ✓ دانلود فوری مقاله پس از پرداخت آنلاین
- ✓ پشتیبانی کامل خرید با بهره مندی از سیستم هوشمند رهگیری سفارشات