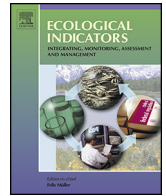




Contents lists available at ScienceDirect

## Ecological Indicators

journal homepage: [www.elsevier.com/locate/ecolind](http://www.elsevier.com/locate/ecolind)



### Short Communication

# BioFTF: An R package for biodiversity assessment with the functional data analysis approach

T. Di Battista <sup>a,\*</sup>, F. Fortuna <sup>a,1</sup>, F. Maturò <sup>b,1</sup>

<sup>a</sup> DISFPEQ, University G. D' Annunzio, Italy

<sup>b</sup> DEA, University G. D' Annunzio, Italy

#### ARTICLE INFO

##### Article history:

Received 14 April 2016

Received in revised form 11 October 2016

Accepted 24 October 2016

Available online xxx

##### Keywords:

Biodiversity profile

Functional biodiversity tools

Functional data analysis

R package

Surface area

#### ABSTRACT

This paper presents the R package BioFTF, which is a tool for statistical biodiversity assessment in the functional data analysis framework. Diversity is a key topic in many research fields; however, in the literature, it is demonstrated that the existing indices do not capture the different aspects of this concept. Thus, a main drawback is that different indicators may lead to different orderings among communities according to their biodiversity. A possible method to evaluate biodiversity consists in using diversity profiles that are curves depending on a specific parameter. In this setting, it is possible to adopt some functional instruments proposed in the literature, such as the first and second derivatives, the curvature, the radius of curvature and the arc length. Specifically, the derivatives and the curvature (or the radius of curvature) highlight any peculiar behaviour of the profiles, whereas the arc length helps in ranking curves, given the richness. Because these instruments do not solve the issue of ranking communities with different numbers of species, we propose an important methodological contribution that introduces the surface area. Indeed, this tool is a scalar measure that reflects the information provided by the biodiversity profile and allows for ordering communities with different richness. However, this approach requires mathematical skills that the average user may not have; thus, our idea is to provide a user-friendly tool for both non-statistician and statistician practitioners to measure biodiversity in a functional context.

© 2016 Elsevier Ltd. All rights reserved.

## 1. Introduction

Biodiversity can be defined as the variability among living organisms (Patil and Taillie, 1979) and is generally related to the apportionment of some quantity into a number of categories. It is recognized as an important feature of healthy ecosystems because it is extremely linked to environmental functions. Many studies have shown that even minor losses in the number of species may reduce the capacity of ecosystems to perform their function (Vackar et al., 2012; McCann, 2002). Indeed, the rapid loss of biodiversity that has occurred over the last decades has made its conservation a key driver of environmental policies (Gordon et al., 2011; Pérez-Vega et al., 2012; Di Battista et al., 2016b; Ricotta et al., 2003; Normandera et al., 2012). The changes in biodiversity are expected to have consequences for human well-being, i.e., estuarine biodiversity (Pinto et al., 2014). In this context, the use of proper tools for biodiversity measurement becomes a fundamental issue. The most common indices used in the literature are: the richness index, the

Shannon index (Shannon, 1948) and the Simpson index (Simpson, 1949). However, when we look for a suitable numerical definition of biodiversity, no single index can adequately summarize this concept, which combines richness (the number of different species) with evenness (the degree to which abundances are equitably divided among species) (Ricotta et al., 2003). As a consequence, different indices may lead to different community rankings (Patil and Taillie, 1982; Lamb et al., 2009; van Striena et al., 2012). Furthermore, different biodiversity measures respond differently to environmental conditions (Azevêdo et al., 2015). For this reason, Hill (1973) proposed a unifying diversity formulation by introducing a parametric family of diversity indices called diversity profiles. Diversity profiles are functions dependent on a parameter that reflects the sensitivities to rare and abundant species; they provide a continuum of possible biodiversity measures (Ricotta et al., 2003) and yield a faithful graphical representation of community diversity (Leinster and Cobbold, 2012). The analysis of the profile graphs provides an immediate biodiversity ranking among communities; indeed, if profiles do not intersect, a higher curve reflects a community with higher biodiversity (Patil and Taillie, 1979).

Because diversity profiles are presented as curves, the functional data analysis (FDA) approach (Ramsay and Silverman, 2005) may be considered to inspect curves' behaviours throughout the

\* Corresponding author.

E-mail address: [dibattis@unich.it](mailto:dibattis@unich.it) (T. Di Battista).

<sup>1</sup> The authors are entered in alphabetical order according to their last names.

reference domain (Gattone and Di Battista, 2009; De Sanctis and Di Battista, 2012; Di Battista and Fortuna, 2013; Di Battista et al., 2014, 2016a,c). In this context, Di Battista et al. (2016b) suggested additional functional tools to improve the interpretation of the diversity profiles and achieve a solution to the ranking issue for communities with intersecting curves. In particular, the authors focused on the analysis of the derivatives, the radius of curvature, the curvature and the arc length. The first and second derivatives reflect the slope and the deceleration of the profiles, respectively. Because they are very sensitive to small variations in the species distributions, they are immediate and direct indicators of the presence of dominant species in a community, i.e. a high relative abundance of the most abundant species. The radius of curvature and the curvature highlight communities' composition because they are good indicators of the lack of balance among species. Finally, the arc length provides a scalar measure that helps in ranking communities with intersecting profiles, given the number of categories. The proposed approach presents several advantages. First, contrary to the classical indices, the diversity profiles jointly consider species richness and species evenness. Second, the derivatives and the radius of curvature (or the curvature) show peculiar profile behaviours for each part of the domain due to their sensibility to small changes in species distribution. Third, the arc length may be used to solve some ranking problems for communities with intersecting profiles. Finally, the combined use of these functional tools provides an analytic instrument to compare communities, supporting the analysis of profile graphs. However, the disadvantage of this method is that it is not possible to order communities with intersecting profiles and different richness. To fulfil this gap, which is still unsolved in the literature, we propose a new functional tool called the surface area. The latter is mathematically computed as the approximate integral of the diversity profile in a fixed domain and represents a suitable solution for ranking communities. This tool is less influenced by the richness than the arc length; thus, it allows us to compare communities that present different numbers of categories.

Although the functional approach provides a deeper analysis of diversity profiles, it requires mathematical skills that the average diversity user may not have. For this reason, we propose a new R package called BioFTF, designed to compute the  $\beta$  diversity profile and its linked biodiversity functional tools. The package aims to make accessible this method to a large community and allows users to analyze biodiversity in an intuitive way. The package focuses on statistical diversity assessment in an ecological framework; however, it may be adopted for measuring the heterogeneity of qualitative data in different research fields.

The paper is organized as follows: Section 2 describes the proposed model by providing a brief overview of the  $\beta$  diversity profile and of its linked functional tools. In the same section, the surface area is introduced. Section 3 presents our package, its structure and its core functions; Section 4 shows some capabilities of BioFTF through the analysis of an example dataset. Section 5 provides the study's conclusions and outlines future developments.

## 2. Methods

This paper focuses on biodiversity assessment through the evaluation of the functional characteristics of the  $\beta$  diversity profile. This section provides a brief overview of the approach and introduces the surface area as an additional functional instrument that is useful to solve the ranking issue.

### 2.1. Diversity profile model

Patil and Taillie (1979, 1982) proposed a general class of diversity indices by defining diversity as the species average rarity within

an ecological community. In particular, we refer to the  $\beta$  diversity profile:

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

where  $(1 - p_i^{\beta})/\beta$  is a rarity measure of the  $i$ -th species,  $i=1, 2, \dots, s$ ; the value of  $\beta$  denotes the relative importance of richness and evenness while  $p_i$  represents the relative abundance of the  $i$ -th species with  $0 \leq p_i \leq 1$  and  $\sum_{i=1}^s p_i = 1$ . Of course, the profile computation depends on the estimates of the species abundances under a suitable sampling design (Schreuder et al., 1993; Barabesi and Fattorini, 1998; Di Battista and Gattone, 2003; Di Battista, 2002, 2003; Gattone and Di Battista, 2004, 2011). Although Eq. (1) is valid for  $-\infty \leq \beta \leq \infty$ , the restriction  $\beta \geq -1$  ensures that  $\Delta_{\beta}$  satisfies some suitable properties (Patil and Taillie, 1982). Moreover, calculating and 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). Mathematically, the various diversity measures obtained by varying  $\beta$  are different moments of the same diversity function which shows a complete diversity picture. The diversity profile is obtained by plotting diversity values,  $\Delta_{\beta}$ , against the scale parameter  $\beta$ . The most common diversity indices are special cases of Eq. (1):  $\beta = -1$  generates the richness index,  $\lim_{\beta \rightarrow 0} \Delta_{\beta}$  represents the Shannon diversity index (Shannon, 1948), and  $\beta = 1$  returns the Simpson index (Simpson, 1949). Specifically, the  $\beta$  profile is a decreasing curve that tends towards a straight line in the case of maximum equitability and becomes more curved when few species prevail over the others. According to these characteristics, it is possible to order communities by comparing the graphs of their profiles. In particular, a higher curve highlights a biological population with higher diversity and vice versa. This ranking is extremely advantageous because it preserves the information provided by the whole domain of the diversity profile. However, it presents a strong limitation: communities with intersecting profiles are not comparable.

### 2.2. Functional diversity tools

The FDA approach addresses observations expressed by functions rather than by scalar measures (Ramsay and Silverman, 2005). Because  $\Delta_{\beta}$  is a function of  $\beta$  in a fixed domain,  $\beta \in [-1, 1]$ , we take advantage of this methodological framework to create new biodiversity indicators. In particular, according to the characteristics of the  $\beta$  profile in Eq. (1), Di Battista et al. (2016b) proposed five functional biodiversity tools: the first and second derivatives, the radius of curvature, the curvature, and the arc length. They are able to provide additional information on the communities and to overcome some drawbacks of the diversity profile approach.

The analysis of the first and second derivatives is an essential phase of the FDA approach, and it may be useful to emphasize differences among curves in an ecological framework. Specifically, the  $\beta$  profile derivatives indicate the presence of dominance or evenness better than diversity profiles because they are more sensitive to small variations in the communities' composition (Di Battista et al., 2016b). The profile slope expressed by the first derivative is a good indicator of the presence of dominant species within a community. For  $\beta$  close to  $-1$ , high absolute values of the first derivative indicate that the  $\beta$  profile decreases quickly by suggesting the dominance of one or very few species in a community. On the contrary, low absolute values of the first derivative mean that living organisms tend to be equally distributed among the species (evenness). The second derivative represents the deceleration of the curve for any given value of  $\beta$ . In particular, for  $\beta$  close to  $-1$ , high values

Download English Version:

<https://daneshyari.com/en/article/6292687>

Download Persian Version:

<https://daneshyari.com/article/6292687>

[Daneshyari.com](https://daneshyari.com)