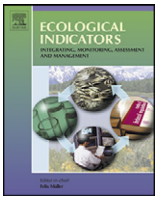
Ecological Indicators 23 (2012) 366–373

Contents lists available at SciVerse ScienceDirect

Ecological Indicators

journal homepage: www.elsevier.com/locate/ecolind



How far can we go in simplifying biomonitoring assessments? An integrated analysis of taxonomic surrogacy, taxonomic sufficiency and numerical resolution in a megadiverse region

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ARTICLE INFO

Article history:
Received 23 May 2011
Received in revised form 16 April 2012
Accepted 21 April 2012

Keywords:
Amazonia
Congruence
Mantel
Procrustean rotation
Spatial patterns
Surrogate groups

ABSTRACT

The need for biodiversity conservation is increasing at a rate much faster than the acquisition of knowledge of biodiversity, such as descriptions of new species and mapping species distributions. As global changes are winning the race against the acquisition of knowledge, many researchers resort to the use of surrogate groups to aid in conservation decisions. Reductions in taxonomic and numerical resolution are also desirable, because they could allow more rapid the acquisition of knowledge while requiring less effort, if little important information is lost. In this study, we evaluated the congruence among 22 taxonomic groups sampled in a tropical forest in the Amazon basin. Our aim was to evaluate if any of these groups could be used as surrogates for the others in monitoring programs. We also evaluated if the taxonomic or numerical resolution of possible surrogates could be reduced without greatly reducing the overall congruence. Congruence among plant groups was high, whereas the congruence among most animal groups was very low, except for anurans in which congruence values were only slightly lower than for plants. Liana (Bignoniaceae) was the group with highest congruence, even using genera presence–absence data. The congruence among groups was related to environmental factors, specifically the clay and phosphorous contents of soil. Several groups showed strong spatial clumping, but this was unrelated to the congruence among groups. The high degree of congruence of lianas with the other groups suggests that it may be a reasonable surrogate group, mainly for the other plant groups analyzed, if soil data are not available. Although lianas are difficult to count and identify, the number of studies on the ecology of lianas is increasing. Most of these studies have concluded that lianas are increasing in abundance in tropical forests. In addition to the high congruence, lianas are worth monitoring in their own right because they are sensitive to global warming and the increasing frequency and severity of droughts in tropical regions. Our findings suggest that the use of data on surrogate groups with relatively low taxonomic and numerical resolutions can be a reliable shortcut for biodiversity assessments, especially in megadiverse areas with high rates of habitat conversion, where the lack of biodiversity knowledge is pervasive.

1. Introduction

Comprehensive and reliable biodiversity data that allow the use of systematic conservation-planning procedures (Margules and Pressey, 2000) are available for only a few areas worldwide. Conversely, most of the species-rich areas are plagued by the absence of biological information (e.g., Hopkins, 2007; Schulman et al., 2007). Brown and Lomolino (1998) and Lomolino (2004) coined the terms “Linnean shortfall” and “Wallacean shortfall”, respectively, to summarize this problem. The first term refers to the lack of information about species identities, whereas the second is related to the lack of data on the spatial distribution of species (see also Whittaker et al., 2005).

The world is experiencing severe human-induced impacts (e.g., Hansen et al., 2000; Vörösmarty et al., 2010), so we may not

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http://dx.doi.org/10.1016/j.ecolind.2012.04.023

have time to solve the Linnean and Wallacean shortfalls before the impacts on biodiversity become irreversible or unmanageable. In addition, carrying out inventories of all biodiversity of megadiverse regions of the planet, apart from being expensive and time-consuming, may be a quixotic task (Magurran and Queiroz, 2010). The huge diversity found in the Amazon would require an inordinately large number of taxonomists for a basic inventory of this diversity (Hopkins, 2007), and many tropical areas are still practically inaccessible, especially in the Amazon region (Schulman et al., 2007).

Because of the Linnean and Wallacean shortfalls, most proposed systematic conservation plans are based on surrogate taxa, which are selected by the availability of data (Rodrigues and Brooks, 2007). However, decisions taken for a particular surrogate group may not be optimum for the conservation of all (unknown) biodiversity in a given area (Franco et al., 2009), and the effectiveness of these decisions is also scale-dependent. Because of the uncertainty about the efficiency of the surrogacy approach, the number of studies testing for community congruence (cross-taxon congruence or community concordance) is increasing steadily (e.g., Paszkowski and Tonn, 2000; Su et al., 2004; Macía et al., 2007). Two communities are said to be concordant when beta-diversity or community structures exhibited by these communities are correlated (e.g., Lopes et al., 2011). A similar response to major environmental gradients is the most common mechanism underlying community congruence (Heino et al., 2003). A good surrogate group should be easy to sample and identify, and have a distribution pattern congruent with those of other taxonomic groups. Independently of other requirements (availability of experts; costs of sampling, identification and enumeration), although rarely tested, congruence is a necessary condition for the reliable use of surrogate groups. Besides the analysis of community congruence, a different set of studies has focused on how well biodiversity patterns, obtained with species-level data, can be reproduced by data on higher taxa, in order to improve the cost-effectiveness of monitoring programs and community analyses in general (e.g., Attayde and Hansson, 2001; Bertrand et al., 2006).

The effects of taxonomic resolution on biodiversity patterns can be tested by combining species into coarser taxonomic classes and by evaluating the similarity between ordination patterns depicted by both species-level and lower-resolution data (Melo, 2005; Anderson et al., 2005). If the patterns are similar, then data for higher taxa can be used to replace species-level data (e.g., Terlizzi et al., 2003) that is more expensive and time consuming to obtain. The effects of numerical resolution (e.g., transforming abundance data into presence–absence data) on biodiversity patterns can be analyzed similarly (Melo, 2005; Carneiro et al., 2010). The reliability of higher taxa data for conservation planning is also scale-dependent, and in general, the effectiveness of surrogates increases with the increase of the spatial extent of the area under study (La Ferla et al., 2002; ter Steege et al., 2006).

Studies in the Amazon region have found cross-taxon correlations between similarity matrices derived from plant groups (Vormisto et al., 2000; Ruokolainen et al., 2007; Macía et al., 2007), but studies evaluating the congruence between floristic and faunistic data are largely lacking (see Paavola et al., 2006; Qian and Ricklefs, 2008 for studies in other regions). Variation in faunistic similarity might be better predicted by floristic similarity than by environmental similarity matrices (Oliver et al., 1998). The reason for this is that data on plant species composition integrate a number of important environmental factors, and because of the direct relationships between animal and plants (Schaffers et al., 2008).

Here we used a comprehensive dataset on the composition of different communities in a 100 km^2 Amazonian reserve to evaluate the congruence in the distribution patterns of 22 taxonomic groups. For those groups with the highest power in predicting the distribution of other groups, we also evaluated the degree to which biomonitoring assessments undertaken at this spatial scale can be further simplified by reducing the taxonomic and/or numerical resolution. Some previous studies have evaluated the use of surrogate groups (e.g., Banks-Leite et al., 2011; Rooney and Bayley, 2012), and the effect of taxonomic (e.g., Greffard et al., 2011; Rimet and Bouchez, 2012) and numerical resolution (e.g., Melo, 2005; Carneiro et al., 2010). However, to the best of our knowledge, no previous study has examined simultaneously the adequacy of surrogate groups, and taxonomic and numerical resolution.

Many investigations (e.g., Andersen et al., 2002) have used indicators for assessments of ecological integrity, but most of these studies focused on biological groups assumed to have strong relationships with particular environmental variables. In this study, we tested whether the distributional patterns of several taxonomic groups that are frequently used in biodiversity monitoring are congruent among themselves. That is, we searched for a biological group that best represented the patterns observed for other groups. After identifying this group, we evaluated whether the taxonomic and numerical resolutions of the best group (i.e., the one with the highest average congruence) could be reduced without loss of surrogacy capacity.

2. Materials and methods

2.1. Study area

This study was undertaken using data on 22 taxonomic groups collected at the Ducke Reserve of the National Institute for Research in the Amazon (INPA), located 26 km northwest of the city of Manaus, state of Amazonas (Fig. 1). The area corresponds to site 1 of the Brazilian Long-Term Ecological Research Program (Brazilian LTER), and is part of the Biodiversity Research Program (PPBio) of the Brazilian Ministry of Science and Technology (MCT). The reserve covers 10,000 ha (10 km × 10 km) of preserved *terra-firme* tropical rain forest, with a closed canopy 30–37 m high and emergents growing to 40–45 m (Costa et al., 2005). A central plateau splits the reserve into two drainage systems (Espírito-Santo et al., 2009) with altitude ranging from 40 to 110 m asl. The mean annual temperature is 26 °C and the mean annual rainfall is 2362 mm. Soils in the reserve vary in a continuum from clayey soils at higher altitudes to sandier soil at lower altitudes (i.e., stream valleys).

2.2. Sampling design and datasets

A research team working in the Brazilian Biodiversity Research Program gathered all datasets used in this study (PPBio; see Magnusson et al., 2005 and http://ppbio.inpa.gov.br/Eng). The basic sampling design used in this program is based on the RAPELD protocol (a combination of the acronyms RAP, for Rapid Assessment, and PELD, short for Long Term Ecological Research Program in Portuguese) with a system of trails and permanent plots in which a diverse range of taxa can be sampled (see Magnusson et al., 2005; Costa and Magnusson, 2010 for a detailed description of the sampling design). The RAPELD grid in the Ducke Reserve is a square 8 km on a side, containing 64 km^2 of trails connecting 72 plots with a distance of 1 km between them (Fig. 1). Each sample plot is 250 m long, and its width varies according to the taxa or life stage being sampled. The centerline of each plot follows an elevation contour line, thus minimizing altitudinal variation within plots. A detailed description of the sampling protocols used to collect the data on composition and abundance of the different taxonomic groups can be found in the metadata available together with individual datasets in the PPBio website (http://ppbio.inpa.gov.br/Eng).