



Assigning indicator taxa based on assemblage patterns: Beware of the effort and the objective!



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ABSTRACT

Environmental managers often use indicator taxa to monitor full biodiversity and hidden environmental factors. For identifying practical indicators from assemblage data collected in the field, it is crucial to remove irrelevant variation, which unfortunately is not a common practice. We demonstrate, based on field data from Estonian forests, (i) how an attractive indicator group of macrofungi, perennial polypores, loses its apparent indicator value when variation in study effort and conspicuous environmental factors have been reduced; (ii) that simply including survey effort variation is sufficient to create significant covariation between species richness of taxon groups, which has often been taken as a justification for indicator assignment. These results imply that standardizing study effort should become a requirement for any field study that reports indicator taxa based on covariance patterns. We encourage researchers to be explicit and critical about the practical value of indicator taxa when compared with direct measurement of habitat conditions.

1. Introduction

The questions of where biodiversity is, and how it responds to the changing environment, have become an everyday part of environmental management. Because full biodiversity is impossible to address in practice, an attractive perspective is to use selected taxon groups or species, which represent other taxa (“biodiversity indicators”) or reveal hidden features or holistic ‘health’ of the environment (“environmental indicators”; Caro, 2010). By now, the literature on indicator species is huge and diverse, ranging from conceptual (e.g., Landres et al., 1988; Sætersdal and Gjerde, 2011), methodological (e.g., McGeoch, 1998; Favreau et al., 2006; Goodsell et al., 2009) and operational problems (Lindenmayer and Likens, 2011) to hundreds of empirical attempts to list indicator species for practical use in marine, freshwater and terrestrial realms (e.g., Rosenberg and Resh, 1993; Villard and Jonsson, 2009; Pereira et al., 2013; Overmars et al., 2013; Halme et al., 2017).

While distinguishing indicator species is thus a popular research activity, its real-world applications place high responsibility on researchers for indicator validity and for clarity of the objective (the characteristic indicated) (e.g., Lindenmayer and Likens, 2010). Warnings given include, notably, that (i) subsets of taxon groups are seldom informative for inferring the distribution of taxonomically and/or ecologically distant groups, except perhaps at extreme spatial scales (Westgate et al., 2014); (ii) surveys of many sensitive indicator species (particularly small organisms with complicated taxonomy) can be so

difficult or expensive that managers reject those as impractical (e.g., Maes et al., 2011); and (iii) direct measuring of habitat factors can be more convenient, reliable, or to serve broader goals than surveys of even well-known taxa (Gjerde et al., 2007; Billeter et al., 2008; Banks-Leite et al., 2011; Lindenmayer and Likens, 2011). The broad implication is that environmental indicators should be adaptive (continuously tested and improved) rather than static (Lindenmayer et al., 2015). More specifically, environmental indicator species should focus on measuring particular complex or cumulative characteristics of the environment (Niemi and McDonald, 2004); and most promising biodiversity indicators should include representative subsets of large poorly known taxon groups such as most invertebrate (e.g., Lovell et al., 2007) and fungal groups (Molina et al., 2011; Unterseher et al., 2012).

Besides wisely chosen objectives, the validity of indicator species also depends on the method of indicator extraction. A basic problem is the variable and incomplete detection of species in field studies (e.g., Iknayan et al., 2014), combined with the necessity of biodiversity surveys to be cost-effective (“optimally incomplete”). A consequence is that few tests of biodiversity indicators are based on near-complete species lists, particularly of the target group (but see, e.g., MacNally and Fleishman, 2004). According to our preliminary scan of literature (based on 107 relevant studies among 738 hits with keywords ‘congruence’ and ‘taxon’ or ‘species’ in the database Scopus, 30 June 2014), around half of indicator extraction studies are prone to unaccounted variation that may undermine their conclusions (examples in Table 1).

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Table 1

Examples of biodiversity indicators as distinguished by analysing subsets of field samples, and potential sources of their bias (as assessed by the authors of the current paper).

Indicator distinguished	Target	Approach and study system	Source ^a	Bias ^b	Variation ^c
Species richness					
“Signal” species of bryophytes	Richness of red-listed bryophytes	Visual searching for species along strip transects in Swedish forests	1	DEO	P*
Perennial polypore fungi	Richness of annual (red-listed) polypores	Visual searching for fruit-bodies in forests in Finland	2	DEO	H
Prosobranch gastropods	Total invertebrate richness on shores	Visual rapid surveys of rocky shores in Australia	3	AT	P
Predatory ants	Richness of leaf litter arthropod groups	Trapping of arthropods in various habitats in Colombia	4	CT	P
Nymphalid butterflies	Total butterfly richness	Visual searching (incl. bait-attraction) of butterflies in the Atlantic Forest in Brazil	5	EOT	
Woodpeckers	Total richness of forest birds	Atlas mapping of birds in 10 × 10 km squares in Poland	6	DEOT	HP
Conspicuous species					
<i>Phengaris arion</i> (butterfly)	Total butterfly richness	Visual transect counts on grasslands in Czech Republic	7	O	
<i>Corvus cornix</i> (bird)	Richness of wetland birds in open lowlands	Transect counts of birds in Poland	8	DEO	HP

^a Sources: 1 – Gustafsson et al., 2004; 2 – Halme et al., 2009; 3 – Smith, 2005; 4 – Cabra-García et al., 2012; 5 – Brown and Freitas, 2000; 6 – Mikusiński et al., 2001; 7 – Spitzer et al., 2009; 8 – Kosicki and Chylarecki, 2014

^b Potential bias: A – variation in study plot size; C – capture effectiveness of traps; D – detectability differences among surveyed habitats; E – variation in study effort; O – different observers pooled; T – temporal differences in the activity of organisms.

^c Conspicuous variation not accounted for: H – main habitats or substrates; P – contrasting habitat types, *discussed in the original publication.

In the clearest case, the data on indicator and target taxa have been collected during the same surveys – then, any variation in survey effectiveness (effort, time or area; detection effectiveness among habitats or observers, etc.) can affect the detection of all subsets of species and produce artifactual covariation between them. This problem of cross-taxon evaluations has been better acknowledged (yet seldom quantified) in broad-scale analyses (Gaston, 2000; Williams et al., 2006).

In this paper, we validate a biodiversity indicator that has been previously extracted from large and representative field material: polypore fungi with perennial fruit bodies (hereafter: perennial polypores), which are among the best detectable fungi (Berglund et al., 2005; Lõhmus, 2009). Based on almost 1500 Fennoscandian surveys of fruit-bodies, Halme et al. (2009) reported perennial polypore species richness to explain nearly 70% of the variation in the richness of other (annual) polypores and, separately, red-listed annual polypores. Their finding could add a valuable tool for forest conservation assessments and monitoring of dead-wood inhabiting biodiversity, given the ecological relationships between polypores, forest structure and other taxon groups (Junninen and Komonen, 2011). Polypores serve some key functions in forest ecosystems: they are among the dominant decomposers of the vast woody biomass, enrich soil with nutrients (Dighton and White, 2017), and play major roles in food-webs (Stokland et al., 2012). Importantly, however, Halme et al.'s (2009) analyses pooled multiple datasets that were heterogeneous in terms of study effort and habitats. To analyse whether such heterogeneity may have affected the detected indicator value of perennial polypore richness, we collected two comparable datasets, which (i) differed in the inclusion of conspicuous environmental variation, and (ii) allowed us to perform the analyses both at fixed and variable efforts.

2. Material and methods

2.1. Datasets

We re-analysed two datasets, which have been collected using similar techniques in hemiboreal forests in mainland Estonia. The survey method was a 4-hour survey of polypore fruit bodies in September–October (top fruiting season in Estonia) in 2-ha plots, which were delineated within relatively homogeneous stands. We have shown that such a combination of effort and area effectively reveals local species pools (Runnel et al., 2015). The fruit bodies that could not be reliably identified in the field were collected and identified either microscopically or (ca. 2% of specimens) by rDNA ITS and LSU sequences, as compared with those available in public reference databases and authors' personal database. Additionally, in every studied plot, line

intersect approach was used to measure the volume of downed woody debris (four to five 50-m transects per plot; the method described by Lõhmus and Kraut, 2010).

Dataset 1 ('mixed-type dataset') was collected all over inland-Estonia and has been documented in detail by Runnel and Lõhmus (2017). It included 23 pairs of forests: an old-growth stand and a nearby mature commercial stand of the same type. The stand pairs represented four distinct types of forest along the moisture and nutrient status gradients: from dry boreal pine forests to mixed meso-eutrophic and eutrophic forests (six replicates of each) and, finally, mobile-water swamps (five replicates). The surveys were carried out in 2005–2006 by the same observer (A.L.).

Dataset 2 ('drained-forest dataset') was collected in 29 Scots pine (*Pinus sylvestris*) dominated, drained peatland forests within ca. 70-km² area in south-western Estonia (ca. 58°20'N, 25°05'E). The area has been described and some preliminary results listed by Runnel et al. (2015). The studied stands differed from each other by age structure (dominant tree cohort 42–118, mean 77 years), the share of downy birch (*Betula pubescens*) in the canopy (0%–33%, mean 11%), and the depth of the peat layer (from 0.3 m to > 1.5 m). No recent signs of timber harvesting were observable in any plot. The polypore surveys were carried out in autumn 2013 by both authors (15 randomly assigned plots by A.L., 14 plots by K.R.). The authors had previous joint experience with the method and the species richness estimates obtained confirmed a lack of between-observer difference (21.9 and 21.4 polypore species per plot, respectively; *t*-test: *t* = 0.5, *p* = 0.63). From this dataset, we used both the 4-h survey results and their subdivision to 30-min intervals (i.e., species accumulation curves) for simulating variation in effort.

2.2. Data processing

Our main approach was to describe plot-scale relationships between the species richness of annual polypores (dependent variable) and of perennial polypores (independent variable) (hereafter: 'species richness relationship'). Polypore species were categorized to either of these taxon groups similarly to Halme et al. (2009). Neither of the species richness values contained zeroes and both were symmetrically distributed around the mean; we therefore used parametric analysis methods for their simplicity. The statistical analyses were performed using STATISTICA 7.1 software.

To explore whether perennial polypores could reflect conspicuous environmental variation (here: broad ecosystem type; plot size; year), we first used simple linear regression to investigate whether the species richness relationship differed between the Dataset 1 (containing a wide gradient of forest types over a region) and Dataset 2 (restricted to one

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