



# A flexible multi-scale approach for standardised recording of plant species richness patterns

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## ABSTRACT

A sound monitoring of appropriate biodiversity indicators is necessary in order to assess the progress towards the internationally agreed target of halting the loss of biodiversity by 2010. However, existing monitoring schemes often do not address species richness as a key component of biodiversity directly or do so with insufficient methods. I provide an overview and assessment of the large variety of different sampling approaches for small-scale plant species richness. Major shortcomings of many of these are (i) non-uniform plot sizes or shapes; (ii) analysis of only one spatial scale despite the scale dependence of nearly all biodiversity parameters; (iii) lack of replication of smaller subplots; and (iv) exclusion of bryophytes and lichens despite their often large contribution to total plant diversity. Based on this review, I propose a new standardised sampling approach for plant diversity patterns at small scales that is applicable for a multitude of purposes and in any biome. In its basic variant, species composition is recorded on nested squares of 0.01 m<sup>2</sup>, 0.1 m<sup>2</sup>, 1 m<sup>2</sup>, 10 m<sup>2</sup>, and 100 m<sup>2</sup>, with all smaller subplots being replicated at least 3-fold and evenly spaced within the next larger plot. Not only terricolous vascular plants, but also bryophytes, lichens, macro-algae as well as non-terricolous taxa should be recorded with the any-part system, i.e. those plants are counted within a plot whose superficial parts reach over it. This approach can be used to assess plant diversity patterns (i) of individual plots of interest, (ii) along environmental gradients, (iii) within specific vegetation types, or (iv) for landscape sectors. In the latter case, the series of nested plots must be placed randomly or systematically, but irrespective of plot homogeneity. The proposed approach allows the calculation of many meaningful biodiversity indicators, while being well compatible with a range of other sampling schemes, but avoiding their shortcomings. As this approach is not very time-consuming in its basic variant, but can easily be extended for specific purposes, I suggest its use for any kind of biodiversity studies and particularly for monitoring.

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## 1. Introduction

Biodiversity is seriously threatened by anthropogenic global change (Sala et al., 2000). At the 2002 World Summit on Sustainable Development in Johannesburg, 190 nations agreed on "... achieving by 2010 a significant reduction in the current rate of biodiversity loss at the global, national, and regional level ... ." (Balmford et al., 2005a, b; EEA, 2007). Biodiversity may be lost due to many different processes, such as climate change, intensification of agriculture on productive sites, abandonment of agriculture on marginal sites, direct habitat loss, habitat fragmentation, and nitrogen deposition (e.g. Sala et al., 2000). Various measures have been taken to counteract these negative tendencies, for example, by establishment of nature reserves, 'agri-environment schemes', or organic farming. However, it is largely unknown whether and

how these numerous presumably negative and positive factors actually influence biodiversity. Moreover, 'biodiversity' is not a single, easy-to-measure figure, but a multi-faceted phenomenon, ranging from genes, over species to ecosystems, including both the number of different 'entities', their composition and spatial variability, and behaving differently for different taxa and at different spatial scales (e.g. Heywood and Watson, 1995; van der Maarel, 1997).

For species diversity as the central dimension of biodiversity, global patterns are well documented and reasonably understood for vascular plants and vertebrates, but only at large spatial scales (10,000 km<sup>2</sup> and more) (Gaston, 2000; Mutke and Barthlott, 2005). In well-surveyed regions as some parts of Europe, for vascular plants and bryophytes data of good quality are available down to the scale of quadrants of topographic map sheets (approximately 30 km<sup>2</sup>) (e.g. Benkert et al., 1996; Meinunger and Schröder, 2007). For smaller scales, such as 1 m<sup>2</sup> or 1000 m<sup>2</sup>, it is presently even in central Europe impossible to answer seemingly trivial questions such as "What is the mean species density?" or "Which are the

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most frequent taxa?" However, these are the scales on which species interact with each other and with their changing environment; thus, processes at these small scales ultimately produce the well-known global patterns.

Nearly all aspects of biodiversity are scale-dependent, the species–area relationship (SAR) being only the most prominent one (Connor and McCoy, 2001; Crawley and Harral, 2001; Turner and Tjørve, 2005; Dengler, 2009). Regarding botanical diversity, spatial scale also affects co-occurrence patterns (e.g. Otýpková and Chytrý, 2006), species turnover along abiotic and land-use gradients (e.g. Reed et al., 1993; Spiegelberger et al., 2006), spatial patterns of diversity metrics (e.g. Kallimanis et al., 2008), species frequency distributions (reviewed in Dengler, 2003), as well as species constancies and thus vegetation classification (Dengler, 2003). Even species diversity patterns that are nearly universal at large scales may be reversed at small scales. Dengler and Löbel (2006) and Dengler and Boch (2008a), for example, found higher plant species richness at plot scale in the hemiboreal compared to the nemoral zone, contrasting to the usually assumed negative diversity trend towards the poles (e.g. Gaston and Spicer, 2004). Similarly, small-scale richness of vascular plants and bryophytes significantly increases in Switzerland from the colline to the montane to the subalpine belt (Koordinationsstelle Biodiversitätsmonitoring Schweiz, 2006), which deviates from the typical elevational decrease at larger scales (e.g. Gaston and Spicer, 2004).

A meaningful set of biodiversity indicators for monitoring is needed in order to assess progress towards the 2010 target of halting biodiversity loss (Balmford et al., 2005a, b; Dudley et al., 2005; see also Dröschmeister, 2000). Strangely, among the many proposed indicators within the framework of the Convention on Biological Diversity (CBD; see Balmford et al., 2005a; EEA, 2007) none addresses species richness directly and the majority even lack a straightforward relation to biodiversity. The coverage of protected areas or forests (two of the proposed indicators), for example, is not necessarily positively related to all components of biodiversity (see Dudley et al., 2005). Even recent biodiversity monitoring schemes that explicitly address plant species richness (e.g. Dröschmeister, 2001; Seidling, 2005) often neglect the scale dependency of biodiversity (by studying only one spatial scale) or the many methodological pitfalls involved in small-scale species richness sampling (for review, see Dengler, 2008).

With this article, I aim at providing an overview of existing major approaches for assessing species diversity and at evaluating their merits and shortcomings. As a result, I will present a new flexible multi-scale sampling approach. My focus is on botanical diversity, representing the one component of ecosystems that usually constitutes the major proportion of biomass, that shapes ecosystem functions and services, and that can be most easily assessed in a near-comprehensive manner (as compared to animals, fungi, and microbes).

## 2. Overview and evaluation of existing approaches

With the following review, I do not intend to list the multitude of published approaches comprehensively, but to discuss some major categories of widely used methodologies for recording local plant diversity patterns.

### 2.1. Phytosociological surveys

Phytosociological records, so-called relevés, presently probably constitute the largest proportion of available data on small-scale plant species richness. Numerous such relevés have been taken according to procedures described in phytosociological textbooks (e.g. Braun-Blanquet, 1964; Westhoff et al., 1973; Dierschke, 1994) in order to describe and classify vegetation, to analyse relation-

ships between community composition and environment, and partly also to monitor vegetation changes. Worldwide, there are several million relevés, partly published, partly unpublished (Ewald, 2001; J. Schaminée and M. Chytrý, 2008, personal communication). In a recent survey, J. Schaminée and M. Chytrý (2008, personal communication) concluded that in Europe alone more than three million relevés exist. These relevés become increasingly available in large regional or national databases, e.g. approximately 460,000 in the Dutch database (Schaminée et al., 2006), 70,000 in the Czech database (Chytrý, 2007), and 50,000 in the largest German database, that of Mecklenburg-Vorpommern (Berg et al., 2004). These high numbers of relevés in combination with their good spatial (e.g. Berg and Dengler, 2004; Schaminée et al., 2006; Chytrý, 2007) and temporal coverage (phytosociological relevés have been taken in a basically similar way since nearly one century) constitute a great, yet largely unused potential for addressing ecological questions and for monitoring environmental change (Ewald, 2001; Dengler et al., 2008). Unfortunately, this potential power of past phytosociological data for biodiversity and other ecological research is diminished by several shortcomings: (i) phytosociological sampling procedures vary in many ways between researchers and are not always clearly documented in the studies (cf. Dengler, 2003); (ii) phytosociologists often place their plots subjectively according to the occurrence of assumed character species (see Glavač, 1996), leading to biases in species richness and species compositional data (e.g. Diekmann et al., 2007); (iii) in phytosociology, a very wide range of plot sizes has been suggested (e.g. Westhoff et al., 1973; Dierschke, 1994) and applied (see Chytrý and Otýpková, 2003), typically differing by a factor of 1000 within and 10,000 between vegetation classes; (iv) according to circumstantial evidence, relevés of larger plots are often rather incomplete (Chytrý, 2001; Dengler et al., 2006).

### 2.2. Whittaker plots and their modifications

In contrast to phytosociological relevés, 'Whittaker plots' have been specifically developed by R.H. Whittaker for sampling and comparing biodiversity patterns (Shmida, 1984; see Table 1). Whittaker plots together with their recent modifications are widely used in North America and in semi-arid regions worldwide. In the original version (Shmida, 1984), a Whittaker plot consists of four different plot sizes, namely 1 m<sup>2</sup>, 10 m<sup>2</sup>, 100 m<sup>2</sup>, and 1000 m<sup>2</sup>, with the 10 m<sup>2</sup> plots replicated twice and the 1 m<sup>2</sup> plots ten times and the plots arranged in a nested manner in the centre of the largest plot. While the 1 m<sup>2</sup> and 100 m<sup>2</sup> plots are squares, the 10 m<sup>2</sup> and 1000 m<sup>2</sup> plots are rectangles with a length–width ratio of 5:2. Two new variants of Whittaker (WH) plots have been suggested by Stohlgren and co-workers: the 'Modified-Whittaker' (MW; see Table 1) and the 'Long-Thin' (LT) plot designs (Stohlgren, 1995, 2007; Stohlgren et al., 1995). Both use the same four plot sizes as the original, but differ in three aspects: (i) they apply (nearly) identical length–width ratios for all sizes, namely 5:2 or 4:1 in MW plots and 10:1 in LT plots; (ii) the subplots below 1000 m<sup>2</sup> are not nested within each other; (iii) the replicates of the smaller areas are placed as far from each other as possible. In the North Carolina Vegetation Survey (Peet et al., 1998; Fridley et al., 2005; see Table 1), the original Whittaker design is modified by adding two smaller plot sizes (0.1 m<sup>2</sup> and 0.01 m<sup>2</sup>), by using square plots for all but the 1000 m<sup>2</sup> areas (which retain the 5:2 shape), and by having four replicates of 10 m<sup>2</sup> size and eight of all smaller sizes. Contrary to MW and LT designs, the smaller plots are fully nested. BIOTA biodiversity observatories, which are widely used for biodiversity monitoring in Africa ([www.biota-africa.org](http://www.biota-africa.org); see Jürgens, 2006), are another variant of Whittaker's fundamental approach. Each observatory consists of an area of 1 km × 1 km, subdivided in one hundred 1-ha grid cells, 20 of which are selected for detailed

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