

WHAT CAN BE INFERRED FROM SPECIES DIVERSITY INDICES?

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Abstract. Species diversity indices, which describe distribution of individuals among species into a single value, are at best questionable tools for community functional analysis. As shown in the article, they cannot be safely used either deductively for the testing of hypotheses, or inductively for the sorting of communities into different functional types.

Since the pioneering papers of Fisher *et al.* (1943) and Simpson (1949), many species diversity indices have been proposed (see Peet 1974, Washington 1984 for reviews, recently *e.g.*, Kvalseth 1991). Essentially, these indices are all designated to describe community dominance structure, that is the distribution of individuals among species in any sample (Fig. 1), into a

single value. Construction of indices is performed in various ways, all converting initial information to a presumptive more workable form by inevitably reducing them. The substantial effort devoted to the mathematical perfection of indices, and their routine usage as an important community characteristic, strongly implies that dominance structure is valuable for under-

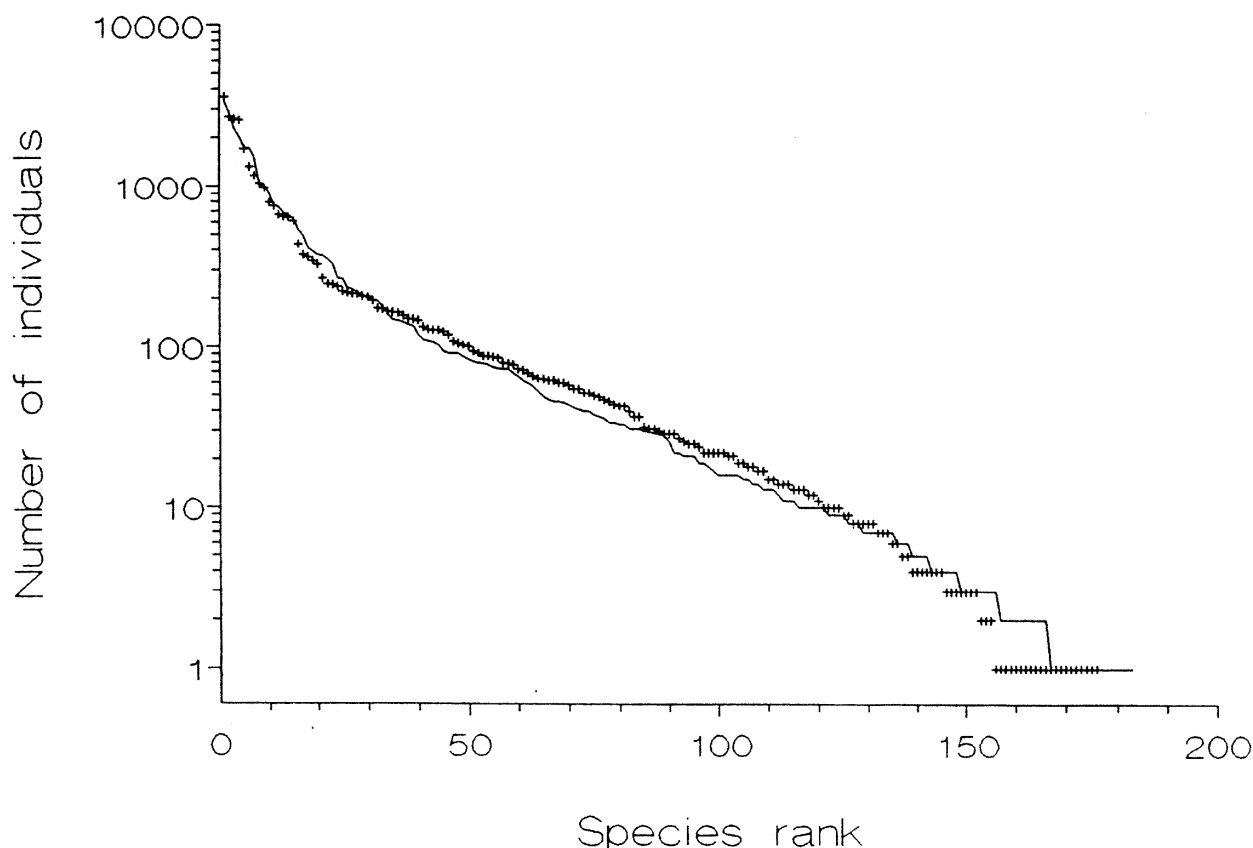


Figure 1. Dominance structure of two moth communities (Lepitoptera, Noctuidae) near Ceske Budejovice, South Bohemia. Total number of individuals of each species in a sample is depicted; for each community, species are ordered in a descending order. Solid line: agriculture landscape, 183 species, 31 937 individuals. Crosses: climax alder carr, 176 species, 31 834 individuals. Each community was sampled daily during the vegetative seasons 1981 - 1989 by a light trap.

standing community organization and function, a major goal of community research. Contrary to this expectation, it is practically impossible to draw any significant conclusions concerning the dynamic processes of a community from its dominance structure, and vice versa.

Various theoretical models that differ widely in their premises concerning community assemblage rules predict the same dominance structure. The log normal distribution of individuals among species may be merely a consequence of the central limit theorem (MacArthur 1960, May 1975), or the result of the sequential breakage of a community niche space (Sugihara 1980), the summation of several species groups with normal distributions (Ugland and Gray 1982), or the hierarchical habitat model (Kolasa and Biesiadka 1984). Similarly, there are several explanations for other distributions, including the broken-stick distribution (MacArthur 1957, Webb 1974, Cohen 1968). Consequently, the dominance structure of real communities cannot be used to test the validity of niche division models even in the case of a perfect agreement between predicted and real data.

This point is illustrated by two species assemblages of Noctuidae (Lepidoptera) from two neighbouring sites in South Bohemia. One is from temporally highly variable agricultural landscape, and the other from the climax ecosystem of an alder carr with constant composition of vegetation (Spitzer and Lepš 1988, Jaroš and Spitzer 1987). The data sets presented in Fig. 1 are based on nine years of continuous sampling. They are fully comparable one to another in the sampling method, time, location, sample size, and species number. The communities differ significantly in the prevailing bionomic strategy of constituent species, but in terms of dominance structure they are indistinguishable. The agricultural landscape community is an assemblage of mainly polyphagous species with population sizes widely fluctuating in time, the community of the alder carr is more habitat specific and temporally constant in composition (Rejmánek and Spitzer 1982, Spitzer *et al.* 1984, Spitzer and Lepš 1988, Wolda *et al.* 1992).

Obviously, as descriptors of community dominance structure, indices of diversity are at best questionable tools for community functional analysis. They cannot be safely used either deductively for the formulation and testing of hypotheses of community assembly rules, or inductively when applied to sorting of sampled communities into functional types according to their dominance structure. Consequently, the causal inter-

pretation of diversity values is very difficult so that their measurement adds a little to the understanding of community organization. Calculations of diversity values so represent a case where perfection of mathematical descriptors is not followed by an adequate progress in our understanding of biological reality which is being described.

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