



PARTITIONING RAPTOR SPECIES DIVERSITY WITHIN THE PLAIN AREA LOCATED IN THE SOUTH OF DOLJ COUNTY, ROMANIA

Mihail Dragoș ȘTEFĂNESCU¹, Mariana Luminița OLARU², Sandu BOENGIU³

¹University of Craiova, Faculty of Biology, Al.I.Cuza 13, 200 585- Craiova, Romania - mihailstefanescu@yahoo.com

²University of Craiova, Faculty of Biology, Al.I.Cuza 13, 200 585- Craiova, Romania – luminitaolaru@yahoo.com

³University of Craiova, Faculty of Biology, Al.I.Cuza 13, 200 585- Craiova, Romania - sboengiu@central.ucv.ro

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SYNOPSIS

Spatial patterns of species diversity within a local habitat vary from one region to another. In order to illustrate this variation we used the additive partitioning of species diversity method. It is a method for decomposing some total amounts of diversity (γ) into the components of mean diversity within samples (α) and diversity among samples (β). Additive partitioning is based on the simple relationship that alpha and beta sum to gamma ($\gamma = \alpha + \beta$). Raptor species diversity was additively partitioned within and among samples (α and β diversity) from hierarchically levels to assess the proportion of the total diversity (γ) found in the plain cultivated areas located in the South of Dolj County.

INTRODUCTION

The general concept of biodiversity can have different meanings. The human activities are greatly reducing biodiversity. This can vary from depleting the number of species at a particular place and time, to homogenizing species composition among regions. Conservation efforts may be misguided unless we pay careful attention to precisely underline how human activities alter species diversity in space and time (Lande et al. 2003).

To generate these insights we need to partition species diversity into components, much like an experimentalist uses Analysis of Variance to partition a variance into components associated with different factors or causes (Lande et al. 2003).

Conservation biologists have recently recognized applications for diversity partitioning in survey design (DeVries et al. 1997). Partitioning of spatially explicit diversity can identify the most important source of diversity and target conservation efforts.

The idea that diversity can be partitioned into additive components is not new. MacArthur et al. (1996) and Levis (1968) developed simple equations for additively partitioning diversity a few years after Whittaker (1960) and decades before Lande (1996), but their equations did not use Whittaker's terms. Ecologists have followed Whittaker (1960) and viewed γ -diversity as being the product, not the sum, of α - and β -diversities.

Beta diversity was introduced by Whittaker to describe changes in species composition and abundance across environmental conditions. Whittaker (1956) defined the diversity within a "community" as "alpha diversity". β -diversity was then taken as the change in the number of species for one place to another along the gradient (Whittaker 1960), and later defined a "species turnover" or changes in species composition from one community to another (Whittaker 1972). Whittaker (1960) reasoned that if one knew the average diversity within a set of communities or sample (α -diversity), then one could obtain the total diversity represented by all samples (γ -diversity).

Lande (1996) appears to have been the first to place the additive partitioning of species diversity in the context of Whittaker's concepts of α -, β -, and γ -diversities. Lande's (1996) additive version treats α -diversity as the average within-sample diversity, regardless of whether diversity is measured by species richness, the Shannon index, or The Simpson index. Likewise, β -diversity is also an average; it is the average amount of diversity not found in a single, randomly-chosen sample.

The present paper analyses the partitioning of raptor species diversity (13 species) within certain plain or agricultural areas located in the South of Dolj County, Romania, aiming at rendering a possible utility of the method with regard to raptors' conservation.

METHODS

The additive partitioning of species diversity is a method for decomposing some total amounts of diversity (γ) into the components of mean diversity within samples (α) and diversity among samples (β). Additive partitioning is based on the simple relationship that alpha and beta sum to gamma ($\gamma = \alpha + \beta$). Moreover, species diversity can be partitioned at each level or scale of hierarchical sampling schemes in which samples at level j are nested within samples at level $j + 1$. In a hierarchical sampling scheme, the α -diversity at level j equals the alpha at level $j-1$ plus the beta at that level; $\alpha_j = \alpha_{j-1} + \beta_{j-1}$. As a result, the total diversity equals the alpha at the lowest level plus the beta at each level; $\gamma = \alpha_1 + \beta_1 + \beta_2 \dots + \beta_N$. Diversity at each level can be expressed as a percentage of the total diversity. Diversity partitioning is also useful for comparing alpha and beta diversity given that the two are measured in the same units.

Null models and associated hypothesis tests have played a central role in the theoretical development of several other concepts in community ecology (Gotelli 2000). We utilized a null hypothesis that observed partitions of species diversity do

not differ from those expected by chance. The null hypothesis tests whether the observed partition of diversity could have been explained by a random distribution of individuals. It may be useful for testing alternative explanations of species diversity that are based on the nonrandom distribution of individuals such as intraspecific aggregation, resource partitioning, and community saturation (Shorrocks and Sevenster 1995).

The null hypothesis assumes that the observed numbers of individuals of each species are randomly placed among samples at the lowest level ($i=1$), and samples containing randomly placed individuals are then grouped together into progressively larger samples at each higher level $i= 2...m$. Thus our null hypothesis is the observed components of diversity (α_1 and β_1) could have been obtained by the random distribution of individuals among samples at all hierarchical levels.

To test this hypothesis, we conduct a simulation procedure that we refer to as individual-based randomization because the number of individuals and species in sample are determined by the random placement of individuals into sample at the lowest level. The randomization procedure uses a reshuffling algorithm to place individuals in samples randomly while preserving the original species-abundance and sample-size distributions. Samples at higher level are obtained by pooling the appropriate samples at lower levels, as when the actual data are partitioned.

Each randomized data set is then partitioned into α and β components at each hierarchical level for the three diversity measure. The randomization process is repeated 1,000-10,000 times to obtain null distributions of the α and β diversity estimates at each hierarchical level. The probability (P value) that a diversity component greater than the observed could be obtained by chance is obtained from the proportion of null values that are greater than the observed value.

For all these operations we utilized the methodology and a computer program, PARTITION, developed by Crist et al 2003.

We illustrate this technique with a hierarchical study of raptor species to test whether observed partitions are significantly different from the null hypothesis across three sampling scales. The largest sampling scale included two regions of plain and cultivated areas in the southern part of Dolj County, Romania. In each region, we selected one study site with different management conditions. Within each site, four habitat types were sampled, for a total of 8 samples.

RESULTS

More than 60 per cent of the total species richness was due to within- and among –habitat components (α_1 and β_1). The component due to site comprises 32.31 per cent four times the component due to regions (7.69 per cent). The expected components of species richness from null hypothesis are also additive to the total richness, and their proportional contributions can be compared directly with the observed values (fig. no. 1). The species richness at the lower sampling levels comprised a greater proportion of the total than in the observed partition.

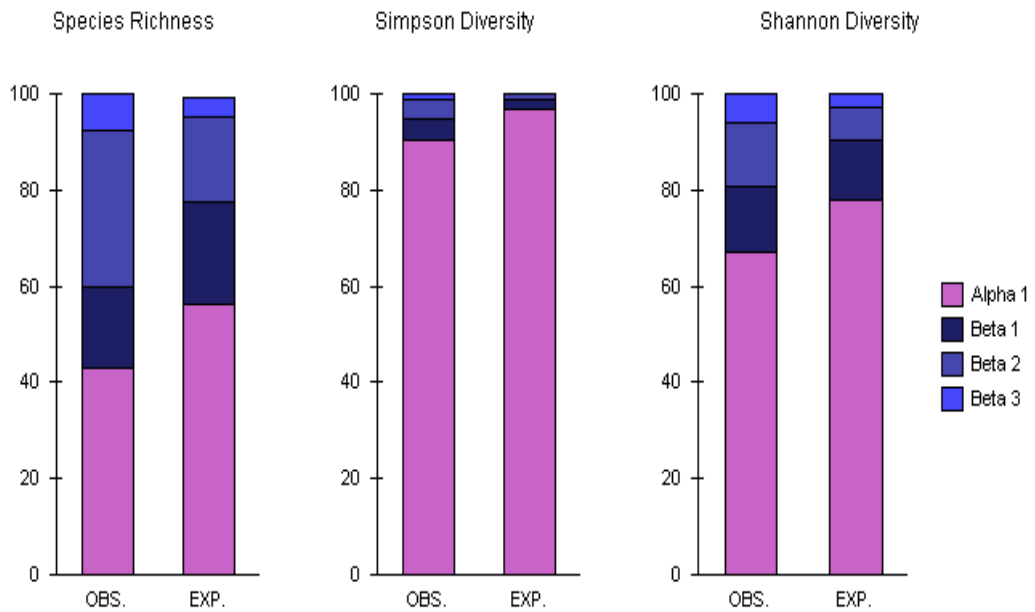


Figure 1: Additive partition of raptor species richness, the Shannon and Simpson index of diversity across three levels (Values are expressed as the percent of the total diversity of raptor species explained by each hierarchical level). The observed partitions are compared with expected values.

A different situation is the partition of Shannon index where α_1 comprised 66.92 per cent of the total raptors diversity. The components due to among habitats (β_1) and sites (β_2) were almost equal (13 per cent) and the component due to among regions (β_3) comprised 5.9 per cent. Despite a great portion of Shannon diversity is found locally within habitats, the observed levels of β diversity (β_2 and β_3) were greater than the value expected from individual-based randomization (table no.1).

Table 1.1 Additive partition of raptor species diversity in a hierarchical sample of plain and cultivated areas in southern part of Dolj County, Romania. There are also shown the expected diversity components on the alternate null hypothesis of no community structure (H).

Diversity component	Species richness		Shannon info.		Simpson diversity	
	Observed	H	Observed	H	Observed	H
among regions β_3	1.0	0.5	0.123*	0.061	0.0078*	0.0008
among site within region β_2	4.2**	2.3	0.277*	0.139	0.0326*	0.0077
among habitats β_1	2.2*	2.8	0.289	0.26	0.0375	0.0161
within habitats α_1	5.6*	7.3	1.394*	1.624	0.7438*	0.7971

* $p \leq 0.05$, ** $p \leq 0.001$

The observed partition of the Simpson index was similar to that from the Shannon index with an even greater importance of α_1 diversity with 90.52 per cent of the total raptor diversity within habitats.

In test of the null hypothesis, species richness was significantly greater than expected for β_2 among sites level ($p \leq 0.001$). Species richness was significantly lower than expected for sampling levels α_1 and β_1 ($p \leq 0.05$). The β_3 among regions level was greater than expected but significantly less ($p = 0.061$). Shannon index null test reveal the same result for α_1 level significantly lower than expected ($p \leq 0.05$). The remaining β components for Shannon index (except β_1) were significantly greater than expected (for β_2 $p = 0.003$ and for β_3 $p = 0.005$). For Simpson index randomization test produce the same pattern of statistical significance as those found with Shannon diversity.

Randomization test show that the β_2 component of species richness among sites are very highly significantly greater than expected by chance indicating that the tendency for different rare raptor species to occur in different sites is not just a random process. Shannon's information occurs mostly at higher levels in the hierarchy, reflecting variation in the geographic distribution among species with intermediate frequencies.

Intraspecific aggregation has a key role in explaining the species coexistence and diversity (Ives 1991 and Legendre 2002). If individual species are aggregated in different habitats, the within-habitat diversity would be lower and among-habitat diversity would be greater than expected by chance. Our raptor diversity partition is consistent with this prediction despite not all tests are significant.

CONCLUSIONS

One of the most operational methods for analysing raptor species diversity across multiple levels is the additive partitioning of species diversity. In our example, More than 60 per cent of the total species richness was due to α_1 and β_1 diversity. According to Shannon index α_1 comprised 66.92 per cent of the total raptor diversity. The observed partition of the Simpson index was similar to that from the Shannon index with an even greater importance of α_1 diversity. The most abundant species were widespread so that the same common species comprise most of α_1 and β_1 diversity. Thus, most rare species were found in a single habitat or site resulting in a small contribution to the α_1 diversity.

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