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# Species richness of a spider community (Araneae): Extrapolation from simulated increasing sampling effort

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**Araneae, spider community, Species richness, biodiversity, island bio-geography, species-area curve, agricultural habitat, apple orchard, pitfall trapping**

**Abstract.** A short and intensive pitfall trapping was performed in an apple orchard to estimate the species richness of the ground-dwelling spider assemblage present. Calculation of the total number of species was achieved by an extrapolation performed in two steps:

1. Establishing a series of species counts corresponding to increasing sampling efforts. Simulation of increasing sampling efforts was achieved by computer sub-sampling.
2. An asymptotic function, derived from the theory of island bio-geography, was established to describe the sampling curve. The asymptotic value of this function provided the estimated total species number, corresponding to a sampling effort that would have covered the whole sampled area.

The method gave a robust and singular result. This method can be useful in comparative biodiversity studies of animal assemblages.

## INTRODUCTION

Different sampling efforts produce different estimates of species richness (Niemelä et al., 1986), but an unbiased estimate is an important characteristic of any animal community (McIntosh, 1967; Peet, 1974). Species richness, although it does not incorporate information on the distribution of individuals among species, is easy to use and is not inferior to diversity indices in describing differences between sites (Wolda, 1983). Species richness is often the simplest measure that allows the rejection of the null hypothesis that two samples have been drawn from the same community (Simberloff, 1978).

To obtain species richness values, independent of sampling effort, one can intrapolate to a standard sample size by rarefaction (Simberloff, 1978) or, as in the present paper, can extrapolate to estimate the total number of species of a given community. The increase in species number as a function of sample size (area sampled) normally results in a saturation curve which can be described by the species-area function of the equilibrium model of island bio-geography (MacArthur & Wilson, 1967).

Here we present an estimation of the species richness of ground dwelling spiders in an apple orchard by simulating a cumulative sampling effort based on the original pitfall trap catches. Fitting a mathematical function to the resulting saturation curve provided an estimate of the total number of spider species present in the orchard.

## MATERIALS AND METHODS

### Study site and trapping method

The study area was in the 5.8 ha apple orchard of the Plant Protection Institute of the Hungarian Academy of Sciences at Juliannamajor, near the north western outskirts of Budapest. The orchard, planted on clay soil, consisted of cultivars "Jonathan", "Golden Delicious" and "Starking". Trapping was performed in the block with cultivar "Jonathan". The surrounding vegetation consisted of other orchards, alfalfa fields and a *Quercetum petreae-cerris* oak forest. The ground-layer vegetation of the orchard was weedy grass occasionally tilled between rows and mowed under the trees. Pest control included 2–4 herbicide and fungicide sprayings during the season, but no insecticides were sprayed.

To sample the spiders active on the ground surface, we used 60 pitfall traps (0.5 l glass jars, 10 cm diameter, with 70% ethylene glycol as preservative) arranged in a grid, 10 meters apart from each other. To gain a "snapshot" picture that represents the community over a short period of time, we used data collected during April–May, 1981 (a total of 1,680 days-trap exposure).

### Computing the total number of species

To estimate the total number of spider species a procedure, described by Stout & Vandermeer (1975), was used. Increase in sampling effort (A) was simulated by involving successively increasing number of traps from the original 60. To calculate the number of species sampled with one trap ($A = 1$), we have randomly selected one trap, took the number of species caught, repeated this procedure 20 times, and calculated the average number of species. To find out the average number in two traps ($A = 2$), we chose a pair of traps randomly, pooled their catch and counted the number of species. The procedure was repeated 20 times and the average number of species was calculated. The same procedure was executed for sets of 3, 4, … 59 traps, repeated 20 times in every case, to gain an average value of the actual species number for each sampling effort. The result of this procedure, plotted as average species number (S) vs. sampling effort (A) is termed as the "empirical curve".

The empirical curve can be described by more mathematical functions. The first function we fitted was the equilibrium equation of the theory of island bio-geography (MacArthur & Wilson, 1967). This equation gives the number of species (S) in relation to the area of an island (A) in an island archipelago, when immigration from the species pool of "T" species and the extinction on the island are in equilibrium:

$$S = a / (A^{-z} + a / T)$$

In the present study "A" is the sampling effort (number of traps considered), "T" is the total number of species in the community (the saturation level of the curve, and also the parameter of interest); "a" and "z" are constant parameters, related to immigration and extinction. In an effort to investigate alternative mathematical functions as well, three other asymptotic functions were also fitted to the data (Table 1). All functions were fitted with an iterative non-linear least squares grid searching procedure. The parameter estimates were finally refined by the Gauss-Newton method (SAS/STAT User's Guide, 1988).

TABLE 1. Equations, parameters, goodness of fit, and asymptote values of the functions fitted to the empirical curve.

| Equation | Parameter estimates | | | Residual SS | Evenness of residual plot* | Estimate of "T" |
|---|---|---|---|---|---|---|
| | $b_0$ | $b_1$ | $b_2$ | | | |
| $y = b_0/(x^{b1}+b_0/b_2)$ (species-area) | 4.59 | –0.77 | 36.97 | 8.34 | even | $b_2 = 36.97$ |
| $y = x/(b_0x+b_1)$ (hyperbolic) | 0.03 | 0.32 | — | 18.02 | poor at low and high As | $1/b_0 = 31.74$ |
| $y = b_0+b_1\exp(b_2x)$ (asymptotic) | 27.53 | –23.02 | –0.06 | 29.68 | poor at low As | $b_0 = 27.53$ |
| $y = \exp(b_0+b_1/x)$ (asymptotic) | 3.36 | –5.43 | — | 104.10 | very poor at low As | $\exp(b_0) = 28.73$ |

*assessed by eye

## RESULTS AND DISCUSSION

The traps caught 246 spiders, belonging to 28 species. Most numerous among them were the wolf spiders (Lycosidae), although the most abundant species was *Zelotes villicus* (Gnaphosidae). The caught species are shown in Table 2. During the experiment, the mean catch/trap was 4.1 (S.D. = 2.04) individuals and 3.5 (S.D. = 1.50) species.

TABLE 2. The dominance and trapping frequency of the spider species caught in the pitfall traps.

| Taxon | dominance (%) | trapping frequency (caught in % of traps) |
|---|---|---|
| *Zelotes villicus* | 18 | 47 |
| *Trochosa ruricola* | 9 | 30 |
| *Pardosa monticola* | 8 | 27 |
| *Pardosa hortensis* | 8 | 23 |
| *Trochosa robusta* | 7 | 23 |
| *Pardosa lugubris* | 7 | 23 |
| *Xysticus kochi* | 7 | 27 |
| *Pardosa riparia* | 7 | 27 |
| *Pardosa agricola* | 4 | 15 |
| *Diplostyla concolor* | 3 | 10 |
| *Alopecosa trabalis* | 3 | 13 |
| *Pardosa agrestis* | 2 | 10 |
| *Centromerus silvaticus* | 2 | 10 |
| *Pachygnatha degeeri* | 2 | 8 |
| *Aulonia albimana* | 2 | 8 |
| *Robertus lividus* | 2 | 7 |
| *Alopecosa pulverulenta* | 1 | 5 |
| *Trochosa terricola* | 1 | 5 |
| *Pardosa pullata* | 1 | 3 |
| *Pisaura mirabilis* | 1 | 3 |
| *Coelotes longispina* | 1 | 3 |
| *Pardosa paludicola* | 0 | 2 |
| *Alopecosa accentuata* | 0 | 2 |
| *Pardosa prativaga* | 0 | 2 |
| *Runcinia lateralis* | 0 | 2 |
| *Agroeca pullata* | 0 | 2 |
| *Enoplognatha thoracica* | 0 | 2 |
| *Harpactea rubicunda* | 0 | 2 |

The random selection procedure performed assumes that the traps at the edge of the area sampled have similar capacity to catch spiders as the traps in the centre of the area. This assumption can be valid only if the catching area of the traps does not overlap, so there is not more interference among traps at the centre than at the edge. Luff (1975) calculated that interference between traps can be of significance only if the grid is small relative to the distance moved by the animals. Data on activity radius of small predatory arthropods (Baars, 1979; Cady, 1984; Franke et al., 1988; Samu & Sárospataki, in press) suggest that at 10 m trap distance interference among traps can be neglected. Traps at the edge and their neighbours inside the grid caught similar number of individuals and species (one-way ANOVA, d.f. = 1.21, $F < 1$, $p > 0.5$).

Of the different asymptotic functions fitted to the data, the species-area function – the one suggested originally by Stout & Vandermeer (1975) – performed the best (Table 1,

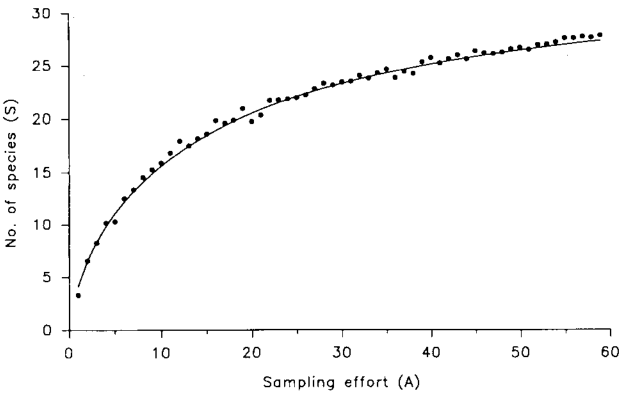

Fig. 1. The species area equation fitted to the empirical curve. Data points represent average species numbers (from 20 replicates) computed for the given sampling effort.

Fig. 1). Fitting this function not only produced the lowest sum of squares, but the fit was also the most even through the whole range of the data, as tested by inspecting the residual plots (Table 1). Using the species-area function, the total number of spider species present in the orchard at the time of the investigation was 37.

The spread of the numbers of species per n traps within each of the 20 replicates decreased from the low sampling efforts (S.D. = 2.4) to large samples (S.D. = 0.4) (Fig. 2a). As the sampling effort increased, the distribution of species number in a replicate became narrower, unimodal, and became skewed at the very end (Fig. 2b). This phenomenon was due to the fact that at smaller sampling efforts the probability that any particular trap was

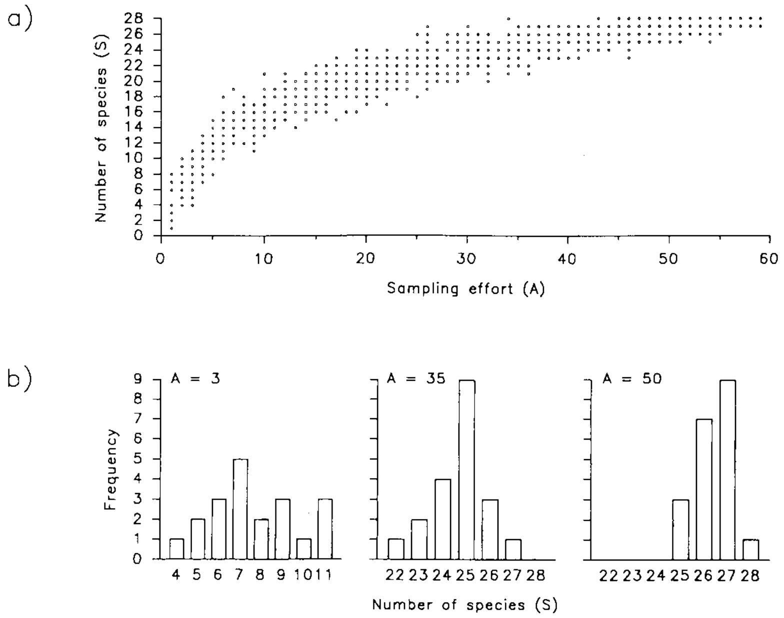

Fig. 2. Spread and distribution of the empirical curve at different sampling efforts. a) Range of species number values in the 20 parallel counts, calculated for each sampling effort. b) Frequency distribution of species counts at three sampling efforts.

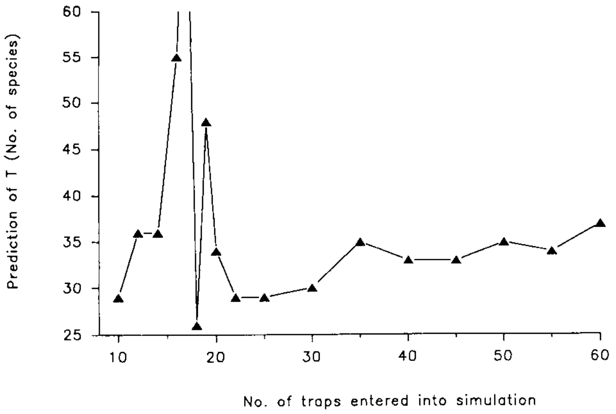

Fig. 3. Change in the predicted number of species as a function of number of traps considered in the starting data set.

chosen more than once was low. At larger sampling efforts, in order to obtain 20 replicates, the repeated use of data from a certain trap became inevitable. Calculating a n average from very similar replicates may be redundant, but omitting these values would not have altered our prediction of the asymptote. This also allowed us to use an identical method over the whole range of sampling effort values.

We also evaluated the ratio of the actual and predicted species number (S/T). This ratio strongly depends on the shape of the curve, which reflects the structure of the community, but also on the actual sampling effort of the study. Stout & Vandermeer (1975) found that for tropical communities, the curve had a gentle but persistent increase; for mid-latitude communities, the curve rose sharply at smaller sampling efforts, overtaking the tropical community curve initially. However, the curve reached its asymptote at lower species number and at smaller sampling effort than the tropical stream communities studied. In that study the S/T values varied from 17–90% (Stout & Vandermeer, 1975). The same ratio was low (33%) in Risch (1979), who applied the same procedure to sweep net samples of insects in maize. S/T ratio for the present study was 75.5%. We think that a high S/T ratio makes the estimate more robust, because the fit is based not only on the strongly ascending, but also the saturating section of the curve. We have simulated the effect of lower S/T ratios by excluding different portions of the original data set from the simulation and thus making S lower. Reducing the number of traps by up to 50% did not influence "T" to a great extent but fewer than 30 traps caused the extrapolation to vary wildly (Fig. 3).

Stout & Vandermeer (1975) based their method on the analogy between their sampling units (rocks in the streams) and real islands. Although the catching area of pitfall traps could be defined as islands, such an analogy is more difficult to justify, since such "islands" would have different area (activity radius) for all species of different mobility. Therefore we propose to interpret the function by directly connecting it to sampling procedures on a community. Preston (1962) and MacArthur & Wilson (1967) pointed out that increasing samples from a community having a log-normal distribution produce the same species-area curve as the one derived from the equilibrium theory. Since distribution of the spider community was significantly different from truncated lognormal distribution fitted to the data ($\chi^2$ = 15.54, d.f. = 4, $p < 0.01$) (Magurran, 1988), there is no evidence that either true insularity or the appropriate niche partitioning processes would exist in the real community, which are the biological assumptions behind the function used. This leaves us with the conclusion that this mathematical function is robust enough to explain the empirical curve, which, in our case, was obtained from a non-lognormal community.

We emphasise that this method estimates only the species richness of a community at a definite short period of time and not the number of species during the whole season. We regard short and intensive trapping as a useful zoological tool especially for comparative purposes and as initial support for decision making in conservation.

During a short sampling period one can ignore differences in the seasonal activity of the species as well as immigration and emigration. Such short-term trappings provide precise "snapshots" of the community studied. To obtain a comprehensive species number estimation, we suggest a series of trapping sessions and estimations of the type described. We are confident that the above method would be useful in many situations where species richness of communities should be compared or tracked through time on the basis of limited samples and data sets.

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