



Figure 13.6. Hypothetical communities with contrasting species-accumulation curves. Habitat A has higher within-sample diversity (e.g., species richness) than habitat B, but it reaches an asymptote more quickly. A within-sample analysis alone may conclude that habitat A is more diverse.

and Beattie (1996b) augment their sample diversity analyses with species-accumulation curves for different sites. In each case the curves provide a powerful and intuitive visual confirmation of the results from within-sample diversity statistics.

Do Relative Abundance Distributions Conform to Biological or Statistical Models?

A decades-long tradition has been to compare sample relative abundance data to mathematical distributions. Some of the distributions are based on particular biological models; others are “statistical” models judged purely on goodness of fit. Three of the most common distributions used to fit relative abundance data are the geometric series, the log-series, and the log-normal. Each has a preferred plot—a method of plotting the data that most clearly demonstrates

the goodness of fit of the data to the model (Magurran 1988).

A sample that fits a geometric series produces a rank abundance plot in which each species abundance is a constant proportion of the preceding species abundance. If a rank-log abundance plot is used, the species fall along a straight line. In contrast, a log-series or log-normal distribution is nonlinear in such a plot. Geometric series distributions have lower evenness than log-series or lognormal. A biological mechanism that could produce a geometric series is the niche preemption hypothesis, in which the first species to arrive at a site monopolizes k percent of the available resources, the next species monopolizes k percent of the remaining resources, and so forth. Species-poor communities sometimes exhibit relative abundance distributions that fit a geometric series. The Berlese data do not conform well to a geometric series (Fig. 13.5); the curve is somewhat concave rather than straight.

A sample that fits a log-series is dominated by a few very common species, similar to the geometric series, but also has many rare species. The preferred plot for the log-series is a frequency histogram for which the horizontal axis is species abundance and the vertical axis is number of species. The highest point of the curve will always be the species known from singletons, with a steep monotonic decrease in numbers of species with higher abundances. Alpha, one of the parameters of the log-series distribution, has been touted as one of the best diversity indexes, mainly because of its low sensitivity to sample size (L. R. Taylor 1978). Magurran (1988) gives recipes for calculating the log-series distribution and evaluating goodness of fit of sample data.

Most species are of intermediate abundance in a sample that fits a lognormal distribution (Fig. 13.7). The preferred plot is a frequency histogram like the plot for the log-series, except that the horizontal axis (abundance class) is a