



Figure 13.8. Contrasting relative abundance distributions for the Berlese data, differing only in how the abundance classes are defined (see text). Each abundance class is a doubling of the previous one. Differences in how singletons and doubletons are distributed in the lowest abundance classes dramatically alter the shape of the distributions.

when plotted using the two different abundance class definitions (Fig. 13.8).

Coddington (pers. comm.) finds fault with both the Ludwig and Reynolds and Magurran methods. The Ludwig and Reynolds method correctly assigns species to abundance classes by splitting ties into adjacent abundance classes, but it is flawed because it includes the 0.5–1 abundance class. This abundance class is under-sampled because the lowest measurable abundance is 1 (the singletons). Magurran's method is flawed because it combines the two lowest abundance classes, and does not account for ties. The Ludwig and Reynolds method underestimates the lowest abundance class; the Magurran method overestimates it. Coddington proposes a modification of the Ludwig and

Reynolds method: use 1–2 as the lowest abundance class instead of 0.5–1. In other words, the lowest abundance class contains half the singletons plus half the doubletons. To see the effect of this method on the Berlese data, ignore the leftmost bar in the upper graph of Fig. 13.8

May (1975) has shown that the lognormal distribution is common in both biological and nonbiological applications (e.g., the distribution of wealth in the United States). The lognormal distribution can be produced by combining the effects of many independent variables, each of which can have any underlying distribution. Thus a lognormal distribution of biological community data may reveal only that many unknown and independent factors are contributing to the observed sample distribution. Alternatively, Sugihara (1980) provided evidence that biological community data fit certain lognormal distributions too well to be explained by multiple independent factors, and he proposed a particular model of community structure that predicted the distributions he observed.

The general problem remains that most data sets are equally well explained by many competing models. Even model distributions as fundamentally different as the log-series and the lognormal have been difficult to distinguish using sample data.

## What Is the Species Richness of a Community?

Conservation biologists and environmental planners may be called upon to evaluate or rank different sites for their conservation value and to monitor changes in conservation value over time. Although not the sole criterion in determining conservation value, community species richness is often considered one of the most important (Gaston 1996). Thus obtaining reliable estimates of species richness is an important goal.