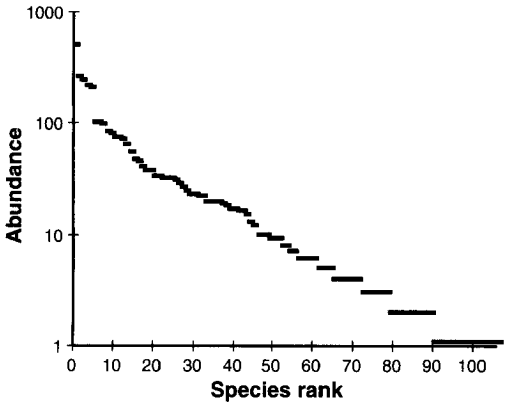

Figure 13.5. Rank abundance plot from Berlese data (see text). The 107 species are ranked from most abundant on the left to least abundant on the right. Abundance is expressed on a log scale.

estimates from other communities or other studies. Thus a diversity value for a single sample has little worth. However, instead of estimating community parameters, diversity indexes can be used to assess differences between groups of samples. This approach follows Taylor's dictum that diversity indexes are only as good as their ability to discriminate the effects of relevant environmental variables (L. R. Taylor 1978). For example, for the Berlese data we may want to know if samples from old-growth forest somehow differ from samples from second-growth forest. We can calculate the value of a diversity index for each sample and compare the sets of values using a *t* test or Mann-Whitney U test.

Common diversity measures are sample species richness (S), alpha (α), the Shannon index (H'), the Simpson index (D), and the Berger-Parker index (d). These measures vary in how they are influenced by the species abundance distribution. Species richness, a measure that ignores evenness, is strongly influenced by the often long tail of rare species. "Dominance" indexes, such as the Simpson and Berger-Parker, are strongly influenced by the relative abundance of the few most abundant species. The Shannon index is influenced by both species richness and the dominant species. Alpha is influenced by the species of intermediate abundance and is relatively insensitive to the rarest and most abundant species.

Alpha is calculated by first estimating x from the iterative solution of

$$\frac{S}{N} = \frac{(1-x)\,(-\ln(1-x))}{x}$$

where S is the number of species in the sample and N is the number of individuals, and then calculating alpha from

$$\alpha = \frac{N(1-x)}{x}$$

The Shannon index is calculated as

$$H' = -\sum p_i \ln p_i$$

where p_i is the proportion of individuals in the ith species.

The Simpson index is calculated as

$$D = \sum \left(\frac{n_i\,(n_i - 1)}{N(N-1)} \right)$$

The higher D the lower the diversity, so the reciprocal of D is often used so that a higher number means higher diversity.

The Berger-Parker index is calculated as

$$d = \frac{N_{\max}}{N}$$

where $N_{\max}$ is the number of individuals in the most abundant species. As in Simpson's index, higher d means lower diversity, so the reciprocal is often used.

Returning to the Berlese data, Table 13.3 shows diversity indexes calculated for each sample. Sample species richness, alpha, and the Shannon index show weak trends toward second growth being more diverse, but the differences are not significant. The two indexes that