

## CAN BIODIVERSITY BE MEASURED INDEPENDENT FROM SAMPLING EFFORT?

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Biodiversity is most frequently expressed as species richness and often in combination with some measure of species abundance distributions. Species richness ( $S$ ) is simply the number of species present in an assemblage and can be modified to include also the total number of individuals in that assemblage. Species abundance distributions describe the number of individuals of each species in an assemblage and how individuals are distributed among species. Uneven species distributions are more commonly recognized as having dominant species. Evaluating species richness and species abundance distributions is dependent on sampling effort, illustrated by species accumulation curves that show ever-increasing effort is needed to discover new species. This requirement also applies when comparing biodiversity indices that must be generated using the same sampling protocols, i.e., sample size and effort, for the comparisons to be valid. Other major drawbacks that apply to most of richness and evenness-based diversity indexes are that there is no statistical framework to determine the departure of measured  $S$  from expectation and richness can vary markedly with different habitat type.

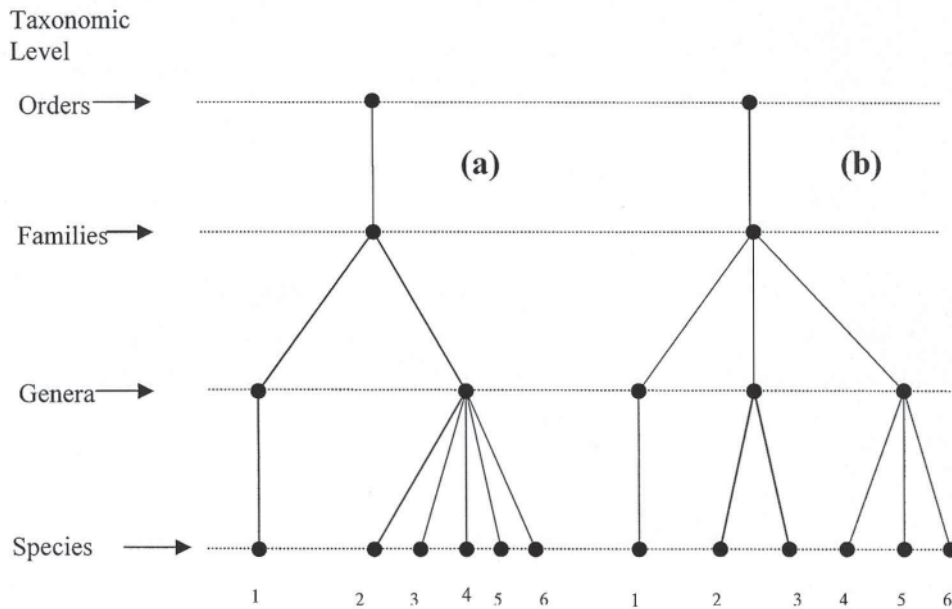
A relatively new index for measuring biodiversity is average taxonomic distinctness (Clarke and Warwick 1998). A nontechnical interpretation of average taxonomic distinctness (abbreviated as either AvTD or  $\Delta^+$ ) is that it is the average distance, based on Linnaean classification, between any two randomly chosen species in a classification tree representing a species assemblage (Figure 1) and is calculated as:

$$\Delta^+ = [\sum_{i < j} \omega_{ij}] / [S(S-1)/2]$$

where  $\omega$  is the distance between species and  $S$  is the number of species present, with  $i$  and  $j$  ranging over these  $S$  species. This metric has properties that overcome the limitations of species richness and evenness-based diversity measures. For example, average taxonomic distinctness of subsets of species chosen at random without replacement from a species assemblage will have the same AvTD as the assemblage they are drawn from, even when  $S$  of the subsets varies in size (Clarke and Warwick 1998). This exercise of choosing subsets of varying  $S$  simulates varying sample sizes. Average taxonomic distinctness, therefore, is not dependent on species richness and consequently is independent of sampling effort.

The present study tested the independence of average taxonomic distinctness from sampling effort a different way, by removing rare species from a species assemblage and observing the effect on the resulting calculated AvTD. The rationale for using rare species was that their discovery is heavily sampling dependent and requires greatest sampling effort. This was a robust procedure for challenging the sampling independent property of AvTD. Species assemblages used in this simulated change in sampling effort were samples from three intertidal areas (2.2–10 acres; 0.9–4.0 hectares) located on the shore of the Gulf of Maine. The samples, ranging from 44–71 species, were epibenthic macroinvertebrates documented in 2005 during a random walk through the intertidal area accompanied with random rock turning. Rare species were selected from a separate data set collected the previous year along line transects (20–230 m) in these same areas. Line transects were divided into continuous quadrats measuring 1 x 0.5 m oriented perpendicular to the shoreline. Sampling effort for line transects at these and three other sites sampled that same year varied from 65–305 minutes and was correlated with number of sample quadrats ( $r = 0.84$ ;  $P < 0.05$ ).

**Figure 1.** Two hypothetical communities with identical species richness ( $S = 6$ ), organized by hierarchical Linnaean classifications into taxonomic trees. Community ‘a’ is less diverse than ‘b’ based on taxonomic relationships with 6 species represented by only two genera as opposed to three in ‘b.’



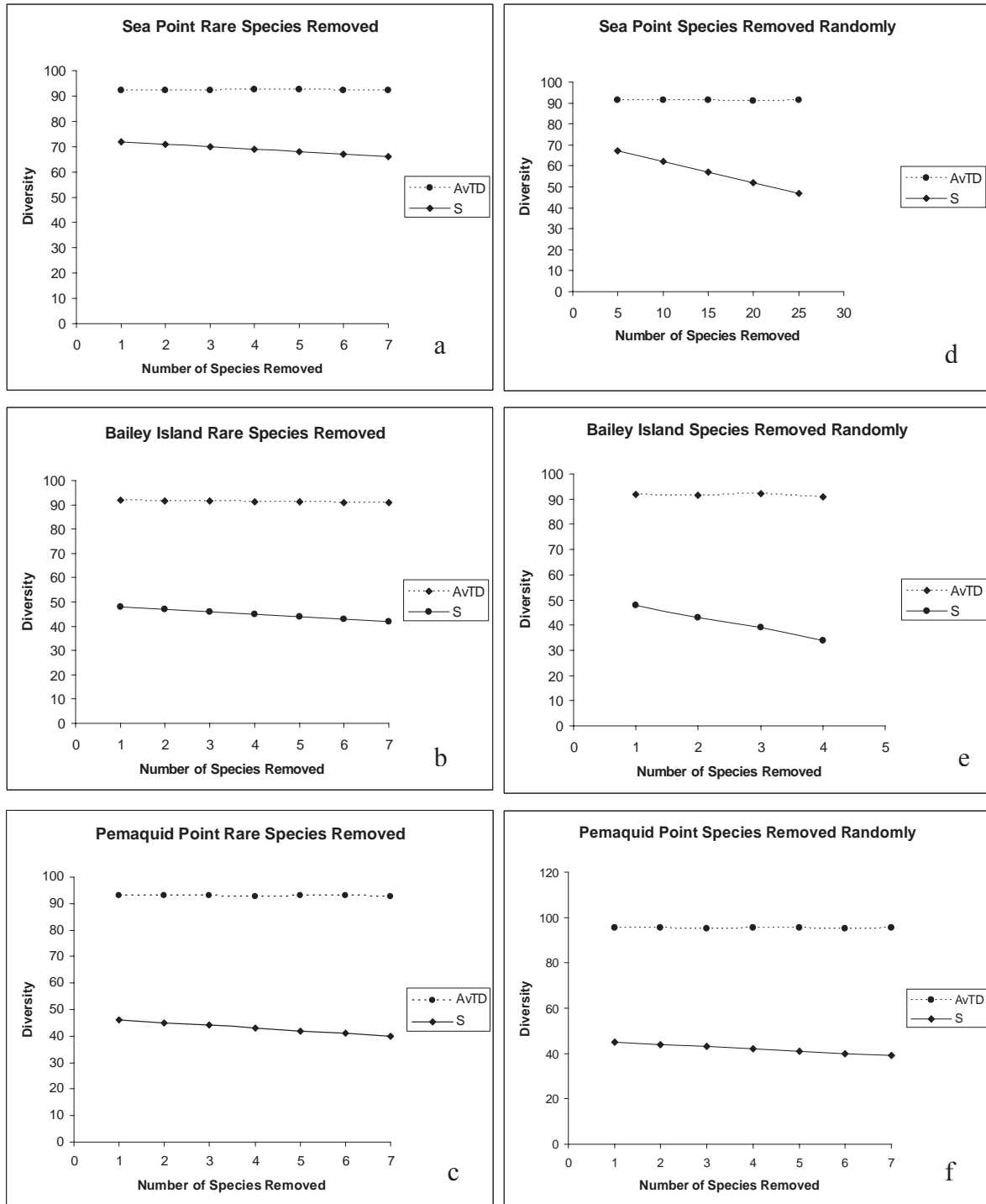
A rare species was defined as one occurring in only 1–2 quadrats. They were then removed, one by one, from their respective species assemblage documented in the 2005 random walk of sample areas. As rare species were removed successively without replacement, average taxonomic distinctness of 2005 samples was barely affected (Figs 2a –c). The absence of affect on AvTD from random removal of species without replacement reported by Clarke and Warwick (1998) was confirmed by repeating their procedure (Figure 2d–f). Since AvTD is barely affected, considerable time can be saved in sampling as shown by the corresponding decrease in sampling time with each quadrat removed (Table 1).

Table 1. The corresponding decrease in sampling time (min) with each reduction in sample quadrat is considerable

Sample Site	Number of Quadrats Subtracted						
	1	2	3	4	5	6	7
Seapoint	1.33	2.66	3.99	5.32	6.55	7.98	9.31
Bailey Island	1.82	3.64	5.46	7.28	9.1	10.92	13.44
Pemaquid Point	2.48	4.96	7.44	9.92	12.4	14.88	17.36

These results confirm that AvTD does not depend on species richness and demonstrate that biodiversity can be measured independent from sampling effort using this metric.

**Figure 2.** (a–c). Removal of species defined as rare by their occurrence in only one quadrat in a line transect has little effect on average taxonomic distinctness (AvTD), although a large effect on species richness (S). (d–f). These results are similar to random removal of species without replacement as previously demonstrated by Clarke and Warwick (1998).



### **Acknowledgements**

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### **Literature Cited**

Clarke, K. R. and R. M. Warwick. 1998. A taxonomic distinctness index and its statistical properties. *Journal of Applied Ecology* 35: 523–531.