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Gordon H. Rodda
U.S. Fish and Wildlife Service

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Diversity

How to Lie with Biodiversity

Biodiversity is the bandwagon of the moment. Unfortunately, the concept is sufficiently complex that almost any population biology study, with almost any conclusion, can be framed as an effort to measure or conserve biodiversity. Based on what I have seen in the literature and heard at recent scientific meetings, here is a primer on some of the more popular ways to bend biodiversity data.

Suppose you wish to claim that a species is disappearing. With the explanation that time and funding were limited, you might present population trajectories based on as few as two estimates of abundance. Perhaps the final abundance estimate was obtained during a drought year. Use a technique for estimating abundance that has untested assumptions. Avoid stating confidence limits. Under these conditions a coin toss would suggest that about half of the species should show declines. If yours does, publish.

If it does not, find a post hoc explanation to account for the result. For example, hypothesize that dry weather reduced or increased activity and distorted your counts. Give your conclusion some statistical rigor by correlating weather phenomena with measures of abundance. But of course don't test the weather hypothesis against an independent data set.

Once you have a hypothesis to account for the apparent influence of weather on abundance, you're all set to model the population dynamics. Gather up a string of weather data from a convenient weather station and model the time to extinction for a population. Time-to-extinction estimates are making a big splash in the conservation community and they don't require any tedious field validation. Few reviewers will notice that this garbage-in-equals-garbage-out exercise provides no new information on the status of the population. With a hypothetical data set you can model whatever extinction time you want.

If you choose to present data on species assemblages, define your assemblage in a way that maximizes investigator convenience. Unfortunately, rare species are difficult to quantify. A popular gambit is to collect data on a few of the commoner species and consider the result representative of the whole assemblage. If you want to

justify habitat disturbance it is generally best to choose early successional species. Area-sensitive forest species should be emphasized by those who want to show that deforestation hurts biodiversity. If this is not convenient, however, one could assume that all species are equally significant; few would notice that global tramp species account for as much biodiversity as do regional endemics. In all probability there is some group of species that can be found to benefit from whatever land-use policy you want to promote.

If you want to go to the effort of quantifying the abundances of all species in an assemblage, simplify your study by basing abundance indices for all species on a single sampling technique. Never mind that there are no techniques that are unbiased among species or among habitats. For example, reptile samplers can rely on an array of pitfall traps and drift fences. Of course, some snake species are rarely caught in pitfall traps, but low estimates of snake abundances do not attract criticism, as it is widely believed that snakes are rare.

If you choose to combine measures of species richness and evenness into a single diversity index, select your index carefully. There are so many measures of diversity that almost any management recommendation can be justified. In some cases, for instance, you may wish to stress how your preferred management prescriptions will improve species evenness in the measured assemblage. If that does not provide the hoped-for answer, you can emphasize within-habitat richness or diversity, using the most supportive of the many available indices. If that still doesn't work, try conflating the concepts of within- and among-habitat diversity. For example, if you want to justify logging of old-growth forest in the face of data showing greater species diversity within old-growth habitats, point out that a combination of old second-growth and recently cleared areas (the combination can be labeled "managed forest") has more species than does old growth alone. It is not hard to pump up species richness measures if you just pool enough habitat types.

Your study (and your management recommendations) will inevitably be linked to your choice of study organism. There is no need to emphasize to readers that

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diametrically opposed management recommendations might have been obtained by studying a different taxon.

If those strategems don't yield comfortable management recommendations, there are always more creative solutions. For example, congressional revulsion to a U.S. public land agency's practice of converting diverse southern hardwood forests to monotypic pine plantations resulted in passage of a law requiring the agency to maintain the level of diversity that is found in forests regionwide. Given the lack of consensus in the scientific community over the best measure of species diversity, Congress left choice of the applicable diversity index up to the managing agency. The agency chose to measure diversity not in number of tree species but in stand age. Thus, for a rotation age of 50 years, maximal diversity was to be achieved by cutting one tenth of the forest area every five years (reforested as a monoculture). Perfect evenness! Such is the beauty of biodiversity; it can be used to justify creation of a monoculture.

Unfortunately, it is easier to add up the ways in which the concept of biodiversity can be misused than it is to present a simple solution to the extremely complex problem of measuring or maintaining biological diversity. The public is unclear on the concept, and scientists cannot give a simple answer. There is broad agreement only that humankind should prevent anthropogenic ex-

tinctions. Perhaps we should build on this consensus rather than undermining it with dubious measurements of biodiversity.

Perhaps we need to recognize that for scientists to combine partial data with advocacy is counterproductive in the long run.

Perhaps conservation biologists need a consensus declaration that short-term, taxonomically narrow, or local diversity studies are inappropriate tools for the long-term conservation of global biodiversity. If anthropogenic declines are our primary concern, perhaps we need to refocus our attention on (1) rangewide status surveys that will provide firm baseline data, (2) evidence that anthropogenic causes are responsible for demonstrable population changes, and (3) identification of the proximate mechanisms that link human activities with species loss. These avenues of study will not be as easy or as much fun as blunderbuss sampling of biodiversity, but they may keep the concept from becoming tawdry through uncritical application.

Gordon H. Rodda

U.S. Fish and Wildlife Service
National Ecology Research Center
4512 McMurry Avenue
Fort Collins, CO 80525, U.S.A.