

A Biodiversity Indicator for Economic Analysis

Yvonne Chen
Shenandoah University

This research models a measurement that could serve as a biodiversity indicator for use in interdisciplinary study. The indicator relies on the phylogenetic variations to benchmark biodiversity, since the functional differences of species are coherent with the phylogenetic variations. Furthermore, the intrinsic and economic value of biodiversity originates from the dynamic functional roles that species exhibit. To conceptualize these observations, the author adopts Linnaean taxonomy—with its focus on phylogenetic attributes when grouping organisms—as the methodology to construct the index and quantify its value. Finally, the article discusses the use of this index in modeling optimization problems and conservation priorities.

INTRODUCTION

The word *biodiversity* has a broad spectrum of definitions: it could refer to the external, full range of species on Earth, the internal, genetic variation within species, or the variations and interactions among ecosystems. At any scale, regardless, biodiversity supports essential productivities of the human society as it provides us with natural resources, recreational uses, cures for diseases, and more. Needless to say, biodiversity is an integrated core of our economic system.

Applying economic techniques to estimate the value of any environmental resource is always a challenging task. In the case of biodiversity, the reason rests not only on the absence of a clearly defined property right, but also its not-directly measurable intrinsic value, which includes all known and unknown benefits of a species. One of the popular methods widely used in solving similar problems is the cost-benefit analysis (CBA). In the case of optimization involving environmental pollution, for example, one can evaluate the cost and benefit of the pollution control to determine the optimal clean up effort. Using the same CBA approach, it is assumed, one should be able to identify optimal biodiversity by weighing its benefit against the cost of conservation. Estimating the costs of conservation, which requires technical expertise and professional knowledge, may be manageable. But how does one go about assessing the value of biodiversity or ecological services?

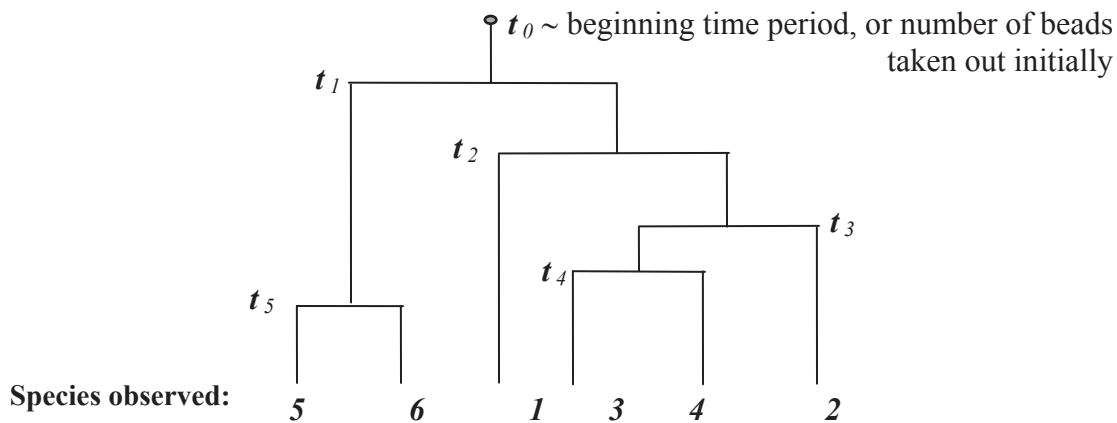
Several approaches have been used to estimate the value of ecological services. The contingent valuation approach relies on using survey to find out consumers' "willingness to pay." However, such method has strong likelihood to produce a bias result (Tietenberg, 1997.) Economists also propose the utility theory: include biodiversity as one type of economic resources, substitutable like capital or labor. However, biodiversity holds an irreplaceable role in the working of an ecological economy. Take the oysters in the Chesapeake Bay as an example. Oyster is not merely a seafood delicacy. Its water-filtering function underpins the whole ecosystem it resides in, and influences various (and economic) aspects of the local economy.

The indicator developed in this paper attempts to address some of these measurement and conceptual issues. The following section provides details on other existing assessments for biodiversity. The subsequent section lays out the groundwork for the proposed biodiversity indicator, in which the system of taxonomic classification is introduced. To conclude the research, the author offers several theoretical examples on model applications and discussions.

LITERATURE REVIEW

The biodiversity indicator constructed in this research was largely inspired by the concepts of Weitzman's bead model (1995). Dr. Weitzman proposed that the genetic evolutionary path is the building block for biodiversity. In his model evolution is likened to tree branching process—it starts small with few branches, and continues to grow larger with new branches and twigs (see Figure 1). Using this branching process, the origin and the status of biodiversity could be explained. A string of beads is used as an analogy for the characteristics of a species, with each species defined by its unique pattern and colors of beads. The beads are accumulated over time by being drawn from a huge bowl that is filled with beads of all possible colors and shapes; i.e., the gene pool. At each unit of time, one bead is drawn from the pool and added to the top of string. Simultaneously, exactly one bead is discarded from the end of string.

**FIGURE 1
WEITZMAN'S BEAD MODEL**



At time t_0 , one type of ancestor species exists. From t_0 to t_1 , $(t_1 - t_0)$ different new beads are accumulated in the string, while the same number of old beads are discarded from the end. The first diversification (bifurcation) takes place at time t_1 , at which two ancestor species are formed. One of these is the common ancestor for species $\{5,6\}$, and the other for species $\{1,3,4,2\}$. The last phase of diversification ends at time t_5 , when ancestor of species $\{5,6\}$ split into two species. The evolution terminates at the current time with six new species 1-6. Each of the six species consists of an equal-length string of beads with some differences in color and pattern. The distance between two species is the number of different beads between them, which is equal to the time elapsed from their most recent common ancestor. Therefore, the total number of different beads contained in the collection of species could be used to define the level of biodiversity.

Although the technique of the bead model is straightforward, its legitimacy is widely disputed (Wilson, 95). Some biologists argued that in order to measure biodiversity, the entire evolutionary history from its process to its time frame needs to be understood first, and much of that information is still inconclusive.

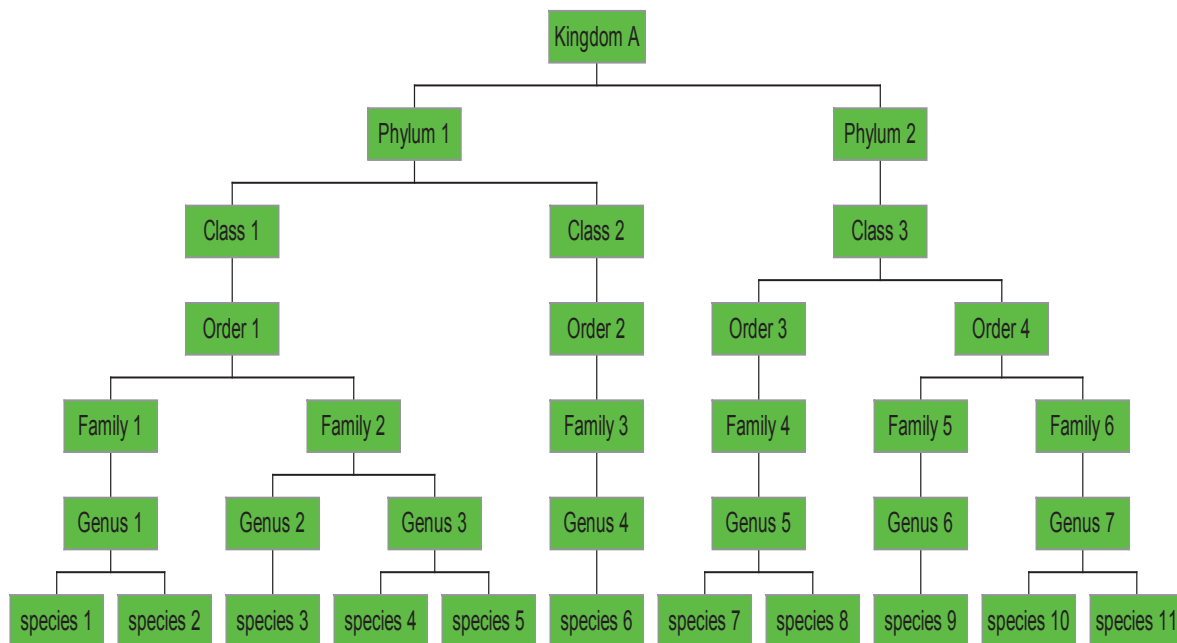
Another widely used biological indices is the Simpson's Index (Hawksworth, 1994), though its application is not without controversy. The index measures the richness of species. That is, it determines the proportion of biomass that each species contributes to the total in a selected area. This index is useful for quantifying number of species in the ecological communities, but it gives little emphasis on how dynamic this system is. A community of ten similar species would have a similar measure as a community with ten diverse species. However, it goes without saying that the first group of species does not have the diversity of the second group. The most significant aspect of biodiversity is at the level of functional differences, not at the level of species richness (Cushman, 96). That is because dynamic interactions are likely to exist among species of different phylogenetic structures in the same ecosystem.

A MODEL FOR BIODIVERSITY

It should be noted that the value of ecological services provided by species (predetermined by its functional role) is far greater than its directly measurable, short-term market value as an economic resource; i.e., oyster as a keystone species in its ecosystem versus as a delicatessen of seafood aficionados. As to the functional difference of species, it is determined by the phylogenetic process. Therefore, the value of biodiversity could be efficiently assessed by examining the functional differences of species and quantifying this diversity with a proxy.

In search of a measuring proxy the author found Linnaean taxonomy a ready tool, since Carl Linnaeus classified organisms based on their phylogeny (evolutionary history). The basic argument for phylogenetic approach is that most organisms share a common ancestry at some time in the past. Phylogenetic differences generally lead to differences in functional roles of the species. It is understandable that the effectiveness of this approach has its limit—by the extent to which the evolutionary history of the species is known. To measure the diversity of an ecological community, the author proposed the following two steps: locate the species on a taxonomy (see Figure 2), and measure their differences in terms of the distances these species are on the taxonomic tree.

**FIGURE 2
LINNAEAN TAXONOMY**



The rationale of this approach is based on the fact that the position of a species on a taxonomic tree indicates a string of unique features of the species (i.e., colorful beads in Weitzman's model), and the relative position, or distance, between species implies the extent of shared characteristics. Assume a taxon consists of two species from different order, family, or genus. Measuring the diversity of this taxon is similar to locating the distance of two "towns" on a map. By assigning a specific value to each taxonomic ranking, we could begin to "map out" the relative distances between species.

However, unlike the distance between two towns, the difference between species is not linear. One level division in taxonomic ranking may suggest countless differences in characteristics of species. There is even a tendency for the variance to diverge as classification advances to higher hierarchy; for instance, differences in phyla are greater than differences in classes. To make amends, the linear distance as measured on the taxonomic tree is replaced by its squared value to denote the difference of species. For example, a measured distance of 5 would be recorded as 5^2 , or 25. Such manipulation is drawn from the statistics concept of variance, where the differences of observations are squared to avoid cancellation of offsetting values. In our case, taking the square of distance could highlight the increasing divergence of species as their distance grows on the taxonomic map. The mathematical format of this indicator is as follows.

Let D stand as the symbol for biodiversity, and $D = \sum d^T(S_i, S_j)^2$, where $d^T(S_i, S_j)$ is the taxonomic distance between species (S) i and j . By taking the square of a taxonomic distance, the difference between species is given more weight. The further the distance, the greater the square value, which implies greater diversity. The remainder properties are listed below.

Axiom 1: The distance between organisms from the same species is defined as zero.

$$d^T(S_i, S_j) = 0, \text{ if } i = j.$$

Axiom 2: The species pair is mathematically interchangeable, but the same pair is recorded only once to avoid iterative computations of the same.

$$d^T(S_i, S_j) = d^T(S_j, S_i); \text{ but if } d^T(S_i, S_j) \neq 0, d^T(S_j, S_i)^2 \equiv 0.$$

Axiom 3: In the event when two (i and j) or more species are from the same hierarchy, only one species is used in measuring the distance with other species (k).

$$D(i, j, k) = d^T(S_i, S_j)^2 + d^T(S_j, S_k)^2 + d^T(S_i, S_k)^2 = d^T(S_i, S_j)^2 + d^T(S_j, S_k)^2.$$

Axiom 4: When species (1, 2, to k) are from the same taxonomic ranking, the distance between species within the group is the same for every pair of species.

$$D(S_i) = (k - 1) d^T(S_1, S_2)^2, \forall i \in [1, k].$$

To obtain D , several steps are developed. The first step is to identify the position of each species on the taxonomic map, and find the group(s) of species with the most immediate taxonomic relation. Next step is to map the rest of the species based on the degree of their taxonomic affinity. Species from the lower hierarchy, which implies greater similarities, will be grouped first, and those that are most unlike will be grouped last. General form of the biodiversity index D is as follows. \rightarrow A group contains n species: $S_i, i = 1, 2, \dots, k, k+1, \dots, l, l+1, \dots, m, m+1, \dots, n$.

$$k \leq l \leq m \leq n.$$

Assume S_1 through S_k are the most similar species. S_{k+1} through S_l are the second most similar ones. S_l through S_m are in the same taxonomic group, while all species from 1 through n belong to a group of higher taxonomic ranking.

Step 1: Subgroup S_i where $i = 1, 2, \dots, k$ are species with the highest resemblance; i.e., belong to the lowest taxonomic hierarchy.

$$D(S_i) = (k - 1) d^T(S_1, S_2)^2, \forall i \in [1, k] \dots \dots \dots (1)$$

Step 2: Subgroup S_i where $i = k+1, k+2, \dots, l$ belong to the second lowest ranking.

$$D(S_i) = (l - k - 1) d^T(S_{k+1}, S_{k+2})^2, \forall i \in [k+1, l] \dots \dots \dots (2)$$

Step 3: The two groups above plus a third subgroup S_i where $i = l+1, \dots, m$ are classified together in a group of higher taxonomic hierarchy.

$$D(S_l, \dots, S_m)$$

$$\begin{aligned}
&= D(S_1, \dots, S_k) + D(S_{k+1}, \dots, S_l) + D(S_1, S_{k+1}, S_{l+1}, \dots, S_m) \dots \text{Axiom 3} \\
&= D(S_1, \dots, S_k) + D(S_{k+1}, \dots, S_l) + (m-l+2-1) d^T(S_{m-l}, S_m)^2 \dots \text{Axiom 4} \\
&= (k-1) d^T(S_1, S_2)^2 + (l-k-1) d^T(S_{k+1}, S_{k+2})^2 + (m-l+1) d^T(S_{m-l}, S_m)^2 \dots (3) \\
&\dots (1) \text{ and } (2)
\end{aligned}$$

Step 4. All species are in the next hierarchy level of taxonomy. S_i where $i \in [1, n]$.

Following axiom 1 and 2, there should be C_2^n “distance” pairs. With axiom 3 and 4, we rule out the iterative computations.

$$\begin{aligned}
D(S_1, \dots, S_n) &= D(S_m, S_{m+1}, \dots, S_n) + D(S_1, \dots, S_m) \dots \text{Axiom 3} \\
&= (k-1) d^T(S_1, S_2)^2 + (l-k-1) d^T(S_{k+1}, S_{k+2})^2 + (m-l+1) d^T(S_{m-l}, S_m)^2 + \\
&\quad (n-m) d^T(S_m, S_{m+1})^2 \dots (3) \text{ and Axiom 4}
\end{aligned}$$

The biodiversity indicator can be written as:

$$D(S_i) = (k-1) d^T(S_1, S_2)^2 + (l-k-1) d^T(S_{k+1}, S_{k+2})^2 + (m-l+1) d^T(S_l, S_m)^2 + (n-m) d^T(S_l, S_{m+1})^2, \forall i \in [1, n] \dots (4)$$

APPLICATIONS AND DISCUSSIONS

Measurement shown below is based on a simple computation technique in which a value of *one* represents the gap between any two nearest taxonomic rankings. If two biological organisms are the same species, then d^T (the taxonomic distance) is set to zero. Two different species of the same genus will have a d^T value of one, and two species from the same family but different genus will have a d^T value of two; i.e., $d^T = 1 + 1$. Species with the same order but different family will have d^T of three; i.e., $d^T = 1 + 1 + 1$. This addition process continues, and d^T increases as lesser similarities are shared between species. A maximum d^T value of seven measures the taxonomic distance between the two most dissimilar living organisms; say, a plant and an animal.

Assume there are three taxa, and each contains four living organisms as follows. Taxon #1: {2, 3, 5, 7}; Taxon #2: {1, 6, 8, 10}; Taxon #3: {4, 7, 9, 11}. The taxonomic location of these species is shown on the taxonomic tree in Figure 2.

To estimate the value of biodiversity, we apply the technique defined in the previous section. The first step is to identify the taxonomic distance between all the pairs in each taxon. For instance, taxon #1 has

$(C_2^4 = \frac{4!}{2! \cdot 2!})$ or six different species pairs to analyze— $d^T(2, 3)$, $d^T(2, 5)$, $d^T(2, 7)$, $d^T(3, 5)$, $d^T(3, 7)$, $d^T(5, 7)$. Next step will be to check for any iterative computation based on Axiom 2 and 3. In this case, species {3, 5} belong to the same family, while {2, 3, 5} belong to the same order. It implies that $d^T(2, 3) = d^T(2, 5)$ and $d^T(2, 7) = d^T(3, 7) = d^T(5, 7)$. Consequently, only $d^T(3, 5)$, $d^T(2, 3)$, and $d^T(2, 7)$ are included in estimating biodiversity of this group.

Let D denote biodiversity. Biodiversity of each taxon is calculated as follows.

$$D_1 = \sum_{\{2,3,5,7\}} d^T(S_i, S_j)^2 = d^T(3,5)^2 + d^T(2,3)^2 + d^T(2,7)^2 = 49.$$

$$D_2 = \sum_{\{1,6,8,10\}} d^T(S_i, S_j)^2 = d^T(8,10)^2 + d^T(1,6)^2 + d^T(1,8)^2 = 77.$$

$$D_3 = \sum_{\{4,7,9,11\}} d^T(S_i, S_j)^2 = d^T(9,11)^2 + d^T(7,9)^2 + d^T(4,7)^2 = 61.$$

Based on the calculations, one could conclude that taxon #2 has the highest biodiversity value of the three groups, despite the fact that each group has the same number of species.

This biodiversity measure approach could also be used to determine the priority of conservation effort. Take taxon #2 as an example. Suppose species 6 and 8 are both endangered, but the resource for conservation is only available for one. Which strategy for conservation is more efficient? Here are two possible scenarios:

A: Let species 8 go extinct.

$$D \text{ for taxon \#2} = \sum_{\{1,6,10\}} d^T(S_i, S_j)^2 = d^T(1,6)^2 + d^T(1,10)^2 = 61.$$

B: Let species 6 go extinct.

$$D \text{ for taxon \#2} = \sum_{\{1,8,10\}} d^T(S_i, S_j)^2 = d^T(8,10)^2 + d^T(1,8)^2 = 52.$$

A higher biodiversity loss clearly links to the extinction of species 6. It could be explained by the fact that species 6, in comparison to species 8, share less characteristics with the others. When extinction occurs on species with little resemblance to the rest of the organisms, a whole lineage of unique genetic characteristics and functions are lost permanently. Therefore, the optimal strategy is A. A case in point is the conservation of the endangered *Ginkgo biloba* (Maidenhair). Dating back to at least 200 million years, this tree has no close biological relatives survived. In addition, its leaf contains a medicinal property that could potentially control the advancement of Alzheimer's disease. These characteristics have made its conservation critical.

CONCLUDING REMARKS

The biodiversity indicator proposed in this research enables us to understand both the functional and utilitarian aspects of the biodiversity. Another contribution of this measurement is it differentiates the ecological importance of species. Instead of considering all species as equal (in terms of their biodiversity importance), this indicator identifies the ecologically more diverse species from the other. Such differentiation is critical as the society often deals with limited resources when practicing conservation biology.

Illustrated in the examples above, the loss of biodiversity could be minimized if prioritizing effort is given to protecting species 6, not species 8. Certainly it would be ideal, but likely infeasible, to allocate sufficient resources into conserving both species. However, part of the characteristics of species 8 could still be found in its ecological cousins (similar relatives), making its extinction a lesser blow to the ecosystem than would be a loss of species 6. The biodiversity indicator, therefore, provides policy makers with an optimization tool in conservation biology and economics.

There are several issues unresolved concerning the accuracy and biasness of this measurement. One of the main challenges is insufficient understanding of functional characteristics of the species, which could compromise the accuracy of this measurement. In addition, problems could arise from sample selection bias. Nevertheless, though this is a work in progress, it is hoped that an indicator such as this could find its contributions in modeling optimization problems in economics, assessing priorities in conservation biology, addressing ecological impact of natural or man-made disasters such as the oil spill, and beyond.

REFERENCES

- Chapman J. and Reiss M., (1992). Ecology: Principles and Applications. Cambridge: Cambridge University Press.
- Collins, A. (2008). "Economic instruments and the conservation of biodiversity," Management of Environmental Quality.
- Cushman, J., Medina, E., Mooney, H., and Schulze, E., eds, (1996). Functional Roles of Biodiversity. New York: Wiley.
- Don and Edward Wilson, eds, (1997). Biodiversity II. Washington, DC: Joseph Henry Press.

Eldredge, N. ed, (1992). Systematics, Ecology, and the Biodiversity Crisis. New York: Columbia University Press.

Hawksworth, D. L., ed, (1994). Biodiversity--Measurement and Estimation. London: Chapman and Hall.

Moran, D. and Pearce, D., (1994). The Economic Value of Biodiversity. London: Earthscan Publications Ltd.

Polasky, S. and Solow, A. (1994). "Measuring Biological Diversity." Environmental and Ecological Statistics 1: 95-107.

Swanson, T., ed, (1995). The Economics and Ecology of Biodiversity Decline. Cambridge: Cambridge University Press.

Tietenberg, T. (1990). "Economic Instruments for Environmental Regulation." Oxford Review of Economic Policy 6(1): 17-33.

Weitzman, M.L. (1992). "On diversity." Quarterly Journal of Economics 57: 363-405.

Wilson, E. (1985). "The Biological Diversity Crisis: a challenge to science." Issues Sci. Technology 2(1): 20-29.