

Measuring and Comparing Biodiversity

1 Diversity of species, phylogeny and function

For an assemblage of individuals, its diversity can be measured in ways different in incorporation of species difference. In species diversity, all species are assumed to be equally distinct. In phylogenetic diversity, evolutionary or phylogenetic differences, *e.g.* taxonomic classification and well-supported phylogenetic tree, is taken into consideration. All else being equal, an assemblage of closely related species is less diverse in terms of phylogeny than an assemblage composed of highly divergent species. In functional diversity, species are described by a set of traits and species difference can be measured by dissimilarities of trait profiles. There are three main approach to functional diversity measures: distance based, dendrogram based and trait-value based.

2 Classic measures of species diversity

Species richness is a simple count of number of species present in an assemblage. It is an intuitive and frequently used diversity index and is a key metric in conservation biology. However, it does not incorporate information about species abundances and is difficult to estimate accurately from small samples.

Shannon index is another measure of diversity, defined as

$$H_{Sh} = - \sum_{i=1}^S p_i \ln p_i \quad (1)$$

where S is species richness and p_i is the relative abundance of i th species.

Gini-Simpson index is another popular measure of diversity, defined as

$$H_{GS} = 1 - \sum_{i=1}^S p_i^2 \quad (2)$$

It gives the probability that two randomly drawn individuals belong to different species.

Species richness, Shannon index and Gini-Simpson index can be united into a family of generalized

indexes, parametrized by a variable $q \geq 0$. The generalized index is defined as

$${}^qH = \frac{1 - \sum_{i=1}^S p_i^q}{q - 1} \quad (3)$$

Thus,

$${}^0H = S - 1 \quad (4)$$

$${}^1H = \lim_{q \rightarrow 1} {}^qH = H_{Sh} \quad (5)$$

$${}^2H = H_{GS} \quad (6)$$

3 Classic measures of phylogenetic diversity

Faith's phylogenetic diversity (PD) (Faith 1992) is a widely used measure of phylogenetic diversity. It is defined as the sum of all branch lengths of a phylogenetic tree connecting all species present in an assemblage. Like species richness, Faith's PD does not incorporate information on species abundance.

Rao's quadratic entropy (Rao 1982) incorporates both phylogeny and species abundances, defined as

$$Q = \sum_{i=1}^S \sum_{j=1}^S d_{ij} p_i p_j \quad (7)$$

where d_{ij} is the phylogenetic distance between i th and j th species.

Allen *et al* (2009) proposed another measure of phylogenetic measure:

$$H_p = - \sum_i L_i a_i \ln a_i \quad (8)$$

where L_i is the length of branch i , a_i is the summed relative abundance of all species descended from branch i .

For an ultrametric tree in which all branch tips are the same distance (denote by depth T) to the root, Faith's PD, Rao's Q and H_p of Allen *et al* can be generalized as (Pavoine *et al* 2009)

$${}^qI = \frac{T - \sum_i L_i a_i^q}{q - 1} \quad (9)$$

Thus,

$${}^0I = \sum_i L_i - T \quad (10)$$

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$${}^1I = \lim_{q \rightarrow 1} {}^qI = - \sum_i L_i a_i \ln a_i \quad (11)$$

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$${}^2I = T - \sum_i L_i a_i^2 \quad (12)$$

37 4 Classic measures of functional diversity (distance-based)

38 Functional attribute diversity (FAD) (Walker *et al* 1999) is the sum of the pairwise distances between
39 species:

$$FAD = \sum_{i=1}^S \sum_{j=1}^S d_{ij} \quad (13)$$

40 where d_{ij} is the functional distance of species i and j .

41 Rao's Q (Equation 7) can be used as a measure of functional diversity, replacing d_{ij} by functional
42 distance. Guiasu (2011, 2012) proposed a weighted Gini-Simpson index for pairs of species as follows:

$$GS_D = \sum_{i=1}^S \sum_{j=1}^S d_{ij} p_i p_j = Q - \sum_{i=1}^S \sum_{j=1}^S d_{ij} (p_i p_j)^2 \quad (14)$$

43 Ricota Szeidl (2009) and de Bello *et al* (2010) transformed Rao's Q for functional diversity to the
44 effective number of species with a maximum species pairwise distance d_{max} . It is the theoretical species
45 richness of a perfectly even assemblage with the same Rao's Q as the original assemblage:

$$Q_e = \frac{1}{1 - Q/d_{max}} \quad (15)$$

46 5 Measure diversity by Hill numbers

47 Measures of species diversity, phylogenetic diversity and functional diversity can be incorporated into a
48 unified framework based on Hill numbers (Chao and Chiu *et al*, 2014) Denote by C an assemblage of
49 entities (species or phylogenetic tree branch segments or species pairs), and by u elements in C . For
50 each u , denote by v_u its attribute value and by a_u its weight (*e.g.* biomass, cover area, abundance). The
51 weighted mean attribute value is

$$\bar{V} = \sum_{u \in C} a_u v_u \quad (16)$$

52 The Hill number of order q is defined as

$${}^qAD(\bar{V}) = \left[\sum_{u \in C} v_u \times \left(\frac{a_u}{\bar{V}} \right)^q \right]^{\frac{1}{1-q}} = \left[\sum_{u \in C} v_u \times \left(\frac{a_u}{\sum_{u \in C} a_u v_u} \right)^q \right]^{\frac{1}{1-q}} \quad (17)$$

53 AD is short for attribute diversity. Further,

$${}^0AD(\bar{V}) = \sum_{u \in C} v_u \quad (18)$$

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$${}^1AD(\bar{V}) = \lim_{q \rightarrow 1} {}^1AD(\bar{V}) = \exp\{-\sum_{u \in C} v_u \frac{a_u}{\bar{V}} \ln \frac{a_u}{\bar{V}}\} \quad (19)$$

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$${}^2AD(\bar{V}) = \frac{1}{\sum_{u \in C} v_u (\frac{a_u}{\bar{V}})^2} \quad (20)$$

References

- [1] Chao, A. , Chiu, C. H. , Jost, L. . (2014). Unifying species diversity, phylogenetic diversity, functional diversity, and related similarity and differentiation measures through hill numbers. *Annual Review of Ecology Evolution Systematics*, 45(1), 297-324.