Anne Chao, Chun-Huo Chiu, Sébastien Villéger, I-Fang Sun, Simon Thorn, Yi-Ching Lin, Jyh-Min Chiang, and William B. Sherwin. 2018.

An attribute-diversity approach to functional diversity, functional beta diversity, and related (dis)similarity measures. ***Ecological Monographs*****.**

Appendix S4: Tabulated summary of two real examples

Table S1. Comparison of functional diversity of three bark treatments and the functional dissimilarity measures among three treatments based on beetle species relative abundance data discussed in the main text. Here d_{min}, d_{mean} and d_{max} refer to the minimum, mean and maximum of the species-pairwise distances in the pooled assemblage.

Diversity order q and threshold level τ	Bark treatment			Dissimilarity among the three treatments	
	Control	Scratched	Debarked	$1-C_{q3}(\Delta(\tau))$	$1-U_{q3}(\Delta(\tau))$
$q = 0$					
$\tau = d_{\text{min}} = 0.0008$	84.00	86.00	61.00	0.279	0.538
$\tau = d_{\text{mean}} = 0.1019$	27.24	29.42	19.74	0.060	0.160
$\tau = d_{\text{max}} = 0.7105$	1.18	1.23	1.15	0.000	0.000
$q = 1$					
$\tau = d_{\text{min}} = 0.0008$	9.81	10.20	8.32	0.118	0.118
$\tau = d_{\text{mean}} = 0.1019$	4.30	4.69	3.75	0.042	0.042
$\tau = d_{\text{max}} = 0.7105$	1.17	1.21	1.14	0.000	0.000
$q = 2$					
$\tau = d_{\text{min}} = 0.0008$	4.46	4.17	3.56	0.066	0.023
$\tau = d_{\text{mean}} = 0.1019$	2.97	3.10	2.53	0.027	0.009
$\tau = d_{\text{max}} = 0.7105$	1.16	1.19	1.14	0.000	0.000

Table S2. Comparison of within-plot functional diversity of two Forest Dynamic Plots in Taiwan (Fushan and Kenting) and between-plot functional dissimilarity measures based on species relative abundance data (10-ha for each plot) discussed in the main text. Here d_{min}, d_{mean} and d_{max} refer to the minimum, mean and maximum of the species-pairwise distances in the pooled assemblage.

Diversity order q and threshold level τ	Individual plot		Dissimilarity between Fushan and Kenting	
	Fushan	Kenting	$1-C_{q2}(\mathit{\Delta}(\tau))$	$1-U_{q2}(\mathit{\Delta}(\tau))$
$q = 0$				
$\tau = d_{\text{min}} = 0.0035$	94	86	0.867	0.929
$\tau = d_{\text{mean}} = 0.1556$	4.56	7.71	0.074	0.137
$\tau = d_{\text{max}} = 0.6077$	1.28	1.23	0.000	0.000
$q = 1$				
$\tau = d_{\text{min}} = 0.0035$	25.19	8.16	0.994	0.994
$\tau = d_{\text{mean}} = 0.1556$	3.35	2.84	0.360	0.360
$\tau = d_{\text{max}} = 0.6077$	1.28	1.21	0.012	0.012
$q = 2$				
$\tau = d_{\text{min}} = 0.0035$	13.47	3.05	1.000	1.000
$\tau = d_{\text{mean}} = 0.1556$	3.21	2.12	0.569	0.397
$\tau = d_{\text{max}} = 0.6077$	1.27	1.20	0.029	0.015

Here we briefly explain why the two types of data (species raw abundances and species within-assemblage relative abundances) lead to different functional alpha, beta and gamma diversities. Our following derivation is for functional gamma diversity; the same reasoning applies to functional alpha and beta diversities. Then in Tables S3 and S4, we compare some numerical differences for the two real-data examples presented in the main text.

(a) Based on species raw abundances n_{ik} (the number of individuals of the *i*-th species in the *k*-th assemblage), it follows from Eq. (6a) of the main text that the functional gamma diversity of order *q* given a specified threshold level τ is simply the Hill number for an assemblage in which there are *S* sub-assemblages: the *i*-th sub-assemblage consists of $v_{i+}(\tau) = n_{i+} / a_{i+}(\tau)$ functional groups, each with group abundance $a_{i+}(\tau)/n_{++}$, *i* = 1, 2, …, *S*, where

$$\frac{a_{i+}(\tau)}{n_{++}} = \sum_{j=1}^{S}[1-f(d_{ij}(\tau))]\frac{n_{j+}}{n_{++}} = \sum_{j=1}^{S}[1-f(d_{ij}(\tau))]\sum_{k=1}^{N}\frac{n_{jk}}{n_{++}}.$$

The attribute contribution of species *i* is $v_{i+}(\tau) = n_{i+} / a_{i+}(\tau)$. Let $p_{ik} = n_{ik} / n_{+k}$ denote the within-assemblage relative abundance of the *i*-th species in the *k*-th assemblage. Then we obtain the following relationship:

$$\frac{a_{i+}(\tau)}{n_{++}} = \sum_{j=1}^{S}[1-f(d_{ij}(\tau))]\sum_{k=1}^{N}\frac{n_{+k}}{n_{++}}p_{jk}. \qquad \text{(S1)}$$

The above relationship is obtained by noting that $\frac{n_{j+}}{n_{++}} = \sum_{k=1}^{N}\frac{n_{+k}}{n_{++}}p_{jk}$, i.e., any species relative abundance in the pooled assemblage is equivalent to size-weighted pooling over the *N* sets of within-assemblage relative abundances. Here the weight for Assemblage *k* in Eq. (S1) is the size-weight, i.e., n_{+k} / n_{++}, *k* = 1, 2, …, *N*.

(b) For within-assemblage relative abundance data, we replace n_{ik} by $p_{ik} = n_{ik} / n_{+k}$ and thus we have $p_{+k} = 1$ for all *k* = 1, 2, …, *N*, and $p_{++} = N$. The functional gamma diversity of order *q* becomes the Hill number for an assemblage in which there are *S* sub-assemblages: the *i*-th sub-assemblage consists of $v^*_{i+}(\tau) = p_{i+} / a^*_{i+}(\tau)$ functional groups, each with group abundance $a^*_{i+}(\tau)/p_{++}$, *i* = 1, 2, …, *S*, where

$$\frac{a_{i+}^{*}(\tau)}{p_{++}} = \frac{a_{i+}^{*}(\tau)}{N} = \sum_{j=1}^{S}[1 - f(d_{ij}(\tau))]\sum_{k=1}^{N}\frac{1}{N}p_{jk}. \tag{S2}$$

Based on the relative abundance matrix [p_{ik}], we have the relationship $\frac{p_{j+}}{p_{++}} = \sum_{k=1}^{N}\frac{1}{N}p_{jk}$. That is, any species relative abundance in the pooled assemblage is equivalent to equal-weighted pooling over the N sets of within-assemblage relative abundances. Comparing the above two equations (Eqs. S1 and S2), we see the difference arises because the raw abundances could yield different total abundances among assemblages while the within-assemblage relative abundances always sum to 1 (i.e., all assemblages have the same weight in computing gamma diversity). This leads to different group abundances for each species, which subsequently leads to different attribute contributions (i.e., $v_{i+}(\tau) \neq v_{i+}^{*}(\tau)$) and thus different gamma diversities.

In the following two tables, we compare functional diversities based on two different types of data (raw abundances and within-assemblage relative abundances) for the real examples presented in the main text. All numerical results reveal that the two types of data generally yield comparable results.

Table S3. Comparison of functional alpha, beta and gamma diversities for three bark treatments (control, debarked, bark-scratched), based on beetle species absolute and relative abundance data discussed in the main text. Here d_{min}, d_{mean} and d_{max} refer to the minimum, mean and maximum of the species-pairwise distances in the pooled assemblage.

Diversity order *q* and threshold level τ	Absolute abundances			Relative abundances		
	Gamma	Alpha	Beta	Gamma	Alpha	Beta
q = 0						
$\tau = d_{\text{min}} = 0.0008$	120	77	1.5584	120	77	1.5584
$\tau = d_{\text{mean}} = 0.1019$	32.9593	29.4429	1.1194	32.1681	28.7349	1.1195
$\tau = d_{\text{max}} = 0.7105$	1.2005	1.2005	1	1.19	1.19	1
q = 1						
$\tau = d_{\text{min}} = 0.0008$	11.0207	8.7159	1.2644	10.7073	9.4058	1.1384
$\tau = d_{\text{mean}} = 0.1019$	4.7079	4.0219	1.1706	4.5151	4.3122	1.047
$\tau = d_{\text{max}} = 0.7105$	1.1861	1.0609	1.1180	1.1766	1.1765	1.0001
q = 2						
$\tau = d_{\text{min}} = 0.0008$	4.4016	3.588	1.2268	4.211	4.026	1.046
$\tau = d_{\text{mean}} = 0.1019$	3.0482	2.5457	1.1974	2.9215	2.8698	1.018
$\tau = d_{\text{max}} = 0.7105$	1.1762	0.9885	1.1899	1.1675	1.1672	1.0002

Table S4. Comparison of functional alpha, beta and gamma diversities of two Forest Dynamic Plots in Taiwan (Fushan and Kenting) based on species absolute and relative abundance data (10-ha for each plot) discussed in the main text. Here d_{min}, d_{mean} and d_{max} refer to the minimum, mean and maximum of the species-pairwise distances in the pooled assemblage.

Diversity order q and threshold level τ	Absolute abundances			Relative abundances		
	Gamma	Alpha	Beta	Gamma	Alpha	Beta
$q = 0$						
$\tau = d_{\text{min}} = 0.0035$	168	90	1.8667	168	90	1.8667
$\tau = d_{\text{mean}} = 0.1556$	7.2420	6.7420	1.0742	7.2788	6.7788	1.0738
$\tau = d_{\text{max}} = 0.6077$	1.3610	1.3610	1	1.3596	1.3596	1
$q = 1$						
$\tau = d_{\text{min}} = 0.0035$	29.6999	14.9064	1.9924	28.5630	14.3366	1.9923
$\tau = d_{\text{mean}} = 0.1556$	4.3501	3.3893	1.2835	4.3237	3.3697	1.2831
$\tau = d_{\text{max}} = 0.6077$	1.3534	1.3392	1.0106	1.3514	1.3405	1.0081
$q = 2$						
$\tau = d_{\text{min}} = 0.0035$	10.9074	5.4542	1.9998	9.9485	4.9747	1.9998
$\tau = d_{\text{mean}} = 0.1556$	3.8882	2.8064	1.3855	3.8105	2.7271	1.3973
$\tau = d_{\text{max}} = 0.6077$	1.3465	1.3218	1.0187	1.3441	1.3244	1.0149