Appendix B: Results using Leinster and Cobbold's index and comparisons with Chao's diversity index

To the best of our knowledge, there are two different generalizations of Hill's numbers that allow to include species' similarity: Chao's diversity index, which is based on (phylogenetic) trees, and Leinster and Cobbold's index (2012), which is based on species distance matrices. Both indices are compatible to the analyses we showed but can yield slightly different results. We expose here the results of the analyzes from the article performed with Leinster and Cobbold's (LC) diversity index and compare them to the results of the analysis performed with Chao's diversity index.

Methods

The diversity index is a function of the *q* parameter, which varied between 0 and $+\infty$ and reflects the effect of dominance on the diversity estimation. The more q increases, the more qD is influenced by dominant species and the less by rare species.

(Eq. 1)

$$
{}^{q}D(p) = \begin{cases} \left(\sum_{i=1}^{N} p_i (\sum_{j=1}^{N} Z_{ij} p_j)^{1-q}\right)^{\frac{1}{1-q}} & q \neq 1\\ exp(-\sum_{i=1}^{N} p_i \times log(\sum_{j=1}^{N} Z_{ij} p_j)) & q = 1 \end{cases}
$$

To calculate the α-diversity for each community, $p = \{p_i\}$ was defined as the vector of the relative abundances of the *N* species occurring in the communities, while to calculate the γdiversity of the meta-community, *p* was defined as the vector of the average relative abundance of the species over all communities. Z contained the similarity measures between species in the community. Note that for $q=0$, ${}^{0}D$ is not equivalent to a presence/absence diversity index, as it is still dependent on species abundances if species are not fully dissimilar. For $q = 2$, ²D is, like Chao's index, equal to a monotonic transformation of Rao's Quadratic Entropy.

Z was calculated as:

$$
Z_{ij}(\delta) = 1 - \frac{d_{ij}(\delta)}{max[d_{ij}(\delta)]}
$$

(Eq. 2) $\left(\begin{array}{c} (i,j) \end{array}\right)$ with Z_{ij} , the similarity measures between species i and *j*, and $d_{ii}(\delta)$ the distances between species i and j after the transformation of the tree with the parameter *δ* (Pagel 1997, Figure B1).

The rest of the methods is identical to the methods detailed in the main article.

Properties – As Chao's diversity index, LC's satisfies the replication principle (Leinster and Cobbold 2012) but only Chao's diversity index has been proven to yield estimates of β-diversity that are set between 1 and the number of studied communities (Chiu and al. 2014). β-diversity calculated from Leinster and Cobbold's index can be below 1 as noticed by Reeve and al. (2014). This complicates the interpretation of the β-diversity as "the equivalent number of fully distinct communities in the meta-community" (adapted from Tuomisto 2010) and goes against the basic requirement of a diversity decomposition framework (Jost 2007).

This behavior may be due to the properties of the species' dissimilarity matrix used to perform the α, β, γ decomposition. As stated by Pavoine (2012), the mean alpha diversity is inferior to the gamma diversity calculated from Rao's quadratic entropy (which is part of LC's generalization of Hill's numbers) only if the species distance matrix is Euclidean. While this is thus valid for Leinster and Cobbold's diversity index for $q = 2$, it has yet to be demonstrated for any positive value of *q*.

Despite this drawback, LC's diversity indices presents the advantage of being simpler and faster to compute than Chao's index, an important criterion when the analysis involves a large number of null model randomizations, a large set of *q* and δ parameter or a large dataset. We recommend to use LC approach here only in the case of Euclidean or ultrametric distances, which are usually the case when considering dated phylogenetic trees or functional distance from functional dendrograms.

Results

The results obtained on the basis of LC's diversity index were overall qualitatively similar to the results obtained with Chao's index (Figure B2 and S3). The trend of increasing SES with increasing q and increasing δ was common to both indices. We can yet notice that the standard effect size (SES) for the phylogenetic β-diversities were overall more positive even for $q = 0$ and did not present a local minimum for high value of q.

Thus our ecological conclusions hold regardless of the diversity index used. Statistically, there are significant discrepancies between both diversity indices. These were mostly confined to the lower values of q (q <2) and very high values of q (q \geq 5).

This is due to a decreased correlation between both indices for these values in particular for intermediate values of δ (0.5 $\leq \delta \leq 2$; Figure B4 & Figure B5). Furthermore, LC's presented a much lower range of values for $q = 0$ and $q = 1$ (Figure B5; the opposite holds for high q values ($q > 2$) as Chao's diversity index seemed to saturate for phylogenetic α -diversities.

References

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Figure B1. Flowchart of the different steps used to model the similarity effect. 1) The original phylogenetic or functional tree of the meta-community species was transformed by Pagel's delta tree transformation (1997). A value of *δ* superior to 1 led to an inflation of close-to-tips branches, while a value inferior to 1 led to an inflation of close-to-root branches; a value of d equal to 1 leaves the tree unchanged. 2) The similarity matrix Z was calculated from the transformed tree. The bottom-right graphic represents the resulting effect of the tree transformation on the relationship between cophenetic distances deduced from the original tree (d_{ij}) and species similarity (z_{ii}) for different value of δ .

The similarity effect

Relationship between original cophenetic distances (d_{ii}) with the interspecific similarity (Z₁) controlled by d.

Figure B2. Standard Effect Sizes (SES) of the functional (left panel) and phylogenetic (right panel) beta-diversity of the meta-community against a tip-shuffling null model, as a function of the strength of the dominance effect (*q*) and the strength of the similarity effect (δ). A low *q* value indicates that rare and dominant species were given about the same weight while a high *q* value indicates that more weight was given to dominant species. A low (respectively high) *δ* value indicates that small (respectively large) species' similarities were given more weight (Figure 1). A low SES value indicates a higher than expected β-diversity, hence a predominant influence of environmental filtering, while a high SES value indicates a lower-than-expected βdiversity, hence a predominant influence of competition resulting in a limiting similarity pattern.

Figure B3. Influence of environment and space on the inter-community pairwise functional and phylogenetic distances, as a function of the strength of the dominance effect (q) and the strength of the similarity effect (δ) . A low q value indicates that rare and dominant species were given about the same weight while a high q value indicates that more weight was given to dominant species. A low (respectively high) δ value indicates that small (respectively large) species' similarities were given more weight (Figure 1). The different lines represent the variance (Adjusted R2) of the β-distances matrix of communities explained by environment only (E/S), spatially autocorrelated environment (SxE) and a pure spatial effect (S/E).

Figure B4. Comparisons of the Guisane valley α-diversities calculated from Leinster and Cobbold's diversity indices and Chao's for various values of q and $\delta = 1$. Functional α -diversities are in black and phylogenetic α -diversities in red.

Figure B5. Correlation coefficient between Guisane valley functional α-diversities calculated from Leinster and Cobbold's diversity indices and Chao's as a function of q and δ parameters. Note that for $q = 2$, both indices are equal and return the equivalent number of Rao's quadratic entropy.

