***Appendix S1. Definition, equations and references for the indices***

Because of the plethora of indices developed so far to measure phylogenetic alpha and beta diversity, we had to select a subset of indices for our analysis. The selection was made to represent the wide variety of aspects of phylogenetic diversity that mathematical indices can capture and the most commonly used indices.

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*B* is the number of branches. *Bt* is the set of branches in the phylogenetic tree. *Bti* is the set of branches in the phylogenetic tree joining species (tip) *i* to the root of the tree. *Lb* is the length of branch *b*. In our paper, we considered *T* as the root to tip distance (all trees were ultrametric so that for any tree this distance was a constant over all tips). *S* is the assemblage species number or species richness. *Rb* is the ‘branch’ range size, i.e. union of range size of the species descending from branch *b*. *Ab* is the branch abundance, i.e. the sum of the abundances of the species descending from branch *b. Pb* is the branch relative abundance, i.e. the sum of the relative abundances of the species descending from branch *b. Sb* is the branch richness, i.e. the number of species descending from branch *b.*

*dij*is the phylogenetic distance between two species *i* and *j.* Unless otherwise specified we defined the distance between two species as the distance from their first common ancestor. In addition we simulated trees with height (*T*) standardized to equal 1 so that the maximal possible distance between two species is 1.

*di min* is the distance of a given species *i* to its closest relative in the assemblage. *pi* is the probability to draw an individual of species *i* from the assemblage or the proportion of species *i* in the assemblage (measured here as a relative abundance). *ni* is the abundance of species *i* in the assemblage.

***ALPHA-diversity indices***

|  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- |
| Links among indices | Index | | Equation | Definition | | Reference |
| **I. Richness indices** | | | | | | |
| **1. Using branch lengths** | | | | | | |
|  | PD  Phylogenetic diversity | |  | Sum of total branch lengths connecting species together | | Faith (1992) |
|  | PDAb  Abundance-weighted PD *sensu* Vellend | |  | Sum of branch lengths, where branches are scaled by proportional abundances of subtending species. Was named PDAw in Vellend *et al.* (2010). | | Vellend *et al.* (2010) |
|  | ΔnPD  Abundance-weighted PD *sensu* Barker | |  | Sum of branch lengths, where branches are scaled by abundances of subtending species. | | Barker (2002) |
|  | PE  Phylogenetic endemism | |  | Sum of total branch lengths connecting species together weighted by their range size | | Rosauer *et al.* (2009) |
|  |  | |  |  | |  |
| **2. Using phylogenetic pairwise distances** | | | | | | |
|  | F  Extensive quadratic entropy | |  | Sum of pairwise distances | | Izsák & Papp (2000); Izsák & Szeidl (2002) |
|  | PSR  Phylogenetic species richness | | with either  *dij*=0.5(*cii*+*cjj*-*cij*) or | Variability in an unmeasured neutral trait multiplied by species richness. *cii* is the sum of branch lengths from species (tip) *i* to the root of the phylogenetic tree; *cij* is the sum of branch lengths from first common ancestor for *i* and *j* to the root. (See section ‘Details on the links between several indices’) | | Helmus *et al.* (2007) |
| **3. Using species phylogenetic isolation index**  A phylogenetic isolation index represents the relative isolation of a given species within a phylogenetic tree. Several indices have been proposed so far but we focus here on the evolutionary distinctiveness index called ‘Fair Proportion’ as proposed by Redding (2003) and Isaac (2007). | | | | | | |
|  | ED  Summed  evolutionary distinctiveness | | with | Sum of species’ evolutionary distinctiveness. Note that, in our case study, this index is not equal to Faith’s PD because the the *EDi* are computed from the regional pool of species and summed across a given assemblage (i.e. a subset of the regional species pool) | | This paper. Also Safi *et al.* (2013).  The *EDi* were defined by Redding (2003) and Isaac (2007) |
|  | AED  Abundance-weighted ED | | with | Abundance-weighted version of ED | | This paper. *AEDi* was defined by Cadotte *et al.* (2010) |
|  |  | |  |  | |  |
| **II. Divergence indices** | | | | | | |
| **1. Using branch lengths** | | | | | | |
|  | avPD  Average phylogenetic diversity | |  | Sum of total branch lengths, where branches are scaled by proportional abundances of subtending species, divided by the number of species | | Clarke & Warwick (2001) |
|  | avPDAb  Abundance-weighted avPD | |  | Sum of total branch lengths connecting species together divided by the number of species | | This paper |
|  |  | |  |  | |  |
| **2. Using phylogenetic pairwise distances** | | | | | | |
| MPD = AvTD  = S/(S–1)\*J | MPD  (also named AvTD and Δ+)  Mean pairwise distances | |  | Mean distances between species | | Clarke & Warwick (1998); Webb *et al.* (2002, 2008); Kembel *et al.* (2010) |
| PSV  Phylogenetic species variability | | MPD with either  *dij* = 0.5(*cii* + *cjj* – *cij*) or | Variability in an unmeasured neutral trait or the relative amount of unshared branch length. *cii* is the sum of branch lengths from species (tip) *i* to the root of the phylogenetic tree; *cij* is the sum of branch lengths from first common ancestor for *i* and *j* to the root. (See Section ‘Details on the links between several indices’) | | Helmus *et al.* (2007) |
| J  Intensive quadratic entropy | |  | Average distance between two randomly chosen species | | Izsák & Papp (2000) |
| With certain definitions of the phylogenetic distances among species (see the definition of PSE)  PSE = *S*/(*S*–1) Rao’s QE | MPDAb = Rao’s QE  Rao’s Quadratic Entropy or abundance-weighted MPD | |  | Quadratic entropy: Simpson’s type diversity index where the product of species relative abundances is weighted by phylogenetic distances. This is also the phylogenetic distance between two randomly chosen individuals [drawn WITH replacement] | | Rao (1982); Clarke & Warwick (1998); Pavoine *et al.* (2005); Hardy & Senterre (2007); Webb *et al.* (2002, 2008); Kembel *et al.* (2010) |
| PSE  Phylogenetic species evenness | | with either  *dij*=0.5(*cii*+*cjj*-*cij*) or | Abundance-weighted PSV*. cii* is the sum of branch lengths from species (tip) *i* to the root of the phylogenetic tree; *cij* is the sum of branch lengths from first common ancestor for *i* and *j* to the root. (See Section ‘Details on the links between several indices’) | | Helmus *et al.* (2007) |
|  | InterMPDAb  (also named Δ\*)  Interspecific MPDAb | | / | ‘Interspecific’ MPDAb: expected phylogenetic distance between two individuals randomly drawn conditionally on the fact that the individuals are from different species | | Clarke & Warwick (1998); Miller *et al.* (2013) |
|  | | | |  | |  |
| **3. Using nearest distances** | | | |  | |  |
|  | MNTD  Mean nearest taxon distance | |  | Mean shortest distance from a species to all others in the assemblage | | Webb *et al.* (2002, 2008); Kembel *et al.* (2010) |
|  | MNTDAb  Abundance-weighted MNTD | |  | Abundance-weighted MNTD: mean shortest distances, adjusted by species’ proportions (i.e. species’ relative abundances) | | Webb *et al.* (2002, 2008); Kembel *et al.* (2010) |
|  |  | |  |  | |  |
| **4. Using phylogenetic isolation index**  A phylogenetic isolation index represents the relative isolation of a given species within a phylogenetic tree. Several indices have been proposed so far but we focus here only on the evolutionary distinctiveness as measured by the index ‘Fair proportion’ (Redding, 2003; Isaac,2007). | | | | | | |
|  | mean(ED)  Mean evolutionary distinctiveness | | with | Mean of species’ evolutionary distinctiveness | | This paper.  The *EDi* were defined by Redding (2003) and Isaac (2007) |
|  | | | | | | |
| **III. Regularity indices** | | | | | | |
| **1. Using phylogenetic pairwise distances** | | | | |  |  |
|  | VPD  (also named VarTD and Λ+)  Variance in pairwise distances |  | | | Variance in pairwise distances | Clarke & Warwick (2001) |
|  | VPDAb  Abundance weighted VPD | () | | | Variance in pairwise distance weighted by species abundances. | This paper |
|  | InterVPDAb  Interspecific VPDAb | () | | | Variance in pairwise distance weighted by species abundances.  *ni* is the abundance of species *i* in the assemblage. | This paper |
|  | | | | |  |  |
| **2. Using nearest distances** | | | | |  |  |
|  | VNTD  Variance in nearest taxon distances | |  | | Variance in nearest pairwise distance | This paper |
|  | VNTDAb  Abundance-weighted VNTD | |  | | Variance in nearest pairwise distance weighted by species abundances | This paper |
|  | PEve  Phylogenetic evenness | | Weighted evenness:  Partial weighted evenness: | | Phylogenetic version of the functional FEve index. First a minimum spanning tree (MST) is computed using the cophenetic distances obtained from the phylogenetic tree. The MST contains *S*–1 branches connecting the *S* species. We denote *l* a branch on the MST, *dist(i,j)* is the length of the branch *l* that connects species *i* and *j*. *ni* is, as defined above, the abundance of species *i* in the assemblage. | Villéger *et al.* (2008); Dehling *et al.* (2014) |
|  |  | |  | |  |  |
| **3. Tree topology** |  | |  | |  |  |
|  | IAC  Imbalance of abundances at the clade level | | with | | IAC quantifies the relative deviation in the abundance distribution from a null case where individuals are evenly partitioned between clade splits. *v* is the number of nodes in the phylogenetic tree.  *ni* is, as defined above, the abundance of species *i* in the assemblage. is the expected abundance species *i* would have if the abundance was randomly split among lineages in the phylogenetic tree at each speciation event. is the number of lineages originating at node *k* in the set *s*(*k*,*root*), which contains the nodes located on the path between node *k* and the root of the phylogenetic tree. *N* is the total assemblage abundance | Cadotte *et al.* (2010) |
|  | IC  Colless index | |  | | Sum of absolute differences in species richness between sister-clades at each internal node. For fully resolved trees, each internal node defines two sister-clades. *S1k* is the number of species descending from the first clade defined by node *k* and *S2k* that of the second clade. *v* is, as defined above, the number of nodes in the phylogenetic tree | Colless (1982) |
|  | γ  Gamma index | |  | | The index characterizes the distribution of branching events within the tree. Trees with γ < 0 have relatively longer branches towards the tips of the phylogeny (tippy trees), whereas trees with γ > 0 have relatively longer inter-nodal distances towards the root of the phylogeny (stemmy trees). *tk* represents an ‘evolutionary period’ (limits are given by two speciation events) or equivalently an internode distance. | Pybus & Harvey (2000) |
|  |  | |  | |  |  |
| **4. Using phylogenetic isolation** | | | | | | |
|  | HED  Entropy measure of evolutionary distinctiveness | |  | Shannon index applied to evolutionary distinctiveness values | | Cadotte *et al.* (2010) |
|  | EED  Equitability of evolutionary distinctiveness | | HED/ln(*S*) | HED controlled for species richness | | Cadotte *et al.* (2010) |
|  | var(ED)  Variance in evolutionary distinctiveness | |  | Variance of species’ evolutionary distinctiveness | | This paper |
|  | HAED  Abundance-weighted version of HED | |  | Abundance-weighted version of HED | | Cadotte *et al.* (2010) |
|  |  | |  |  | |  |
| **IV. Parametric indices** | | | | | | |
| **1. Unified frameworks** | | | | | | |
| *Entropies: unified by Pavoine* et al*. (2009): “Tsallis Number” (for ultrametric phylogenetic trees)* | | | | | | |
| *General formula of the framework* | Iq  Rarity-adjustable index of PD | | with | *tk* represents an ‘evolutionary period’ (limits are given by two speciation events). *q* is the factor that tunes the weight given to rare *versus* abundant species. *Pi* represents the relative abundance of lineage *i* descending from this period (sum of the relative abundances of the species descending from this lineage) | | Pavoine *et al.* (2009) |
| *q = 2* | I2=Rao’s QE if patristic distances among species are used in Rao’s QE (see Section ‘Divergence’) | | | | | |
| *q → 1* | I1=Hp  Phylogenetic entropy | |  | Phylogenetic entropy | | Allen *et al.* (2009) |
| *q= 0* | I0 = *PD* – *T* (See Section ‘Richness’) | | | | | |
|  | | | |
| **2. Hill numbers adapted to measure phylogenetic diversity** | | | | | | |
| *2A. Chao et al. framework* | | | |  | |  |
| *First version of the framework* |  | |  | Represents the ‘mean effective number of species’ over any time interval of interest. *Lb*represents length of branch *b* while *Pb*is the sum of the relative abundances of species descending from branch *b* | | Chao *et al.* (2010) |
| *q=2* |  | |  | 2*D(T)* = 1/(1–Rao’s *QE*/*T*). See Chao *et al.* (2010) for details | | Chao *et al.* (2010) |
| *q→1* |  | |  | See above for the definition of *Hp* | | Chao *et al.* (2010) |
| *q=0* |  | |  | (see ‘Richness section’) | | Chao *et al.* (2010) |
| *Second version of the framework* |  | |  | ‘Effective number of lineages’ | | Chao *et al.* (2010) |
|  |  | |  |  | |  |
| *2B.*  *Leinster & Cobbold framework* | | | | | | |
| *General formula of the framework* |  | | with | (*Zp*)*i* is the expected similarity between an individual of the *i*th species and an individual chosen at random. The phylogenetic similarity for two species *i* and *j* is given by *Zij*. Here *pi* refers to abundance of species *i*. ***p*** is the vector of species’ relative abundances. Here we used *Zij* = 1 – *dij* | | Leinster & Cobbold (2012) |
|  |  | |  |  | |  |
| *2C. Scheiner framework* | | | | | | |
|  | *qD(P)* | |  | Hill numbers applied to species relative evolutionary distinctiveness. For *q*=0, this index reduces to *S* | | Scheiner (2012) |
|  |  | |  | Abundance-weighted version of q*D(P)* | | Scheiner (2012) |
|  |  | |  |  | |  |

***BETA-diversity indices***

|  |  |  |  |  |  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- | --- | --- | --- | --- | --- |
| Class of indices | | Index | Equation | | Definition | | | Reference | | |
| **I. Richness indices (presence–absence data only)** | | | | | | | | | | |
|  | | Phylosor (PhylosorAb)  Phylogenetic Sørensen index |  | | Generalization of Sørensen index. *BLij* is the branch length common to both communities *i* and *j*, and *BLi* and *BLj* are the total lengths of assemblage *i* and *j*, respectively. So phylosor represents the proportional shared branch length between two communities. Branches can be weighted by abundances | | | Bryant *et al.* (2008) | | |
|  | | Unifrac (UnifracAb) | *BLij / (BLi + BLj – BLij)* | | Generalization of Jaccard index (same notations as above). Branches can be weighted by abundances. | | | Lozupone & Knight (2005) | | |
|  | | Faith’s PDβ |  | | Same notations as above. *BL*0 is the branch lengths not present in the two communities *I* and *j* but present in the region (pool) | | | Nipperess *et al*. (2010) | | |
| *Pavoine & Ricotta (2014) generalization of species turnover measures* | | Although the Pavoine & Ricotta (2014) indices can incorporate abundance data, we chose to apply them here to presence–absence data, so that they represent ‘richness indices’. In the equations below, *xi* & *zj* are presences/absences of species in the two compared communities. When formulated with absolute abundances, they are also ‘richness indices’; when formulated with relative abundances they are ‘divergence indices’.  *σij* = 1 – *δij* with *δij*being a measure of pairwise phylogenetic similarity among species. The phylogenetic distances should be between 0 and 1 and satisfy certain mathematical properties (see Pavoine & Ricotta, 2014, for calculations of phylogenetic similarities). | | | | | | | | |
|  | | SJaccard |  | | Generalization of Jaccard measure of species turnover | | | Pavoine & Ricotta (2014) | | |
|  | | SOchial |  | | Generalization of Ochial measure of species turnover | | | Pavoine & Ricotta (2014) | | |
|  | | SSorensen |  | | Generalization of Sørensen measure of species turnover | | | Pavoine & Ricotta (2014) | | |
|  | | SSokal-Sneath |  | | Generalization of Sokal & Sneath measure of species turnover | | | Pavoine & Ricotta (2014) | | |
|  | | Sβ |  | | Standardized version of Rao’s DAb. | | | Pavoine & Ricotta (2014) | | |
|  | |  |  | |  | | |  | | |
| **II. Divergence indices (using pairwise distances among species)** | | | | | | | | | | |
| **1. Presence/absence data** | | | | | | | | | | |
| *1A. Decomposition into α, β, γ diversities* | | | | | | | | | | |
|  | | ΠST  MPD-based proportional β-diversity |  | | | Additive decomposition of MPD. is MPD measured in the regional pool.  is the average MPD within communities. See details in Hardy & Senterre (2007). Note that we used the coefficients described by the authors, not their estimators | | Hardy & Senterre (2007) | | |
| *1B. Direct Dissimilarities* | |  |  | | |  | |  | | |
| *Using all distances* | | Dpw = COMDIST = Rao’s D  MPD-based β-diversity |  | | | Mean phylogenetic distance between a species from assemblage 1 and a species from assemblage 2. Webb *et al.*’s COMDIST = Swenson’s Dpw. *S*1and *S*2are the numbers of species in communities 1 and 2, respectively | | Webb *et al.* (2008); Swenson (2011) | | |
| *Using nearest distances* | | Dnn = COMDISTNT  MNTD-based β-diversity |  | | | COMDISTNT uses the minimum pairwise distance (MNTD) for each taxon in a sample to all taxa in the other sample and calculates the mean. Same notations as above. ‘*k* *in 1*’ means species *k* from assemblage 1. Webb *et al.*’s COMDISTNT = Swenson’s Dnn. | | Webb *et al.* (2008); Swenson (2011) | | |
|  | | PCD  Phylogenetic community dissimilarity | with  and | | | *PSV* is the α-diversity phylogenetic metric described earlier. *tr* is the trace of the matrix. Communities 1 and 2 have *n*1 and *n*2 species, respectively. *C*11, *C*22 and *C*12 represent the covariance matrix of species of assemblage 1, 2 or between species of the two communities, respectively. PSVpool is the unconditional PSV calculated for all *N* species in the species pool, Cpool is their phylogenetic covariance matrix and  is the mean conditional  for a community *i,* given the composition of *nj* species randomly drawn from the species pool | | Ives & Helmus (2010) | | |
| **2. Abundance data** | |  |  | | |  | |  | | |
| *2A. Decomposition into α, β, γ diversities* | | | | | | | | | | |
|  | | Hβ  Phylogenetic β-entropy |  | | | Additive decomposition of Allen et al. (2009) phylogenetic entropy (Hp). *Hγ* is calculated in the regional pool and *Hα* is the average diversity within communities | | Mouchet & Mouillot (2011) | | |
|  | | PST  Rao's QE-based proportion abundance-weighted β-diversity |  | | | Additive decomposition of Rao’s QE*.*  is Rao’s QE calculated in the regional pool and the average value of Rao’s QE calculated per assemblage. Note here that we used the coefficients described by the authors, not their estimators | | Hardy & Senterre (2007) | | |
|  | | BST  InterMPDAb-based proportion abundance-weighted β-diversity |  | | | Additive decomposition of interMPDAb. This index is similar to Pst but does not consider conspecific individuals comparisons (i.e. interMPDAb is used instead of Rao’s QE) | | Hardy & Senterre (2007); Hardy & Jost (2008) | | |
|  | | Rao’s DISC  Raos' QE-based dissimilarity coefficient |  | | | Rao’s dissimilarity coefficient based on Rao's QE; *pi1* is the relative abundance of species *i* in assemblage 1, and *pj*2 the relative abundance of species *j* in assemblage 2. | | Rao (1982) | | |
| *2B. Direct dissimilarities* | |  |  | | |  | |  | | |
| *Using all distances* | | DpwAb  (also named Dpw’)  Partially abundance-weighted version of the average species dissimilarity between two assemblages |  | | | Abundance-weighted version of Dpw/COMDIST. *S*1and *S*2are the numbers of species in communities 1 and 2, respectively | | Swenson (2011) | | |
|  | | COMDISTAb = Rao’s DAb  Average species dissimilarity between two assemblages |  | | | Alternative abundance-weighted version of Dpw/COMDIST. *pi1* is the relative abundance of species *i* in assemblage 1, and *pj*2 the relative abundance of species *j* in assemblage 2 | | Rao (1982); Webb *et al*. (2008) | | |
| *Using nearest distances* | | DnnAb  (also named Dnn’)  Average nearest-neighbour distance between two assemblages |  | | | Abundance-weighted version of Swenson’s Dnn/COMDISTNT. *S*1and *S*2are the numbers of species in communities 1 and 2, respectively | | Webb *et al*., (2008); see Weiher & Keddy (1995) in a functional context | | |
|  | |  |  | |  | | |  | | |
| **III. Parametric indices** | | | | | | | | | |
| **1. Equivalent numbers** | |  |  | | |  | |  | | |
| We also used Chiu *et al.*’s (2014) decomposition of Chao *et al.*’s (2010) adaptation of Hill numbers to phylogenetic diversity where  See Chiu *et al.* (2014) for definitions of parameters. | | | | | | | | | | |
| **2. Entropy** |  | | |  | | |  | |  | |
|  | Iqβ  Entropy-based parametric phylogenetic β-diversity | | | Iqγ–Iqα | | | Additive decomposition of Iq. Iqγ is Iq measured in the regional pool. Iqα is the average Iq within communities. | | Pavoine *et al*. (2009) | |

***Details on the links between several indices***

Among the indices that use phylogenetic distances among species, some are very general in the definition of these distances (for example it might be sufficient that they are non-negative, however they have been calculated), others slightly restrict the choice of the distances (for example distances bounded between 0 and 1) and others impose a way of calculating the phylogenetic distances as for Helmus *et al*. (2007) PSV and PSE indices.

We start below with notations defined by Helmus *et al.* (2007).

PSV is a special case of MPD:



*n* is the number of tips (species), tr(**C**) is the trace of **C** (sum of diagonal values) (see below for the definition of **C**), is the sum of all values in **C**.



First scenario:

**C** is the matrix of covariances. Let us assume that there is no loss of generality but to make it more concrete that they are Brownian covariances. *cii* = sum of branch lengths from tip *i* to root; *cij* = sum of branch lengths from first common ancestor for *i* and *j* to root. .



Let



Here *dij* is half the sum of branch lengths in the shortest path that connects two tips (half patristic distances). For the dated tree, this would be the time to first common ancestor.

Second scenario:

PSV is applied to **Z**, i.e. the matrix of correlations. We still assume no loss of generality but to make it more concrete we use Brownian covariances. *cii* = sum of branch lengths from tip *i* to root; *cij* = sum of branch lengths from first common ancestor for *i* and *j* to root.

*zii* = 1. *zij* =



.



Let , *dij* is bounded between 0 and 1 (see Pavoine & Izsák, 2014, for an application of as an index of phylogenetic similarities among species)



Here *dij* is one minus the phylogenetic correlation between two tips *i* and *j*.

In both scenarios, Helmus *et al*.’s (2007) measure PSR is equal to



PSE is a special case of Rao’s QE:



*n* is the number of tips; *mi* is the abundance of tip *I*; *m* is the sum of abundances across tips=; *m*/*n* is the average abundance per tip and **M** is the vector of *mi* for all *i.*



First scenario:

**C** is the matrix of covariances (see notations above).



Let *pi* be the relative abundance for tip *i*,



Let



Here (as above for PSV) *dij* is half the sum of branch length in the shortest path that connects two tips (half patristic distances). For a dated tree, this would be the time to first common ancestor.



where **p** is the vector of all *pi*.

Second scenario:

PSE is applied to **Z**, the matrix of correlations (see definition above for PSV). We still assume no loss of generality but to make it more concrete we use Brownian covariances. *cii* = sum of branch lengths from tip *i* to root; *cij* = sum of branch lengths from first common ancestor for *i* and *j* to root.

*zii* = 1. *zij* =



Let , *dij* is bounded between 0 and 1 (see Pavoine & Izsák, 2014 for an application of as an index of phylogenetic similarities among species)



Here *dij* is one minus the phylogenetic correlation among two tips. is Rao's QE applied to the *dij*'s and the vector of all *pi*.

