Measure	Reference	Description
Colless' Index (I_c)	Colless (1982)	Comparison of the number of tips either 'side' of each node with the number in a perfectly balanced tree.
PD (Phylogenetic Distance)	Faith (1992)	Sum of the branch lengths in a phylogeny.
MPD (Mean Phylogenetic Distance)	Unknown	The mean of PD; some use the median phylogenetic distance (*e.g.*, Maitner *et al.*, 2012).
Δ (taxonomic diversity index)	Warwick & Clarke (1995)	Extension of the Shannon index, with weighting according to the absolute taxonomic distance between individuals.
Δ^+ (taxonomic distinctiveness index; TDI_D+	Warwick & Clarke (1995)	Essentially Δ divided by the value of Δ given the simplest possible taxonomic structure (all species in the same genus).
γ	Pybus & Harvey (2000)	γ values < 0 suggest internal nodes are closer to the root than expected. The converse cannot be tested with γ.
LTT (Lineages Through Time) Plot	Martin (2002)	Number of lineages through time in a phylogeny. Not a metric (rather a plot), but Martin (2002) suggest departure from a curve generated under a Yule null model indicates overdispersion or clustering.
PSV (Phylogenetic Species Variability)	Helmus *et al.* (2007)	Compares branch lengths of species with the variance expected under the Brownian motion of a neutral trait across a phylogeny. Claims specifics of the model are independent of Brownian model.
PSR (Phylogenetic Species Richness)	Helmus *et al.* (2007)	Product of *PSV* and phylogeny size.
Corrected *PD* (regPD)	Vamosi & Vamosi (2007)	Residuals of regression of *PD* on species richness. Intended to control for the confound of species richness and phylogenetic diversity.
E_{ED}	Cadotte *et al.* (2010a)	Equitability of an entropic measure of diversity of species' evolutionary distinctiveness.
Phylogenetic Eigenvector Methods (PE)	Diniz-Filho *et al.* (2011)	Sum of the axes retained in a principal coordinate analysis of a phylogenetic distance matrix is related to phylogenetic imbalance; in our analyses, we used the first two axes. See Freckleton *et al.* (2011) for a discussion of issues with the approach in comparative analysis.
EPD (Expected Phylogenetic Diversity)	O'Dwyer *et al.* (2012)	Sum, across all potential sizes of clade, of the product of a clade having at least one species present in a community and the sum of all branch lengths in all clades of that size. Since analytical null expectations can be generated, this facilitates the examination of extremely large phylogenies without time-consuming null randomisations.

Table 1 Phylogenetic *shape* measures, in (approximate) order of publication. The abbreviations used in the chapter's Fig. 2 are given in the 'Measure' column.

Measure	Reference	Description
F_{ST}	Martin (2002)	Standard population genetics method, showing how differentiated samples are. Re-purposed by Martin (2002) for use in concert with the *P test*, to study the phylogenetic scale of clustering.
P_{ST}	Hardy & Senterre (2007)	An extension of Simpson's index to incorporate phylogenetic relatedness. Assesses how much of a site's diversity is explained by turnover within sites. Part of the framework mentioned in Π_{ST} below.
Π_{ST}	Hardy & Senterre (2007)	Part of a family of measures partitioning and examining hierarchical partitioning of evenness (and shape). Many other terms are defined, but they are (acknowledged to be) redefinitions of measures described elsewhere in these tables; interested readers should consult Hardy & Senterre (2007) for more details.
PSE (Phylogenetic Species Evenness)	Helmus *et al.* (2007)	As *PSV*, but with polytomies with branch lengths of zero and sizes equal to the frequency of members of the community added to the phylogeny.
Phylogenetic Entropy (Hp)	Allen *et al.* (2009)	The product of two species co-occurring and their natural logarithm of their phylogenetic relatedness. Generalisation of the Shannon Index.
$H_\alpha, H_\beta, H_\gamma$	Mouchet & Mouillot (2011)	An extension of the phylogenetic entropy concept of Allen *et al.* (2009).
$PD_\alpha, PD_\beta, PD_\gamma$	Cadotte *et al.* (2010b)	PD_α is the *MPD* within sites, PD_γ is the sum of the branch lengths connecting all species across sites, and PD_β is $PD_\gamma PD_\alpha$. Uses the Lande (1996) partitioning of diversity; note that PD_α is constructed from *MPD*, not *PD*.
PAE (Phylogenetic Abundance Evenness)	Cadotte *et al.* (2010a)	A scaled measure of the product of species frequency and each species' terminal branch length.
IAC	Cadotte *et al.* (2010a)	Relative per-node imbalance in the distribution of individuals. Can be thought of as an abundance-weighted form of I_C; ignores branch lengths.
E_{AED}	Cadotte *et al.* (2010a)	Equitability of an abundance-weighted entropic measure of diversity of species' evolutionary distinctiveness. Similar to E_{ED}.

Table 2 Phylogenetic *evenness* measures, in (approximate) order of publication. The abbreviations used in the chapter's Fig. 2 are given in the 'Measure' column.

Measure	Reference	Description
NRI (Net Relatedness Index)	Webb (2000); Webb *et al.* (2002)	Null randomisations' mean *MPD* subtracted from an observed assemblage's *MPD*, scaled by the standard deviation of those null randomisations. The 2000 definition is based on nodal distance.
NTI (Nearest Taxon Index)	Webb (2000); Webb *et al.* (2002)	Null randomisations' mean smallest between-species phylogenetic distance *MPD* subtracted from an observed assemblage's mean least phylogenetic distance, scaled by the standard deviation of those null randomisations. The 2000 definition is based on nodal distance.
SES_{MPD} (Standardised Effect Size of Mean Phylogenetic Distance)	Kembel (2009)	The negation of *NRI* (Webb *et al.*, 2002).
SES_{MNTD} (Standardised Effect Size of Mean Phylogenetic Distance)	Kembel (2009)	The negation of *NTI* (Webb *et al.*, 2002).
SES_{PD} (Standardised Effect Size of Phylogenetic Diversity)	Proche *et al.* (2006)	Null randomisations' mean *PD* subtracted from an observed assemblage's *PD*, scaled by the standard deviation of those null randomisations.
Summed number of state changes	Chazdon *et al.* (2003)	Reconstructed number of state changes in community presence across the phylogeny; fewer changes indicate greater phylogenetic conservatism (and so phylogenetic clustering). Many methods for ancestral state reconstruction exist, this is the first example we found of it being used in a community phylogenetic context.
D	Fritz & Purvis (2010)	Sum of differences in independent contrasts of species' presence/absence, scaled according to random and Brownian expectation.
INND/*MIPD* (Inverse Nearest Neighbour Distance/Mean of Inverse Pairwise Distances)	Ness *et al.* (2011)	As *NRI*/*NTI* (Webb *et al.*, 2002), but using the *inverse* of phylogenetic distance. Assumes a non-linear relationship between ecological and phylogenetic distance.
Standardised *PD* (*stdPD*)	Mi *et al.* (2012)	Difference between observed *PD* of subsets of a sample and the total *PD* of that sample. Used to examine influence of rare species on *PD* by regressing *stdPD* against the rank abundance distribution.

Table 3 Phylogenetic *dispersion* measures. The abbreviations used in the chapter's Fig. 2 are given in the 'Measure' column.

Measure	Reference	Description
Quadratic Diversity (raoDkk)	Rao (1982)	Sum of the product of the proportions of sites where two species are present, and their phylogenetic relatedness. Generalisation of the Simpson Index.
P Test	Maddison & Slatkin (1991); Martin (2002)	Compares distribution of sequences unique to each community within the phylogeny and compares the number of evolutionary transitions required for this distribution with a null model. A parsimony-based approach adapted from the cladistic literature by Martin.
Θ^+	Clarke & Warwick (1998); Clarke *et al.* (2006)	As Γ^+, but each samples minimum distances are kept listed separately and then averaged. Related to the Bray-Curtis index.
Γ^+	Izsak (2001); Clarke *et al.* (2006)	Mean of the smallest taxonomic distances between species in each sample. Related to the Bray-Curtis index.
Δ_C (raoDkk)	Singleton (2001)	Compares curves of number of unique sequences within a sample against a cut-off for sequence dissimilarity. Designed for bacterial systems and rRNA.
UniFrac	Lozupone & Knight (2005)	The fraction of total branch length that two communities share. Can thus create a distance matrix for all communities to which one can apply multivariate statistics. Widely used by the microbiological community, but ignored by the wider ecological community.
PhyloSor	Bryant *et al.* (2008)	Fraction of branch length shared among communities. So-called because of its derivation from the Sørensen's index.
βNRI / βNTI	Webb *et al.* (2008)	Mean phylogenetic distance (or mean nearest-relative phylogenetic distance) between communities. Terminology from Fine & Kembel (2011), who called *NRI* and *NTI* αNTI and αNRI to emphasise the links between them.
PCD	Ives & Helmus (2010)	An extension of *PSV* that partitions dissimilarity into phylogenetic and non-phylogenetic components.

Table 4 Phylogenetic *dissimilarity* measures, in (approximate) order of publication.

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