

Summary Statistics	Information	Citation/Package in R
Mean BL	mean of community phylogeny branch lengths	base r package
Var BL	variance of community phylogeny branch lengths	
Mean Reg BL	mean of regional phylogeny branch lengths	
var reg bl	variance of regional phylogeny branch lengths	
mean bl dif	difference between regional and community mean branch lengths	
var bl dif	difference between regional and community variance of branch lengths	
Mean tr	mean of community traits	
Var tr	variance of community traits	
Mean Reg tr	mean of regional traits	
var reg tr	variance of regional traits	
mean tr dif	difference between regional and community mean of traits	
var tr dif	difference between regional and community variance of traits	
Moran I	Moran's I	Paradis E., Claude J. & Strimmer K. 2004. APE: analyses of phylogenetics and evolution in R language. Bioinformatics 20: 289-290.
Age	age of community tree	
Colless	Colless' index of a tree	Michelle Kendall, Michael Boyd and Caroline Colijn (2018). phyloTop: Calculating Topological Properties of Phylogenies. R package version 2.1.1. https://CRAN.R-project.org/package=phyloTop
Sackin	The Sackin's index is computed as the sum of the number of ancestors for each tips of the tree.	
nLTT	This function takes two ultrametric phylogenetic trees, calculates the normalized Lineage-Through-Time statistic for both trees and then calculates the exact difference between the two statistics.	Janzen,T. Hoehna,S., Etienne,R.S. (2015) Approximate Bayesian Computation of diversification rates from molecular phylogenies: introducing a new efficient summary statistic, the nLTT. Methods in Ecology and Evolution. doi: 10.1111/2041-210X.12350
Msig	mean of squared contrasts	Pennell MW, FitsJohn RG, Cornwell WK, Harmon LJ. 2015. Model Adequacy and the macroevolution of Angiosperm functional traits. The American Naturalist.
Cvar	The coefficient of variation (standard deviation/mean) of the absolute value of the contrasts.	
Svar	of the contrasts against their expected variances (following Garland et al. 1992).	
Shgt	of the contrasts against node depth (after Purvis and Rambaut 1995).	
Dcdf	test from comparing the distribution of contrasts to that of a normal distribution with mean 0 and standard deviation equal to the root of the mean of squared	
Kurtosis	kurtosis of community traits	Lukasz Komsta and Frederick Novomestky (2015). moments: Moments, cumulants, skewness, kurtosis and related tests. R package version 0.14. https://CRAN.R-project.org/package=moments
Skewness	skewness of community traits	
amp.loc	amplitude of peak 1 in trait data	Sathish Deevi and 4D Strategies (2016). modes: Find the Modes and Assess the Modality of Complex and Mixture Distributions, Especially with Big Datasets. R package version 0.7.0. https://CRAN.R-project.org/package=modes
amp.amp	amplitude of peak 2 in trait data	
bimode	bimodality coefficient in trait data	
bi.rat	bimodality ratio in trait data	
mod.val	mode value in trait data	
mod.len	mode length in trait data	