Shifts in taxonomic and functional composition of trees along rainfall and phosphorus gradients in central Panama

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Supplementary Methods

Null model – The null model to standardize the functional turnover metric consisted of shuffling trait values at the tips of the functionally based dendrogram so that each species was randomly reassigned a trait value from the 550-species meta-community. We then calculated randomized functional turnover values (β_{sim}) using a modified version of the function "beta.core" (baselga 2010, Baselga & Orme 2012) (see code below). We shuffled trait values and recalculated randomized functional turnover (β_{sim}) values 999 times, subtracted the mean randomized values from the observed values, and divided by the standard deviation of the randomized values to compute standardized functional turnover. Positive standardized values indicate that functional turnover is higher than expected by chance. For these analyses, LMA, LA, and MH were log-transformed to correct for skewness.

Variance partitioning – For the variance partitioning analyses using taxonomic information, we calculated the Jaccard dissimilarity index across all 72 sites to quantify taxonomic composition (Jost, Chao & Chazdon 2011). To obtain spatial variables, we performed a principal coordinates of neighborhood matrix (PCNM) analysis on the latitudes and longitudes of the 72 sites using the function 'varpart', package 'vegan' version 2.5-6 in R (Borcard & Legendre 2002). This analysis decomposes the spatial relationship among sites using a principal coordinate analysis (Borcard & Legendre 2002). We selected all principal coordinates with positive eigenvectors and correlated these variables with latitude and longitude. The first five principal coordinates were significantly correlated with latitude or longitude so we retained these five spatial coordinates as predictor variables in models explaining functional and taxonomic variation.

Code

Parameters:
- sumSi: the sum of the species richness values of all sites
- St: the total richness in the dataset
- a: the multiple-site analog of the shared species term
- shared: a matrix containing the number of species shared between pairs of sites
- not.shared: a matrix containing the number of species not shared between pairs of sites: b, c
- sum.not.shared: a matrix containing the total number of species not shared between pairs of sites: b+c
- max.not.shared: a matrix containing the total maximum number of species not shared between pairs of sites: max(b,c)
- min.not.shared: a matrix containing the total minimum number of species not shared between pairs of sites: min(b,c)
- comm: community matrix (species= columns, communities=rows)
- tree: functional dendrogram

```
library(picante)
```
Function:
```
functional.betapart.core <- function (comm, tree)
```

```r
{
 if (is.null(tree$edge.length)) {
   stop("Tree has no branch lengths, cannot compute UniFrac")
 }
 if (!is.rooted(tree)) {
   stop("Rooted phylogeny required for UniFrac calculation")
 }
 comm <- as.matrix(comm)
 s <- nrow(comm)
 phylodist <- matrix(NA, s, s)
 rownames(phylodist) <- rownames(comm)
 colnames(phylodist) <- rownames(comm)
 shared <- matrix(NA, s, s)
 rownames(shared) <- rownames(comm)
 colnames(shared) <- rownames(comm)
max.not.shared <- matrix(NA, s, s)
 rownames(max.not.shared) <- rownames(comm)
 colnames(max.not.shared) <- rownames(comm)
 min.not.shared <- matrix(NA, s, s)
 rownames(min.not.shared) <- rownames(comm)
 colnames(min.not.shared) <- rownames(comm)
 comm_comb <- matrix(NA, s * (s - 1)/2, ncol(comm))
 colnames(comm_comb) <- colnames(comm)
 i <- 1
 for (l in 1:(s - 1 )) {
   for (k in (l + 1 ):s) {
     comm_comb[i, ] <- comm[l, ] + comm[k, ]
     i <- i + 1
   }
 }
 pdcomm <- pd(comm, tree)
 pdcomm_comb <- pd(comm_comb, tree)
 i <- 1
 sumSi <- sum(pdcomm[,1]) # sum of branch length of all sites
 St <- pd(t(colSums(comm)), tree) ## total (branch length) in the dataset
 a <- sumSi - St[,1]
 for (l in 1:(s-1)) {
   pdl <- pdcomm[l, "PD"]
   for (k in (l + 1):s) {
     pdk <- pdcomm[k, "PD"]
     pdcomb <- pdcomm_comb[i, "PD"]
     pdsharedlk <- pdl + pdk - pdcomb
     phylodist[k, l] = (pdcomb - pdsharedlk)/pdcomb
     shared[k, l] <- pdsharedlk
     #sum.not.shared[k, l] <- pdcomb - pdsharedlk
     max.not.shared[k, l] <- max(pdk, pdl)
     min.not.shared[k, l] <- min(pdk, pdl)
     i <- i + 1
   }
 }
 max.not.shared <- as.matrix(as.dist(max.not.shared))
 min.not.shared <- as.matrix(as.dist(min.not.shared))
 shared <- as.matrix(as.dist(shared))
 diag(shared) <- pdcomm[,1]
 not.shared <-  abs(sweep(shared, 2, diag(shared)))
 diag(not.shared) <- 0
 sum.not.shared <- not.shared +t( not.shared)
 output <- list(unifrac= phylodist,sumSi=sumSi, St=St, a=a, shared=shared,
           not.shared=not.shared,sum.not.shared=sum.not.shared,
           max.not.shared=max.not.shared, min.not.shared=min.not.shared  )
```

```
class(output) <- "betapart"
return(output) }
```

References

Baselga, A. (2010). Partitioning the turnover and nestedness components of beta diversity. *Global Ecology and Biogeography*, *19*(1), 134–143. doi: 10.1111/j.1466-8238.2009.00490.x

Baselga, A., & Orme, C. D. L. (2012). Betapart: An R package for the study of beta diversity. *Methods in Ecology and Evolution*, *3*(5), 808–812. doi: 10.1111/j.2041-210X.2012.00224.x

Borcard, D. & Legendre, P. (2002) All-scale spatial analysis of ecological data by means of principal coordinates of neighbour matrices. *Ecological Modelling*, **153**, 51–68.

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