**Measuring other dimensions of biodiversity: phylogenetic and functional diversity**

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There are multiple dimensions of biodiversity that characterize taxonomic, functional and phylogenetic diversity. In other words, there are multiple ways of being different (species) or diverse (sites). A species is different from other species in its identity but also in how it functions and its evolutionary history. So when we examine the diversity at a site, we’re not only looking at the specific (taxonomic) diversity but also how each species contributes to energy flow through the system (functional) and the shared evolutionary history (phylogenetic) between species at the site. While taxonomic diversity metrices are historically popular, they assume that all species are equivalent. Also, taxonomic diversity is not a good proxy for the other forms of diversity i.e., functional and phylogenetic (Lean & Maclaurin 2016). In contemporary times, this idea of quantifying all three forms of biodiversity has become increasingly recognized and valued in uncovering eco-evolutionary patterns of speciation and coexistence and it is gaining utility in conservation prioritization (Faith, 1992; Cadotte et al., 2012). We have addressed taxonomic diversity in previous lectures. In this lecture we will focus on functional and phylogenetic diversity metrices only.

**Phylogenetic diversity** – total branch length of species on a phylogeny represents evolutionary relatedness and amount of “features” diversity at a given site (Faith 1992). Some authors argue that phylogenetic diversity is a good proxy for functional diversity, but the extent to which this is true varies across space, leaving the debate unresolved. There are multiple ways of quantifying phylogenetic diversity at a site, each represent different types of information. 1. Phylogenetic diversity (PD) 2. Mean pairwise distance (MPD) 3. Mean nearest taxon distance (MNTD). In this lecture, we will focus on PD only.

Note that there are several indices for quantifying PD out there, and redundancies abound (Schweiger et al 2008). Note also that there is a difference between phylogenetic analysis/inference and community phylogenetics through Phylogenetic Comparative Methods (PCM). Whereas the field of phylogenetics reconstruct the evolutionary relationships among species, using morphology, genetics, fossils etc. One of the products of phylogenetic reconstruction is phylogenetic trees. PCMs on the other hand study diversification by using phylogenies to control/account for evolutionary history. Under PCMs, we can examine and quantify the amount of relatedness using metrics like PD. So, one subdiscipline produces phylogenies, the other makes use of phylogenies.

**Functional diversity** – total differences or distance between species in functionally relevant traits that represent how energy flows through the system. There are two major approaches a) functional group approach that assigns species to categories based on behavioral and morphological characteristics, b) functional trait approach that measures the real values of a suite of functionally relevant morphological, physiological, behavioral traits that capture diet and habitat use – both key aspects of energy flows within a community (Villéger et al., 2008; Legras et al., 2018). There are multiple functional diversity indices (Mouchet et al., 2010; Schleuter et al., 2010).

We will rely on the ‘picante’ and ‘ape’ packages and use data collected during my masters in southern Nigeria. I sampled bats at three localities – Okomu National Park, Ososo, and Emu that represent three levels of disturbance: mature forest, regenerating forest/farm mosaic and farmland respectively. The community data is reported in Tanshi et al. (2019). The phylogenetic tree can be obtained from the Vertlife project at this website: <http://vertlife.org/phylosubsets/>

**Exercise**:

We will work with three datasets today: (1) Phylogenetic tree, downloaded from Vertlife. (Go check out Vertilife, where you can download a list of species that you work with or are curious about. It’s a pretty cool tool.) (2) Sample data, a site x species community matrix. (3) Trait data.

Step 1:

Library, data, clean up - set your working directory and library all the required packages.

#install.packages("picante")  
#install.packages("ape")  
#install.packages("FD")  
  
library(ape)  
library(picante)

library(FD)

#Read phylogenetic tree  
NGBat.Tree <- read.nexus("NigBatTree.nex")

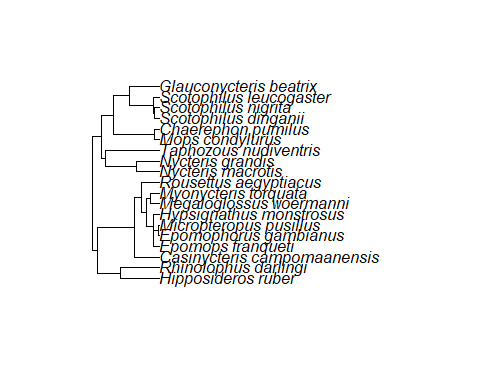
The tree file is in the nexus format, which needs to be read in with the function read.nex. However, further analysis will need a tree that this a “phylo” object, so you need to convert our nex tree into a phylo object.

Use the code to kill two birds; convert to phylo object and extract one tree. Note that Vertlife outputs a min of 100 trees. It’s usual to try to get a consensus tree, but for this, we will just extract the first tree.

#convert tree to phylo object, and restrict to just one tree (ideally consensus tree)  
NGBat.phylo <-as.phylo(NGBat.Tree[[1]])

Go ahead and plot the tree.

#plot the data  
plot(NGBat.phylo, label.offset=0.3)



Does it represent current knowledge of evolutionary relationships within the group? I’ve examined this tree and found it to be representation of the current bat phylogeny.

Now view the tree dataset. Hint, view (). What is it made up of?

#Read community data  
NGBat.samp <-read.csv("NGBat.samp.csv", header = TRUE)

Check the data out – hint: class(), str().

How many species are found across all three sites? Is it the same as the number on the tree? Do the names on both tree and sampling data match up?

Check to see that R is happy with species labels on both datasets using the match.phylo.comm function.

#Match species labels on tree and community data  
NGBat.match <- match.phylo.comm(NGBat.phylo, NGBat.samp)

## [1] "Dropping taxa from the community because they are not present in the phylogeny:"  
## [1] "Species" "Chaerephon\_aloysiisabaudiae"  
## [3] "Eidolon\_helvum" "Lavia\_frons"   
## [5] "Lissonycteris\_angolensis" "Mimetillus\_moloneyi"   
## [7] "Nycteris\_arge" "Saccolaimus\_peli"   
## [9] "Scontonycteris\_zenkeri"

The tree is lacking some species that are present in the data, but these were dropped to allow exact matching.

Did you assign the output of this operation? What is this new object comprised of?

#assign corrected/sorted/matched datasets to original files  
NGBat.phylo <- NGBat.match$phy  
NGBat.samp <- NGBat.match$comm

#Calculate phylogenetic diversity  
NGBat\_PD <- pd(NGBat.samp, NGBat.phylo, include.root=FALSE)

Check the data out. What parts of the data did you examine? What should you be looking out for with respect to the tree and sampling dataset?

Step 2:

Phylogenetic diversity We will compute Faiths Phylogenetic Diversity (PD), using the function pd. The function returns PD and SR – species richness.

#Calculate phylogenetic diversity  
NGBat\_PD <- pd(NGBat.samp, NGBat.phylo, include.root=FALSE)

Step 3:

Functional diversity

# Read trait data  
NGBat.trait <- read.csv("NGBat.traits.csv", header = TRUE, row.names = 1)

Check the data out. What parts of the data did you examine? What should you be looking out for in the trait data with respect to the tree and sampling datasets?

To examine functional diversity, we will use the dbFD (distance-based Functional Diversity indices).

# Read trait data  
NGBat.trait <- read.csv("NGBat.traits.csv", header = TRUE, row.names = 1)  
  
  
#Alphabetically order the community data by columns  
NGBat.samp2 <- NGBat.samp[ , order(names(NGBat.samp))]  
  
#Compute functional diversity stats for NGbats  
NGBat\_FD <- dbFD(NGBat.trait, NGBat.samp2)

## FRic: No dimensionality reduction was required. The 2 PCoA axes were kept as 'traits'.

NGBat\_FD

## $nbsp  
## [1] 6 8 9  
##   
## $sing.sp  
## [1] 6 8 9  
##   
## $FRic  
## [1] 0.5036933 1.0650968 1.8966689  
##   
## $qual.FRic  
## [1] 1  
##   
## $FEve  
## [1] 0.3244629 0.4335603 0.4075947  
##   
## $FDiv  
## [1] 0.5489446 0.5695161 0.8975667  
##   
## $FDis  
## [1] 0.6431067 0.6344256 1.2967192  
##   
## $RaoQ  
## [1] 0.7678687 1.0512673 1.9526734  
##   
## $CWM  
## FA BM  
## 1 55.59820 36.48468  
## 2 60.30364 42.08545  
## 3 64.65161 58.27097

You get a number of values from this function, but we will focus on: FRic, FEve, FDiv and FDis. Which of the landuse types is most functionally rich?

**References**

Cadotte, M. W., Dinnage, R., & Tilman, D. (2012). Phylogenetic diversity promotes ecosystem stability. Ecology, 93(sp8), S223-S233.

Faith DP (1992) Conservation evaluation and phylogenetic diversity. Biol Conserv 61:1–10. <https://doi.org/10.1016/0006-3207(92)91201-3>

Lean, C., & Maclaurin, J. (2016). The value of phylogenetic diversity. In Biodiversity conservation and phylogenetic systematics (pp. 19-37). Springer, Cham.

Legras, G., Loiseau, N., & Gaertner, J. C. (2018). Functional richness: Overview of indices and underlying concepts. Acta Oecologica, 87, 34-44.

Mason, N. W., de Bello, F., Mouillot, D., Pavoine, S., & Dray, S. (2013). A guide for using functional diversity indices to reveal changes in assembly processes along ecological gradients. Journal of Vegetation Science, 24(5), 794-806.

Mouchet, M. A., Villéger, S., Mason, N. W., & Mouillot, D. (2010). Functional diversity measures: an overview of their redundancy and their ability to discriminate community assembly rules. Functional Ecology, 24(4), 867-876.

Schleuter, D., Daufresne, M., Massol, F., & Argillier, C. (2010). A user's guide to functional diversity indices. Ecological monographs, 80(3), 469-484.

Schweiger, O., Klotz, S., Durka, W. et al. A comparative test of phylogenetic diversity indices. Oecologia 157, 485–495 (2008). <https://doi.org/10.1007/s00442-008-1082-2>.

Tanshi, I., A. E. Ogbeibu, and P. J. J. Bates. 2019. Complementary bat (Mammalia: Chiroptera) survey techniques uncover two new country records for Nigeria. Journal of Threatened Taxa, 11: 14788–14801. <https://www.researchgate.net/publication/337603758_Complementary_bat_Mammalia_Chiroptera_survey_techniques_uncover_two_new_country_records_for_Nigeria>

Villéger, S., Mason, N. W., & Mouillot, D. (2008). New multidimensional functional diversity indices for a multifaceted framework in functional ecology. Ecology, 89(8), 2290-2301.

**Assignment:** due March 16th

Let’s return to the grassland dataset. The tree and trait data are provided, available from Steve Kembel’s website. Read in all your data. Play with the tree.

As this is a big tree and checking species names may make you cross-eyed, skip confirming species names here. Plus, the data is well used and clean, so everything is as it should be. How would you attempt to answer the following questions?

Q1. Which is the most phylogenetically diverse site? Is there a positive or negative relationship between species richness and phylogenetic diversity? Use the plot function.

Q2. What inferences can you draw about the relationship between PD and SR For sites with > 20 species?

Q3. What is the functional diversity at the five most species rich sites?

Q3. Is there a relationship between PD and FRic?

Q4. What do these results mean with respect to the relationship between these three dimensions of biodiversity? Is one a proxy for the other?