

# Measuring functional diversity in R

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In the ‘diversity lab’ we examined the effects of coffee farm management intensity on bird *taxonomic* diversity. This time we will consider whether management intensity affects bird *functional* diversity.

Taxonomic diversity quantifies the variety of bird species found in a community, and includes both the number and evenness of species abundance. Ecologists have found that communities with greater species diversity often have greater ecosystem functioning, and that much of this difference can be attributed to greater functional diversity. Functional diversity measures the variety of species traits found in a community. For instance, consider a plant community that includes two species, one of which is adapted to dry conditions and the other is adapted to wet conditions. The wet-adapted species is more productive (i.e., grows faster) in wet years, whereas the dry-adapted species is more productive in dry years. If there is substantial year to year variation in precipitation, then the two species community will be more productive than either one by itself. In contrast, a two species community where both species are equally drought tolerant will not necessarily be more productive than either alone, at least in the face of variable precipitation. Of course, plant communities encounter a wide variety of environmental conditions in addition to precipitation, including soil nutrient availability, pH, light availability, temperature minimum and maximum, grazing intensity, and disturbance intensity, among others. From this long list it is clear that the number of potential niches in a community could be quite large. If there were only one suitable position (and of course there could be more) along each of these axes, that would mean there are  $2^8$  or 256 possible niches to be filled. This may explain why some tree communities may have up to 1000 species in a single hectare (about 2 acres) and why there are millions of plant species on the planet.

Today however we are interested in bird species diversity and bird functional diversity in coffee farms. How might bird functional diversity contribute to an ecosystem function, and, what functions do birds perform, anyway? Two functions that we considered are pest control and ecotourism. Birds consume pests in a number of ways. Some, such as Passerines (songbird) eat insects that might be herbivores on coffee plants. Others, such as hawks might eat rodents. Thus a variety of prey items or food types within a bird community may be beneficial if you want to control pests. Also, pests might occur at multiple heights in a forest canopy, so a variety of foraging heights might increase pest control. Finally, larger birds eat larger prey, so a variety of bird sizes might increase pest control. So, we have three traits, foodtype (e.g., insects, rodents, nectar, fruit), foraging height (ground=1, shrub layer=2, lower canopy=3, middle canopy=4, upper canopy=5), and bird length, that might be good to include in an index of functional diversity. For

ecotourism, bird diversity might contribute to in a couple ways. A greater variety of color might be attractive to birders, and it might be good if a locale had both rare and common species, as it's always nice to see some familiar birds as well as something new. So, we have two traits that might contribute to ecotourism, bird color and abundance. Of course, these are also traits that can be obtained from bird guides fairly easily.

To analyze bird functional diversity, we will use three approaches, Petchey's FD, Rao's Q, and convex hull volume. Petchey's FD measures diversity by constructing a dendrogram of the entire community based on the available traits and then calculates the total branch length of individual communities superimposed on the dendrogram. Rao's Q measures the average pairwise distance between *individuals* in trait space and thus incorporates the abundance of a given trait as well as the difference between trait values. Convex hull volume measures the total volume that a community inhabits in trait space. For instance, if one bird community has species that ranged from 4 to 8 cm, while a second community had species that ranged from 4 to 12 cm, the second community would occupy twice the trait space of the first. Adding more traits simply adds more dimensions, and the volume for a community is simply the product of the range for each dimension. Convex hull volume does not work that well for categorical variables, so we will only use the continuous variables for this index. It also often makes sense to log-transform a variable if it is a measurement like size. When log-transformed, for instance using base 2, a doubling in size is equal to a one unit change on the log scale. Thus two communities that have size variation over a factor of 2 would have equal volume. For instance a community that ranges from 4 to 8 cm and another that range from 8 to 16.

Below, we show you how to compute each of these measures of functional diversity. You can then determine whether management intensity affects functional diversity. At various points through the exercise we will stop to ask questions about what we have found.

Note that this lab requires Dan Flynn's 'All\_functions.R' and the following additional R packages: lattice, geometry, reshape, and rgl.

WINDOWS USERS NOTE: For some reason, 'geometry' does not show up when you try to download it from within R. However you can install it by downloading the zipfiles from r-project -> cran -> your favorite mirror -> windows -> contrib -> your current version (2.6?) . Note that packages are sorted funny with caps first, lower case second, so scroll down. Now within R 'install from local zip files' from menu.)

```
# script to analyze the functional diversity of coffee bird data
library(vegan)
library(cluster)
library(lattice)
```

```
source("FD_Calculators.R")
birdTraits <- read.csv("Bird_traits_annon.csv", header=TRUE)
```

```

head(birdTraits)
hist(birdTraits$Length_cm)
birdTraits$logLen=log2(birdTraits$Length_cm)
hist(birdTraits$logLen)
# lets drop a few of these because they are redundant or contain
little info
birdTraitsr <- subset(birdTraits, select = c("Common", "logLen",
      "foodtype1", "forageHt",
      "sColor", "abun"))

# Now get abundance data from last week
birds <- read.csv("Coffee Bird List I.csv")
head(birds)
birds <- birds[, c(-1,-2)]
for (i in (2:length(birds))) {birds[,i]=ifelse(birds[,i]==0, NA,
birds[,i])}      # must convert 0's to NA

birds=merge(birdTraitsr, birds, by="Common")
head(birdsr)
rownames(birdsr) <- birdsr[, "Common"];
head(birdsr)

# note on indexing. The brackets are a convenient way to index an
object, array, or dataframe.
# Today we will lump all our data in a single dataframe,
"birdsr", and use indexing to utilize parts of that dataframe.
# The brackets contain two entries separated by a comma.
# The first entry indexes the rows, and the second indexes the
columns.
# In you can use most any sort of expression in either spot. In
the command above, we select only the column called "common" and
assign those values to the row names. Below, we select just the
farm abundance columns, or just the trait columns. When we work
with convex hulls below, we will doubly index the dataframe
birdsr: "birdsr[, trtcols][bighull, 2]". See below for more.

FDall=Calculate.FD(landfile=birdsr[,7:13],
traitfile=birdsr[,2:6])
Qall=Calculate.Q(landfile=birdsr[,7:13], traitfile=birdsr[,2:6])
FDall
Qall

FDdf=data.frame(Site=names(FDall), FD=as.numeric(FDall))
Qdf=data.frame(Site=names(Qall), Q=as.numeric(Qall))

```

```

management <- read.csv("Coffee_Bird_Management.csv")
head(management)
management = merge(management, FDdf)
management = merge(management, Qdf)
management$ab=c('a','b','a','b','a','b','b')

quartz()
xyplot(FD~Management.index, groups=ab, data=management,
auto.key=list(x=0.1, y=.95, border=TRUE))
summary(lm(FD~Management.index, data=management))
quartz()
xyplot(Q~Management.index, groups=ab, data=management,
auto.key=list(x=0.1, y=.95, border=TRUE))
summary(lm(Q~Management.index, data=management))

# so lets plot the functional dendrograms for individual
locations to see how FD compares between farms
# here is how we build the tree for all species present
cluster.distances <- daisy(
  birdsr[,2:6],
  metric="gower")

tree = hclust(cluster.distances)
tree <- as.dendrogram(tree)

quartz(width=6, height=12) # on windows use windows() instead of
quartz()
par(mar = c(5, 4, 4, 18)) # this sets the margins of the plot as
a number of lines, clockwise beginning at the bottom

plot(tree,
  main = "",
  horiz = TRUE,
  leaflab = "none", # this suppresses the automatic labeling of
the leaves
)

# now we simply add leaf labels for the community (farm) of
interest
mtext(as.character(row.names(birdsr)[order.dendrogram(tree)]), 4,
las = 1, at = 1:length(birds$Common), # this orders the row names
(=common names) as in the tree

```

```

col = ifelse(is.na(birdsr$Forest_A)[order.dendrogram(tree)],
"grey50", "black")) # and this makes the leaf label grey if the
species is missing, black if present
# let's add a title too
title("functional dendrogram for Forest_A")

# you can now repeat this for each community (farm) you can open
a new graphics window for each (quartz()) or write them to pdf
pdf() try ?pdf for more info.

# Question: how do the dendrograms of FD compare? Are there any
clusters that are under or over represented on any farms?

# A third approach to quantifying functional diversity is to
calculate the convex hull volume that a community occupies in
multidimensional trait space.
# In this case we will calculate hull volume using just the 3
numeric traits

# here we will need the rgl and geometry packages
# geometry will allow us to calculate the volume of n-dimensional
convex hulls
# rgl is a 3d viewer so we can see the results
library(rgl)
library(geometry)
library(reshape)
# first we need to change the format of birds (only the abundance
data) from 'wide' to 'long'
birdsLong=melt(birdsr[,c(1,7:13)], id="Common",
variable_name="community", na.rm=TRUE)
head(birdsLong)

rgl.open() # this opens a new rgl window
rgl.viewpoint(fov=10, zoom=1.5, theta=340, phi=0) # this sets
the angle of view
rgl.bg(color="white") # this sets the background color

# so, here is the plan. First we will make a hull of all of the
species, and compute its volume.
# convex hull volume only works with continuous variables, so we
will only use log(length), forage height, and abundance
# Next we will make hulls of the individual communities and
compare those volumes as a fraction of the entire community

```

```

head(birdsr)
# first we can construct and plot the full hull
trtcols=c("logLen","forageHt","abun")
rgl.clear( type = "shapes" )
# First we use convhulln from the geometry package to find the
convex hull of the cloud of species points in 3d trait space.
# The convex hull is simply the set of points that encloses all
other points
# That same hull can be defined as the set of facets or triangles
(half-spaces in geometry-ese) that encloses the set of points.
# In this case "bighull" is the set of triangles that represents
the convex hull. Each column contains 3 numbers that represent
the row number indices of the three points that bound each
triangle in the original dataframe birdsr.
bighull = t(convhulln(birdsr[, trtcols], options="QJ"))
rgl.triangles(birdsr[, trtcols][bighull, 1], birdsr[,
trtcols][bighull, 2], birdsr[, trtcols][bighull,
3],col="blue",alpha=.8)
# Here we are using rgl to plot the individual triangles that
form the convex hull.
# The three indices of birdsr (eg, birdsr[, trtcols][bighull, 1])
each references one trait, such that the first 3 of each plot one
facet, the second three the next facet, etc.
axis3d(c('x'), color= "black", labels=c(2,4,8,16,32))
axis3d(c('y'), color= "black", labels=c(1:5))
axis3d(c('z'), color= "black", labels=c(1:5))
title3d(main="Full community", sub=NULL, "Length (cm)", "Foraging
Height", "Abundance", color= "black", line=3)

```

# if you click and drag of the RGL device (the hull) you can rotate it. Remind us to show you a movie made using this approach!

```

# now, we can plot each individual hull for the farms
# we will use a loop to make the code more compact
# this should make 7 windows with two 3d hulls in each.
# The light blue is the full community and the dark green is the
individual farm
vol=list()
for (i in levels(birdsLong$community)) { # i="Forest_A"
  rgl.open() # this opens a new rgl window
  rgl.viewpoint(fov=10, zoom=1.5, theta=340, phi=0) # this

```

```

sets the angle of view
  rgl.bg(color="white") # this sets the background color
  rgl.triangles(birdsr[, trtcols][bighull, 1], birdsr[,
trtcols][bighull, 2], birdsr[, trtcols][bighull,
3],col="blue",alpha=.2)

  splist= birdsLong[birdsLong$community==i, "Common"]
  commhull = t(convhulln(birdsr[birdsr$Common%in%splist,
trtcols], options=paste("FS TO ",i,".txt", sep="")))
  rgl.triangles(birdsr[birdsr$Common%in%splist,
trtcols][commhull, 1], birdsr[birdsr$Common%in%splist,
trtcols][commhull, 2], birdsr[birdsr$Common%in%splist,
trtcols][commhull, 3],col="green",alpha=.8)
  axis3d(c('x'), color= "black", labels=c(2,4,8,16,32))
  axis3d(c('y'), color= "black", labels=c(1:5))
  axis3d(c('z'), color= "black", labels=c(1:5))
  title3d(main=i, sub=NULL, "Length (cm)", "Foraging Height",
"Abundance", color= "black", line=3)
}

```

# well, that was fun. Now, notice that there are several rgl  
# windows. You can rotate the hulls by clicking and dragging on  
# them.

# But wait, what are the volumes of these hulls?

# Note that the volume is returned in the console, but there  
seems to be no way to get it as an object in R.

# Fortunately, there is a method to write the output to a file,  
which we can then read in as an R object.

```
management$vol=NULL # first make an empty container for the
volumes
```

# now loop through the farms and calculate the volume for each.

```
for (i in levels(birdsLong$community))
{management[management$Site==i, "vol"]=scan(paste(i,".txt",
sep=""))[4]}
```

```
xyplot(vol~Management.index, groups=ab, data=management)
```

# Clearly, there is no effect of management intensity on this  
measure of diversity either.

# Further questions:

# In your estimation, does farm management affect bird species or  
functional diversity?

# How might this analysis be improved?

# Are there any additional traits you would include if you could  
obtain them?