

Measuring and comparing beta diversity

Hi there,

Beta diversity can be understood as the difference in the composition of species between communities. Moreover, beta diversity can be seen as the sum of two components: turnover and nestedness. Turnover is the difference between communities solely in relation to which species occur in them. Nestedness represents how much the species composition of a site with a lower species richness is a subset of a site with higher species richness. Today we are going to see how to calculate and compare values of beta diversity based both on presence/absence and abundance data. Additionally, we'll see how to partition beta diversity into their turnover and nestedness partitions.

First of all, install and load "vegan" and "betapart" packages.

```
install.packages("betapart")
install.packages("vegan")
library(betapart)
library(vegan)
```

Download the following file:

<https://www.mediafire.com/?6jer766yzc5p0h1> [<https://www.mediafire.com/?6jer766yzc5p0h1>]

Load the file, which presents species occurring in 6 communities.

```
comm <- read.csv(choose.files(), row.names=1, sep=";")
```

Now, consider that the first three communities are from undisturbed forest fragments, while the other three are from disturbed forest fragments. We can then create an object indicating these groups. Note that we will repeat "undisturbed" three times, and then "disturbed" also three times. We will use this object later in "betadisper".

```
groups <- factor(c(rep(1,3), rep(2,3)), labels = c("undisturbed", "disturbed"))
```

Jaccard and Sorensen indices do not consider the abundance of species. So, they can only use the presence/absence matrix. To transform our community data matrix to a presence/absence matrix, use:

```
presabs <- ifelse(comm > 0, 1, 0)
```

Now, we'll calculate the Jaccard index and its partitions of turnover and nestedness. We can calculate Sorensen index instead by using the argument `index.family="sorensen"` .

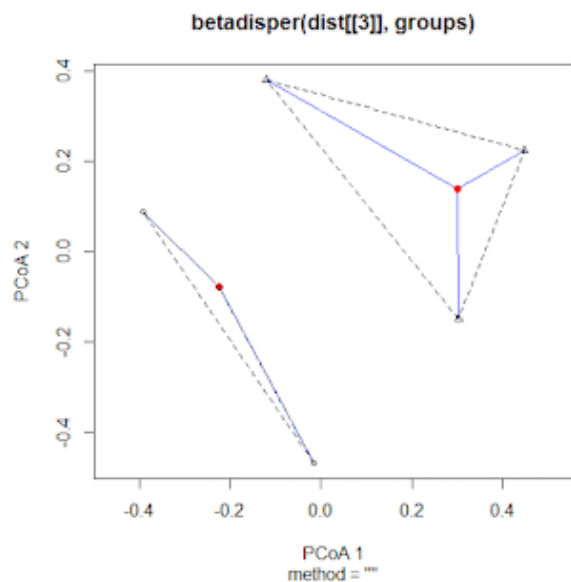
```
dist <- beta.pair(presabs, index.family="jaccard")
```

To get the pairwise Jaccard index turnover partition between communities, type: `dist[[1]]`. To get nestedness partition, type: `dist[[2]]`. To get all beta diversity: `dist[[3]]`.

If we want to compare the beta diversities of communities aggregated by the treatments of "undisturbed" and "disturbed", we can use "betadisper" analysis.

```
bd <- betadisper(dist[[3]], groups)
```

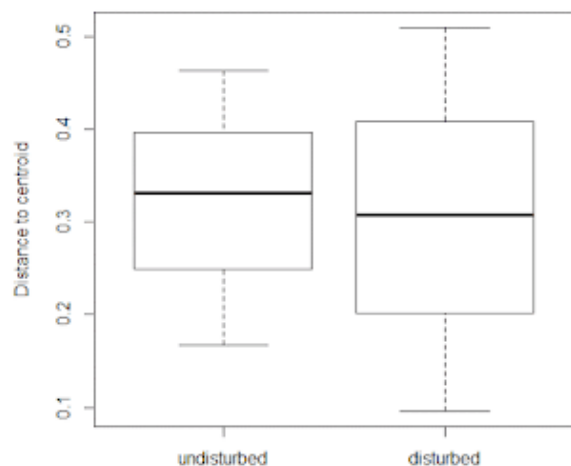
```
plot(bd)
```



[<https://4.bp.blogspot.com/-IRX3SuVDInY/V8l3k5XlrVI/AAAAAAAAABVM/jA4KG0qOsUY7LLYnM72HaF77DSffsvDaACLcB/s1600/betadisperjac.png>]

The betadisper plot indicates that there is a difference in species compositions from undisturbed and disturbed forest fragments. Let us first do a boxplot to observe the distance of values of beta diversity of each treatment in relation to their centroids (basically, this indicates homogeneity in how communities of a given treatment differ from each other). Then, we'll perform an ANOVA to test if treatments are significantly different.

```
boxplot(bd)
```



[<https://2.bp.blogspot.com/-0zQRbLGmRv8/V8l78mP3h1I/AAAAAAAAABVk/MXCoettAFYwFbcyDVRCfRXYLbkoNulunQCLcB/s1600/boxplotbd.png>]

```
anova(bd)
```

	Df	Sum Sq	Mean Sq	F value	Pr(>F)
Groups	1	0.002644	0.0026444	0.1708	0.7006

Residuals 4 0.061912 0.0154780

Observe that, in our example, treatments (disturbed and undisturbed forest fragments) do not differ significantly in relation to how communities vary from each other.

TO CALCULATE BETA DIVERSITY USING ABUNDANCE-BASED DATA

The approach is the same we used before, but where we used "beta.pair", use "bray.part" function. The function will calculate beta diversity (and its partitions) based on Bray-Curtis dissimilarity index.

```
dist<-bray.part(comm)
```

However, read <http://onlinelibrary.wiley.com/doi/10.1111/2041-210X.12029/abstract> [<http://onlinelibrary.wiley.com/doi/10.1111/2041-210X.12029/abstract>] for more information concerning the use of this index.

Finally, take a look at "phylo.beta.pair" and "functional.beta.pair" from "betapart" package to see how we can also calculate phylogenetic and functional beta diversities.

This is it for now.

Till' next time!

Posted 27th August 2016 by [José Hidasí](#)

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