CompoundTest

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How to test for a compound topology using the restricted null model

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See README for further info.

Summary

1. PREPARING THE DATA {#1}

#Set the working directory setwd(dirname(rstudioapi::getActiveDocumentContext()$path))

#Delete all previous objects rm(list= ls())

#Clear the console cat("\014")

#Load the required packages and functions. library(bipartite) source("RestNullModel.R") source("PosteriorProb.R")

#Load the data data<-as.matrix(read.table("net1.txt", head=TRUE))

#Visualize the data data

#Check the data dim(data) class(data)

#Visualize the raw matrix visweb(data)

2. MODULARITY ANALYSIS

#Compute modularity Mod <- bipartite::computeModules(data)

#Recover the partitions Part <- bipartite::module2constraints(Mod) row.Part <- Part[1:nrow(data)] col.Part <- Part[(nrow(data)+1):(nrow(data)+ncol(data))]

#Test for the significance of modularity with a Monte Carlo procedure

#Generate randomized matrices nulls <- nullmodel(data, N=9, method="r2d")

#Calculate the modularity of the randomized matrices mod.nulls <- sapply(nulls, computeModules) like.nulls <- sapply(mod.nulls, function(x) x@likelihood)

#Calculate the z-score of the randomized distribution (z <- (data.mod@likelihood - mean(like.nulls))/sd(like.nulls))

#Plot the observed modularity value against the distribution of randomized values plot(density(like.nulls), xlim=c(min((data.mod@likelihood), min(like.nulls)), max((data.mod@likelihood), max(like.nulls))), main="Observed vs. randomized") abline(v=(Mod@likelihood), col="red", lwd=2)

#Estimate the P-value mean(like.nulls) sd(like.nulls) Mod@likelihood praw <- sum(like.nulls>(Mod@ likelihood)) / length(like.nulls) ifelse(praw > 0.5, 1-praw, praw)

3. NESTEDNESS ANALYSIS

#Calculate the desired nestedness metric (here WNODA) for the original network. obs <- unlist(bipartite::nest.smdm(x = data, constraints = Part, #Input the modular structured recovered from step 2 weighted = T, #By considering the edge weights, you are choosing WNODA decreasing = "abund"))

#Check the scores obs

4. RESTRICTED NULL MODEL ANALYSIS

#Calculate constrained interaction probabilities considering the network's modular structure Pij <- PosteriorProb(M = data, R.partitions = row.Part, C.partitions = col.Part, #Input the modular structured recovered from step 2 Prior.Pij = "degreeprob", #Choose the null model Conditional.level = "modules") #Choose the kind of constraints

#Check what those probabilities look like Pij

#Generate randomized networks with the null model of your choice, considering the interaction probabilities calculated before. nulls <- RestNullModel(M = data, Pij.Prob = Pij, #Recover the probabilities calculated in the previous command Numbernulls = 9, #This step may take long, so start experimenting with low values Print.null = T, allow.degeneration = F, #Choose whether you allow orphan rows and columns to be removed or not return.nonrm.species = F, connectance = T, byarea = T, R.partitions = row.Part, C.partitions = col.Part)

#Calculate the same nestedness metric for all randomized networks null <- sapply(nulls, function(x) bipartite::nest.smdm(x = x, constraints = Part, weighted = T, decreasing = "abund")) WNODA.null <- unlist(null[3,]) WNODAsm.null <- unlist(null[8,]) WNODAdm.null <- unlist(null[9,])

#Plot the observed nestedness value against the distribution of randomized values par(mfrow = c(1,3)) plot(density(WNODA.null), xlim=c(min(obs[3], min(WNODA.null)), max(obs[3], max(WNODA.null))), main="Observed vs. randomized", xlab = "WNODA matrix") abline(v=obs[3], col="red", lwd=2) plot(density(WNODAsm.null), xlim=c(min(obs[8], min(WNODAsm.null)), max(obs[8], max(WNODAsm.null))), main="Observed vs. randomized", xlab = "WNODAsm matrix") abline(v=obs[8], col="red", lwd=2) plot(density(WNODAdm.null), xlim=c(min(obs[9], min(WNODAdm.null)), max(obs[9], max(WNODAdm.null))), main="Observed vs. randomized", xlab = "WNODAdm matrix") abline(v=obs[9], col="red", lwd=2)

#Estimate the P-values

#Nestedness in th entire network praw.WNODA <- sum(WNODA.null>obs[3]) / length(WNODA.null) p.WNODA <- ifelse(praw.WNODA > 0.5, 1- praw.WNODA, praw.WNODA) # P-value p.WNODA

#Nestedness within the modules praw.WNODAsm <- sum(WNODAsm.null>obs[8]) / length(WNODAsm.null) p.WNODAsm <- ifelse(praw.WNODAsm > 0.5, 1- praw.WNODAsm, praw.WNODAsm) # P-value p.WNODAsm

#Nestedness between the modules praw.WNODAdm <- sum(WNODAdm.null>obs[9]) / length(WNODAdm.null) p.WNODAdm <- ifelse(praw.WNODAdm > 0.5, 1- praw.WNODAdm, praw.WNODAdm) # P-value p.WNODAdm

5. PLOTTING THE NETWORK

par(mfrow = c(1,1))

#Sort the matrix in a way that facilitates visualizing the compound topology data.comp <- bipartite::sortmatrix(matrix = data, topology = “compound”, sort_by = “weights”, row_partitions = row.Part, col_partitions = row.Part)

#Assign colors for the modules modcol <- rainbow((length(unique(Part))), alpha=1)

#Plot the matrix plotmatrix(data.comp$matrix, row_partitions = data.comp$row_partitions, col_partitions = data.comp$col_partitions, border = T, binary = F, modules_colors = modcol, within_color = modcol, between_color = “lightgrey”)

6. SOURCE STUDIES

#If you want to understand the background of those new analyses before using them, read the following studies. The first three paved the ground for the analysis of compound topologies developed later by our lab.

1. Lewinsohn, T. M., P. Inácio Prado, P. Jordano, J. Bascompte, and J. M. Olesen. 2006. Structure in plant-animal interaction assemblages. Oikos 113: 174–184. Available at: http://doi.wiley.com/10.1111/j.0030-1299.2006.14583.x.

2. Bezerra, E. L. S., I. C. Machado, and M. A. R. Mello. 2009. Pollination networks of oil-flowers: a tiny world within the smallest of all worlds. J. Anim. Ecol. 78: 1096–1101. Available at: http://www.ncbi.nlm.nih.gov/pubmed/19515098.

3. Flores, C. O., S. Valverde, and J. S. Weitz. 2013. Multi-scale structure and geographic drivers of cross-infection within marine bacteria and phages. ISME J. 7: 520–532. Available at: http://www.nature.com/doifinder/10.1038/ismej.2012.135 [Accessed June 9, 2016].

4. Pinheiro, R. B. P., G. M. F. Félix, A. V Chaves, G. A. Lacorte, F. R. Santos, É. M. Braga, and M. A. R. Mello. 2016. Trade-offs and resource breadth processes as drivers of performance and specificity in a host–parasite system: a new integrative hypothesis. Int. J. Parasitol. 46: 115–121. Available at: http://www.sciencedirect.com/science/article/pii/S0020751915002933.

5. Felix, G. M., R. B. P. Pinheiro, R. Poulin, B. R. Krasnov, and M. A. R. Mello. 2017. The compound topology of a continent-wide interaction network explained by an integrative hypothesis of specialization. bioRxiv 236687. Available at: https://doi.org/10.1101/236687.

6. Pinheiro, R. B. P. 2019. As topologias de redes de interações ecológicas e suas origens. PhD Thesis, Federal Univesity of Minas Gerais. URL: http://hdl.handle.net/1843/33333.

7. Pinheiro, R. B. P., G. M. F. Felix, C. F. Dormann, and M. A. R. Mello. 2019. A new model explaining the origin of different topologies in interaction networks. Ecology 100: e02796. Available at: https://doi.org/10.1002/ecy.2796.

8. Mello, M. A. R., G. M. Felix, R. B. P. Pinheiro, R. L. Muylaert, C. Geiselman, S. E. Santana, M. Tschapka, N. Lotfi, F. A. Rodrigues, and R. D. Stevens. 2019. Insights into the assembly rules of a continent-wide multilayer network. Nat. Ecol. Evol. 3: 1525–