R code for analysis

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#Bipartite network of fly families and the habitats they visit

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library(vegan)

library(bipartite) #this package contains the "nested" stat which looks at all possible ways to analyze nestedness

library(ggplot2)

library(gridGraphics)

library(readr)

## Insert raw csv file for species data

rawhabitatdata1 <- read\_csv("rawhabitatdata1.csv", col\_types = cols(Laboratory = col\_skip()))

#data is a presence/absence matrix, where "1" indicates a species lives in a particular habitat

rawhabitatdata1[is.na(rawhabitatdata1)] <- 0

#Change all the NAs to "0", as this means the species were not found in that habitat and data must be binary

View(rawhabitatdata1)

# x is the species (without the names or r thinks the x column is not numeric)

#y are the different habitat types

########### calculating nestedness ############

########## first we will see if there is nestedness between SPECIES and habitats ##########

nested(rawhabitatdata1, method = "ALL", rescale = FALSE, normalised = TRUE)

## temperature is 2.339996 so data IS nested

# Temperature measures the order in which species' extinction or colonization would occur in the system

#####The data is nested since the value is 'colder' (closer to zero) - so there is a fixed order of extinction

#AKA, the generalists would survive but the specialists would die first

#### further proof the data is nested

out1 <- nestedtemp(rawhabitatdata1)

plot(out1, kind = "incid")

nestedness(rawhabitatdata1)

#calculate null models to compare original models to

oecosimu(rawhabitatdata1, nestedtemp, "r0")

#non-sequential algorithm for binary matrices that preserves the site (row) frequencies.

oecosimu(rawhabitatdata1, nestedtemp, "c0")

#non-sequential algorithm for binary matrices that preserves species frequencies (Jonsson 2001).

oecosimu(rawhabitatdata1, nestedtemp, "r00")

#non-sequential algorithm for binary matrices that only preserves the number of presences (fill)

#essentially this compares the original to a null community

########## nestedness between FAMILIES and habitats ##########

fhabitat <- read.csv("Desktop/Literature review/Flies and flower shapes/fhabitat.csv")

row.names(fhabitat) <- c("Anthomyiidae", "Bibionidae", "Bombyliidae","Calliphoridae", "Ceciomyiidae",

"Ceratopogonidae", "Drosophilidae", "Ephydridae", "Fanniidae", "Milichiidae",

"Muscidae", "Opomyzidae", "Rhiniidae", "Rhinophoridae", "Sarcophagidae",

"Scathophagidae", "Sciomyzidae", "Sepsidae", "Simuliidae", "Stratiomyidae",

"Syrphidae", "Tabanidae", "Tachinidae", "Tephritidae", "Ulidiidae")

View(fhabitat)

fhabitat <- t(fhabitat)

#switches rows with columns

nestedtemp(fhabitat)

#matrix is 6.21 so it is nested

out2 <- nestedtemp(fhabitat)

plot(out2, kind = "incid")

#calculate null models to compare original models to

oecosimu(fhabitat, nestedtemp, "r0")

#non-sequential algorithm for binary matrices that preserves the site (row) frequencies.

oecosimu(fhabitat, nestedtemp, "c0")

#non-sequential algorithm for binary matrices that preserves species frequencies (Jonsson 2001).

oecosimu(fhabitat, nestedtemp, "r00")

#non-sequential algorithm for binary matrices that only preserves the number of presences (fill)

#essentially this compares the original to a null community

#### making the figure ######

## Insert raw csv file for family data WITHOUT LABORATORY HABITAT

library(gridGraphics)

library(bipartite)

new\_fhabitat <- grid.grabExpr(grid.echo(function() visweb(fhabitat, labsize = 0.8)))

View(new\_fhabitat)

# shift the left axis labels to the right

new\_fhabitat[["children"]][["graphics-plot-1-left-axis-labels-1"]][["x"]] <- unit(0.75, units = "in")

# shift the bottom axis labels upwards

new\_fhabitat[["children"]][["graphics-plot-1-bottom-axis-labels-1"]][["y"]] <- unit(0.1, units = "in")

dev.new(width=11, heighxt=5, noRStudioGD=T)

grid.newpage(); grid.draw(new\_fhabitat)