

Rarity Index

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Script to calculate the rarity index

To define species rarity we combined estimates of local abundance (LA), geographical range (GR), and habitat breadth (HB) of each species. The rarity index for a species i (RI_i) is calculated by the following formula:

$$RI_i = \frac{[(LA_i \times w_{la}) + (GR_i \times w_{gr}) + (HB_i \times w_{hb})]}{(w_{la} + w_{gr} + w_{hb})}$$

where w_{la} , w_{gr} and w_{hb} are the weighting parameters for local abundance, geographical range and habitat breadth, respectively. The weighing parameter for each metric x was calculated by the following formula:

$$w_x = \frac{1}{2} + \left[\left(\frac{1 - |r_{x1}|}{2} \right) + \left(\frac{1 - |r_{x2}|}{2} \right) \right]$$

where r_{x1} and r_{x2} are the Pearson's correlation coefficients between the given metric x and each of the other two metrics.

We obtained LA, GR and HB for each dung beetle species and construct an object with these three parameters. We first log-transformed each metric and then standardized the data by dividing each value by the maximum value across all species

```
rarity <- read.csv("rarity_parameters.csv", h=T)

parameters <- rarity[,3:5]
transformed <- log(parameters+1)
names(transformed) <- c("LogLA", "LogGR", "LogHB")
scaled.GR <- transformed$LogGR/max(transformed$LogGR)
scaled.HB <- transformed$LogHB/max(transformed$LogHB)
scaled.LA <- transformed$LogLA/max(transformed$LogLA)
scaled <- data.frame(rarity$sp, scaled.GR, scaled.HB, scaled.LA)
```

To obtain weighting parameters, first we ran Pearson's correlations to get r_x values:

```
#Correlations between variables

library(stats)

correlations <- cor(scaled[2:4], method="pearson")

rlahb <- correlations[2,3]
rlagr <- correlations[1,3]
rgrla <- correlations[3,1]
rgrhb <- correlations[2,1]
rhbla <- correlations[3,2]
rhbgr <- correlations[1,2]
```

And then used the r_x values to calculate the w factors:

```
Wla <- 1/2+(((1-rlagr)/2)+((1-rlahb)/2))  
Wgr <- 1/2+(((1-rgrla)/2)+((1-rgrhb)/2))  
Whb <- 1/2+(((1-rhbgr)/2)+((1-rhbba)/2))
```

Finally, we calculated the Rarity Index for each species:

```
RI <- ((scaled$scaled.LA*Wla)+(scaled$scaled.GR*Wgr)+(scaled$scaled.HB*Whb))/(Wla+Wgr+Whb)  
RI <- data.frame(rarity$sp, RI)
```