Comparison of EcoIndicators and IndVal methods for indicator species analysis

Site

We analysed a data set collected in the northeast of the Buenos Aires province, in experimental plots of the National University of Luján (UNLu) and in rural plots of the localities of Open Door, Cortines and General Rodríguez (Buenos Aires, Argentina). Sampling was carried out seasonally from 2008 to 2014.

Different sites were chosen according to their use history: (A), with a history of use between 17 and 31 years applying conventional tillage and reduced tillage; (G) livestock soils with a use history of 15 years with sheep and cattle grazing: (N) Naturalized soils, with no agricultural or livestock use for at least 30 years. A total of 99 sampling units of each type of use were analysed for the evaluation of indicator species. We aggregated species by the taxonomic category of order.

Indicator species analysis

1. Load the required packages

```
devtools::install github('lsaravia/EcoIndicators')
## Skipping install of 'Ecoindicators' from a github remote, the SHA1 (045a59bf) has not changed since
    Use `force = TRUE` to force installation
library(Ecoindicators)
library(labdsv) # indval function
## Loading required package: mgcv
## Loading required package: nlme
## This is mgcv 1.8-42. For overview type 'help("mgcv-package")'.
## This is labdsv 2.1-0
## convert existing ordinations with as.dsvord()
##
## Attaching package: 'labdsv'
##
  The following objects are masked from 'package:stats':
##
##
       density, loadings
2. Read data
macromesofauna <- read.table("../data/macromesofauna.txt", header = TRUE)
```

3. Call the function select_indicator_species.

Arguments

• Community data: fauna[,-1] to exclude the Landuse column

- group: the samples grouping by Landuse.
- $\alpha = 0.05$

macromesofauna.indicatorspecies <- select_indicator_species(macromesofauna[,-1], group = macromesofauna
macromesofauna.indicatorspecies\$names</pre>

```
## [1] "Geophilomorpha" "Lithobiomorpha" "Coleoptera" "Dermaptera"
## [5] "Diptera" "Hemiptera" "Hymenoptera" "Isopoda"
## [9] "Collembola" "Megascolecidae"
```

4. Call the function indval.

Use the same arguments.

```
macromesofauna.indval <- indval(macromesofauna[,-1],clustering = macromesofauna$Landuse)
sort(macromesofauna.indval$indcls,decreasing = T)</pre>
```

##	Collembola	Isopoda	Acari	Hymenoptera
##	0.34276343	0.31876374	0.31492522	0.21094550
##	Hemiptera	Diptera	Lumbricidae	Coleoptera
##	0.16470677	0.15742794	0.13519814	0.11981982
##	Lithobiomorpha	Geophilomorpha	Dermaptera	Acanthodrilidae
##	0.11313131	0.09719840	0.07575758	0.06989247
##	Megascolecidae	Diplopoda	Lepidoptera	Symphyla
##	0.05387205	0.04565132	0.03703704	0.03703704
##	Araneae	Stylommatophora	Protura	Orthoptera
##	0.03194738	0.03142536	0.02938476	0.02308802
##	Blattodea	Gordioidea	Scolopendromorpha	Psocodea
##	0.02203857	0.02188552	0.01010101	0.01010101
##	Diplura			
##	0 01010101			

5. Show the indicator species names shared by the two methods.

shared <- names(sort(macromesofauna.indval\$indcls,decreasing = T)) %in% macromesofauna.indicatorspecie
shared.sig <- macromesofauna.indval\$pval[names(sort(macromesofauna.indval\$indcls,decreasing = T))[shared.sig</pre>

##	Collembola	Isopoda	${ t Hymenoptera}$	Hemiptera	Diptera
##	TRUE	TRUE	TRUE	TRUE	TRUE
##	Coleoptera	${\tt Lithobiomorpha}$	Geophilomorpha	Dermaptera	Megascolecidae
##	FALSE	TRUE	TRUE	TRUE	TRUE

Results

Applying both methods, results coincided in nine indicator species, finding a total of 10 species with a value of p < 0.05.

References

Duhour, A.; Falco, L.; de la Vega, H.; Coviella, C.; Velazco, N.; Sandler, R.; Rionda, M.; Porres, M. D. & Saravia, L. Ecoindicators, un programa para el análisis de especies indicadoras. Revista del Museo de La