GSC on Biodiversity. MAGIC

GLOBAL SCIENCE COMMUNITY ON BIODIVERSITY

Universidad Autónoma de Santo Domingo
UASD

Área de Investigación
Instituto Geográfico Universitario
UASD

Santo Domingo, República Dominicana
11 de febrero de 2016

GSC on Biodiversity. MAGIC

BIODIVERSITY CONCEPTS

- First mention of the 'biological diversity' concept is attributed to **Gerbilskii and Petrunkenvitch** (1955), who referred it in the context of **intraspecific in behaviour and life history**
- Biodiversity contraction was apparently first proposed by Walter Rosen in 1985.
- UNEP defines biological diversity as the **variability among living organisms** from all sources including, terrestrial, marine and other aquatic systems, and the ecological complexes of which they are part; this includes **diversity within species, between species and of ecosystems**

GSC on Biodiversity. MAGIC

BIODIVERSITY CONCEPTS

- As proposed by Magurran (2004), biodiversity is "the **variety and abundance** of species in a defined unit of study"
- So, for biodiversity measurement, **richness** (the variety) is important, but **relative abundance** is also a necessary component

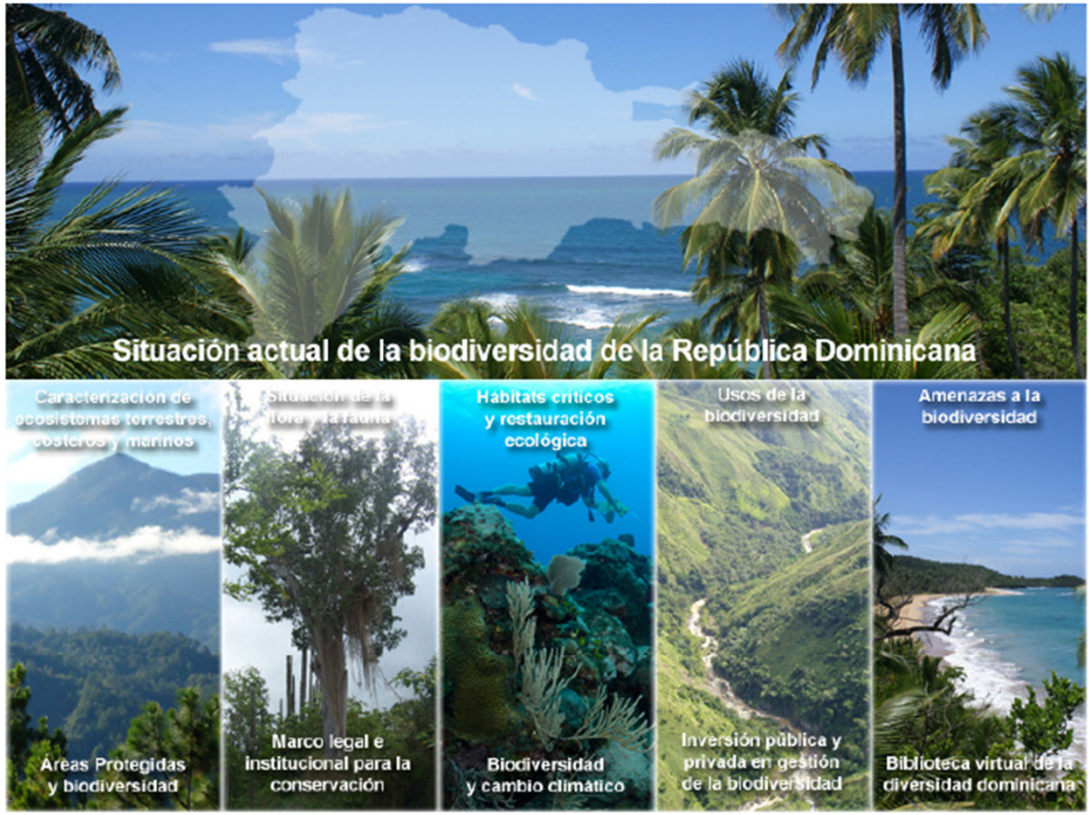
GSC on Biodiversity. MAGIC

WHAT ARE WE FOCUSED ON AT UASD/IGU?

- **Focal group: woody plants**, *Cactaceae* and palms in dry, semideciduous and rainforests
- **Measurement of biodiversity**, considering both components, relative abundance and richness
- Application of **statistics and spatial statistics** to biodiversity and its relation to **geology and geomorphology**

JARDÍN BOTÁNICO NACIONAL
"Dr. Rafael Ma. Moscoso"
INICIO
SOBRE NOSOTROS
DEPARTAMENTOS
DOCUMENTOS
TRANSPARENCIA
La Caoba, Swietenia mahagoni "Árbol Nacional"

Aumento de la capacidad de adaptación ecosistémica en las Reservas de Biosfera fronterizas en la República de Haití y la República Dominicana (CAReBios)



Informe semiestructurado (segunda entrega)
Contrato 83205496/ Número de referencia 13.2036.5-002.00

Equipo facilitador:
Dra. Liliana Betancourt Fernández
Dr. Alejandro Herrera Moreno
Lic. Brígido Peguero

Santo Domingo, Noviembre 2015

Punto origen		Punto final					
X: 266039	Y: 2003784	X:	Y:	Orientación:		Parcela:	COV_1
Datum:	WGS84			Altimetria:	1200		
				Fecha:	30/7/2013	PROY.:	Bahoruco
Responsables:	Rafael Cámara, Teodoro Clase, María Cámara					Hoja:	1
País: RD	Estado/Com. Autóno	Municipio:	Polo			Lugar:	Cortico

Grupo de Estudios tropicales y Cooperación al desarrollo

UNIVERSIDAD DE SEVILLA

Aplicación elaborada por Dr. Rafael CAMARA ARTIGAS. Departamento de Geografía Física y Análisis Geográfico Regional. Universidad de Sevilla. España, 2011

								individuos con DAP<2 cm		individuos con DAP>2 cm										
N	Distancia al inicio (cm)	distancia izquierda (cm)	distancia derecha (cm)	altura (cm)	flor	fruto	seco	Diametro Mayor (cm)	Diametro menor (cm)	Radio mayor (cm)	Radio menor (cm)	dap1	dap2	dap3	dap4	dap5	dap6	dap7	dap8	dap9	dap10
88	0	0	0	1000						600	400	155									
1061	140	—	36	600						400	200	8									
1061	0	0	0	800						130	50	5									
549	127	—	80	210				70	70	[illegible]	[illegible]	1,5									
1062	30	50	—	60				20	12												
1063	320	—	40	250						60	60	2									
549	400	30		170				60	40	[illegible]											
549	450	—	21	300						35	35										
1061	420	100	—	20						110	50										
87	430	80	—	120				50	40												
549	480	10	—	110				46	22												
1063	500	24	—	400						90	90	6									
1062	520	—	40	170				40	20												
623	560	—	60	120				46	20												
1064	510	—	30	70				50	12												
642	530	—	40	50				20	10												
1065	560		60	80																	

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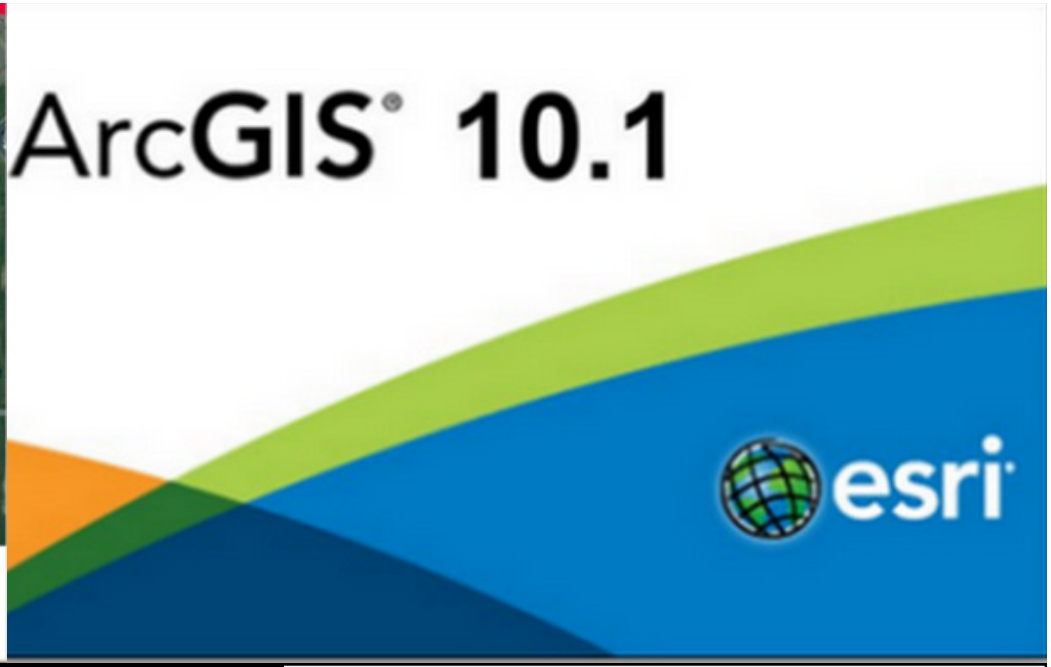
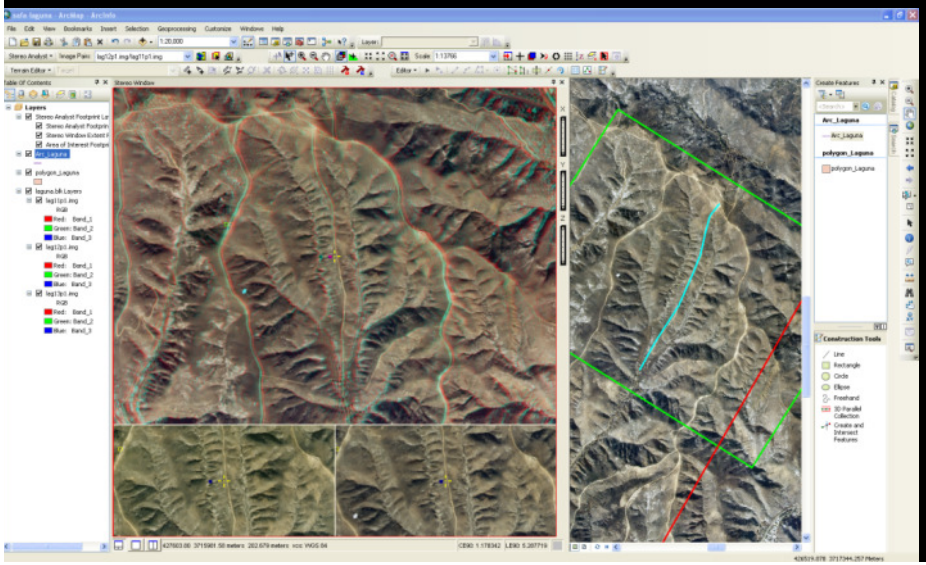
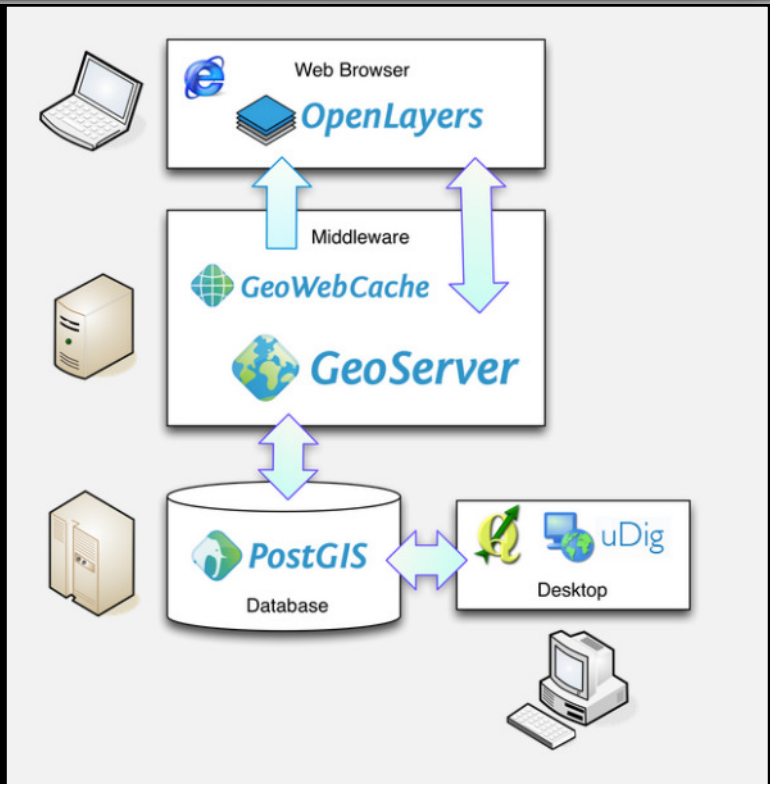

ArcGIS 10.1
esri




Web Browser
OpenLayers
Middleware
GeoWebCache
GeoServer
PostGIS
Database
uDig
Desktop

About R
What is R?
Contributors
Screenshots
What's new?

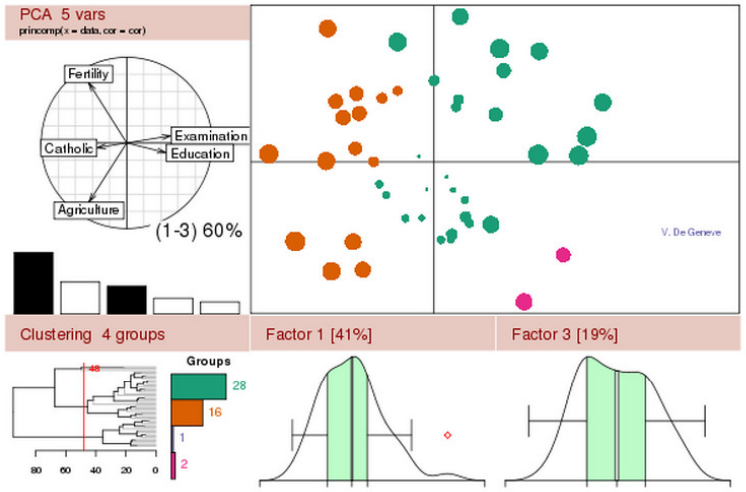
Download, Packages
CRAN

R Project
Foundation
Members & Donors
Mailing Lists
Bug Tracking
Developer Page
Conferences
Search

Documentation
Manuals
FAQs
The R Journal
Wiki
Books
Certification
Other

Misc
Bioconductor
Related Projects
User Groups
Links

The R Project for Statistical Computing



Getting Started:

- R is a free software environment for statistical computing and graphics. It compiles and runs on a wide variety of UNIX platforms, Windows and MacOS. To **download R**, please choose your preferred CRAN mirror.
- If you have questions about R like how to download and install the software, or what the license terms are, please read our answers to frequently asked questions before you send an email.

News:

- **R version 3.1.0** (Spring Dance) has been released on 2014-04-10.
- **R version 3.0.3** (Warm Puppy) has been released on 2014-03-06.
- **The R Journal Vol.5/2** is available.
- **useR! 2013**, took place at the University of Castilla-La Mancha, Albacete, Spain, July 10-12 2013.

http://www.r-project.org/

Vegan: ecological diversity

Jari Oksanen

Id: diversity-vegan.Rnw 2807 2013-12-05 11:50:52Z jarioksa processed with vegan 2.0-10 in R Under development (unstable) (2013-12-11 r64449) on December 12, 2013

Abstract

This document explains diversity related methods in **vegan**. The methods are briefly described, and the equations used them are given often in more detail than in their help pages. The methods discussed include common diversity indices and rarefaction, families of diversity indices, species abundance models, species accumulation models and beta diversity, extrapolated richness and probability of being a member of the species pool. The document is still incomplete and does not cover all diversity methods in **vegan**.

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1 Diversity indices 1

2 Rarefaction 2

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4 Species abundance models 4
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The **vegan** package has two major components: multivariate analysis (mainly ordination), and methods for diversity analysis of ecological communities. This document gives an introduction to the latter. Ordination methods are covered in other documents. Many of the diversity functions were written by Roeland Kindt, Bob O'Hara and Péter Sólymos.

Most diversity methods assume that data are counts of individuals. The methods are used with other data types, and some people argue that biomass or cover are more adequate than counts of individuals of variable sizes. However, this document mainly uses a data set with counts: stem counts of trees on 1 ha plots in the Barro Colorado Island. The following steps make these data available for the document:

```
> library(vegan)
> data(BCI)
```

1 Diversity indices

Function `diversity` finds the most commonly used diversity indices (Hill, 1973):

$$H = -\sum_{i=1}^{S} p_i \log_b p_i \quad \text{Shannon–Weaver} \quad (1)$$

$$D_1 = 1 - \sum_{i=1}^{S} p_i^2 \quad \text{Simpson} \quad (2)$$

$$D_2 = \frac{1}{\sum_{i=1}^{S} p_i^2} \quad \text{inverse Simpson} \quad (3)$$

where p_i is the proportion of species i, and S is the number of species so that $\sum_{i=1}^{S} p_i = 1$, and b is the base of the logarithm. It is most common to use natural logarithms (and then we mark index as H'), but $b = 2$ has theoretical justification. The

Package 'vegan'

September 25, 2013

Title Community Ecology Package

Version 2.0-9

Date September 25, 2013

Author Jari Oksanen, F. Guillaume Blanchet, Roeland Kindt, Pierre Legendre,Peter R. Minchin, R. B. O'Hara, Gavin L. Simpson, Peter Solymos,M. Henry H. Stevens, Helene Wagner

Maintainer Jari Oksanen <jari.oksanen@oulu.fi>

Depends permute, lattice, R (>= 2.14.0)

Suggests MASS, mgcv, cluster, scatterplot3d, rgl, tcltk

Description Ordination methods, diversity analysis and other functions for community and vegetation ecologists.

License GPL-2

URL http://cran.r-project.org, http://vegan.r-forge.r-project.org/

NeedsCompilation yes

Repository CRAN

Date/Publication 2013-09-25 09:56:27

R topics documented:

vegan-package 4
add1.cca 5
adipart 7
adonis 11
anosim 14
anova.cca 16
as.mlm.cca 19
BCI 21

Package 'BiodiversityR'

January 20, 2014

Type Package

Title GUI for biodiversity, suitability and community ecology analysis

Version 2.4-1

Date 2014-01-16

Author Roeland Kindt

Maintainer Roeland Kindt <R.KINDT@CGIAR.ORG>

Description This package provides a GUI (Graphical User Interface, via the R-Commander) and some utility functions (often based on the vegan package) for statistical analysis of biodiversity and ecological communities, including species accumulation curves, diversity indices, Renyi profiles, GLMs for analysis of species abundance and presence-absence, distance matrices, Mantel tests, and cluster, constrained and unconstrained ordination analysis. A book on biodiversity and community ecology analysis is available for free download from the website. In 2012, methods for (ensemble) suitability modelling and mapping were expanded in the package.

License GPL-2

URL http://www.r-project.org,
http://www.worldagroforestry.org/resources/databases/tree-diversity-analysis

Depends R (>= 3.0.0), tcltk

Imports Rcmdr (>= 1.9-4)

Suggests vegan (>= 1.17-12), permute, lattice, MASS, mgcv, cluster,car, RODBC, rpart, effects, multcomp, ellipse, maptree, sp,splancs, spatial, akima, nnet, dismo, raster (>= 2.0-31),rgdal, gbm, randomForest, gam, earth, mda, kernlab, e1071,tools

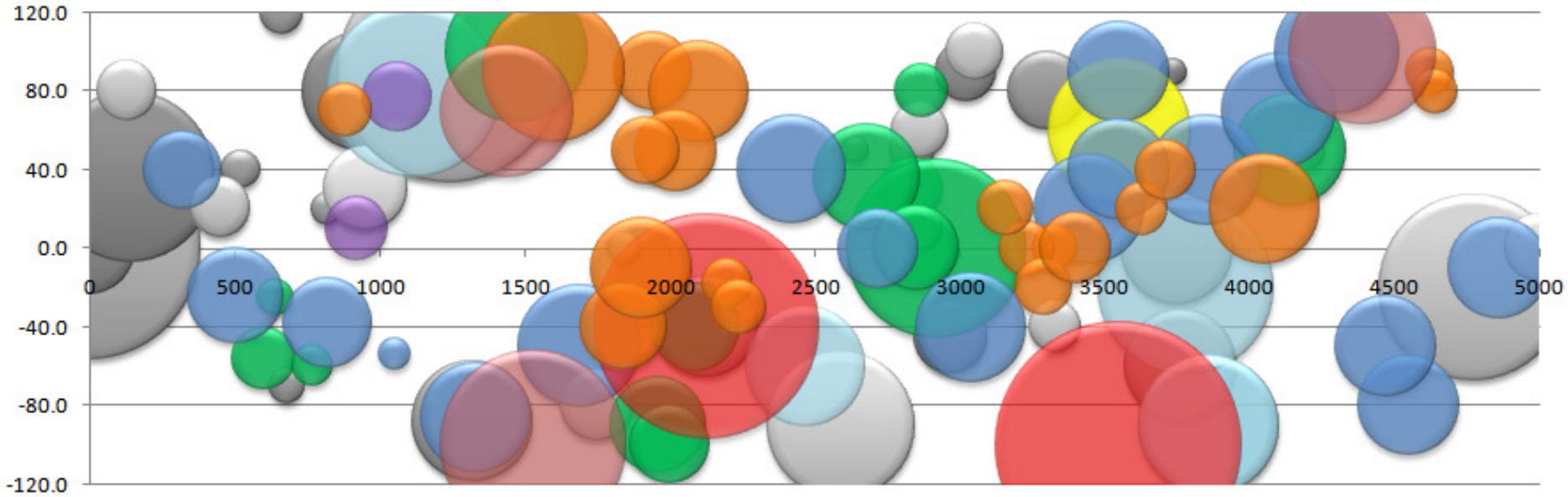
NeedsCompilation no

Repository CRAN

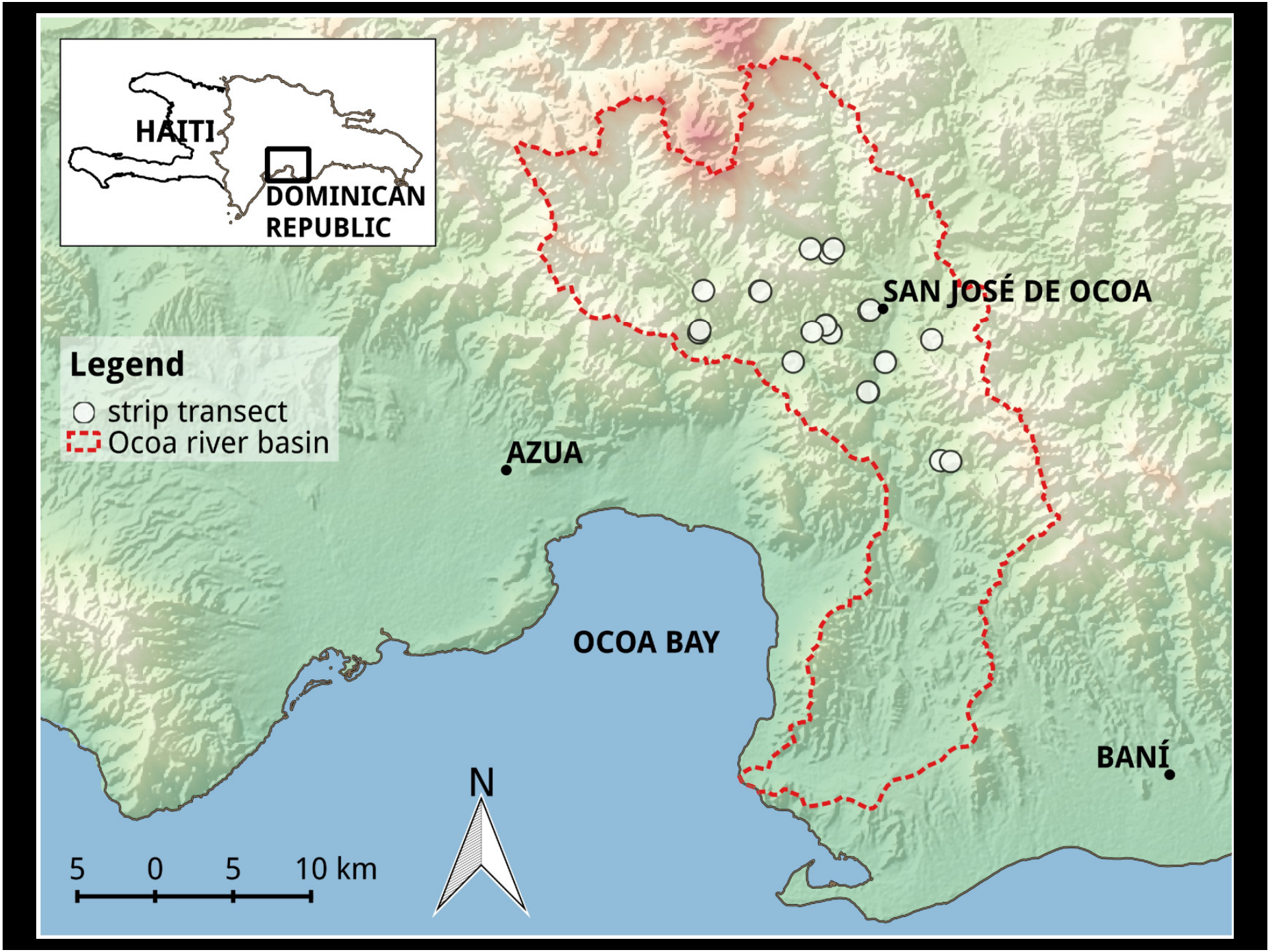
Date/Publication 2014-01-20 09:36:08

```
#ANÁLISIS DE DIVERSIDAD PARA LA COMUNICACIÓN "Bosques en régimen tropical y con contraste estacional de la cuenca del rí

#CARGA DE PAQUETES
library(grDevices)
library(moments)
library(RODBC)
library(reshape)
library(vegan)
library(BiodiversityR)

#LECTURA DESDE LA BASE DE DATOS
canal<-odbcConnectAccess("D:/proyecto_FONDOCyT/flora_vegetacion/Ocoa/consolidado_flora.mdb")
d<-sqlQuery(canal,paste("select *from c_tabla_abundancia_para_R"))
d.env<-sqlQuery(canal,paste ("select *from t_env"))
odbcCloseAll()
str(d)

#CANTIDAD DE ESPECIES SEGÚN FAMILIA
canal<-odbcConnectAccess("D:/proyecto_FONDOCyT/flora_vegetacion/Ocoa/consolidado_flora.mdb")
famesp<-sqlQuery(canal,paste("select *from c_fami_esp_2"))
hist(famesp$cant_esp,col=200,xlab='cantidad de especies',ylab='cantidad de familias',main='Cantidad de familias según nú
odbcCloseAll()

#EXCLUYENDO MUESTREOS CUYA VEGETACIÓN (BOSQUES NUBLADOS Y PINAR) NO CORRESPONDE AL OBJETO DE ESTUDIO DEL ARTÍCULO (BOSQU
d<-subset(d, !(sitio %in% c('VNv_1','MNv_1')))
d.env<-subset(d.env, !(sitio %in% c('VNv_1','MNv_1')))

#CANTIDAD DE ESPECIES SEGÚN GÉNERO
d$especie<-factor(d$especie)
d$genero<-sub(" .*", "", d$especie)
unique(desp$genero)
desp<-d[,c(3,13)]
str(desp)
desp<-unique(desp)
str(desp)
length(unique(desp$genero))
sort(tapply(desp$especie,desp$genero,length))
table((tapply(desp$especie,desp$genero,length)))
hist(tapply(desp$especie,desp$genero,length),col=200,xlab='cantidad de especies',ylab='cantidad de géneros',main='Cantid

#CONVERSIÓN DE LA TABLA DE ABUNDANCIAS A UNA MATRIZ DE COMUNIDAD DE R
d<-cast(d,sitio~especie,fun.aggregate=length,value="Id")
str(d)
rownames(d)<-d$sitio
head(d)[1:4]
d<-d[,2:192]
str(d)
```

Diagrama de burbujas del transecto COV_1



- Symplocos domingensis Urb.
- Badiera fuertesii Urb.
- Eupatorium gabbii Urb.
- Myrcia deflexa (Poir.) DC.
- Persea krugii Mez
- Myrsine coriacea (Sw.) R.Br.
- Alsophila minor (D.C. Eaton) Tryon
- Psychotria berteroana DC.
- Cecropia schreberiana Miq. & Mart.
- Calyptranthes selleanus Urb. & Ekm.
- Gomidesia lindeniana O. Berg
- Renealmia jamaicensis (Gaertn.) Horan.
- Rondeletia conferta Urb. & Ekman
- Magnolia hamorii Howard
- Prestoea montana (Graham) Nicholson
- Weinmannia pinnata L.
- Schefflera tremula (Krug & Urb.) Alain
- Cestrum coelophlebium O.E.Schulz
- Lasianthus bahorucanus Zanoni
- Ocotea foeniculacea Mez
- Collecteria seminervis (Urb.& Ekm.) D.W. Taylor
- Ocotea patens (Sw.) Alain
- Brunellia comocladifolia Bonpl.


HAITI
DOMINICAN REPUBLIC
Legend
strip transect
Ocoa river basin
SAN JOSÉ DE OCOA
AZUA
OCOA BAY
BANÍ
N
5 0 5 10 km

Índice	Fórmula
Índice de Shannon	$H = -\sum p_i ln(p_i)$
Índice de Gini-Simpson	$R = GS = 1 - \sum_{i=1}^{S} p_i^2$
Índice de Fisher-alpha	$f = \frac{\alpha x^n}{n}$
Índice de equidad de Pielou (*J-evenness*)	$J' = \frac{H'}{H'_{max}}$

p_i = abundancia relativa de la especie i, calculada a partir de:
n_i/N, donde n_i es la abundancia de la especie i, y N es la abundancia total
S = riqueza o número de especies
α = parámetro de diversidad
x = parámetro dependiente de N y $\alpha = N/(N - \alpha)$
H' = índice de Shannon
H'_{max} = valor máximo del índice de Shannon = $ln(S)$

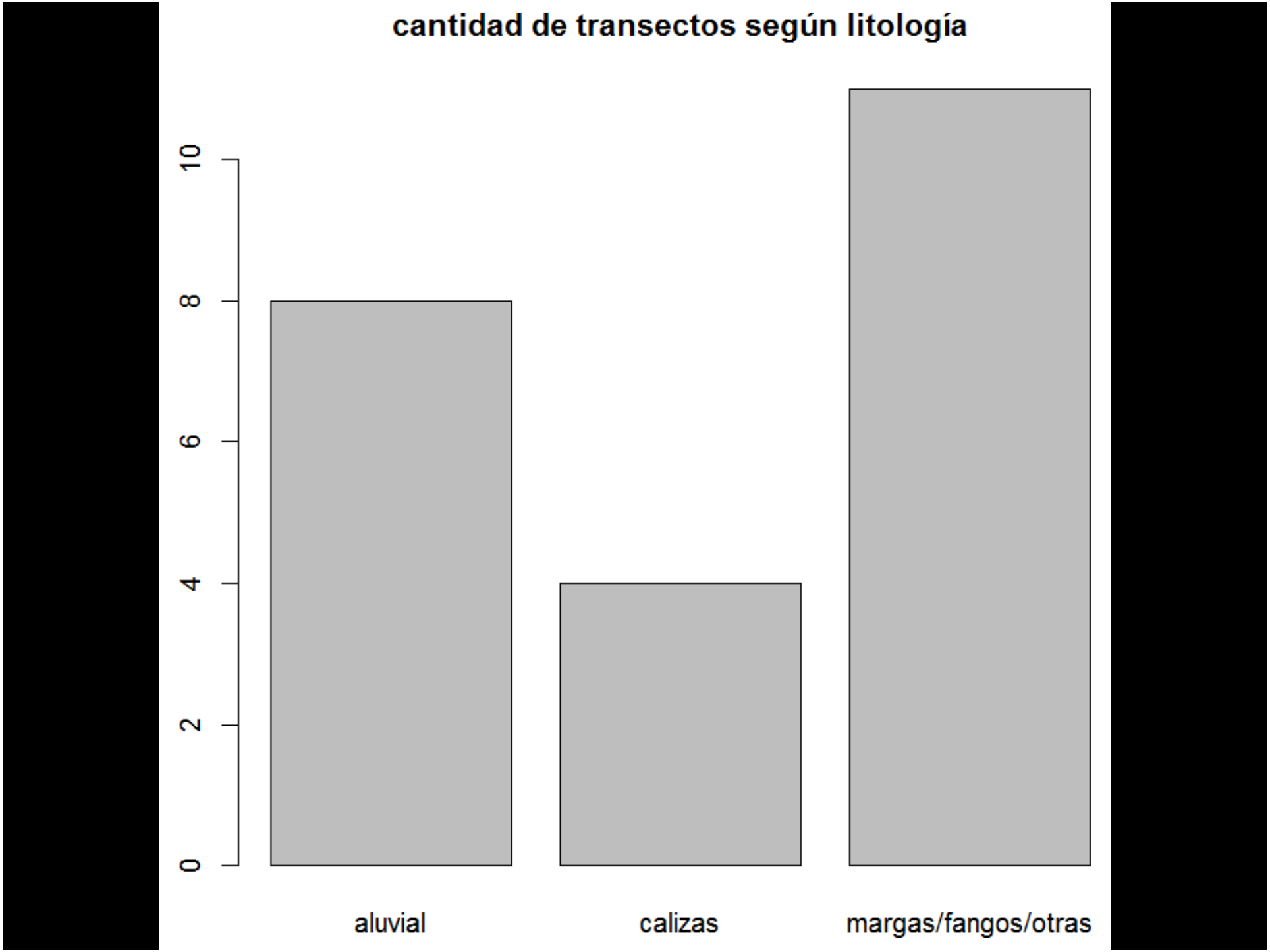
http://www.geografiafisica.org/2016/02/11/curso-r-biodiversidad-uasd-us-de-enero-de-2016/

https://gist.github.com/geofis/5c9ce0f780a10cbb7972

Bookmarks | Biogeografia, flora | Estadistica regresior | GEO202 | Huracanes, meteorc | La Isabela | Teledeteccion y SIG | Varios | Bases de datos

```
111 dev.new() #GENERA UNA VENTANA GRAFICA INDEPENDIENTE. ESTA SENTENCIA SE REPITE MUCHO A LO LARGO DEL SCRIPT, Y EN LO ADELANTE APAR
112 barplot(sort(rowSums(d),decreasing=T),las=3,ylim=c(0,100),ylab='abundancia (número de individuos)',main='Abundancia por transect
113
114 ##ÍNDICES DE BIODIVERSIDAD USANDO vegan PASO A PASO
115 diversity(d) #CALCULA EL ÍNDICE DE SHANNON
116 diversity(d,'simpson') #CALCULA LA EQUIDAD DE SIMPSON (1-D), DENOMINADO TAMBIÉN "GINI-SIMPSON"
117 diversity(dfv) #CALCULA EL ÍNDICE DE SHANNON PARA LA MATRIZ DE COMUNIDAD POR FORMACIÓN VEGETAL
118 diversity(dfv,'simpson') #CALCULA LA EQUIDAD DE SIMPSON (1-D), DENOMINADO TAMBIÉN "GINI-SIMPSON" PARA LA MATRIZ DE COMUNIDAD POR
119 diversity(drb) #CALCULA EL ÍNDICE DE SHANNON PARA LA MATRIZ DE COMUNIDAD POR RÉGIMEN BIOCLIMÁTICO
120 diversity(drb,'simpson') #CALCULA LA EQUIDAD DE SIMPSON (1-D), DENOMINADO TAMBIÉN "GINI-SIMPSON" PARA LA MATRIZ DE COMUNIDAD POR
121
122 ##ÍNDICES CALCULADOS MASIVAMENTE Y ANEXADOS A MATRIZ AMBIENTAL
123 indicesmasivo <- cbind(parcela=rownames(d),as.data.frame(sapply(c("Shannon","Simpson","inverseSimpson","Logalpha","Berger","Jeve
124 colnames(indicesmasivo)[2:ncol(indicesmasivo)]<-c('Shannon','Gini_Simpson','inverso_de_Simpson','Fisheralpha_Logalpha','Berger_F
125 indicesmasivo
126 d.env <- merge(d.env,indicesmasivo) #ANEXA LOS ÍNDICES GENERADOS A LA MATRIZ AMBIENTAL
127
128 ##LOGARITMOS, TAMBIÉN ANEXADOS
129 logindicesmasivo <- cbind(parcela=rownames(d),as.data.frame(sapply(c("Shannon","Simpson","inverseSimpson","Logalpha","Berger","J
130 colnames(logindicesmasivo)[2:ncol(logindicesmasivo)]<-paste('log',c('Shannon','Gini_Simpson','inverso_de_Simpson','Fisheralpha_L
131 logindicesmasivo
132 d.env <- merge(d.env,logindicesmasivo) #ANEXA LOS ÍNDICES GENERADOS A LA MATRIZ AMBIENTAL
133 d.env
134
135 ##ESTIMADOR DE RIQUEZA CHAO1
136 estimadorchao1 <- data.frame(parcela=rownames(d),chao1=sapply(rownames(d),function(x) chao1(d[x,]))) #GENERA UNA TABLA CON EL ES
137 d.env <- merge(d.env,estimadorchao1) #ANEXA LOS VALORES GENERADOS A LA MATRIZ AMBIENTAL
138
139 ##DIVERSIDAD DE RENYI
140 renyi(d) #VALORES DE DIVERSIDAD DE LA MATRIZ DE COMUNIDAD POR TRANSECTO PARA CADA NÚMERO DE HILL
```

Source code:
https://gist.github.com/geofis/5c9ce0f780a10cbb7972


cantidad de transectos según litología
0
2
4
6
8
10
aluvial
calizas
margas/fangos/otras

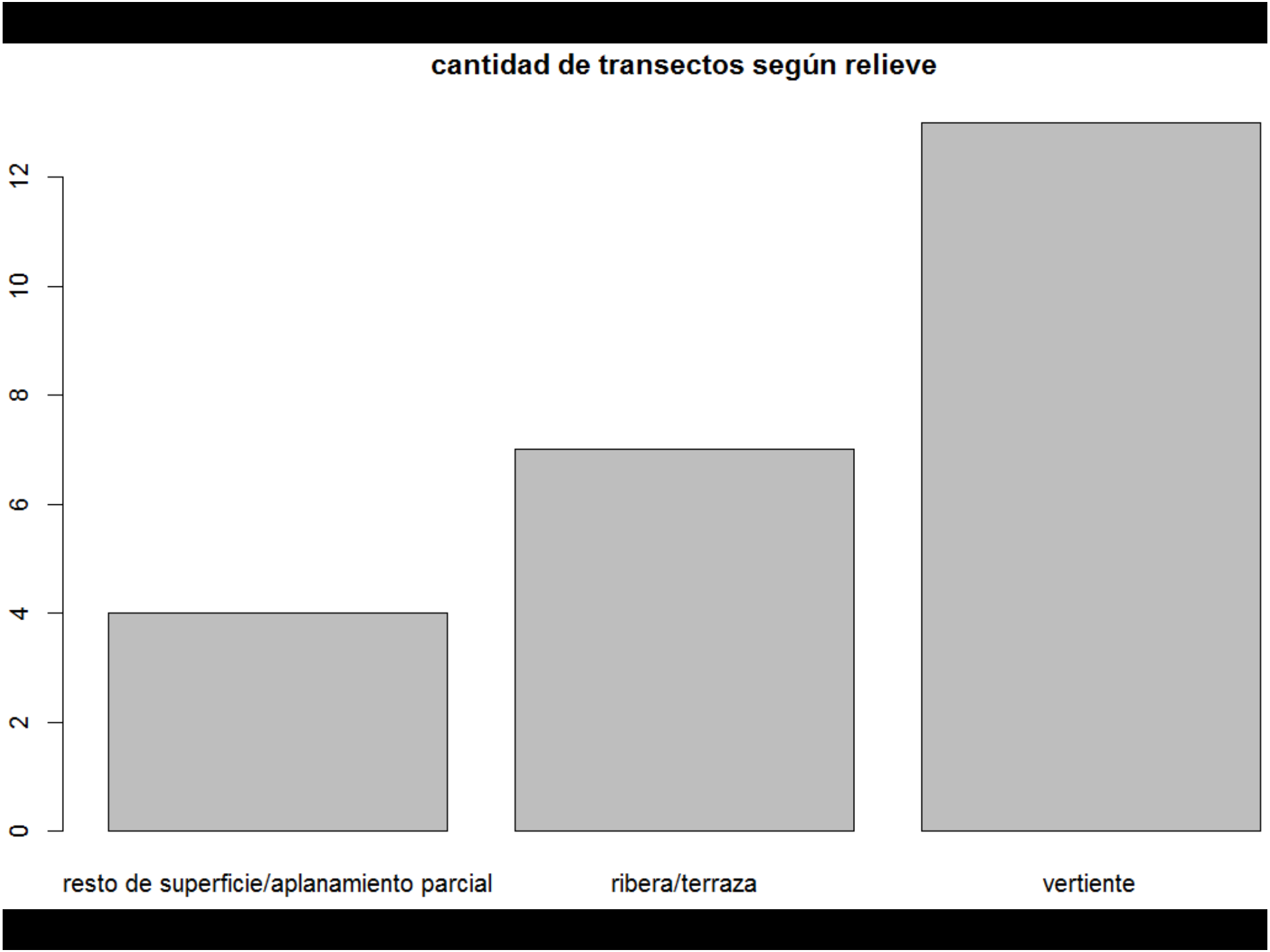

cantidad de transectos según relieve
0
2
4
6
8
10
12
resto de superficie/aplanamiento parcial
ribera/terraza
vertiente

Tabla 6. Tabla de rango-abundancia, mostrando los primeros 12 registros

especie	rango	N	abundancia relativa (%)	abund. relativa acumulada (%)
Coccoloba diversifolia Jacq.	1	121	5.4	5
Randia aculeata L.	2	106	4.7	10
Coccothrinax argentea (Lodd. ex Schult. & Schult. f.) Sarg. ex K. Schum.	3	100	4.4	15
Bursera simaruba (L.) Sarg.	4	86	3.8	18
Eugenia foetida Pers.	5	85	3.8	22
Acacia skleroxyla Tussac	6	78	3.5	26
Savia sessiliflora (Sw.) Willd.	7	78	3.5	29
Chrysophyllum oliviforme L.	8	68	3	32
Leucaena leucocephala (Lam.) de Wit	9	54	2.4	35
Coccoloba buchii O.C. Schmidt	10	53	2.4	37
Nectandra coriacea (Sw.) Griseb.	11	52	2.3	39
Swietenia mahagoni (L.) Jacq.	12	50	2.2	41

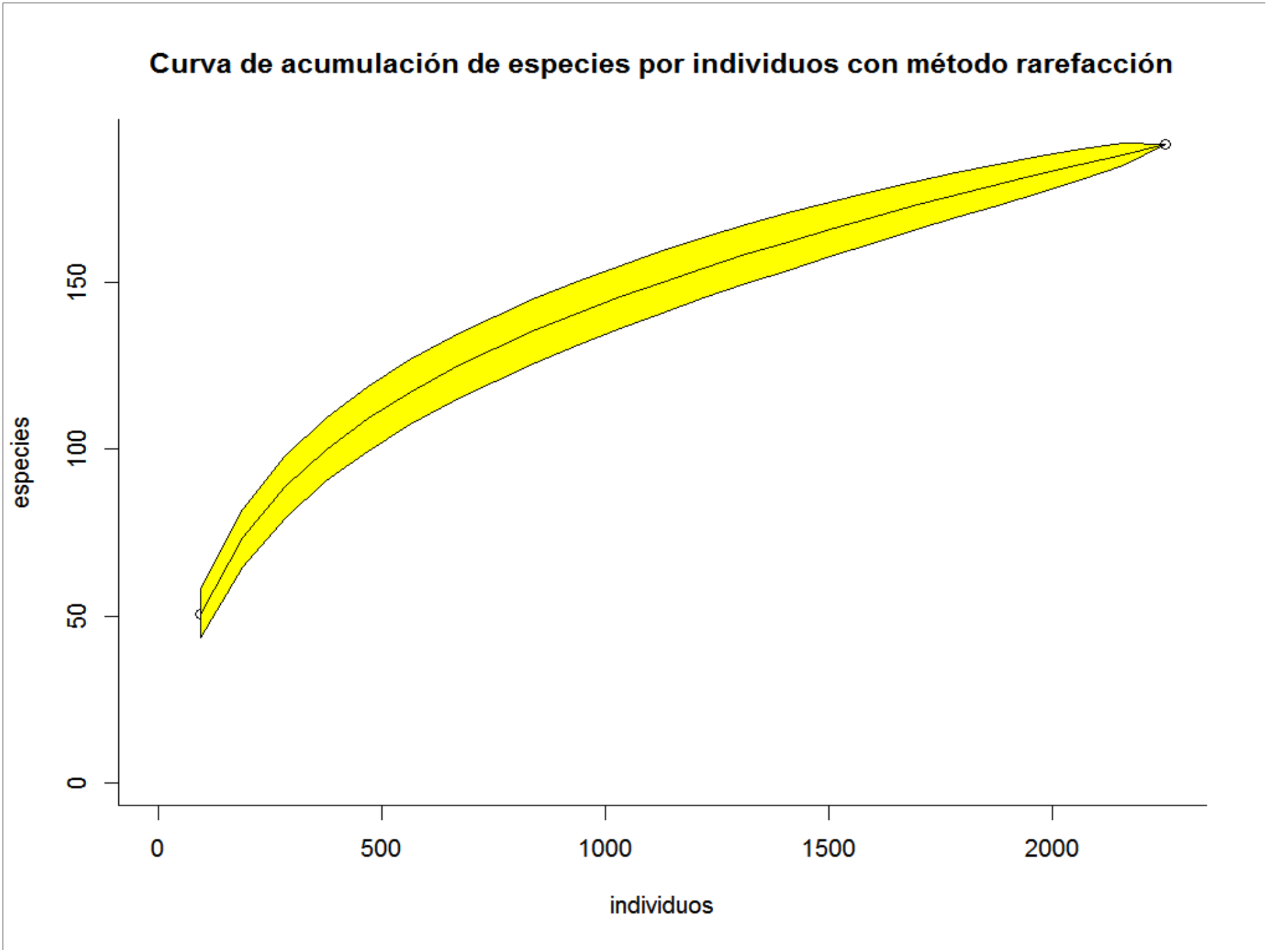

Curva de acumulación de especies por individuos con método rarefacción
especies
0
50
100
150
0
500
1000
1500
2000
individuos

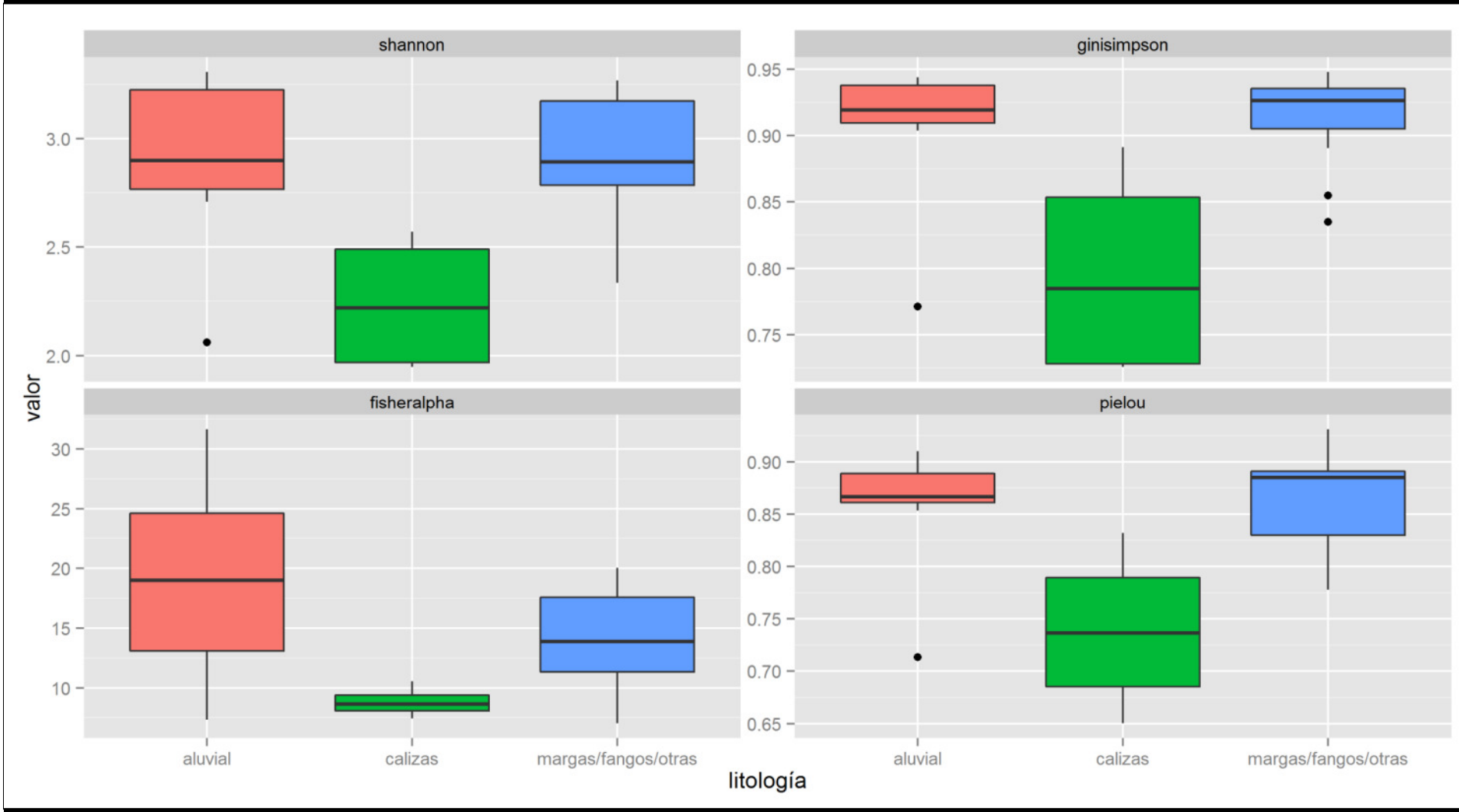
Tabla 11. Resultados de la aplicación de 8 pruebas de Chi cuadrado para evaluar independencia entre los niveles de biodiversidad y la litología/geomorfología

biodiversidad / **grupos**	**niveles de biodiversidad (alta o baja[1]) en base a media del índice de…**			
	…Shannon	**…Gini-Simpson**	**…Fisher-alpha**	**…Pielou**
litología	X^2=6.49, P=0.05	X^2=9.52, **P=0.01**	X^2=4.27, P=0.15	X^2=8.64, **P=0.01**
geomorfología	X^2=1.74, P=0.47	X^2=6.09, **P=0.04**	X^2=3.06, P=0.22	X^2=7.67, **P=0.03**

[1] Por índices, se clasificó a cada muestreo como de "biodiversidad baja" o "biodiversidad alta", en función de si el valor era menor o mayor a la media, respectivamente.

Tabla 12. Valores de P de las pruebas ANOVA y Kruskal-Wallis para índices de diversidad *alpha*, en función de grupos litológicos y geomorfológicos (tratamientos)

índices factores físicos	Shannon	Gini-Simpson	Fisher-alpha	Pielou
Litología	F = 6.1 num df = 2 denom df = 8.49 **P = 0.02**	KW X^2 = 6.83 df = 2 **P = 0.03**	F = 11.14 num df = 2 denom df = 12.41 **P < 0.01**	KW X^2 = 7.17 df = 2 **P = 0.03**
Geomorfología	F = 2.7 num df = 2 denom df = 8.52 P = 0.12	F = 2.83 num df = 2 denom df = 7.17 P = 0.12	F = 3.40 num df = 2 denom df = 8.39 P = 0.08	F = 3.00 num df = 2 denom df = 7.39 P = 0.11
H_0: las medias o medianas de los índices son iguales para cada tratamiento de los factores físicos				


shannon
ginisimpson
fisheralpha
pielou
valor
litología
aluvial
calizas
margas/fangos/otras
3.0
2.5
2.0
0.95
0.90
0.85
0.80
0.75
30
25
20
15
10
0.70
0.65

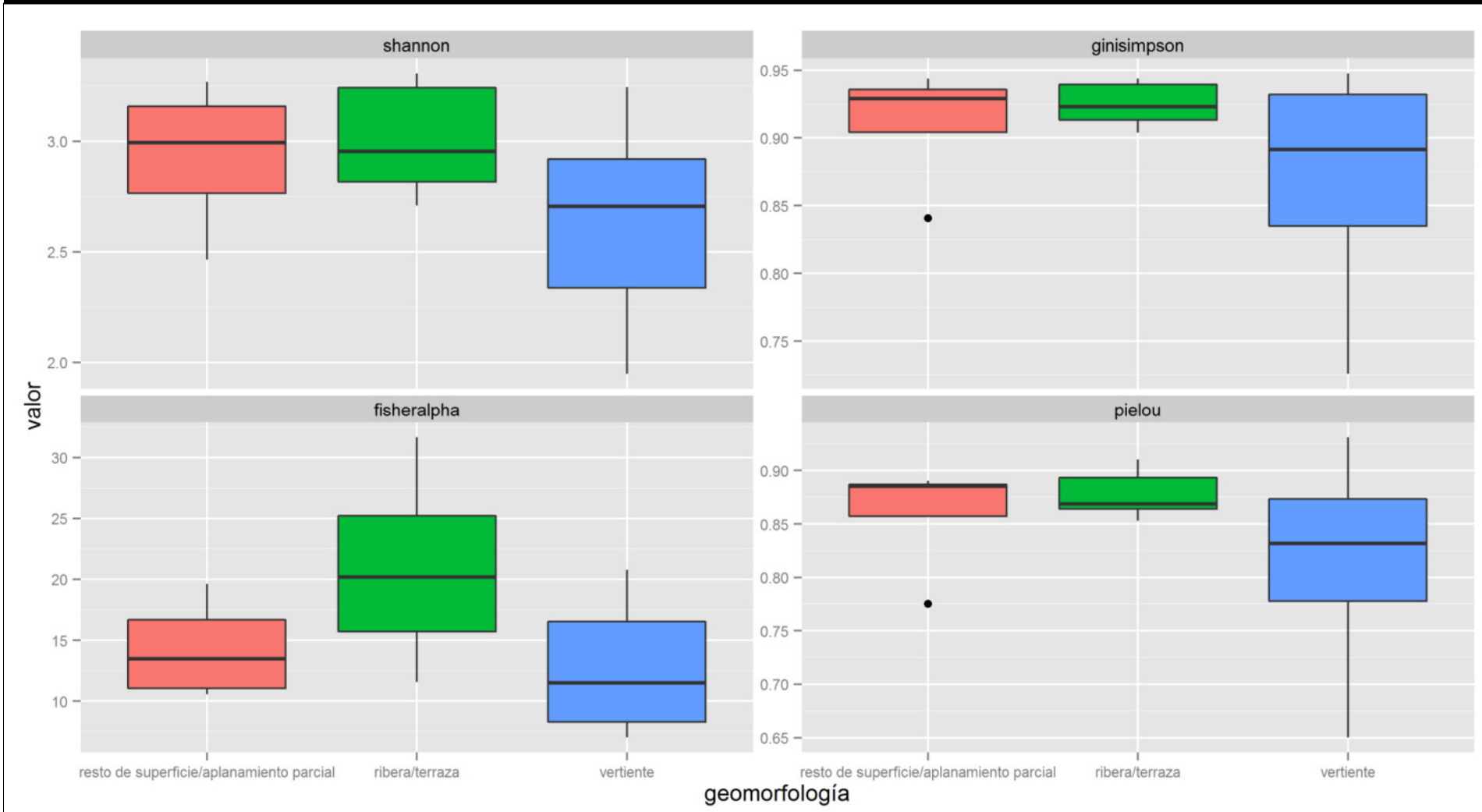

shannon
ginisimpson
fisheralpha
pielou
valor
3.0
2.5
2.0
0.95
0.90
0.85
0.80
0.75
30
25
20
15
10
0.90
0.85
0.80
0.75
0.70
0.65
resto de superficie/aplanamiento parcial
ribera/terraza
vertiente
geomorfología

Tabla 15. Prueba de homogeneidad de Chi cuadrado aplicada a riquezas de bosques sobre litologías y relieves, rarificadas al tipo de menor abundancia

riquezas / grupos	riqueza original	riqueza rarificada al de menor abundancia
grupos litológicos	-	-
margas/fangos	125	83
aluvial	105	83
calizas	66	66
prueba X^2	-	**$X^2 = 2.49$, df = 2, P = 0.29**
grupos geomorfológicos	-	-
vertientes	144	95
riberas/terrazas	100	92
superficies/cimas	73	73
prueba X^2	-	**$X^2 = 3.29$, df = 2, P = 0.19**

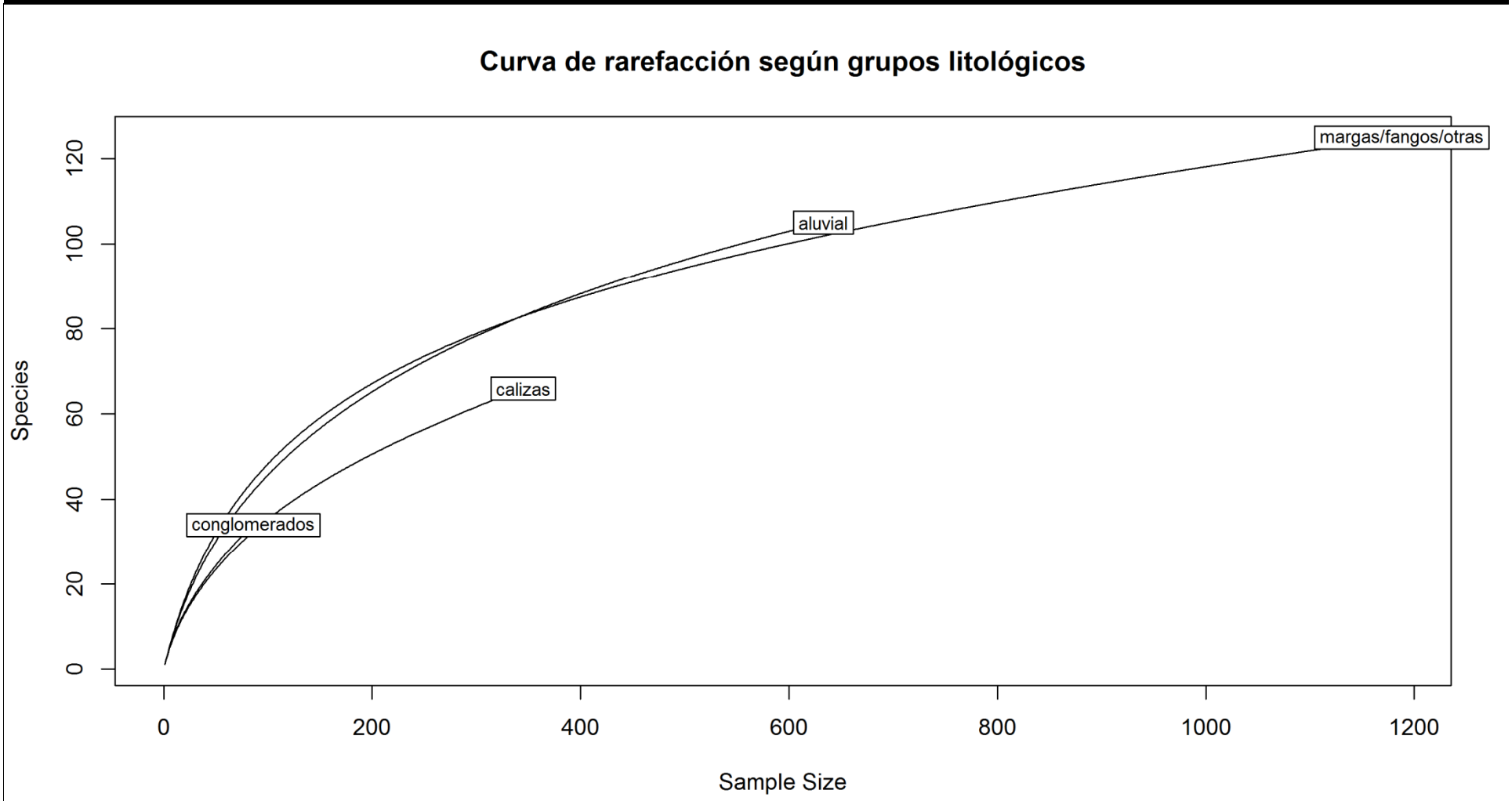
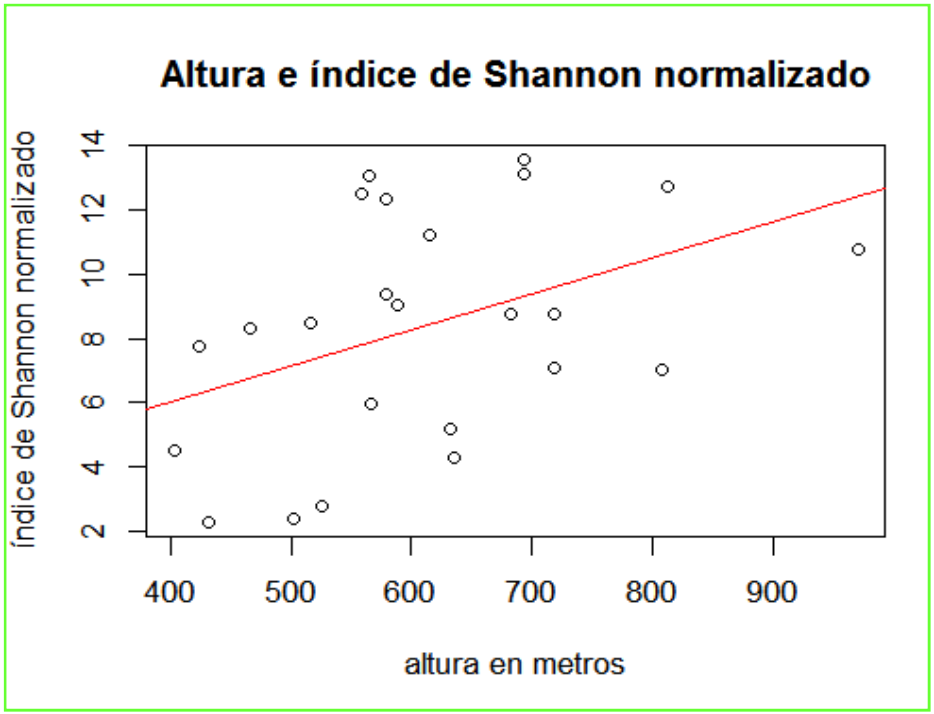
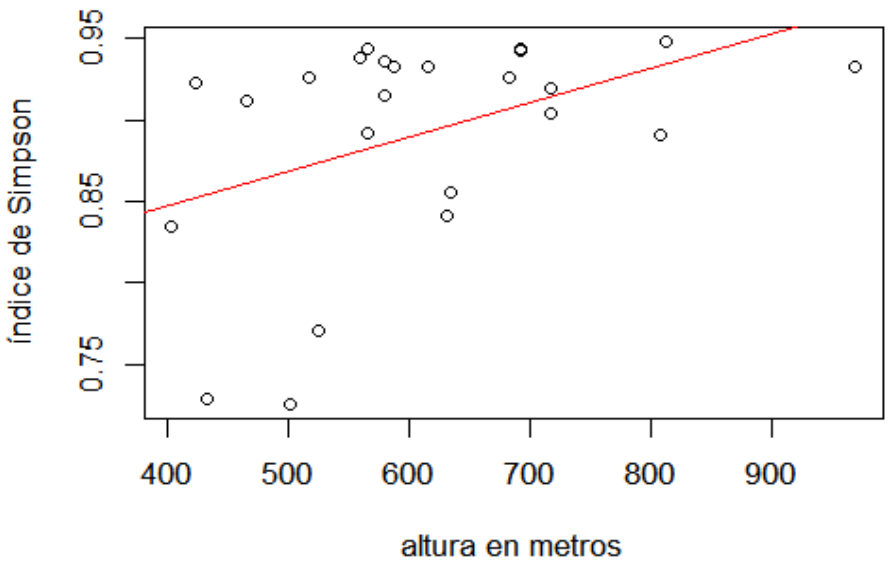

Curva de rarefacción según grupos litológicos
Species
Sample Size
0
20
40
60
80
100
120
0
200
400
600
800
1000
1200
margas/fangos/otras
aluvial
calizas
conglomerados

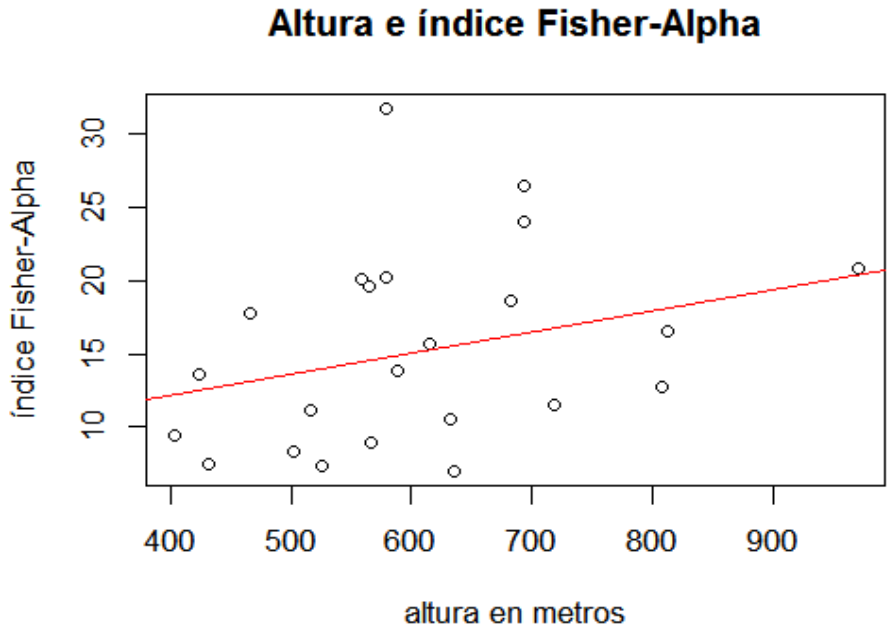
Tabla 16. Análisis de correlación con prueba de asociación entre índices de diversidad *alpha* y variables espaciales (coordenadas, altura y pendiente). Ver comentarios en el texto

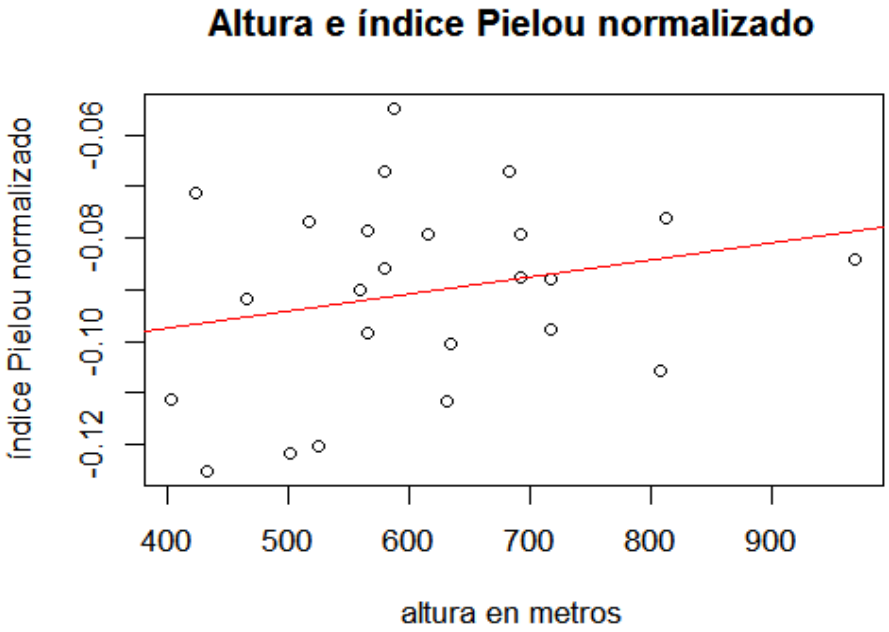
índices variables espaciales	Shannon (norm)	Gini-Simpson[1]	Fisher-Alpha	Pielou (norm)
x (prueba SW, n.s.)	r=-0.34 n.s.	rho=-0.31 n.s.	r=-0.40 P=0.05	r=-0.15 n.s.
y (prueba SW, n.s.)	r=0.09 n.s.	rho=0.16 n.s.	r=0.12 n.s.	r=0.18 n.s.
altura en metros (prueba SW, n.s.)	r=0.42 P<0.05	rho=0.39 n.s.	r=0.30 n.s.	r=0.24 n.s.
pendiente normalizada (datos no normalizados para Gini-Simpson)	**r=-0.51** **P<0.05**	rho=-0.40 P=0.05	**r=-0.60** **P<0.01**	r=-0.40 P=0.06

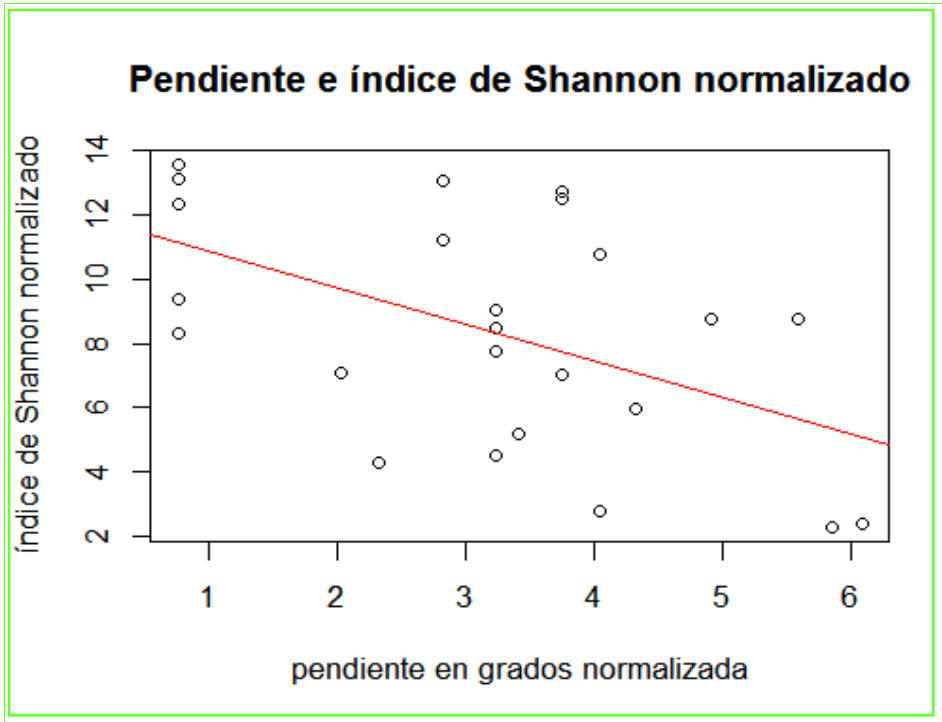
[1] Prueba de asociación con el método de Spearman, porque los datos transformados con el método Box-Cox no superaron la prueba de normalidad de Shapiro-Wilk. En los demás casos se usó la prueba de asociación con el método de Pearson

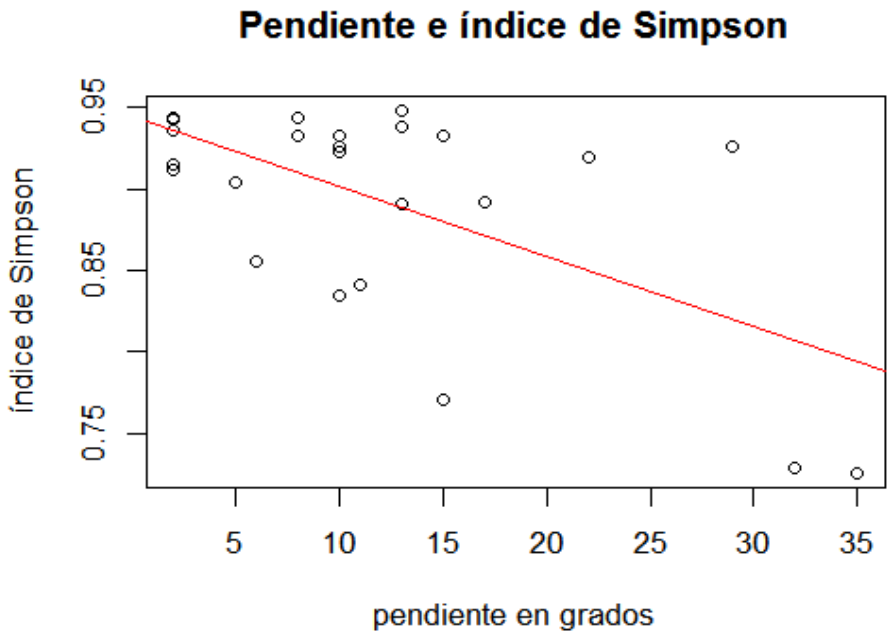

Altura e índice de Shannon normalizado
índice de Shannon normalizado
2
4
6
8
10
12
14
400
500
600
700
800
900
altura en metros

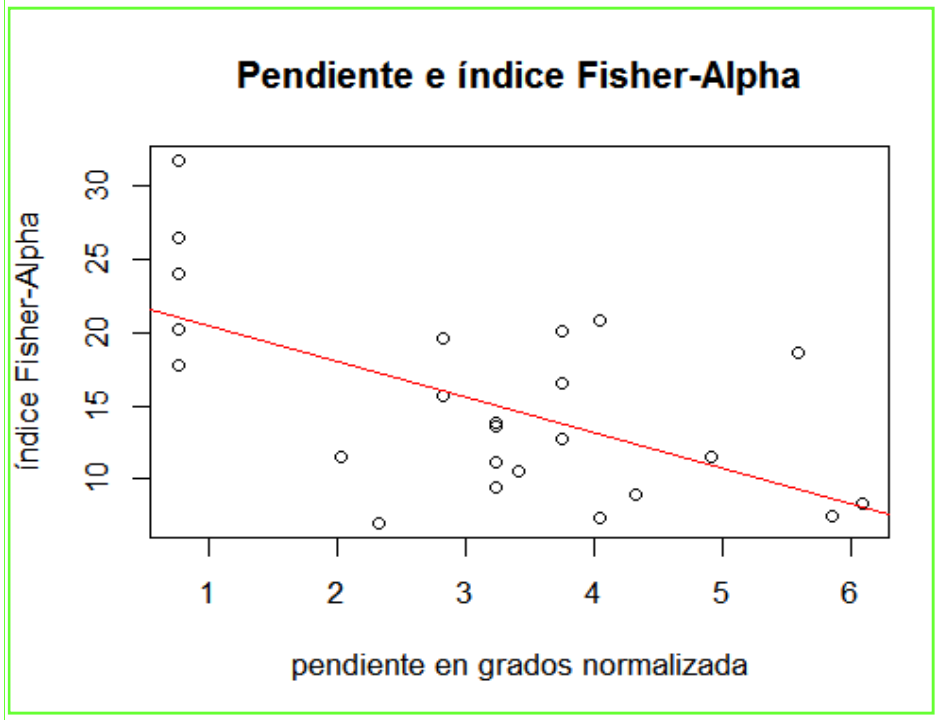

Altura e índice de Simpson
índice de Simpson
0.75
0.85
0.95
400
500
600
700
800
900
altura en metros

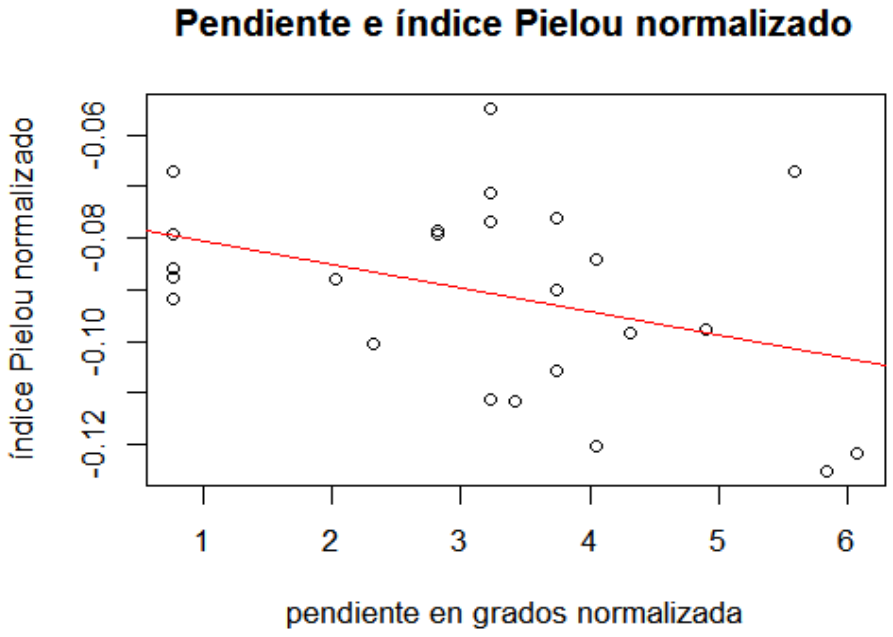

Altura e índice Fisher-Alpha
índice Fisher-Alpha
10
15
20
25
30
400
500
600
700
800
900
altura en metros


Altura e índice Pielou normalizado
índice Pielou normalizado
-0.12
-0.10
-0.08
-0.06
400
500
600
700
800
900
altura en metros


Pendiente e índice de Shannon normalizado
índice de Shannon normalizado
pendiente en grados normalizada


Pendiente e índice de Simpson
índice de Simpson
pendiente en grados


Pendiente e índice Fisher-Alpha
índice Fisher-Alpha
pendiente en grados normalizada


Pendiente e índice Pielou normalizado
índice Pielou normalizado
pendiente en grados normalizada

GSC on Biodiversity. MAGIC

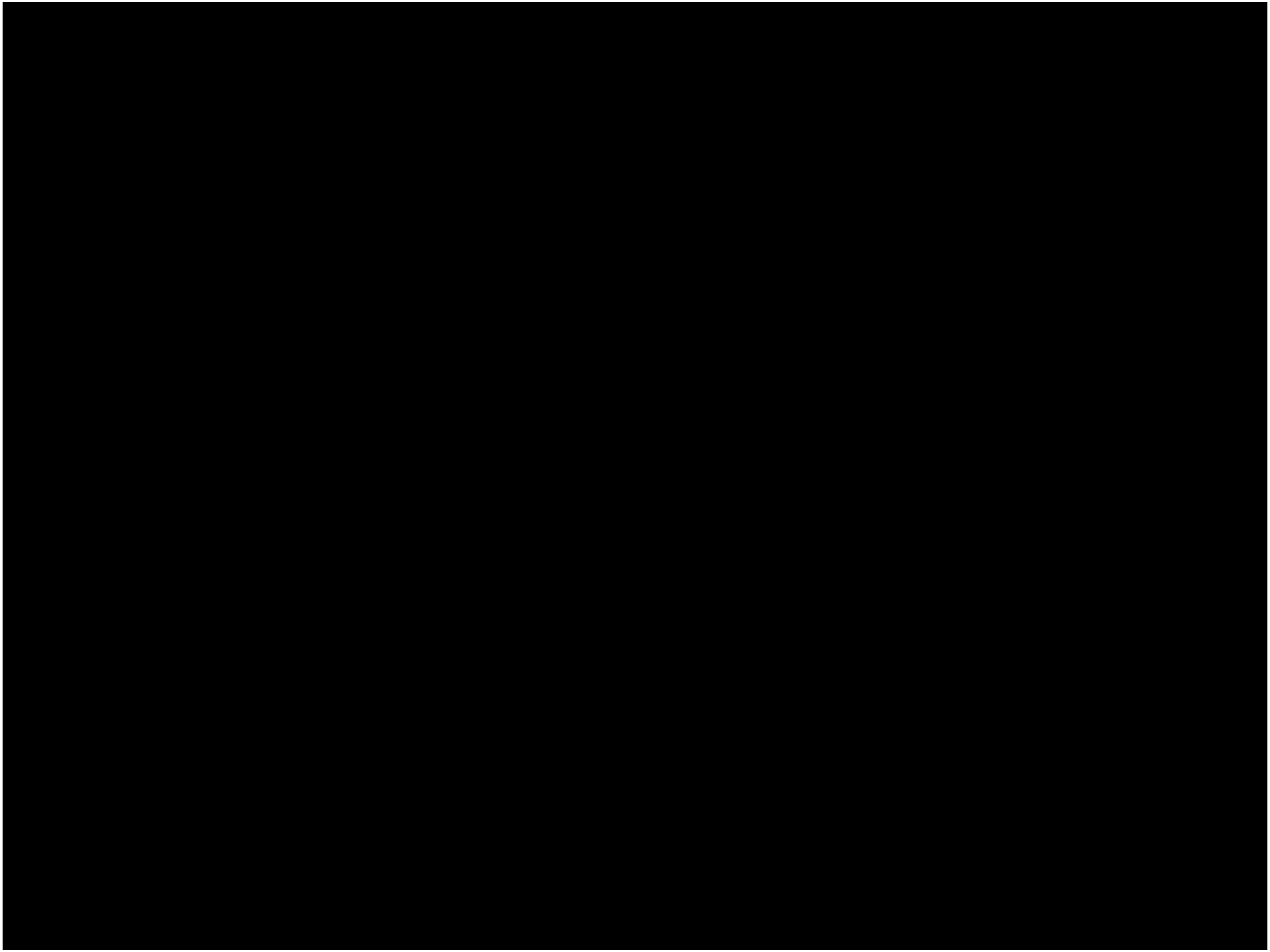
CONCLUSSIONS

- In semideciduous forests, biodiversity measured by alpha-indices varies mainly **because of relative abundance changes**
- Richness appears to be relatively **homogeneous across different rocks substrates and landforms**

GSC on Biodiversity. MAGIC

CONCLUSSIONS

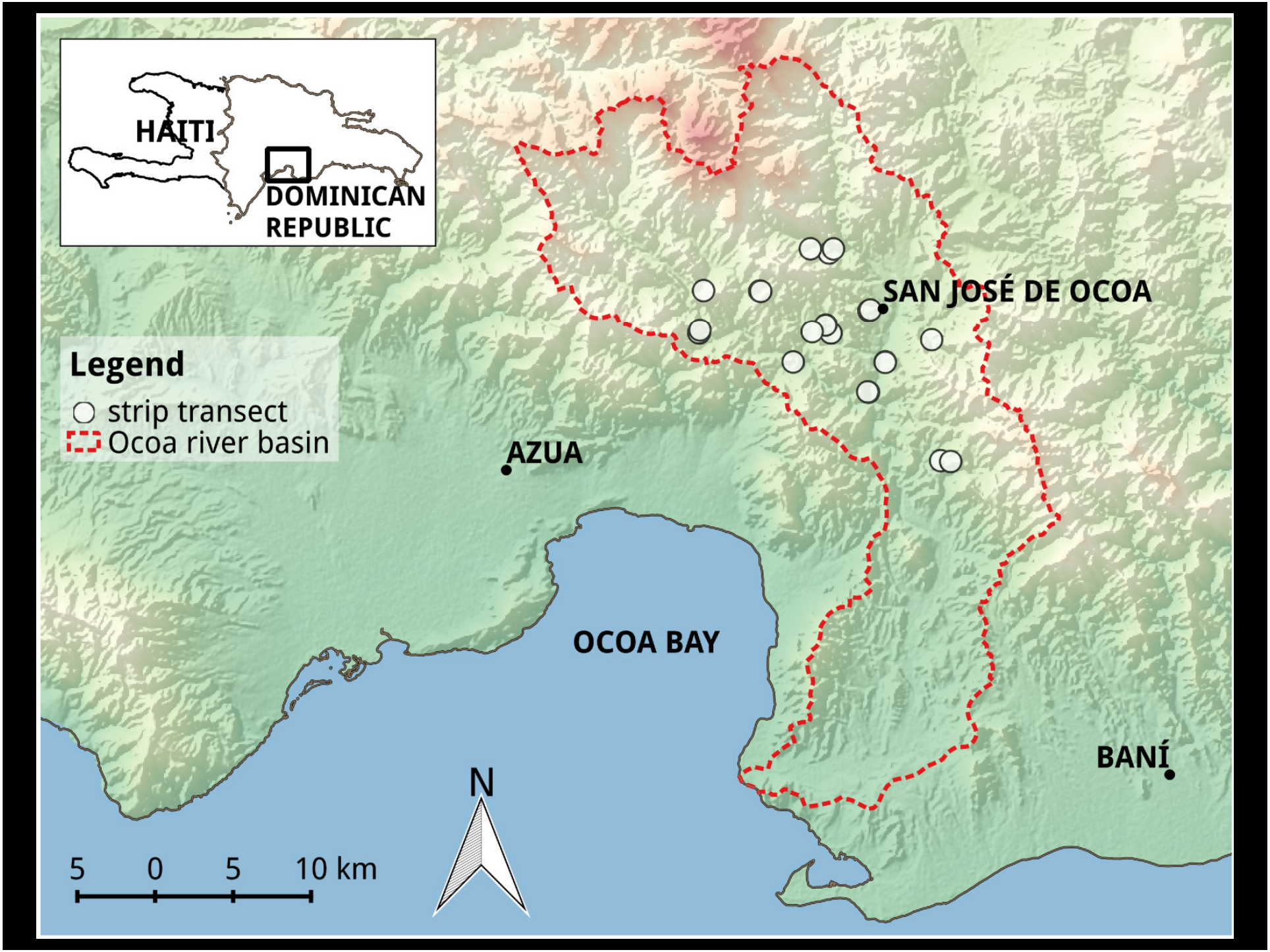
- **Maximum** biodiversity occurs in forests on **marlstones** and **alluvial** deposits
- **Minimum** biodiversity takes place in forests on **limestones**

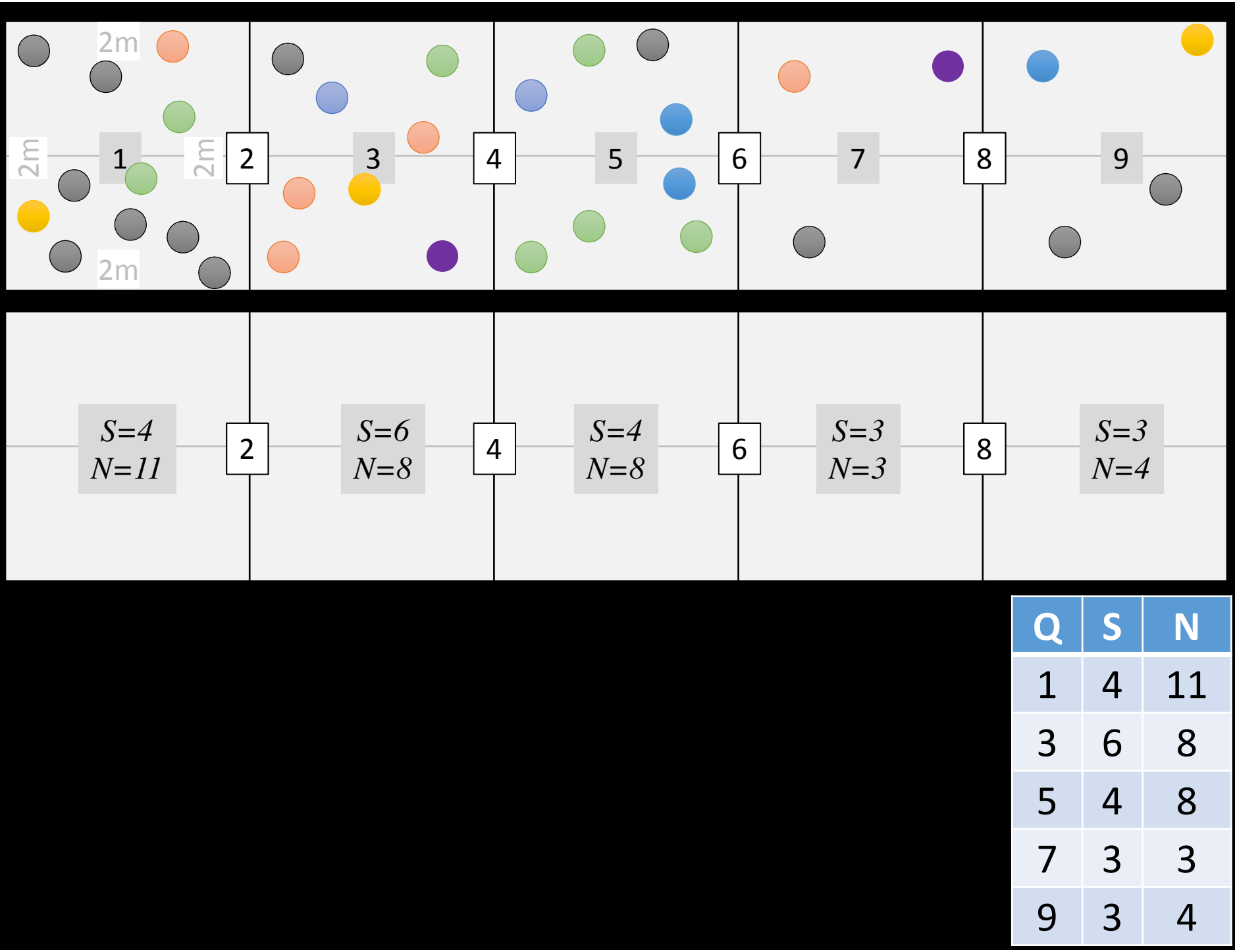


GSC on Biodiversity. MAGIC

GEOSTATISTIC

- It is statistics applied to the **study of spatio-temporal data**
- It gets support from **statistical models based on random functions** theory which models **uncertainty** related to spatial distribution


HAITI
DOMINICAN REPUBLIC
Legend
strip transect
Ocoa river basin
SAN JOSÉ DE OCOA
AZUA
OCOA BAY
BANÍ
N
5 0 5 10 km



Q	S	N
1	4	11
3	6	8
5	4	8
7	3	3
9	3	4

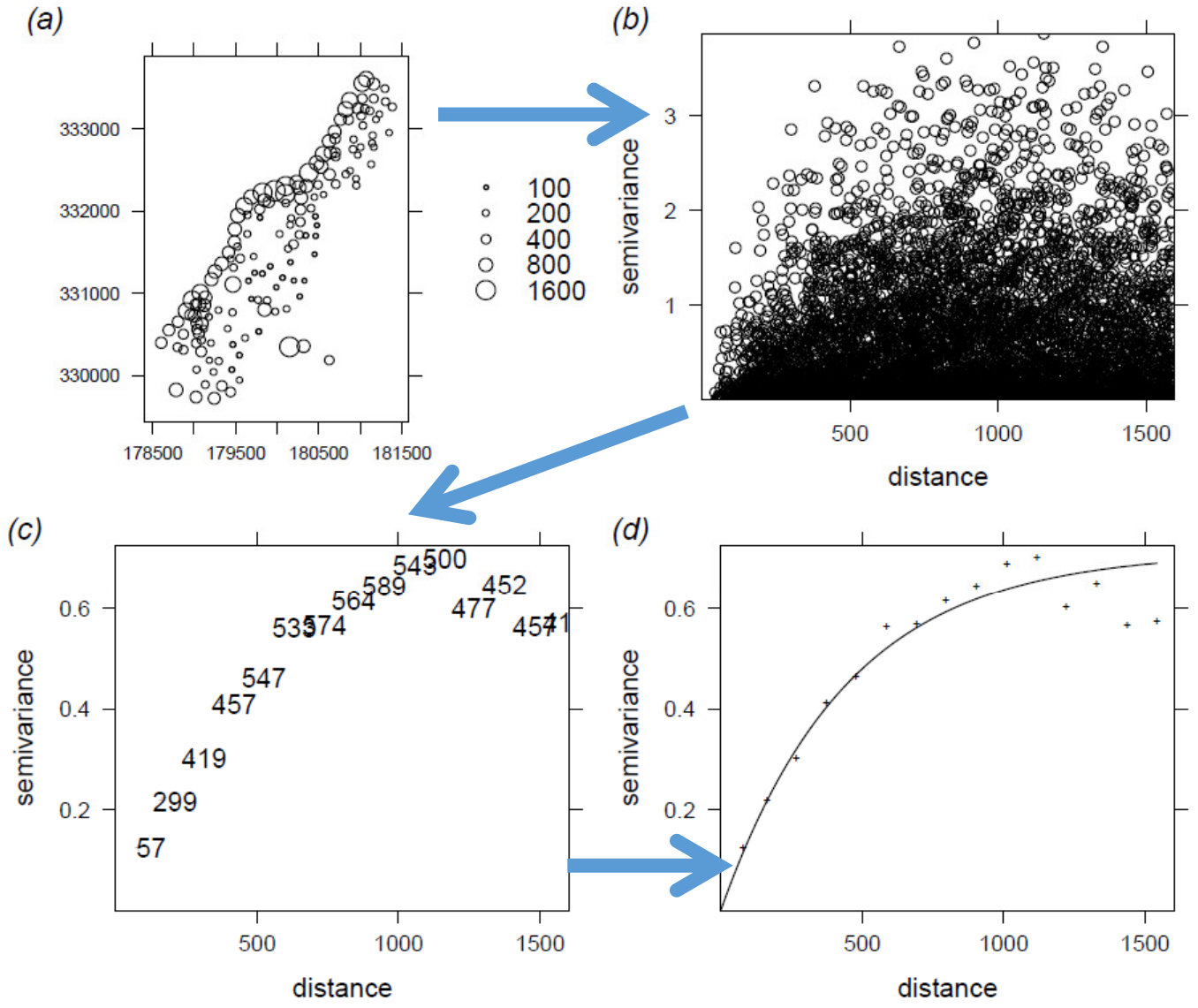
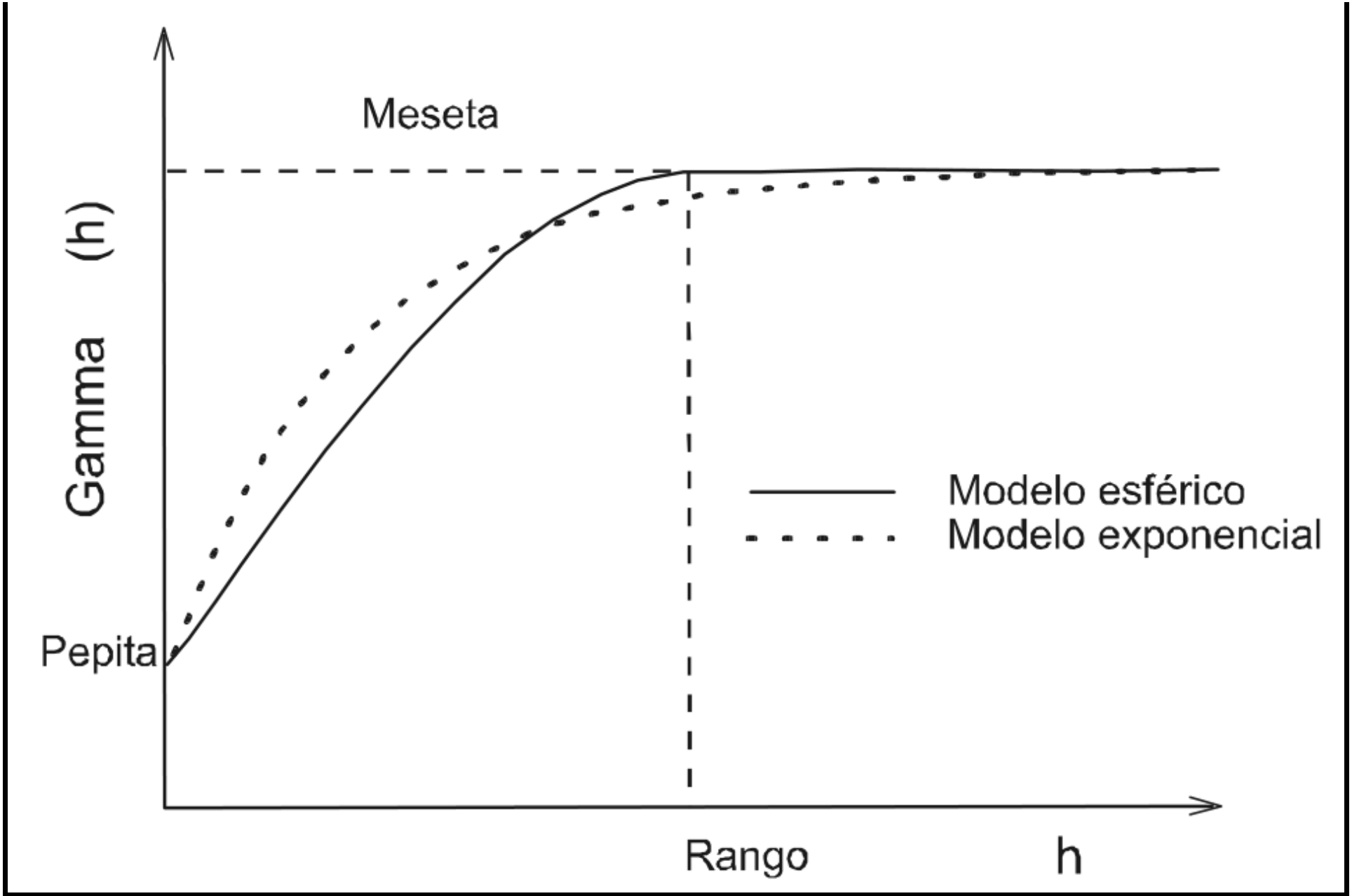
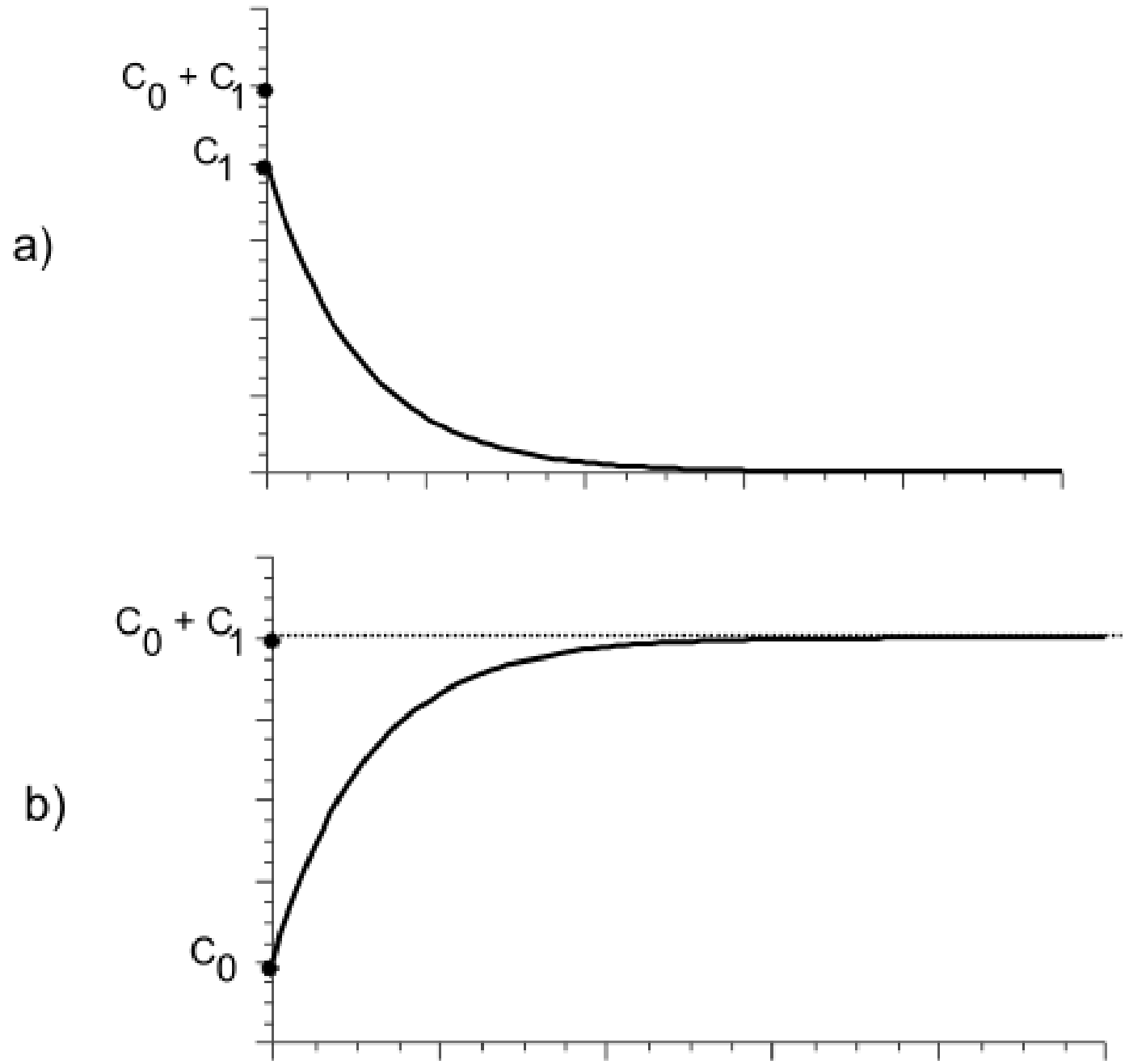


Fig. 1.9: Steps of variogram modeling: (a) sampling locations (155) and measured values of the target variable, (b) variogram cloud showing semivariances for all pairs (log-transformed variable), (c) semivariances aggregated to lags of about 100 m, and (d) the final variogram model fitted using the default settings in gstat. See further p.130.

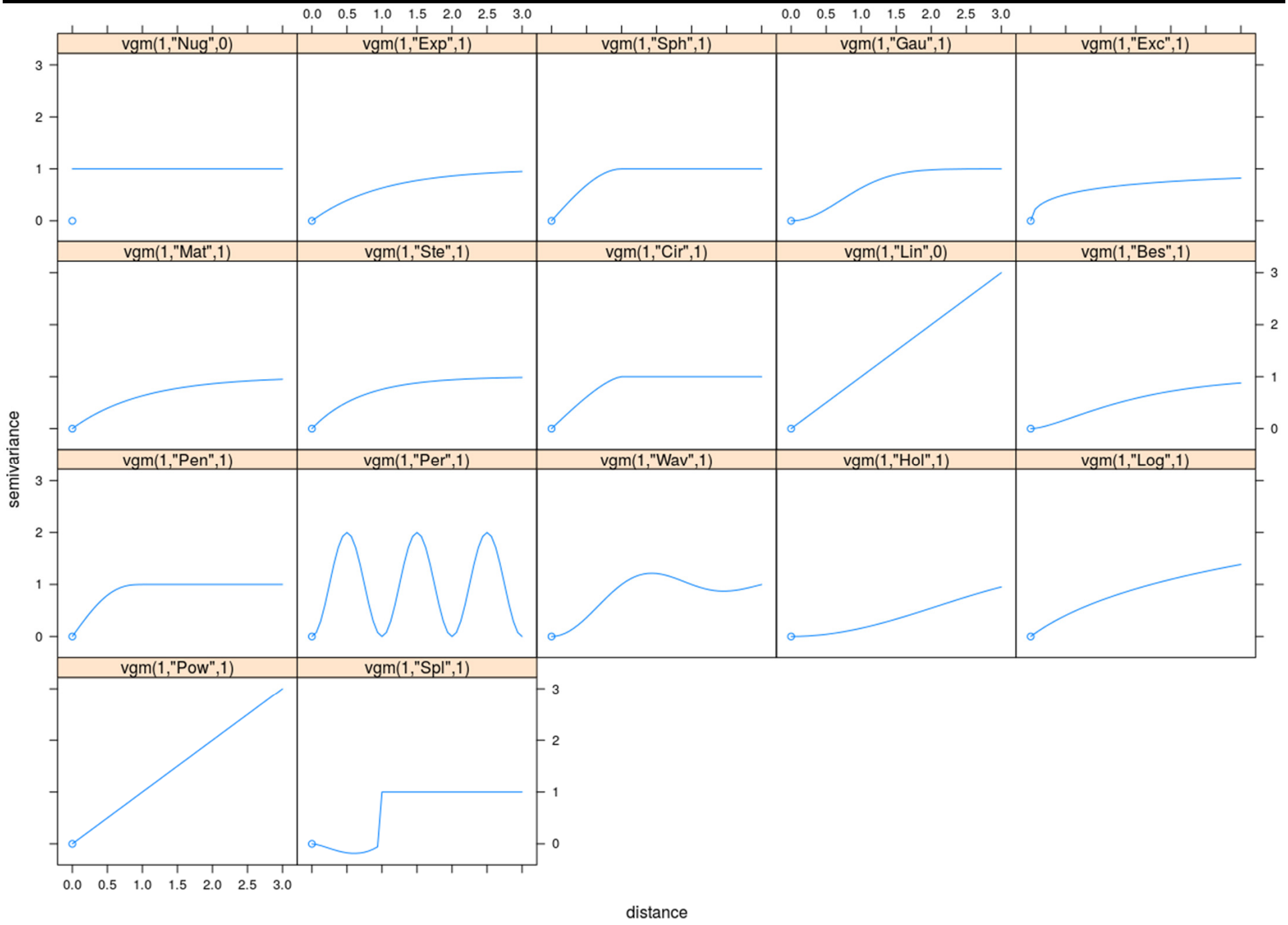
Tomado de: Hengl (2009)

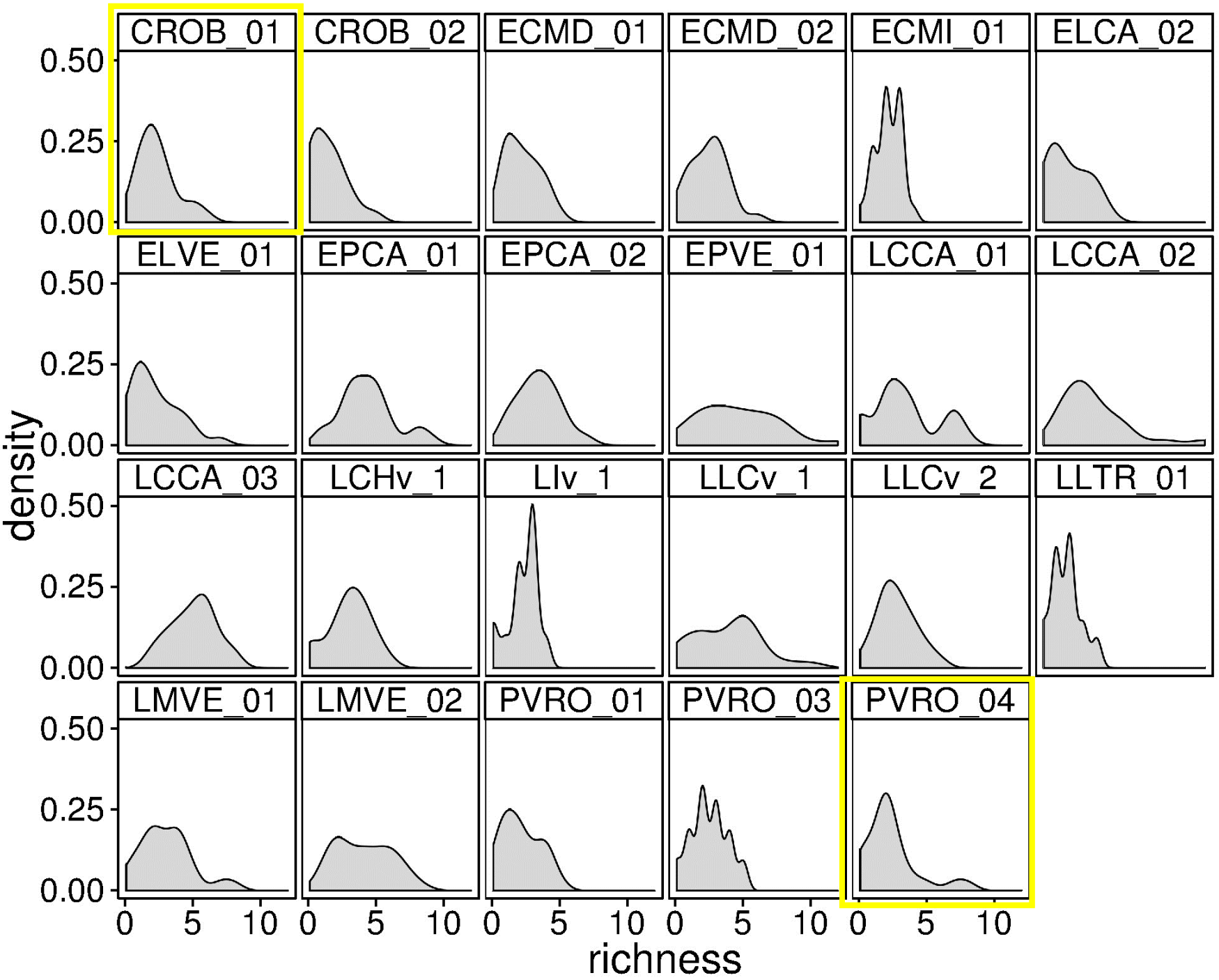


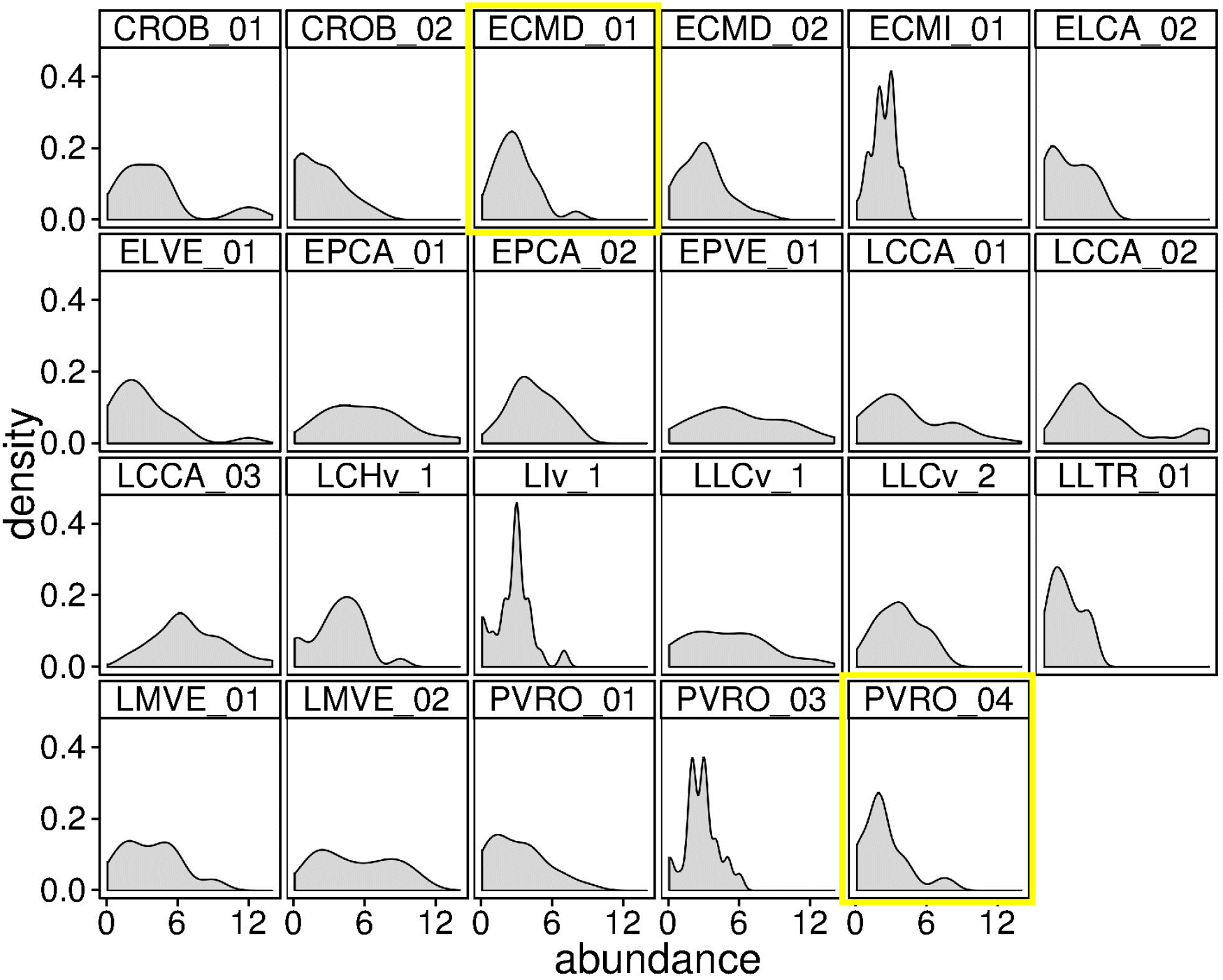
Tomado de: Alperín, M. I., Borges, V. G., & Sarandón, R. (2015)

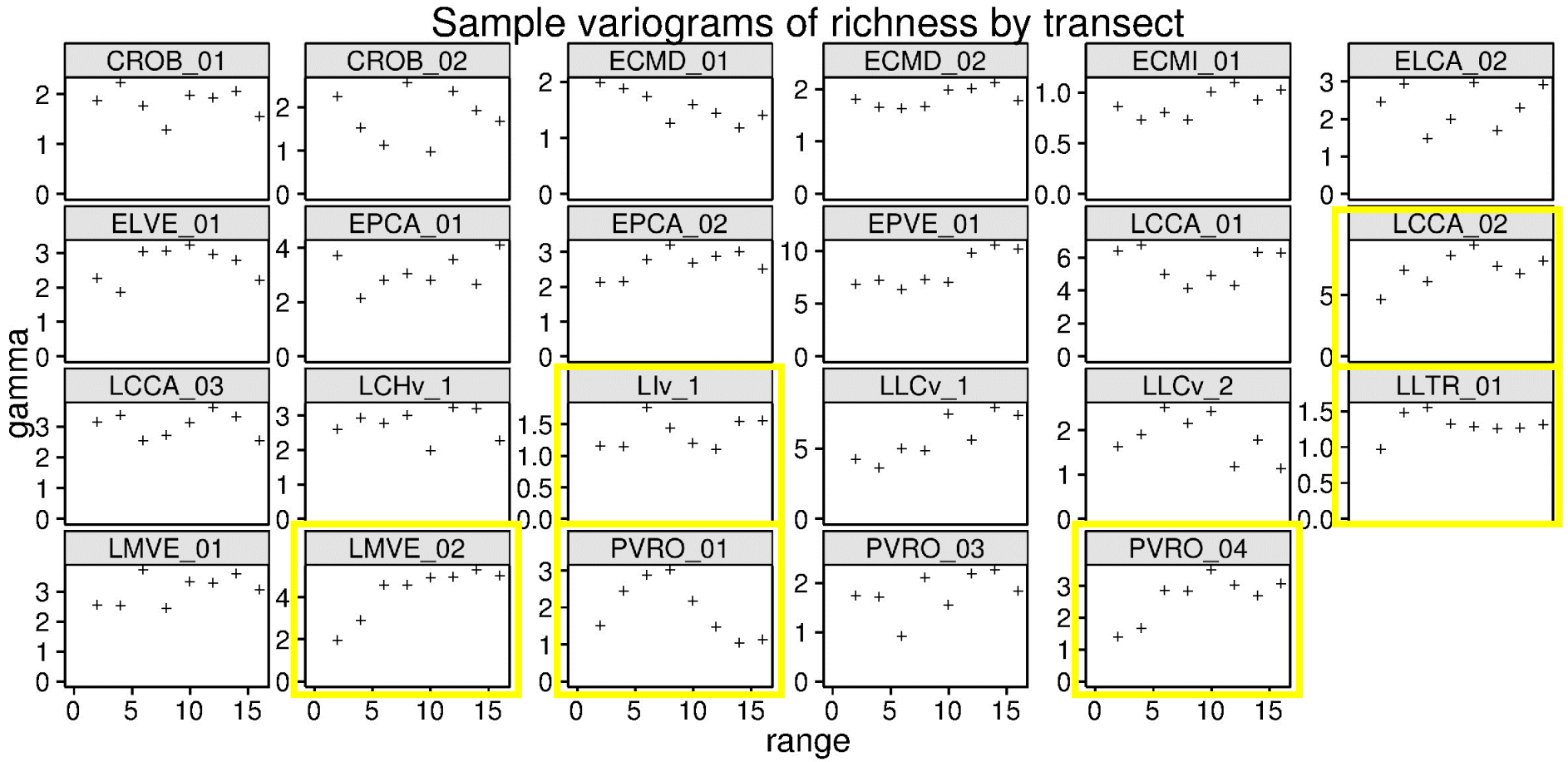


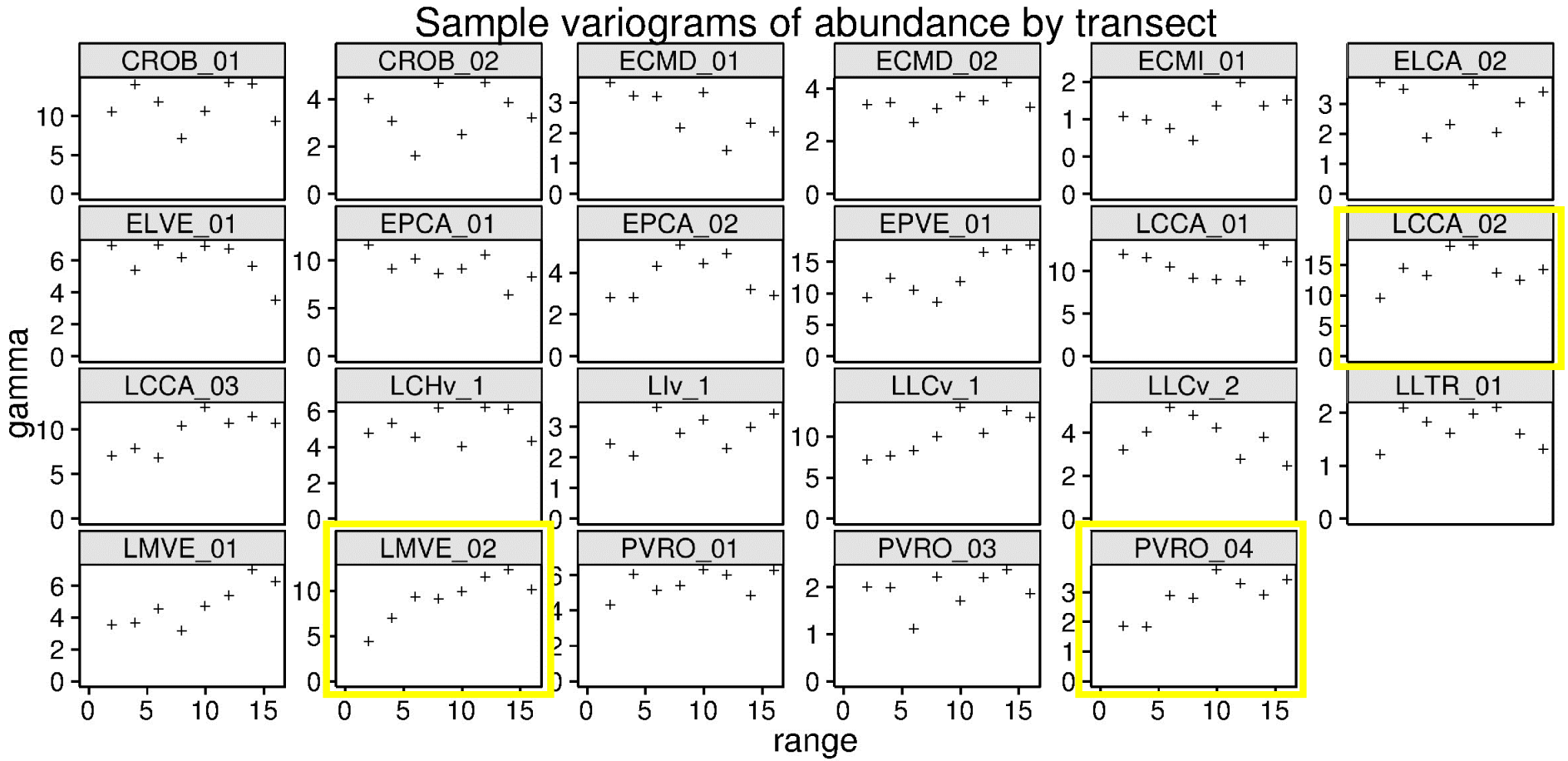
Tomado de: Olaya 2014

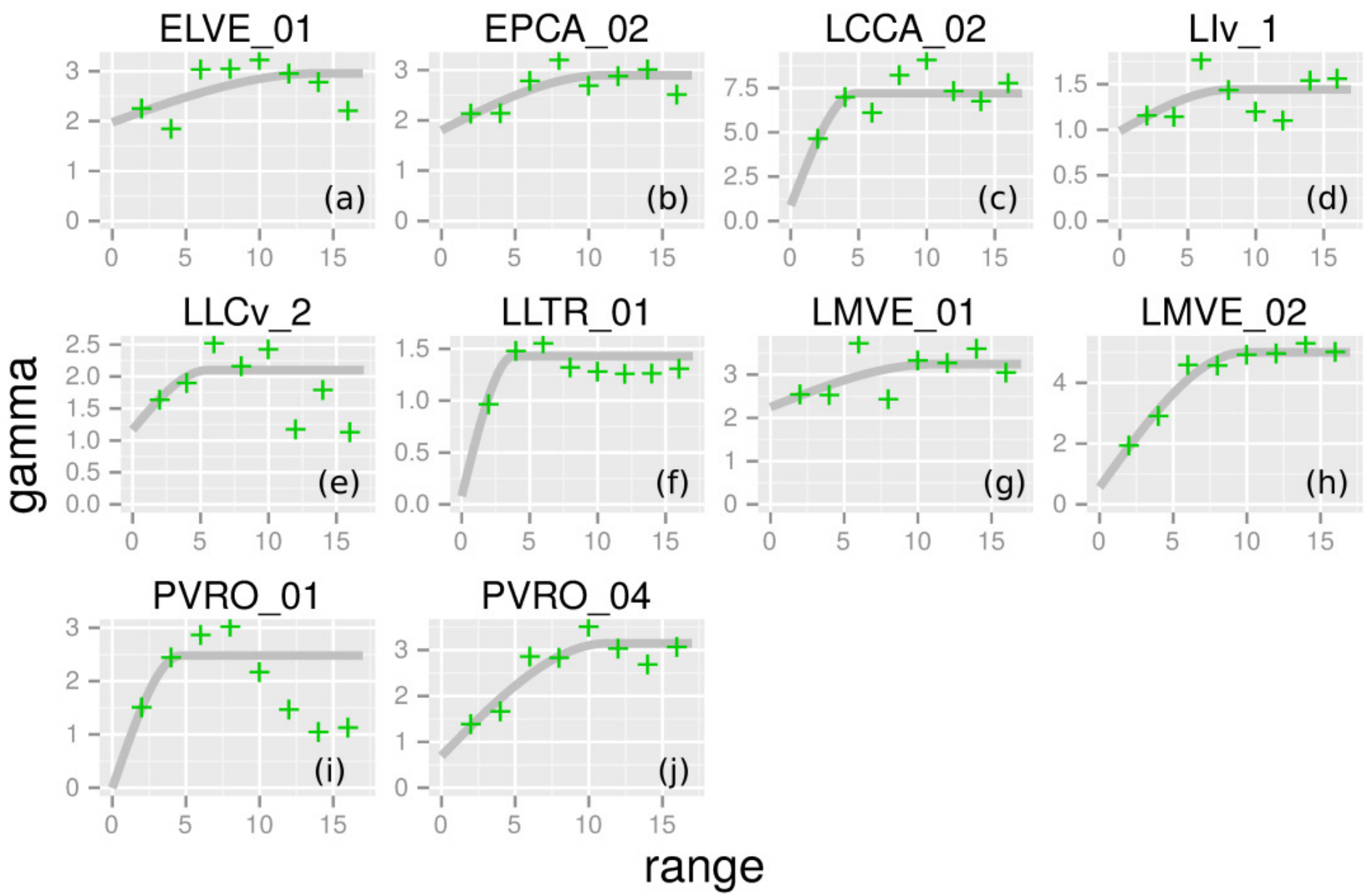

vgm(1,"Nug",0)
vgm(1,"Exp",1)
vgm(1,"Sph",1)
vgm(1,"Gau",1)
vgm(1,"Exc",1)
vgm(1,"Mat",1)
vgm(1,"Ste",1)
vgm(1,"Cir",1)
vgm(1,"Lin",0)
vgm(1,"Bes",1)
vgm(1,"Pen",1)
vgm(1,"Per",1)
vgm(1,"Wav",1)
vgm(1,"Hol",1)
vgm(1,"Log",1)
vgm(1,"Pow",1)
vgm(1,"Spl",1)
semivariance
distance
0.0 0.5 1.0 1.5 2.0 2.5 3.0
0 1 2 3

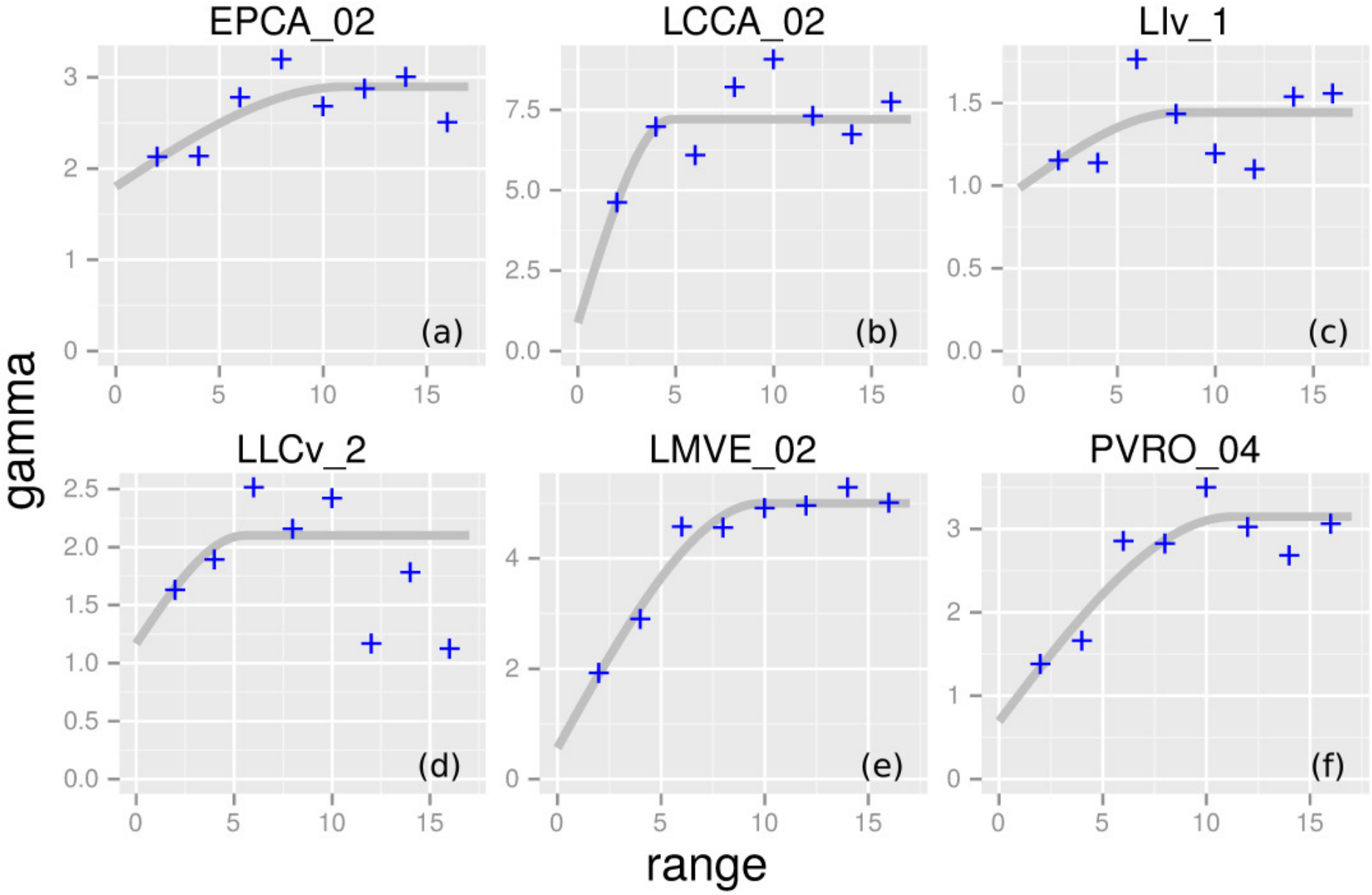

CROB_01
CROB_02
ECMD_01
ECMD_02
ECMI_01
ELCA_02
ELVE_01
EPCA_01
EPCA_02
EPVE_01
LCCA_01
LCCA_02
LCCA_03
LCHv_1
LIv_1
LLCv_1
LLCv_2
LLTR_01
LMVE_01
LMVE_02
PVRO_01
PVRO_03
PVRO_04
density
0.00
0.25
0.50
0
5
10
richness

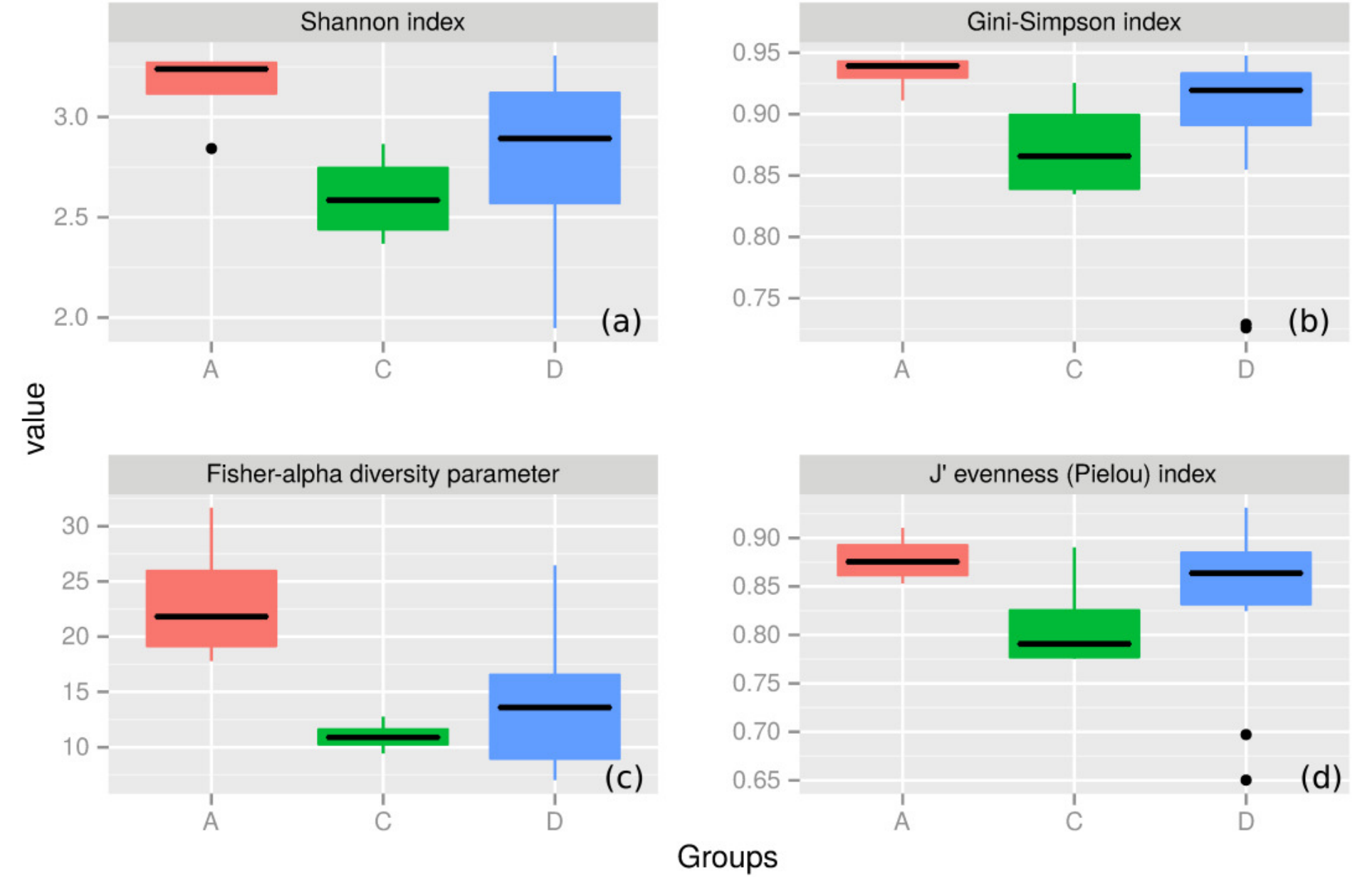

CROB_01
CROB_02
ECMD_01
ECMD_02
ECMI_01
ELCA_02
ELVE_01
EPCA_01
EPCA_02
EPVE_01
LCCA_01
LCCA_02
LCCA_03
LCHv_1
LIv_1
LLCv_1
LLCv_2
LLTR_01
LMVE_01
LMVE_02
PVRO_01
PVRO_03
PVRO_04
density
0.0
0.2
0.4
0
6
12
abundance


Sample variograms of richness by transect
CROB_01
CROB_02
ECMD_01
ECMD_02
ECMI_01
ELCA_02
ELVE_01
EPCA_01
EPCA_02
EPVE_01
LCCA_01
LCCA_02
LCCA_03
LCHv_1
LIv_1
LLCv_1
LLCv_2
LLTR_01
LMVE_01
LMVE_02
PVRO_01
PVRO_03
PVRO_04
gamma
range


Sample variograms of abundance by transect
CROB_01
CROB_02
ECMD_01
ECMD_02
ECMI_01
ELCA_02
ELVE_01
EPCA_01
EPCA_02
EPVE_01
LCCA_01
LCCA_02
LCCA_03
LCHv_1
LIv_1
LLCv_1
LLCv_2
LLTR_01
LMVE_01
LMVE_02
PVRO_01
PVRO_03
PVRO_04
gamma
range


ELVE_01
EPCA_02
LCCA_02
LIv_1
LLCv_2
LLTR_01
LMVE_01
LMVE_02
PVRO_01
PVRO_04
(a)
(b)
(c)
(d)
(e)
(f)
(g)
(h)
(i)
(j)
gamma
range


EPCA_02
LCCA_02
LIv_1
LLCv_2
LMVE_02
PVRO_04
(a)
(b)
(c)
(d)
(e)
(f)
gamma
range


Shannon index
Gini-Simpson index
Fisher-alpha diversity parameter
J' evenness (Pielou) index
(a)
(b)
(c)
(d)
value
Groups
A
C
D
3.0
2.5
2.0
0.95
0.90
0.85
0.80
0.75
30
25
20
15
10
0.70
0.65

Grupo	Códigos	Atributos

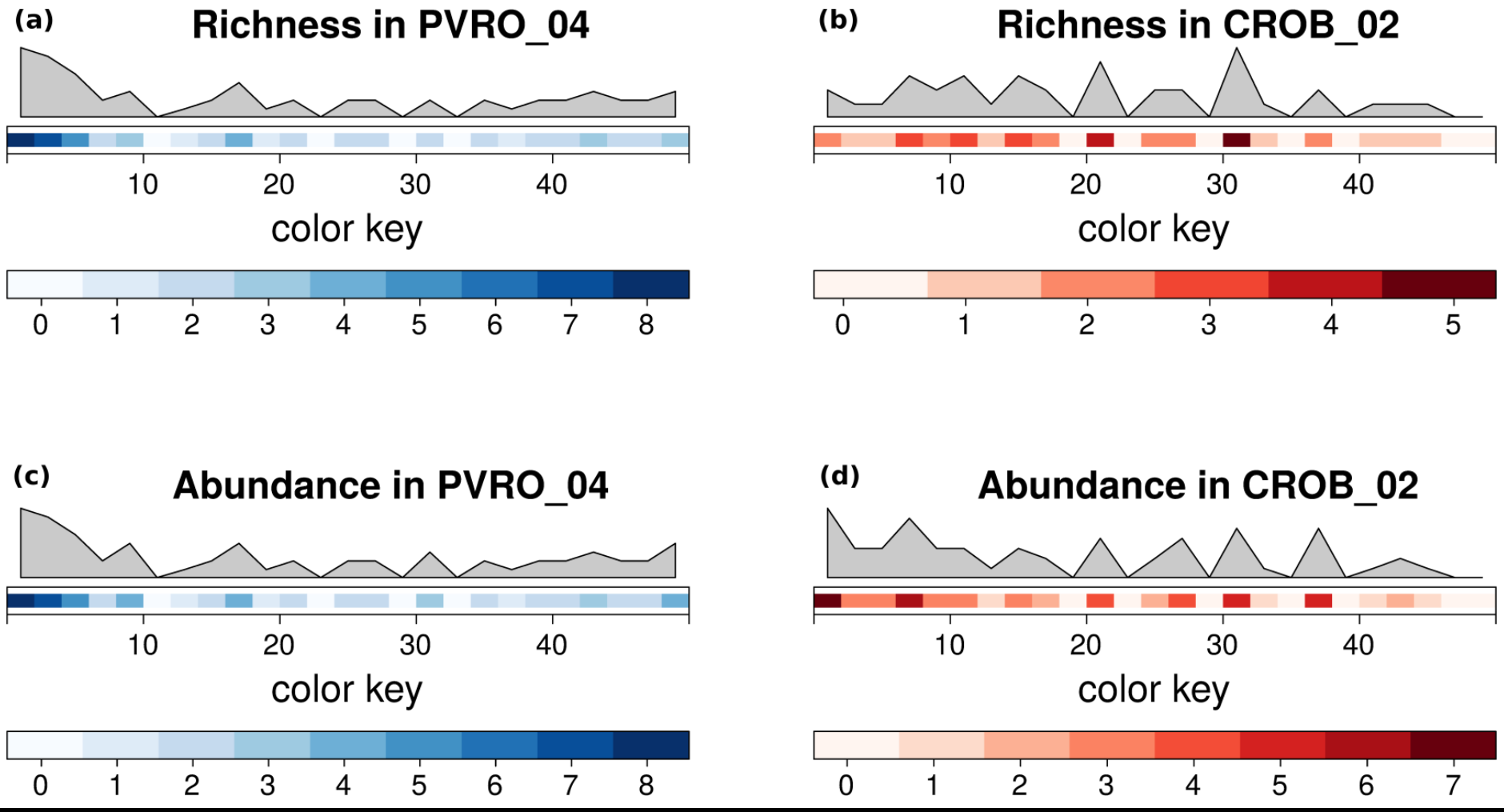
1	LCCA_02, LIv_1, LMVE_02, PVRO_04	• **Spatial:**
		  • **Null** or small nugget effect
		  • **Gradual increase** of semivariance in fitted variograms for both, richness and abundance, which means spatial autocorrelation for these variables
		• **Non-spatial:**
		• **Highest mean Fisher–alpha** diversity parameter, and many singletons reported at quadrat level.
		• Dominant species are **not characteristics of secondary vegetation**. Forests are at least 30 years old
		• Two transects were protected by **fences**.
		• **No livestock evidence** found
		• Three transects were located over river banks/terraces

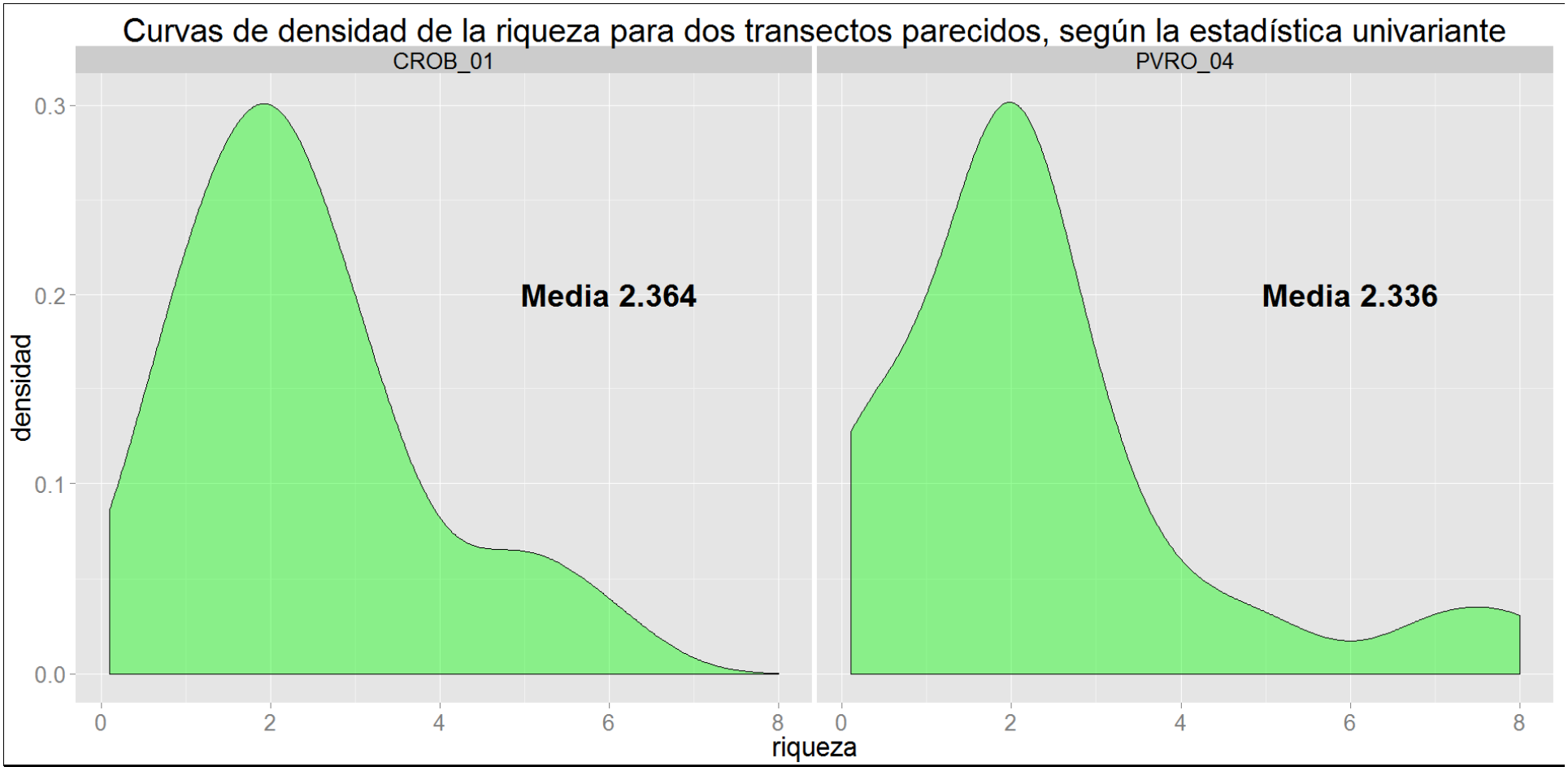
2	PVRO_01, LLTR_01	• **Spatial:**
		  • Gradual increase of semivariance only for richness variograms, and for abundance, results were singular fits
		  • This means high spatial autocorrelation only for richness, but not for abundance
		• **Non-spatial:**
		• **Lowest mean Fisher–alpha** diversity
		• Dominant species were those **characteristics of secondary vegetation**
		• One transect was 12 years old
		• **Fences were absent** and livestock evidence was reported

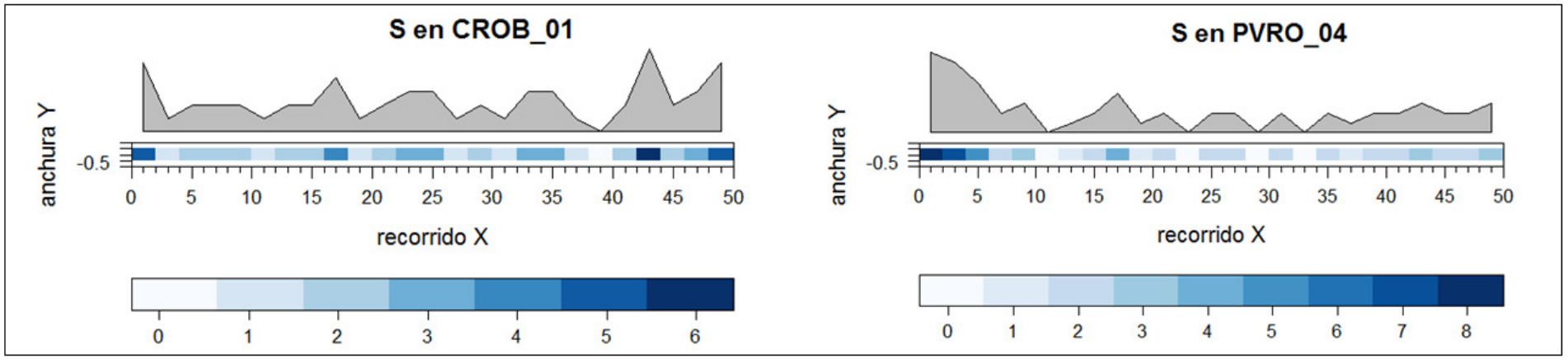
Group	Codes	Attributes

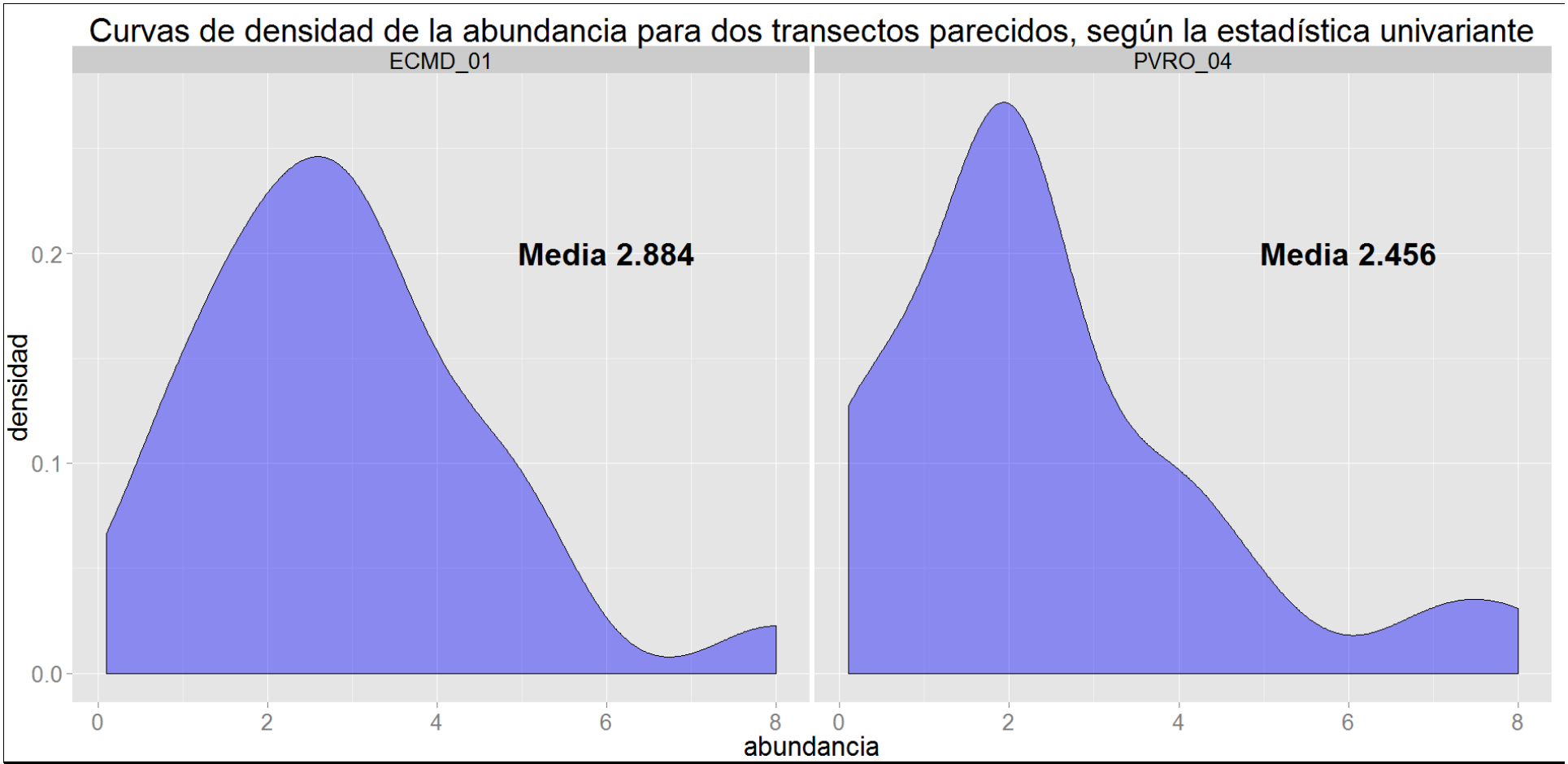
3	ELVE_01, EPCA_02, LLCv_2, LMVE_01	• **Spatial:**
		  • **Convergent variograms** with relatively high nugget effect and without gradual semivariance increase. This means low spatial autocorrelation and high infracell variability
		• **Non-spatial:**
		  • **Moderate mean Fisher–alpha** diversity
		  • **Fences** were **absent**
		  • **Livestock evidence** was reported
		  • Located over **marlstone** and in slopes

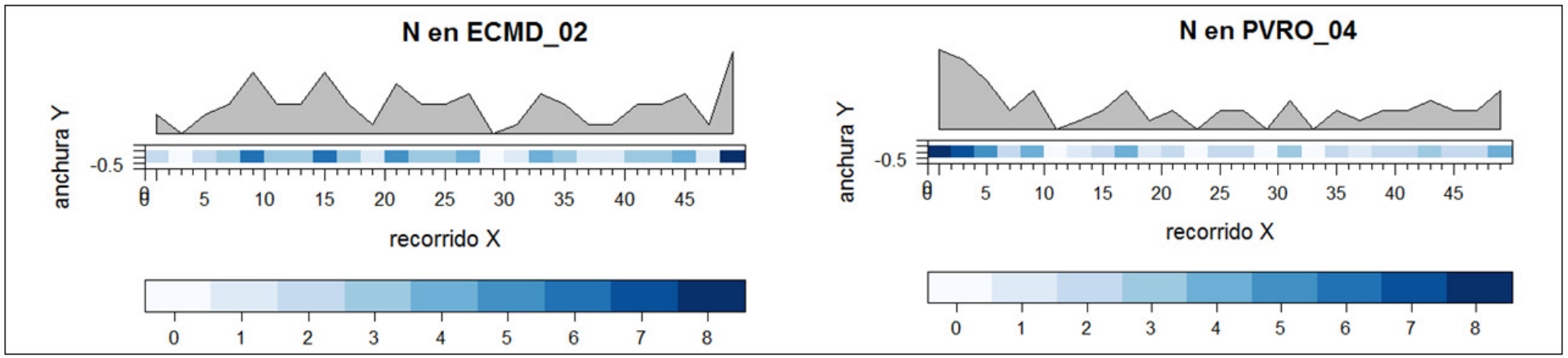
4	CROB_01, CROB_02, ECMD_01, ECMD_02, ECMI_01, ELCA_02, EPCA_01, EPVE_01, LCCA_01, LCCA_03, LCHv_1, LLCv_1, PVRO_03	• **Spatial:**
		  • Singular fit in variograms for both, richness and abundance, which results in **no spatial autocorrelation**
		• **Non-spatial:**
		  • Moderate mean **Fisher–alpha diversity**
		  • **Fences were absent**
		  • **Livestock evidence** was reported
		  • Frequently found on **slopes and river banks/terraces**


(a)
Richness in PVRO_04
10
20
30
40
color key
0
1
2
3
4
5
6
7
8
(b)
Richness in CROB_02
10
20
30
40
color key
0
1
2
3
4
5
(c)
Abundance in PVRO_04
10
20
30
40
color key
0
1
2
3
4
5
6
7
8
(d)
Abundance in CROB_02
10
20
30
40
color key
0
1
2
3
4
5
6
7


Curvas de densidad de la riqueza para dos transectos parecidos, según la estadística univariante
CROB_01
PVRO_04
Media 2.364
Media 2.336
densidad
riqueza
0.0
0.1
0.2
0.3
0
2
4
6
8


S en CROB_01
S en PVRO_04
anchura Y
recorrido X
-0.5
0
5
10
15
20
25
30
35
40
45
50
0
1
2
3
4
5
6
7
8


Curvas de densidad de la abundancia para dos transectos parecidos, según la estadística univariante
ECMD_01
PVRO_04
Media 2.884
Media 2.456
densidad
0.0
0.1
0.2
0
2
4
6
8
abundancia


N en ECMD_02
N en PVRO_04
anchura Y
-0.5
0
5
10
15
20
25
30
35
40
45
recorrido X
0
1
2
3
4
5
6
7
8

GSC on Biodiversity. MAGIC

CONCLUSSIONS

- At quadrat level, geostatistical analysis discovered patterns hidden to univariate statistics, and **reinforced the role of Fisher–alpha parameter as a sensitive measure of diversity**

GSC on Biodiversity. MAGIC

CONCLUSSIONS

- **Mature forests without livestock**, and located over **river banks/terraces**, exhibit:
  - **High spatial autocorrelation of richness and abundance**
  - Harbor great diversity measured by Fisher–alpha parameter at transect level
  - Show prevalence of singletons at quadrat level.
- These communities seems to be **local "biodiversity hotspots"**, but unfortunately they are **not included in any conservation unit** at present time.