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How to determine best diversity ordering method for a community data set?

Kürşad ÖZKAN [1]✤[iD], Serkan GÜLSOY [1iD], Ahmet MERT [1iD], Ali ŞENOL [1iD]

[1] Isparta University of Applied Sciences, Faculty of Forestry, 32260, Isparta, Turkey

ECOLOGY

ABSTRACT

Background: We conducted a study about how to determine best diversity ordering method for a community data set. Using 12 hypothetical and one ecological datasets, we tested the performances of 20 diversity ordering (*divo*) methods based on four criteria. Number of intersections (*ints*) amongst the diversity curves was taken the most important criterion into account. We defined the other criteria considering whether parametric values of a *divo* method contains *SHD* (species richness, Shannon entropy and Simpson index), potentially *uSHD* (unbiased values of *SHD*), and potentially true species diversity, *tSHD* (bias corrected values as effective number of *SHD*). All the criteria were collected into an equation called the relative selection value, rVd_i.

Results: According to the rVd_i values of hypothetical community data sets, the best performances in seven community data sets were provided by N_a. This was followed by intrinsic diversity related methods with five community data sets. For ecological data set, the best results were obtained from the methods, (i,M_i), $(\log i, k_i)$ and N_a with the rVd_i values of 6.883, 6.881 and 6.859, respectively.

Conclusion: Findings suggest that the characteristics of community data sets play important role in defining the best diversity ordering method. This tells us that diversity is certainly a multifaceted phenomenon for a single community but perhaps it is a single phenomenon for a group of communities.

Keywords: complexity, diversity measures, entropy, diversity profile, numbers equivalent, species-distribution abundance, community

HIGHLIGHTS

The problem of diversity index choice is well-known in the literature.
The solution is to use of diversity ordering methods or one-parametric diversity index families.
Numerous diversity ordering methods have been used for drawing diversity profiles of ecological assemblages.
Choosing the best diversity ordering method is another well-known problem.
Various features, especially number of intersections amongst the diversity curves, play essential role in the selection of the best diversity ordering method for a community data set.

INTRODUCTION

Biodiversity plays an essential role for balance, health, dynamism, stability, productivity, and sustainability of the ecosystems. It is therefore the central topic in many scientific disciplines such as conservation biology, environmental ecology, and biogeography (Pärtel et al., 2011; Özkan and Berger 2014). The importance of biodiversity was better understood especially after the Rio Declaration in 1992 and the Lisbon Conference in 1998 (Neumann and Starlinger 2001) and, the number of studies dealing with biodiversity has been steadily increasing since then.

As reported by Peet (1974), biodiversity, in essence, has always been defined by using the measures. An enormous number of diversity measures have been proposed in the literature. All these measures are broadly divided into three groups which are known as species richness indices, heterogeneity indices and species abundance models (Özkan, 2016). From those diversity measures, species richness (Peet, 1974), Shannon's entropy (Shannon, 1948), and Simpson's diversity index (Simpson, 1949) are the most popular metrics. Species richness solely presents the number of species whereas the letter two combine measures of richness together with abundance or incidence data (Abrams et al., 2021; Liu et al., 2007).

As stated by Patil (2014), while diversity increases according to one index, it may decrease according to the other index. This situation demonstrates the difficulties in quantifying biodiversity in a single number (Daly et al. 2018; Abrams et al., 2021). In other words, the question of which diversity index is best remains unanswered. To overcome this shortcoming, some researchers have preferred to define the representative diversity measure using principal component analysis (PCA) (Wilsey et al., 2005; Morris et al., 2014) or produce a component diversity equation derived from different diversity indices (Negiz and Özkan, 2019). Such approaches are reasonable but more or less information loss is inevitable in diversity estimations. To avoid from this information loss, the several other researchers have proposed to use parametric families of diversity indices.

Parametric families of diversity indices can also be called diversity profile techniques or diversity ordering methods. Those methods are divided into 4 groups as reported by Liu et al., (2007). They are intrinsic diversity-based methods, rank type index based method, expected number of species based methods and information based methods. The group of intrinsic diversity-based methods is basically composed of four method which are right tail-sum method (Patil and Taillie, 1979; 1982), logarithmic dominance plot (Tóthmérész, 1995), majorization method (Solomon, 1979) and k- dominance plot (Shaw et al., 1983). Rank type index-based method includes only one method that called rank type index (Patil and Taillie, 1982). Hulbert's family of diversity index (Hulbert, 1971) and Hulbert-Smith-Grassle index of order w (Patil and Taillie, 1979) are found in the group of the expected number of species-based methods. The widest diversity profile group is composed of information-based methods which includes Rényi's generalized entropy (Tóthmérész, 1995), Tsallis generalized entropy (Tsallis, 2002), Hill's diversity number of α (Hill, 1973), Daróczy's

entropy of type α (Daróczy, 1970), Numbers equivalent (Patil and Taillie, 1979, 1982) and diversity index of degree (Patil and Taillie, 1979, 1982). We can also join Landsberg Vedral entropy (Beck, 2009), information function (Bromiley et al., 2010), Kaniadakis entropy (Kaniadakis and Scarfone 2002; Sparavigna 2015), Arimoto entropy (Arimoto, 1971), Bookee and Lubbe's entropy (Bookee and Lubbe, 1980; Hooda and Sharma, 2008), Simpson entropy (Grabchak et al., 2017) and nonextensive Gaussion (Oikonomou and Tirnakli, 2009) in this group since they are the members of information theoretic measures.

It is obvious that more than one dozen methods have been used for drawing diversity profiles of ecological assemblages. In this case, a new question arises about which diversity ordering method is best. To response to this question, the studies conducted by Tóthmérész (1995) and Liu et al. (2007) are of great importance. According to their studies, the evaluation criteria in the selection of the best diversity ordering method is essentially based on number of intersections that occurrences throughout the diversity profiles in a community data set.

Number of intersections probably plays the most important role for selection of best method. However, it is not a unique evaluation criterion. For selection of best method, there are other characteristics to be questioned or considered. In this context, the questions given in the following items should be responded for a diversity ordering method to be selected or used.

1. Does the diversity ordering method to be used contain *SHD* (species richness (*S*), Shannon entropy (*H*) and/or Simpson index (*D*)) values?

2. Does the diversity ordering method to be used have unbiased forms of *S, H* and/or *D* (*uSHD*)?

3. Does effective number of species (true diversity) corresponding to *S, H* and *D*, (*tSHD*) can be obtained from the diversity ordering method considered to be used?

For a community data set, if number of intersections of a diversity ordering method has a greater value than those of the other diversity ordering methods, and for that method, all the answers to the questions of the items 1, 2 and 3 are "yes", then it is certainly the most suitable diversity ordering method for that community data set.

As can be understood in the light of the information given, for selection of best method, our approach is based on not only the number of intersections but also the other characteristics of diversity profiles. In the present study, for a community data set, we discuss how to select the best one among the diversity ordering methods considering all the characteristics mentioned above.

MATERIAL AND METHODS

We use the terms "community", "assemblage" and "sampling plot" interchangeably in this article. In the present study, evaluation material consists of 12 hypothetical community data sets (HS$_1$–HS$_{12}$) and one real ecological data set. Each of hypothetical data sets contains 5 communities and varied number of species (see supplementary files Table A1). Real ecological data set includes vegetation data taken from Yazili Canyon Nature Park, a small-scale district in the Mediterranean region of Turkey.

Table 1. Diversity ordering methods.

Group1	Intrinsic diversity-based methods	References
Right tail-sum method	$(i, T_i) = \left(i, \sum_{j=i+1}^{S} p_{[j]}\right), i = 1, 2, \dots, S - 1$	Patil and Taillie (1979; 1982)
Logarithmic dominance plot	$(\log i, \ L_i) = \left(\log i, \sum_{j=i+1}^{S} p_{[j]}\right), i = 1, 2, \dots, S - 1$	Tóthmérész (1995)
Majorization method	$(i, M_i) = \left(i, \sum_{j=1}^{i} p_{[j]}\right), i = 1, 2, \dots, S$	Solomon (1979)
k- dominance plot	$(\log i, k_i) = \left(\log i, 100 \sum_{j=1}^{i} p_{[j]}\right), i = 1, 2, \dots, S$	Shaw et al. (1983)
Group 2	**Rank type index-based method**	
Rank type index	$\Delta_\rho^{(\text{rank})} = \sum_{i=1}^{S} \left(1 - \sum_{j=1}^{i} p_{[j]}\right) \rho^{i-1} , \rho \geq 0$	Patil and Taillie (1982)
Group 3	**Expected number of species-based methods**	
Hulbert's family of diversity index	$s(m) = \sum_{i=1}^{S} [1 - (1 - p_i)^m], m \geq 1$	Hulbert (1971)
Hulbert-Smith-Grassle index of order *w*	$\Delta_\omega^{\text{HSG}} = \sum_{i=1}^{S} (1 - p_i [1 - (1 - p_i)^\omega]), \omega \geq 0$	Patil and Taillie (1979)
Group 4	**Information based methods**	
Rényi's generalized entropy	$H_\alpha = \left[\ln\left(\sum_{i=1}^{S} p_i^\alpha\right)\right]/(1 - \alpha), \quad \alpha \geq 0, \alpha \neq 1$	Tóthmérész (1995)
Tsallis generalized entropy	$H_q^T = (1 - \sum_{i=1}^{S} p_i^q)/(q - 1), q \geq 0, q \neq 1$	Tsallis (2002)
Hill's diversity number of *α*	$N_\alpha = \left(\sum_{i=1}^{S} p_i^\alpha\right)^{1/(1-\alpha)}, \alpha \geq 0, \alpha \neq 1$	Hill (1973)
Daróczy's entropy of type *α*	$H^{(\alpha)} = (\sum_{i=1}^{S} p_i^\alpha - 1)/(2^{1-\alpha} - 1), \alpha \geq 0, \alpha \neq 1$	Daróczy (1970)
Numbers equivalent	$S_\beta = \left(\sum_{i=1}^{S} p_i^{\beta+1}\right)^{-1/\beta}, \beta \geq -1, \beta \neq 0$	Patil and Taillie (1979, 1982)
Diversity index of degree *β*	$\Delta_\beta = (1 - \sum_{i=1}^{S} p_i^{\beta+1})/\beta, \beta \geq -1, \beta \neq 0$	Patil and Taillie (1979, 1982)
Kaniadakis entropy	$S_\kappa = -\sum_{i=1}^{S} ([p_i^{1+\kappa} - p_i^{1-\kappa}]/2\kappa), -1 > \kappa > 1, \kappa \neq 0$	Kaniadakis and Scarfone (2002), Sparavigna (2015)
Landsberg- Vedral entropy	$S_q^L = (1/q - 1)[(1/\sum_{i=1}^{S} p_i^q) - 1], q \neq 1$	Beck (2009)
Information function	$I_q(P) = (1/q - 1)\left(\sum_{i=1}^{S} (p_i^q/q - 1)\right), q \neq 1$	Bromiley et al. (2010)
Arimoto entropy	$A_\alpha(P) = (2^{\alpha-1} - 1)^{-1}\left[\left(\sum_{i=1}^{S} p_i^{\frac{1}{\alpha}}\right)^\alpha - 1\right], \alpha > 0, \alpha \neq 1$	Arimoto (1971)
Boekee and Lubbe entropy	$H_R(P) = (R/R - 1)\left[1 - \left(\sum_{i=1}^{S} p_i^R\right)^{\frac{1}{R}}\right], R > 0, R \neq 1$	Bookee and Van der Lubbe (1980), Hooda and Sharma (2008)
Generalized Simpson entropy	$\zeta_r = \sum_{i=1}^{S} p_i (1 - p_i)^r , r = 1, 2, \dots$	Grabchak et al. (2017)
Nonextensive Gaussian	$S_q^G = \ln_q^T\left(\prod_{i=1}^{S} (1/p_i)^{p_i}\right)$ where $\ln_q^T(x) := (x^{1-q} - 1)/(1 - q), \ q \neq 1$	Oikonomou and Tirnakli, (2009)

This data set consists of 107 sampling plots and totally 180 species (see supplementary files Table A2). The nature park located in Mediterranean region of Turkey (37° 27' 22" N-37° 29' 37" N and 30° 54' 16" E-30° 58' 26" E) covers an area of approximately 600 hectares and has a karstic land structure between 100-400 m altitude. Brutian pine (*Pinus brutia* Ten.) and Oak species (*Quercus* sp.) are dominant species in the study area. The nature park is rich in endemic species with twenty-four endemic plant taxa (Özkan and Süel, 2008; Mert and Özkan, 2017). During the field survey in Yazili Canyon Nature Park, plant species composition of each plot was recorded using the Braun–Blanquet scores. Those scores were then transformed to relative cover (r: 0.01; +: 0.02; 1: 0.04; 2: 0.15; 3: 0.375; 4: 0.625; 5: 0.875) prior to analysis (Fontaine et al., 2007). We used those transformed values throughout the present study.

We totally employed 20 diversity ordering (*divo*) methods. The names, the equations and the references belonging to the methods are given in Table 1 which has been rearranged by joining the methods, S_κ, S_q^L, $I_q(P)$, A_a (P), H_R (P), ζ_r and S_q^G from the table called "Methods for diversity ordering" given by Liu et al., (2007). In Table 1, S is the number of species in an assemblage, p_i is the relative abundance of *i-th* species and $p_{[j]}$ refers to the relative abundance of the *j-th* most abundant species.

The scale values of (i, T_i), (log i, L_i), (i, M_i) and (log i, k_i) are standart which range from 1, 0, 1 and 0 to S-1, log(S-1), S and log$S$, respectively. Those of the other *divo* methods were defined in wide ranges (Table 2). For S_κ, we considered the recommended positive parameter value range (0>K>1) (Kaniadakis and Scarfone, 2004). We employed the same parameter values for $s(m)$ and Δ_ω^{HSG} between 1 to 30, for H_a, H_q^T, N_a and $H^{(a)}$ ranging from a, $q \to 0$ to 5, and for I_q (P),

S_q^G and S_q^L from $q \to 0$ to 2. The beginning parameter values of $H_R(P)$ and $A_a(P)$ were defined by setting R= 0.5 and a=0.01, respectively because the value of the R parameter equal to almost 0 is most likely cause to obtain very large $H_R(P)$ values and, $A_{a \to 0}(P)$ may have a greater value than $A_{a_{q > a \to 0}}(P)$ value which wouldn't satisfy the condition corresponding to ever-increasing curve with increasing its parameter value.

The beginning scale value of S_β and Δ_β can take an integer value, β=-1. However, those of H_d, H_q^T, N_a and $H^{(a)}$ do not integer $(a, q \to 0)$. Therefore, we used $\beta \to$-1 as the beginning scale values of S_β and Δ_β corresponding to the those of H_d, H_q^T, N_a and $H^{(a)}(a, q \to 0)$. For ζ_r, minimum parameter value is standard, equal to 1 (Grabchak et al., 2017). Therefore, we terminated the maximum of ζ_r at the value of 12.

Relative value of *i-th divo* method (Rd_i) is defined as

$$Rd_i = 100 \left(\frac{ints_i}{\sum ints_i} \right)$$

Which is for hypothetical data sets. For ecological (Yazili Canyon Nature Park) data set, 10000 iterations were run. Each iteration result consists of number of intersections computed using the *divo* methods from randomly selected 16 sampling plots amongst 107 sampling plots. After calculating total number of intersections for each of the methods, their relative values were computed by the following equation.

$$Rd_i = 100 \left(\frac{\sum_{t=1}^{T} ints_i}{\sum_{t=1}^{T} \sum ints_i} \right), t = 1, 2, \ldots, T \tag{1}$$

Where Rd_i also refers to *ints%* of *i-th divo* method employed in evaluating the ecological data set.

We determined the weights in favor of number of intersections since it is the most important criterion. For

Table 2. The scale parameter values of the *divo* methods in Group 2, 3 and 4.

Methods	The scale parameter values										
$\Delta_\rho^{(rank)}$	ρ =0	0	0.01	0.02	0.1	0.2	0.4	0.6	0.8	1	1.2
$s(m)$, Δ_ω^{HSG}	m, ω =1	2	3	5	10	12	15	18	22	25	30
H_a, H_q^T, N_a and $H^{(a)}$	$a, q \to 0$	0.1	0.2	0.4	0.6	0.8	$\to 1$	2	3	4	5
S_β, Δ_β	$\beta \to$-1	-0.9	-0.8	-0.6	-0.4	-0.2	$\to 0$	1	2	3	4
S_κ	$\kappa \to 0$	0.1	0.2	0.3	0.4	0.5	0.6	0.7	0.8	0.9	$\to 1$
$I_q(P)$, S_q^G and S_q^L	$q \to 0$	0.1	0.2	0.3	0.4	0.5	$\to 1$	1.2	1.4	1.7	2
A_a (P)	a =0.01	0.1	0.2	0.3	0.4	0.5	$\to 1$	1.2	1.4	1.7	2
H_R (P)	R= 0.5	$\to 1$	1.5	2	3	4	5	6	8	10	12
ζ_r	r =1	2	3	4	6	7	8	9	10	11	12

selecting the best method, the weights of the characteristics (i.e., number of intersections, *SHD*, *uSHD* and *tSHD*) are 0.8, 0.1, 0.05 and 0.05, respectively. The following equations are used to find the best *divo* method for a community data set.

$$Vd_i = 0.8\left(\frac{Rd_i}{max.\ Rd_i}\right) + 0.1(SHD) + 0.05(bcSHD) + 0.05(bctSHD) \quad (2)$$

Vd_i is the selection value of *i-th divo* method. Relative value of Vd_i is

$$rVd_i = 100\frac{Vd_i}{\sum Vd_i} \quad (3)$$

From the *divo* methods, the best selection is obtained by

$$rVd_i^* = \max(rVd_1, rVd_2, \dots, rVd_i),\ i = 1,2,\dots,20 \quad (4)$$

Where *T* is total number of iterations (*t*=1,2,...*T*), $ints_i$ is number of intersections of *i-th divo* method at *t-th* iteration. *SHD* refers to species richness (*S*), Shannon entropy (*H*) and Simpson index (*D*). *uSHD* is bias corrected values of *S*, *H* and *D* and, *tSHD* refers to true *S*, *H* and *D* values. *SHD* value is 0.1×(1/3) if a *divo* computes solely any one of species richness (*S*), Shannon entropy (*H*) and Simpson index (*D*). *SHD* value is 0.1×(2/3) if a *divo* computes any two of *S*, *H* and *D*, It is 0.1 if all of *S*, *H* and *D* can

be obtained from a diversity ordering method and, 0, otherwise. If bias corrected diversity measures (*uSHD*) can be obtained from a *divo*, the numerical weight value is 0.05 and if a *divo* method provides true species diversity (*tSHD*), its contribution value is 0.05.

None of *S*, *D* and *H* values are found in the profile of $\Delta_p^{(rank)}$(Patil and Taillie, 1982). (*i*,*T*), (log *i*,*L*), (*i*,*M*), (log*i*,*k*), *s*(*m*), Δ_ω^{HSG}, S_κ, S_q^L, $A_\alpha(P)$, $H_R(P)$, ζ, and S_q^G contain only one of *S*, *D* and *H* values (Patil and Taillie,1979 and 1982; Tóthmérész, 1995; Solomon, 1979; Shaw et al.,1983; Hulbert, 1971; Kaniadakis and Scarfone, 2002; Beck, 2009; Arimoto, 1971; Bookee and Van der Lubbe, 1980; Grabchak et al. 2017; Oikonomou and Tirnakli, 2009). $I_q(P)$ consists of *S* and *H* (Bromiley et al., 2010) and, H_α, H_q^T, N_α, $H^{(\alpha)}$, S_β and Δ_β profiles include all of *S*, *D* and *H* values (*SHD*) (Liu et al., 2007). Additionally, H_q^T and N_α contain unbiased *S*, *D* and *H* values (*uSHD*) (Marcon et al., 2014; Chao and Jost, 2015). In these two methods, effective number of species (true diversity) (*tSHD*) can only be provided by N_α (Chao and Jost, 2015) (Table 3).

All the values of diversity ordering methods and their number of intersections were computed by using spreadsheet software programs which were created by the authors of the present paper.

Table 3. The weights of the *divo* methods.

Measures	*SHD*	*uSHD*	*tSHD*
$\Delta_p^{(rank)}$	0	0	0
(*i*,*T*), (log *i*,*L*), (*i*,*M*), (log *i*,*k*), *s*(*m*), Δ_ω^{HSG}, S_κ, S_q^L, $A_\alpha(P)$, $H_R(P)$, ζ, S_q^G	0.0333	0	0
$I_q(P)$	0.0666	0	0
H_α, $H^{(\alpha)}$, S_β, Δ_β	0.1	0	0
H_q^T	0.1	0.05	0
N_α	0.1	0.05	0.05

RESULTS

Hypothetical community data sets

The results of the hypothetical community data sets (HS) are given in Table 4. For the hypothetical community set 1 (HS₁), Figure 1 illustrates that except for the C_5 curve based on S_q^L method, all diversity curves show ever decreasing or increasing trend with increasing the values of scale parameters.

It is worth mentioning that maximum number of intersections (*ints*) obtained from a diversity ordering method is equal to $(n^2-n)/2$ where *n* is the number of communities in a community data set. It means that all the community pairs are non-separable. The number of intersections takes the maximum value equal to 10 for a data set consisting of 5 communities. From the hypothetical data sets, the maximum of number of

intersections was provided by the Group 1 methods from HS_2 and HS_{11} (Table 4). For HS_1, the greatest number of intersections was obtained by intrinsic diversity-based methods and generalized Simpson entropy. From those methods, the calculated number of intersections is 8 and, they have the same separable community pairs (C_1 and C_4 and, C_2 and C_3). *s*(*m*) and Δ_ω^{HSG} are the second ranks. Both of the methods indicate separable four pairs of communities (C_1 and C_4 and, C_2 and C_3 and, C_2 and C_5 and, C_3 and C_4). Rank type index and information theoretical measures, except for S_κ and S_q^G, have the same number of intersections with the same separable community pairs (C_1 and C_4 and, C_2 and C_3 and, C_2 and C_5 and, C_3 and C_4 and, C_4 and C_5). The number of non-separable community pairs (C_1 and C_3 and, C_1 and C_5 and, C_2 and C_4 and, C_3 and C_5) of S_κ is equal to 4 and, all the communities are separable in accordance with the method, S_q^G (Figure 1).

As can be seen in Table 4, number of intersections (*ints*) of the *divo* methods is varied. (i, M_i) and $(\log i, k_i)$ have greatest total *ints* at the value of 83. (i, T_i) and $(\log i, L_i)$ are the second-ranked methods which have a total *ints* value of 78. These methods are followed by H_d H_q^T, N_d $H^{(a)}$, S_β and Δ_β with the same value of 68. The total *ints* values of the others (i.e., $s(m)$, Δ_ω^{HSG}, $\Delta_\rho^{(rank)}$, S_κ, $S_{q'}^L$ $I_q(P)$, $A_a(P)$, $H_R(P)$ and ζ), except for $S_{q'}^G$ range between 41 and 63. All the communities into the hypothetical data sets are separable according to S_q^G method. Its total number of intersections is therefore equal to 0 (Table 4).

Table 5 gives the rVd_i and rVd_i^* results of hypothetical community sets. According to rVd_i^* values, N_a is the method with highest performance at six community data sets (HS_3, HS_6, HS_8, HS_9, HS_{10} and HS_{12}). This is followed by (i, T_i), $(\log i, L_i)$, (i, M_i) and $(\log i, k_i)$, with 5 data sets (HS_1, HS_2, HS_4, HS_5 and HS_{11}). $A_a(P)$ gets the Vd_i^* twice and, $H_R(P)$ and ζ_r only once.
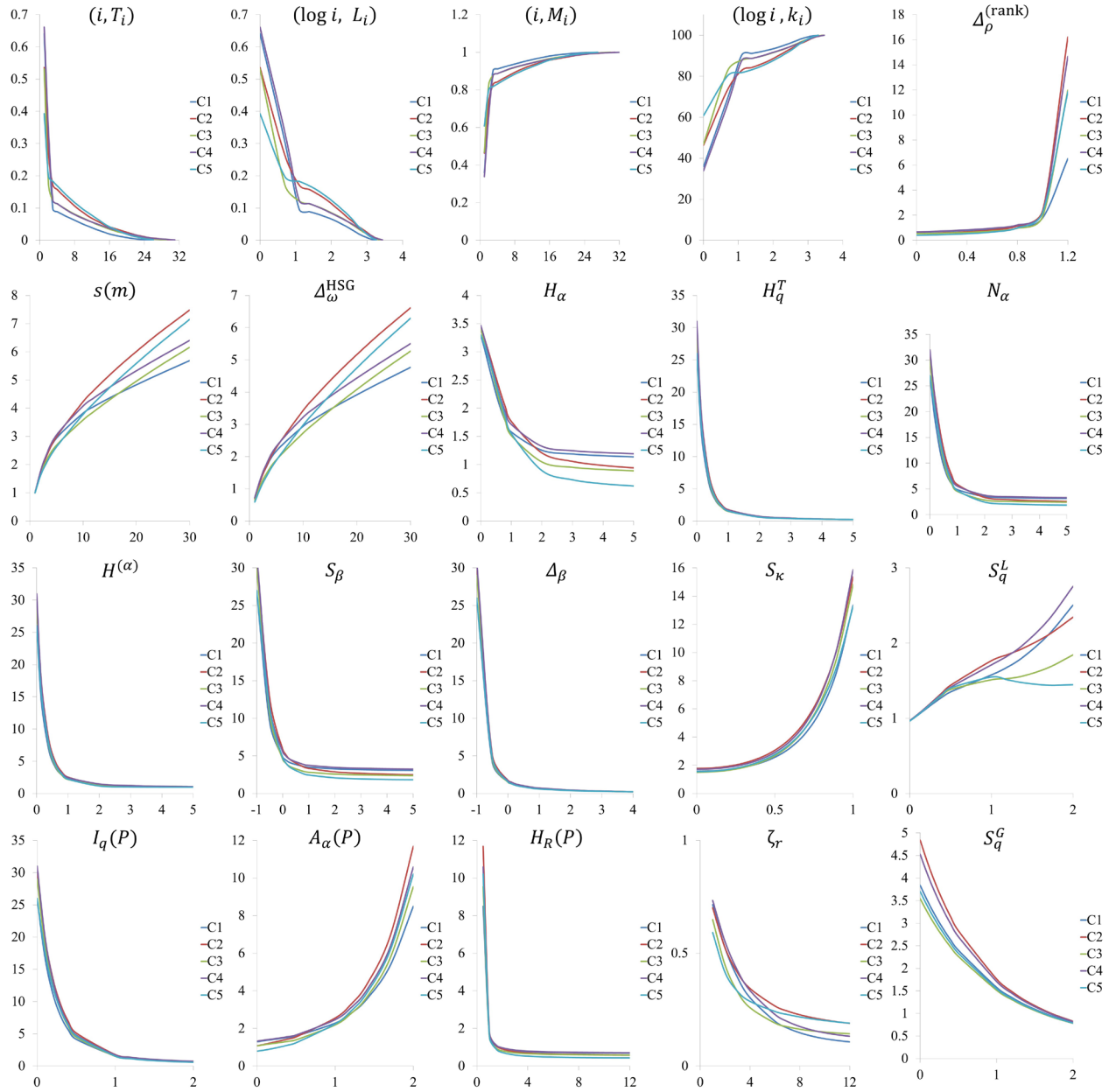

Figure 1. The graphical results of the *divo* methods for HS₁.

Table 4. The number of intersections (*ints*) for each diversity ordering (*divo*) method of the hypothetical community sets.

Measures	HS_1	HS_2	HS_3	HS_4	HS_5	HS_6	HS_7	HS_8	HS_9	HS_{10}	HS_{11}	HS_{12}	$\Sigma ints_i$
(i,T_i)	8	10	6	5	2	9	5	6	5	6	10	6	78
$(\log i, L_i)$	8	10	6	5	2	9	5	6	5	6	10	6	78
(i, M_i)	8	10	7	5	2	9	5	6	7	6	10	8	83
$(\log i, k_i)$	8	10	7	5	2	9	5	6	7	6	10	8	83
$\Delta_\rho^{(rank)}$	5	7	6	5	2	7	5	4	2	6	9	4	62
$s(m)$	6	5	5	0	0	9	2	2	1	5	4	2	41
Δ_ω^{HSG}	6	5	5	0	0	9	2	2	1	5	4	2	41
H_a	5	7	6	3	1	8	4	6	7	6	7	8	68
H_q^T	5	7	6	3	1	8	4	6	7	6	7	8	68
N_a	5	7	6	3	1	8	4	6	7	6	7	8	68
$H^{(a)}$	5	7	6	3	1	8	4	6	7	6	7	8	68
S_β	5	7	6	3	1	8	4	6	7	6	7	8	68
Δ_β	5	7	6	3	1	8	4	6	7	6	7	8	68
S_κ	4	5	5	3	1	6	2	3	7	5	4	6	51
S_q^L	5	7	6	3	1	8	3	5	7	6	5	7	63
$I_q(P)$	5	7	6	3	1	8	3	5	7	6	5	7	63
$A_a(P)$	5	4	4	3	2	8	4	3	0	5	10	3	51
$H_R(P)$	5	4	4	3	2	8	4	3	0	4	9	3	49
ζ_r	8	8	5	1	1	9	2	2	1	5	5	2	49
S_q^G	0	0	0	0	0	0	0	0	0	0	0	0	0

Table 5. rVd_i and rVd_i^* values of hypothetical community sets.

Measures	HS_1	HS_2	HS_3	HS_4	HS_5	HS_6	HS_7	HS_8	HS_9	HS_{10}	HS_{11}	HS_{12}
(i,T_i)	**6.77**	**6.98**	5.30	**7.82**	**7.70**	5.52	6.63	6.37	5.16	5.38	**6.84**	5.10
$(\log i, L_i)$	**6.77**	**6.98**	5.30	**7.82**	**7.70**	5.52	6.63	6.37	5.16	5.38	**6.84**	5.10
(i, M_i)	**6.77**	**6.98**	6.15	**7.82**	**7.70**	5.52	6.63	6.37	7.10	5.38	**6.84**	6.71
$(\log i, k_i)$	**6.77**	**6.98**	6.15	**7.82**	**7.70**	5.52	6.63	6.37	7.10	5.38	**6.84**	6.71
$\Delta_\rho^{(rank)}$	4.06	4.69	5.06	7.51	7.40	4.13	6.36	4.08	1.95	5.17	5.91	3.22
$s(m)$	5.14	3.63	4.46	0.31	0.31	5.52	2.81	2.29	1.26	4.52	2.90	1.88
Δ_ω^{HSG}	5.14	3.63	4.46	0.31	0.31	5.52	2.81	2.29	1.26	4.52	2.90	1.88
H_a	4.87	5.53	5.79	5.44	4.62	5.38	5.88	6.88	7.67	5.81	5.42	7.25
H_q^T	5.28	5.95	6.16	5.91	5.08	5.71	6.28	7.26	8.10	6.14	5.83	7.65
N_a	5.68	6.37	**6.53**	6.38	5.55	**6.04**	**6.68**	**7.64**	**8.52**	**6.46**	6.24	**8.05**
$H^{(a)}$	4.87	5.53	5.79	5.44	4.62	5.38	5.88	6.88	7.67	5.81	5.42	7.25
S_β	4.87	5.53	5.79	5.44	4.62	5.38	5.88	6.88	7.67	5.81	5.42	7.25
Δ_β	4.87	5.53	5.79	5.44	4.62	5.38	5.88	6.88	7.67	5.81	5.42	7.25
S_κ	3.52	3.63	4.46	4.82	4.01	3.76	2.81	3.31	7.10	4.52	2.90	5.10
S_q^L	4.33	4.97	5.30	4.82	4.01	4.94	4.08	5.35	7.10	5.38	3.56	5.91
$I_q(P)$	4.60	5.25	5.55	5.13	4.31	5.16	4.35	5.61	7.39	5.60	3.83	6.17
$A_a(P)$	4.33	2.96	3.62	4.82	**7.70**	4.94	5.35	3.31	0.28	4.52	**6.84**	2.68
$H_R(P)$	4.33	2.96	3.62	4.82	**7.70**	4.94	5.35	3.31	0.28	3.66	6.19	2.68
ζ_r	6.77	5.64	4.46	1.81	4.01	5.52	2.81	2.29	1.26	4.52	3.56	1.88
S_q^G	0.27	0.28	0.25	0.31	0.31	0.22	0.27	0.25	0.28	0.22	0.27	0.27
rVd_i^*	**6.77**	**6.98**	**6.53**	**7.82**	**7.70**	**6.04**	**6.68**	**7.64**	**8.52**	**6.46**	**6.84**	**8.05**

Ecological data set

After 10.000 iterations, calculated relative values of the total number of intersections (*ints%*) and rVd_i of each *divo* method is given in Figure 2. As expected, the greatest *ints%* values belong to intrinsic diversity related methods (i.e., (i,M_i), $(\log i,k_i)$, (i,T_i) and $(\log i,L_i)$). Majority of the member of information theoretical measures, H_d $H_{q'}^T$ N_d $H^{(a)}$, S_β and Δ_β ranks second. Those are followed by $S_{q'}^L$ $I_q(P)$,

$A_a(P)$, $H_R(P)$ and $\Delta_p^{(rank)}$. The methods, $s(m)$, Δ_ω^{HSG}, S_K, ζ_r and in particular S_q^G indicate insufficient performance.

The methods, (i,M_i), $(\log i,k_i)$ and N_d have very close rVd_i values with 6.865 (rVd_i^*), 6.862 and 6.841, respectively. This is followed by (i,T_i) and $(\log i,L_i)$ with the same value of 6.672. Majority of information theoretical measures, H_d $H_{q'}^T$ $H^{(a)}$, S_β and Δ_β also indicate good performances ranging the values between 6.017 and 6.429. The Vd_i values of the other methods are less than 0.5 (Figure 2).
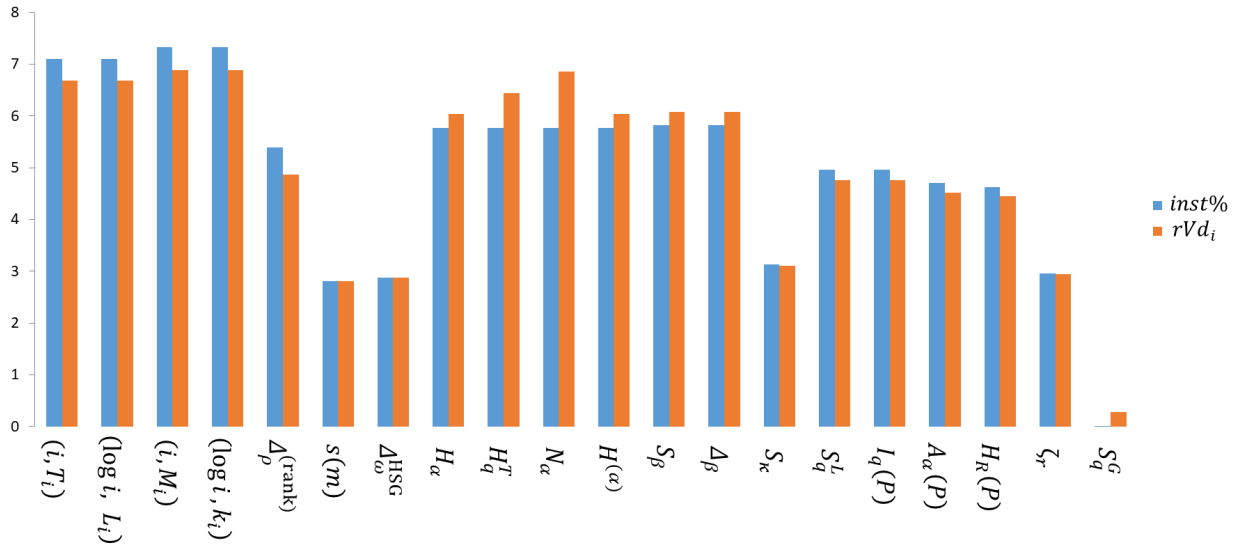
Figure 2. *ints%* and rVd_i values of the ecological data set ($\sum ints\% = \sum rVd_i = 100$).

DISCUSSION

We tested 20 diversity ordering methods using different (12 hypothetical and one ecological) community data sets. Among the methods, S_q^L (Beck, 2009) and S_q^G (Oikonomou and Tirnakli, 2009) are unfavorable for drawing diversity profiles of sampling plots or communities since S_q^L curves do not show always monotonically increasing trend with incresing the scale parameter values (Figure 1) and, almost all the community curves obtained from S_q^G are separable (Figure 1 and 2).

Apart from S_q^L and $S_{q'}^G$ findings indicate that the methods that have the lowest number of intersections are $s(m)$, Δ_ω^{HSG}, S_K and ζ_r. Moreover, $s(m)$ and Δ_ω^{HSG} contains only species richness ($s(\infty)=S$, $\Delta_\infty^{HSG}=S-1$) (Hulbert, 1971; Patil and Taillie, 1979), S_K only Shannon entropy ($S_{K\to0}=H=-\sum_{i=1}^{S}p_i \ln p_i$ where p_i is the relative abundance value of *i*-th species) (Kaniadakis and Scarfone, 2002) and ζ_r only Simpson index, $D=\sum_{i=1}^{S} p_i^2$, using the equation, $D^\zeta=1/(1-\zeta^{1/r})$ where $D^1=1/(1-\zeta)=D$ (Grabchak et al. 2017) and, to the best of our knowledge, none of them have estimators proposed or improved for *uSHD* or *tSHD* values.

According to the *ints* values, the performances of the methods, $\Delta_p^{(rank)}$, $I_q(P)$, $A_a(P)$ and $H_R(P)$ are better than $s(m)$, Δ_ω^{HSG}, S_K and ζ_r. $\Delta^{(rank)}$ includes none of *SHD* (Patil and Taillie, 1982), $A_a(P)$, $H_R(P)$ only H ($A_{a\to1}(P)=H/\ln2$ and $H_{R\to1}(P)=H$) (Arimoto, 1971; Bookee and Van der Lubbe,1980), and $I_q(P)$ both S and H ($I_{q\to0}(P)=S-1$ and $I_{q\to1}(P)=H$) (Bromiley

et al., 2010). *uSHD* or *tSHD* cannot be defined by all these methods. Therefore, except for $I_q(P)$, their *ints%* values lower than their rVd_i values.

The greatest *ints* or *ints%* values were provided by (i,M_i) and $(\log i,k)$. Those are followed by (i,T_i) and $(\log i,L)$. All of those methods are found in intrinsic diversity-related methods (Group 1). As stated by Liu et al., (2007), the methods, (i,M_i) and $(\log i,k)$ are almost entirely attributed to each other because the x-coordinates are only log-transformed and, the y-coordinates are positively linearly transformed in the latter. (i,T_i) and $(\log i,L)$ are equivalent. The only difference between them is that the x-coordinates are log transformed in the latter.

The curves of Group 1 methods comprise only species richness corresponding to $S-1$, $\log (S-1)$, S and $\log S$ for (i,T_i), $(\log i,L_i)$, (i,M_i) and $(\log i,k_i)$, respectively. Hence, their performance values (rVd_i) are lower than their *ints%* values. Moreover, intrinsic diversity-related methods directly rank dominance rather than diversity (Liu et al., 2007). Although we did not consider this characteristic in defining rVd_i values, this is a disadvantage for application of Group 1 methods in creating diversity profiles of communities.

As expected, H_d $H_{q'}^T$ N_a and $H^{(a)}$, S_β and Δ_β have the same *ints%* values since they are monotonic transformations of each other (Chao and Jost, 2015). Δ_β is identical to H_q^T when putting $q=\beta+1$ (Ricotta 2003 and 2005) and, $S_\beta=N_{a+1}$ ($a=\beta$) in Hill's notation (Patil and Taillie, 1982).

The findings of all the information theoretical measures indicate that rVd_i values are greater than $ints\%$ values because they include all of S ($H_{\alpha=0} = N_{\alpha=0,} = S_{\beta=-1} = S$, $H_{q=0}^T = H^{(\alpha=0)} = \Delta_{\beta=-1} = S-1$), H ($H_{\alpha\to1} = H_{q\to1}^T = \Delta_{\beta\to0} = H$, $N_{\alpha\to1} = S_{\beta\to0} = e^H$, $H^{(\alpha\to1)} = H/\ln 2$) and D ($H_{\alpha=2} = -\ln D, H_{q=2}^T = \Delta_{\beta=1} = 1-D$, $N_{\alpha=2} = S_{\beta=1} = 1/D$ $H^{(\alpha=2)} = 2(1-D)$) values into their profiles (Liu et al., 2007). Among those methods, the better performances were obtained by H_q^T and N_a because they also have bias-corrected forms and, N_a has a greater rVd_i value than H_q^T since it gives the richness/diversity results as effective number of species based on unbiased S, H and D (Marcon et al., 2014; Chao and Jost, 2015).

CONCLUSIONS

In our opinion, selection of a diversity profile for a community data set should be based on not only number of intersections but the other factors which were explained throughout the present study.

Based on the studies conducted by Tóthmérész (1995) and Liu et al. (2007), we assume that the larger the number of intersections between diversity profiles of communities, the lower the separability between them in terms of diversity. That provides the most accurate results to decide the separable communities.

Species richness, Shannon entropy and Simpson index are the most commonly used measures to estimate species diversity (Lewis et al., 1998; Ricotta et al., 2003; Pallmann et al., 2012; Di Battista et al., 2016; Grabchak et al. 2017; Daly et al., 2018; Abrams et al., 2021). Therefore, presences of the values belonging to those indices within the numerical value range of a diversity profile at the fixed scale values are of great importance as a selection criterion.

Numerous studies have been performed to propose the bias corrected forms of S (Chao and Lee, 1992; Gotelli and Chao, 2013; Chao and Chiu, 2016), H (Zahl, 1977; Chao et al., 1993; Grassberger, 2003; Özkan, 2020) and D (Lande, 1996; Chen et al., 2018; Nielsen et al., 2003; Droissart et al., 2012). On this context, the fact that a diversity ordering method has a potential to obtain unbiased SHD values gives a significant advantage for its selection.

Complete agreement was reached in an Ecology forum that using numbers equivalents or effective number instead of the classical diversity indices (entropies) such as Shannon entropy should be used in any diversity partitioning (Ellison, 2010). Unbiased forms of effective number have also been proposed by Gotelli and Chao (2013) and Chao and Jost (2015). This means a significant contribution to the relative selection value of a *divo* method that makes unbiased estimations of SHD as effective number. On this context, there is only one *divo* method that is called Hill numbers (Hill, 1973; Jost, 2006).

We defined the weights of the criteria mentioned above in the frame of literature, our scientific information and experiences. Scientific information and experiences are different from person to person. Therefore, number of criterion and their weights may be differently evaluated by different scientists. For selecting the best method, the better way is probably application of analytical hierarchical process, AHP (Saaty, 1987). However, for AHP application, the weights of the factors or characteristics relative to each other should be determined by the experts studying on biodiversity computing. Further studies will probably improve the evaluation criteria in selection of the most suitable *divo* method for community datasets. Besides, it is worth noting that there are several the other parametric family of measures not used in the present study such as Abe entropy (Beck, 2009), Sharma-Mittal entropy (Akturk and Bagci, 2007), Havrda-Charvat entropy (Kumar and Choudhary, 2012), Deng entropy (Deng, 2016) and generalized Deng entropy (Gao et al., 2019; Liu et al., 2019) and so on. Those methods can also be evaluated whether they are favorable for a diversity ordering method or not.

The results obtained from the present study indicate that the characteristics of community data sets are important to define the best diversity ordering method. This allows us to establish the following sentence that diversity is certainly a multifaceted phenomenon for a single community, but probably a single phenomenon for a community data set. Hence, employment of the selection criteria such as *ints*, *SHD*, *uSHD* and *tSHD* is important for more accurate and objective assessments of diversities in ecological community data sets.

AUTHORS' CONTRIBUTION

Project Idea: KÖ
Funding: KÖ, SG, AM, AŞ
Database: KÖ, SG, AM, AŞ
Processing: KÖ, SG, AM, AŞ
Analysis: KÖ, SG, AM, AŞ
Writing: KÖ, SG, AM, AŞ
Review: KÖ, SG, AM, AŞ

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SUPPLEMENTARY FILES

Table A1. Hypothetical community data sets.

HS$_1$[C$_1$: 462, 428, 271, 10, 9, 9, 8, 8, 8, 8, 7, 7, 7, 6, 6, 6, 4, 4, 3, 3, 3, 2, 1, 1, 1, 1, 1, **C$_2$**: 336, 196, 68, 10, 10, 9, 9, 9, 8, 7, 7, 6, 5, 5, 5, 4, 3, 3, 3, 3, 3, 3, 2, 2, 1, 1, 1, 1, 1, 1, **C$_3$**: 453, 347, 49, 9, 8, 8, 8, 7, 6, 6, 6, 6, 6, 5, 5, 5, 4, 4, 3, 3, 3, 3, 3, 2, 2, 2, 1, 1, 1, 1, **C$_4$**: 349, 335, 220, 10, 10, 9, 9, 7, 7, 6, 6, 5, 5, 5, 5, 4, 4, 4, 4, 3, 3, 3, 3, 2, 2, 1, 1, 1, 1, 1, 1, **C$_5$**: 396, 127, 10, 9, 9, 9, 8, 8, 7, 7, 6, 6, 6, 6, 6, 5, 4, 4, 3, 3, 2, 2, 1, 1, 1, 1], **HS$_2$[C$_1$**: 489, 280, 275, 10, 9, 9, 8, 8, 8, 8, 8, 7, 6, 4, 4, 4, 3, 3, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, **C$_2$**: 325, 275, 71, 10, 10, 9, 8, 8, 7, 7, 6, 6, 6, 6, 5, 5, 4, 4, 4, 3, 3, 3, 3, 2, 2, 1, 1, 1, 1, 1, **C$_3$**: 479, 61, 30, 10, 10, 9, 9, 8, 8, 7, 6, 6, 6, 5, 4, 4, 3, 3, 2, 2, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, **C$_4$**: 396, 127, 10, 9, 9, 9, 8, 8, 7, 7, 6, 6, 6, 6, 6, 5, 4, 4, 4, 3, 3, 2, 2, 2, 1, 1, 1, 1, **C$_5$**: 274, 272, 64, 10, 10, 10, 10, 9, 9, 8, 7, 6, 6, 6, 5, 5, 5, 4, 4, 3, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1], **HS$_3$[C$_1$**: 424, 387, 374, 10, 10, 10, 10, 9, 9, 9, 9, 8, 8, 8, 8, 6, 6, 5, 4, 4, 4, 3, 3, 2, 1, 1, 1, 1, **C$_2$**: 469, 248, 24, 10, 9, 9, 8, 8, 8, 7, 7, 7, 7, 6, 5, 5, 5, 4, 3, 3, 3, 3, 2, 2, 2, 1, 1, 1, 1, 1, 1, **C$_3$**: 468, 435, 419, 406, 376, 373, 367, 360, 356, 348, 339, 308, 277, 253, 246, 235, 225, 213, 195, 192, 189, 181, 166, 136, 129, 120, 104, 93, 77, 54, 50, 19, **C$_4$**: 497, 260, 242, 10, 8, 8, 7, 6, 6, 5, 5, 4, 4, 4, 4, 3, 3, 3, 3, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, **C$_5$**: 496, 61, 30, 9, 9, 8, 8, 8, 7, 7, 7, 7, 6, 6, 6, 5, 3, 3, 2, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1], **HS$_4$[C$_1$**: 499, 349, 302, 10, 10, 9, 8, 8, 8, 7, 7, 7, 6, 6, 6, 6, 5, 5, 4, 4, 4, 4, 4, 4, 3, 3, 2, 2, 1, 1, 1, 1, 1, 1, 1, **C$_2$**: 424, 387, 374, 10, 10, 10, 10, 9, 9, 9, 9, 8, 8, 8, 8, 6, 6, 5, 4, 4, 4, 3, 3, 2, 1, 1, 1, 1, **C$_3$**: 307, 113, 113, 113, 113, 113, 13, 13, 13, 13, 13, 13, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 2, 2, 2, **C$_4$**: 473, 374, 288, 10, 10, 10, 9, 8, 8, 7, 6, 6, 5, 5, 5, 4, 4, 3, 3, 3, 1, 1, 1, 1, **C$_5$**: 274, 123, 2, 2, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1], **HS$_5$[C$_1$**: 151, 134, 22, 10, 8, 8, 8, 8, 7, 7, 6, 6, 6, 5, 5, 5, 4, 4, 4, 3, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, **C$_2$**: 375, 372, 83, 10, 10, 10, 9, 8, 8, 8, 7, 7, 6, 6, 6, 5, 5, 4, 2, 2, 2, 1, 1, 1, 1, 1, 1, **C$_3$**: 386, 367, 161, 10, 10, 10, 9, 8, 8, 7, 7, 7, 6, 6, 6, 6, 5, 5, 4, 3, 3, 3, 3, 3, 3, 1, 1, 1, 1, 1, 1, **C$_4$**: 231, 128, 43, 9, 8, 8, 8, 8, 8, 7, 7, 7, 6, 6, 6, 5, 5, 5, 5, 4, 4, 2, 1, 1, 1, 1, 1, **C$_5$**: 122, 45, 14, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 6, 6, 6, 6, 6, 6, 6, 1, 1,], **HS$_6$[C$_1$**: 396, 127, 10, 9, 9, 9, 8, 8, 7, 7, 6, 6, 6, 6, 6, 5, 4, 4, 4, 3, 3, 2, 2, 2, 1, 1, 1, **C$_2$**: 275, 87, 10, 10, 10, 9, 9, 9, 7, 7, 7, 6, 6, 6, 6, 5, 5, 4, 3, 3, 3, 3, 2, 1, 1, 1, 1, **C$_3$**: 463, 388, 370, 10, 10, 10, 9, 8, 8, 8, 6, 6, 5, 5, 5, 4, 3, 2, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, **C$_4$**: 466, 220, 168, 10, 10, 10, 10, 8, 8, 8, 6, 5, 5, 5, 3, 3, 3, 2, 2, 2, 1, 1, 1, 1, 1, **C$_5$**: 423, 322, 248, 10, 9, 8, 7, 7, 7, 6, 6, 5, 5, 5, 4, 4, 3, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1,], **HS$_7$[C$_1$**: 232, 165, 12, 10, 10, 9, 9, 9, 8, 8, 7, 7, 7, 7, 7, 6, 5, 4, 4, 3, 3, 3, 3, 2, 2, 1, 1, 1, 1, 1, 1, 1, **C$_2$**: 470, 337, 94, 10, 9, 9, 9, 9, 9, 8, 8, 7, 7, 7, 5, 4, 4, 4, 4, 4, 3, 3, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, **C$_3$**: 491, 487, 481, 479, 474, 460, 447, 418, 389, 362, 344, 340, 313, 313, 309, 237, 207, 203, 199, 195, 181, 174, 154, 148, 146, 125, 108, 94, 82, 80, 68, 66, 58, 38, 22, 5, **C$_4$**: 374, 315, 88, 10, 10, 10, 10, 9, 9, 8, 7, 7, 7, 6, 6, 6, 6, 6, 6, 5, 5, 4, 4, 2, 2, 1, 1, 1, 1, **C$_5$**: 463, 388, 370, 10, 10, 9, 8, 8, 8, 6, 6, 5, 5, 5, 4, 3, 3, 2, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1,], **HS$_8$[C$_1$**: 499, 455, 454, 436, 412, 412, 372, 295, 244, 212, 184, 145, 145, 68, 64, 55, 53, 28, **C$_2$**: 491, 487, 481, 479, 474, 460, 447, 418, 389, 362, 344, 340, 313, 313, 309, 237, 207, 203, 199, 195, 181, 174, 154, 148, 146, 125, 108, 94, 82, 80, 68, 66, 58, 38, 22, 5, **C$_3$**: 386, 367, 161, 10, 10, 10, 10, 9, 8, 8, 7, 7, 7, 6, 6, 6, 5, 5, 4, 3, 3, 3, 3, 3, 1, 1, 1, 1, 1, 1, **C$_4$**: 463, 388, 370, 10, 10, 10, 9, 8, 8, 8, 6, 6, 5, 5, 5, 4, 3, 2, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, **C$_5$**: 325, 275, 71, 10, 10, 9, 8, 8, 7, 7, 6, 6, 6, 6, 5, 5, 4, 4, 4, 3, 3, 3, 3, 2, 2, 1, 1, 1, 1, 1,], **HS$_9$[C$_1$**: 487, 482, 467, 439, 418, 367, 347, 339, 315, 287, 262, 254, 252, 184, 165, 145, 142, 134, 10, **C$_2$**: 499, 455, 454, 436, 412, 412, 372, 295, 244, 212, 184, 145, 145, 68, 64, 55, 53, 28, **C$_3$**: 285, 280, 191, 10, 10, 9, 9, 9, 8, 8, 7, 6, 6, 6, 4, 4, 3, 3, 3, 3, 2, 1, 1, 1, 1, 1, 1, 1, **C$_4$**: 496, 61, 30, 9, 9, 8, 8, 8, 7, 7, 7, 7, 6, 6, 6, 5, 3, 3, 2, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, **C$_5$**: 17, 17, 17, 13, 13, 13, 13, 13, 13, 13, 13, 13, 13, 13, 13, 13, 13, 12, 12, 12, 12, 12, 12, 12, 12, 12, 12, 12, 12, 12,], **HS$_{10}$[C$_1$**: 374, 315, 88, 10, 10, 10, 10, 9, 9, 8, 7, 7, 7, 6, 6, 6, 6, 6, 5, 5, 4, 4, 2, 2, 1, 1, 1, **C$_2$**: 375, 372, 83, 10, 10, 10, 9, 8, 8, 8, 7, 7, 6, 6, 6, 5, 5, 4, 2, 2, 2, 1, 1, 1, 1, 1, 1, **C$_3$**: 307, 113, 113, 113, 113, 113, 13, 13, 13, 13, 13, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 7, 2, 2, 2, **C$_4$**: 396, 127, 10, 9, 9, 9, 8, 8, 7, 7, 6, 6, 6, 6, 6, 5, 4, 4, 4, 3, 3, 2, 2, 2, 1, 1, 1, **C$_5$**: 479, 61, 30, 10, 10, 9, 9, 8, 8, 7, 6, 6, 6, 5, 4, 4, 3, 3, 2, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1,], **HS$_{11}$[C$_1$**: 217, 163, 14, 10, 9, 9, 9, 8, 8, 7, 6, 6, 6, 5, 5, 5, 4, 4, 3, 2, 2, 2, 1, 1, 1, 1, 1, 1, **C$_2$**: 375, 372, 83, 10, 10, 10, 9, 8, 8, 8, 7, 7, 7, 6, 6, 6, 5, 5, 4, 2, 2, 2, 2, 1, 1, 1, 1, 1, **C$_3$**: 499, 349, 302, 10, 10, 9, 8, 8, 8, 7, 7, 6, 6, 6, 6, 5, 5, 4, 4, 4, 4, 4, 3, 2, 2, 1, 1, 1, 1, 1, 1, **C$_4$**: 231, 128, 43, 9, 8, 8, 8, 8, 8, 7, 7, 7, 7, 6, 6, 6, 5, 5, 5, 5, 5, 4, 4, 2, 1, 1, 1, 1, 1, **C$_5$**: 424, 387, 374, 10, 10, 10, 10, 9, 9, 9, 9, 8, 8, 8, 8, 6, 6, 5, 4, 4, 4, 3, 3, 2, 1, 1, 1, 1,], **HS$_{12}$[C$_1$**: 423, 322, 248, 10, 9, 8, 7, 7, 7, 6, 6, 5, 5, 5, 4, 4, 3, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1, 1, 1, **C$_2$**: 459, 412, 298, 10, 10, 9, 9, 8, 8, 8, 6, 6, 4, 4, 4, 4, 3, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, 1, **C$_3$**: 489, 280, 275, 10, 9, 9, 8, 8, 8, 8, 8, 7, 6, 4, 4, 4, 4, 3, 3, 2, 2, 2, 2, 1, 1, 1, 1, 1, 1, **C$_4$**: 424, 387, 374, 10, 10, 10, 10, 9, 9, 9, 9, 8, 8, 8, 8, 6, 6, 5, 4, 4, 4, 3, 3, 2, 1, 1, 1, 1, **C$_5$**: 17, 17, 17, 13, 13, 13, 13, 13, 13, 13, 13, 13, 13, 13, 13, 13, 12, 12, 12, 12, 12, 12, 12, 12, 12, 12, 12, 12,]]

Table A2. Ecological data set.

C_1: 0.15, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.01, 0.01, 0.01, 0.01, 0.01, C_2: 0.375, 0.15, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.01, C_3: 0.625, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.01, 0.01, 0.01, C_4: 0.625, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_5: 0.375, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_6: 0.625, 0.15, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, 0.01, 0.01, 0.01, 0.01, C_7: 0.375, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, C_8: 0.375, 0.15, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, C_9: 0.625, 0.15, 0.15, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, C_{10}: 0.625, 0.15, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, C_{11}: 0.625, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, C_{12}: 0.625, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{13}: 0.625, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{14}: 0.375, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, C_{15}: 0.625, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, C_{16}: 0.375, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, 0.01, C_{17}: 0.15, 0.15, 0.15, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{18}: 0.15, 0.15, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, 0.01, 0.01, 0.01, 0.01, 0.01, 0.01, 0.01, C_{19}: 0.375, 0.375, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, 0.01, C_{20}: 0.375, 0.15, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, C_{21}: 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, C_{22}: 0.375, 0.15, 0.15, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, C_{23}: 0.375, 0.15, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, C_{24}: 0.625, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{25}: 0.375, 0.15, 0.15, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, C_{26}: 0.375, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, C_{27}: 0.375, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, C_{28}: 0.375, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{29}: 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, C_{30}: 0.625, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, 0.01, 0.01, 0.01, C_{31}: 0.375, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, 0.01, 0.01, 0.01, 0.01, 0.01, C_{32}: 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{33}: 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{34}: 0.375, 0.375, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{35}: 0.625, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{36}: 0.625, 0.15, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{37}: 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{38}: 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{39}: 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{40}: 0.375, 0.15, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{41}: 0.625, 0.15, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{42}: 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{43}: 0.15, 0.15, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{44}: 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, C_{45}: 0.375, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{46}: 0.375, 0.375, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{47}: 0.625, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{48}: 0.375, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, C_{49}: 0.375, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, C_{50}: 0.375, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, C_{51}: 0.375, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, C_{52}: 0.625, 0.15, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, 0.01, 0.01, 0.01, 0.01, C_{53}: 0.375, 0.15, 0.15, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, C_{54}: 0.375, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{55}: 0.15, 0.15, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{56}: 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{57}: 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{58}: 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{59}: 0.375, 0.15, 0.15, 0.15, 0.15, 0.15, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{60}: 0.15, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, C_{61}: 0.15, 0.15, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{62}: 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{63}: 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{64}: 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{65}: 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{66}: 0.375, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{67}: 0.375, 0.375, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{68}: 0.375, 0.15, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{69}: 0.375, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{70}: 0.375, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02,

Table A2.(continuation)   Ecological data set.

C_{71}: 0.15, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{72}: 0.625, 0.15, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, C_{73}: 0.375, 0.15, 0.15, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{74}: 0.625, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{75}: 0.375, 0.375, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{76}: 0.15, 0.15, 0.15, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{77}: 0.375, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, 0.01, C_{78}: 0.375, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, 0.01, 0.01, C_{79}: 0.625, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{80}: 0.375, 0.15, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{81}: 0.375, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, C_{82}: 0.375, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{83}: 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, C_{84}: 0.625, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, C_{85}: 0.375, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{86}: 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, C_{87}: 0.375, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{88}: 0.375, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{89}: 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{90}: 0.625, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, C_{91}: 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, C_{92}: 0.375, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{93}: 0.375, 0.15, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, C_{94}: 0.375, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, C_{95}: 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, C_{96}: 0.15, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, C_{97}: 0.15, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, C_{98}: 0.15, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, 0.01, 0.01, 0.01, 0.01, 0.01, C_{99}: 0.375, 0.15, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, 0.01, 0.01, 0.01, 0.01, 0.01, 0.01, C_{100}: 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.01, 0.01, C_{101}: 0.625, 0.15, 0.04, 0.04, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, C_{102}: 0.15, 0.15, 0.15, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, C_{103}: 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.01, C_{104}: 0.375, 0.04, 0.02, 0.02, 0.02, 0.02, 0.01, 0.01, 0.01, 0.01, 0.01, C_{105}: 0.15, 0.15, 0.04, 0.02, 0.02, 0.02, 0.01, 0.01, 0.01, 0.01, 0.01, 0.01, C_{106}: 0.15, 0.04, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.01, 0.01, C_{107}: 0.375, 0.15, 0.04, 0.04, 0.04, 0.02, 0.02, 0.02, 0.02, 0.02, 0.01