

Investigating the effects of distribution patterns on ecological indices of plant species in a simulated environment

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Abstract

Species diversity is a combination of species richness with species evenness. It helps us differentiate between communities or areas that have the same number of different species, but not in the same abundance. The spatial distribution pattern of plant species is an important topic in plant ecology, the assessment of which is an essential part of research into plant communities. This study aimed to investigate the differences between richness, diversity, and evenness indices obtained for random, uniform, and clumped distribution patterns. For this investigation, three plant distribution patterns were simulated and then random sampling was performed with 10 plots of the size 1 m² for each pattern, each with five repeats for greater accuracy. Finally, the number of species, the Margalef index, and the Menhinick index for richness, the Simpson index and the Shannon-Wiener index for diversity, and the Simpson index, the Shannon-Wiener index, and the Pielou index for evenness were computed and compared. The results of the analysis of variance showed a significant difference between richness, diversity, and evenness indices in different distribution patterns. Accordingly, Shannon-Wiener diversity is the best index when the management objective is more concerned with rare species. Also, Simpson's diversity, would be more appropriate where dominant species are more important.

Keywords: Simulation; Richness; Evenness; Diversity; R software

1. Introduction

Species diversity is one of the most important indicators of change in ecosystems and a major component of biodiversity. Species diversity is widely used in environmental assessment and vegetation studies as a straightforward measure of the condition of ecosystems (Soule, 1986; Magurran, 1988; Primack, 1993). Being a combination of species richness with species evenness (Duncan, 1991; Harrison *et al.*, 2004; Kindt and Coe, 2005; Mesdaghi, 2005; Gardener, 2014; Daly *et al.*, 2018), species diversity represents both the number of species and the abundance of each species that are present within a particular location or community (Speight, 2008). This definition helps us differentiate between communities or areas that have the same

number of different species, but not in the same abundance. First used by McIntosh in 1967, species richness is an older and simpler way to measure diversity. The effect of species richness on diversity is quite clear and it is said to be the simplest measure of diversity (Purvis and Hector, 2000; Gotelli and Chao, 2013) because when comparing two communities, the one with the larger number of species will be more diverse (Ejtehadi *et al.*, 2009). The term species richness simply refers to the number of different species in a given area and time period (Duncan, 1991; Goreaud *et al.*, 1997; Harrison *et al.*, 2004; Mesdaghi, 2005; Daly *et al.*, 2018). To determine species richness, one only has to create a list of species present in the area and count them (Omidzadeh *et al.*, 2014). Species richness can be used as a response variable in various types of analysis (Duncan, 1991). Two assumptions underlie the definition of richness (Marcon *et al.*, 2015). First that a classification of type exists and is known. If such a classification would not exist,

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any richness calculation would become difficult since it might not be clear to which class or taxon any particular individual belongs. The second assumption is that each class is equally distinct, so that no two classes are more or less similar than any others (Ogunseitan, 2005; Daly *et al.*, 2018). Another component of species diversity is evenness, which it represents the degree to which individuals are split among species with low values indicating that one or a few species dominate, and high values indicating that relatively equal numbers of individuals belong to each species (Morris, 2014). There are three terms for measuring diversity on the spatial scale: alpha, beta, and gamma. Alpha diversity is the intra-habitat diversity, which is defined as the mean number of species in a series of randomly selected samples in a habitat (McMurry, 2000). This study is focused on this type of diversity. Beta diversity or inter-habitat diversity shows the difference in species composition or changes in diversity from one habitat or community to another. Gamma diversity or regional diversity is diversity in a large unit or area or an entire landscape. Gamma diversity can be partitioned into alpha and beta components (Daly *et al.*, 2018).

To measure species diversity, one needs to sample the studied habitat or community. To do so, an appropriate number of plots with appropriate dimensions must be selected based on the distribution of species. There are various indices for measuring diversity, among which Shannon-Wiener and Simpson diversity indices are the most widely accepted and extensively used in ecological studies (Krebs, 1999).

The spatial distribution pattern of plant species is an important topic in plant ecology and the assessment of this distribution is an essential part of research into plant communities (Ludwig and Reynolds, 1988; Magurran, 1988; Dale, 1998; Malhado, 2004). A broad knowledge of the spatial distribution of plant species is a prerequisite for many vegetation studies, as it helps us choose the methods that are most accurate as well as convenient for measuring plants' quantitative characteristics such as canopy cover and density. The spatial distribution pattern refers to how individuals of one species are located relative to each other (Dale, 1998; Malhado, 2004). Plant distribution pattern assessments also play a key role in assessing evenness and unevenness of habitats, type of reproduction, competition, and behavioral patterns (selective and non-selective) and also determining which methods are most suitable for measuring each quantitative

characteristic (e.g. canopy cover, density, etc.) (Ludwig and Reynolds, 1988; Magurran, 1988; Buschini, 1999; Moghadam, 2003).

In nature, species generally have one of the following three distribution patterns: random, clumped, and uniform (Ludwig and Reynolds, 1988; Magurran, 1988; Dale, 1998; Malhado, 2004; Baddeley, 2008), and in each pattern, the presence of each individual is important (Baddeley, 2016; Gotelli, 2018). Random distribution patterns can appear in two forms, homogeneous and heterogeneous. A random distribution is said to be homogeneous if individuals are dispersed all over the studied area and is said to be heterogeneous if they are actually clustered in certain parts of the area. A clumped distribution is a heterogeneous random distribution where there is a strong interdependence between points close to each other. Essentially, distribution patterns represent the relative location of a group of data points or individuals over the studied domain. These points can be vegetation covers, animal nests, earthquake epicenters, flu outbreaks, etc. (Baddeley, 2008). These points may be distributed in a two-dimensional plane or a three-dimensional space and can have a temporal distribution as well as spatial distribution. In this study, distribution is two-dimensional and limited to the spatial domain.

As mentioned, plants generally have a random, clumped, or uniform distribution pattern, but these patterns are not equally frequent in nature. For example, it is uncommon to spot a uniform distribution in nature. Meanwhile, sampling of natural habitats requires dedicating significant time and costs. Therefore, In the present paper, we attempt to (1) simulate distribution patterns of plant species, and (2) analyze the relationship between different diversity indices in simulated spatial patterns.

2. Materials and Methods

2.1. Simulation of plant distribution patterns

This study was performed without field sampling and instead by using R software to simulate different situations in terms of the distribution of plant species. The study used the Vegan package for the analysis of plant communities and the Sp, Agricola, and Spatstat packages for the spatial analysis, including the creation, modification, and plotting of point distributions, exploratory data analysis, simulation of point process models, hypothesis

testing, and the preparation of residual plots (Baddeley, 2008). First, a 10×10 frame was created with the SP package, and the three plant distribution patterns were simulated inside it. For each plant distribution pattern, 10 sampling plots were defined and sampling was repeated 5 times.

2.1.1. Random distribution

To create a random distribution, 10 artificial species were defined and each was assigned a

letter (*a, b, c, d, e, f, g, h, i, j*) and a color. A total of 100 trees (10 per species) were defined with the random distribution as shown in Fig. 1. The 10 species were assigned to these 100 trees in a way that became the dominant species and *j* became the rare species. An image of the random distribution simulated in R software is illustrated in the following Fig. In this distribution, the location of each individual is independent of and unaffected by other individuals.

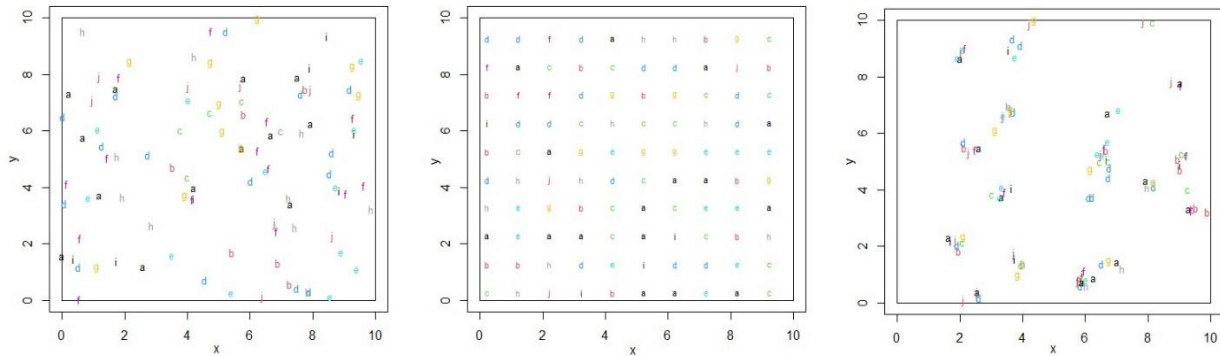


Fig. 1. Simulated plant distribution patterns (right=random, center=uniform, and left=clumped)

After randomly placing the 100 trees in the frame, the next step was to sample the generated population. This was done by placing 10 plots of

1 m² at random locations in the frame (Fig. 2). In this step, plots with different sizes (0.5, 1, 1.5, 2, 2.5, and 3 m²) were used.

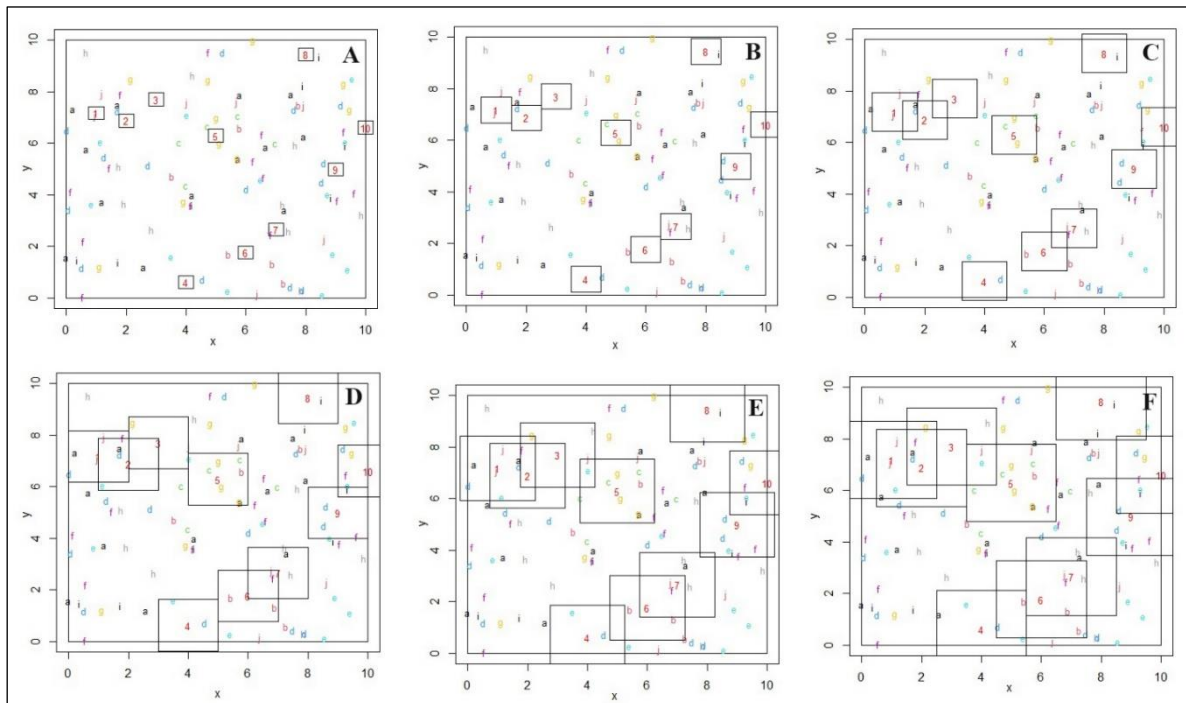


Fig. 2. Random sampling from the random distribution pattern with plots of different sizes. A=0.5; B=1; C=1.5; D=2; E=2.5; F=3m²

2.1.2. Uniform distribution

In this non-random distribution, each individual has its own domain and therefore all individuals are positioned at equal distances from each other. As mentioned, it is uncommon to observe this pattern in nature. To simulate a uniform distribution, the steps previously

described for random distribution were repeated, but this time the 100 trees were placed in the 10×10 frame at regular intervals (Fig. 1). As before, random sampling was performed with 10 plots. For this distribution pattern, too, sampling was performed with plots of different sizes (Fig. 3).

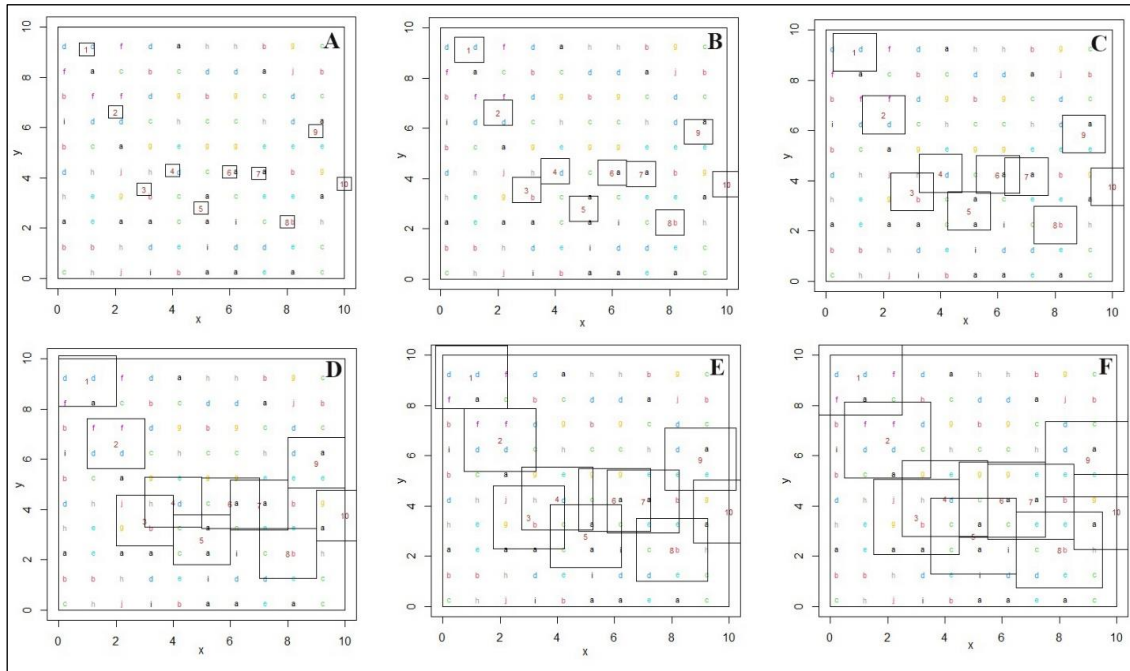


Fig. 3. Random sampling from the uniform distribution pattern with plots of different sizes. A=0.5; B=1; C=1.5; D=2; E=2.5; F=3m²

2.1.3. Clumped distribution

The other non-random distribution is the clumped distribution, which represents the clustering of individuals in more desirable parts of the study area. In this distribution, individuals tend to be present in specific parts of the environment (Fig.1). The spatstat package provides several functions for creating clumped distribution, including rThomas, rMatClust, rVarGamma, and rNeymanScott. In this study, the rThomas function was used for this purpose. The location of random points and sampling plots were determined in the same way as explained earlier. For this distribution, too, sampling was done with 10 plots of different areas (Fig. 4).

2.2. Determination of richness, evenness, and diversity indices for the three distribution patterns

In this step, the goal was to compare the indices of the three distribution patterns with

each other. To compare the richness indices, first, rarefaction had to be performed. Rarefaction is a statistical method for estimating the number of species required in a random sample taken from individuals in a group (Kindt and Coe, 2005). In other words, the frequency of data should be adjusted based on the minimum frequency. Then, the normality of the data was tested. In this study, species richness was measured by three indices, namely the number of species, the Margalef index, and the Menhinick index, diversity was measured by two indices, namely the Simpson index and the Shannon-Wiener index, and evenness was measured by three indices, namely the Simpson index, the Shannon-Wiener index, and the Pielou index. As previously explained, 10 random sampling plots were used for each distribution pattern and sampling was repeated five times to improved accuracy. The results of the Friedman test, the formula of the indices, and the values obtained for these indices for each distribution are given in Table 4 the indices were computed using the Vegan package, where

species richness and species diversity are computed by the specnumber function and the diversity function respectively.

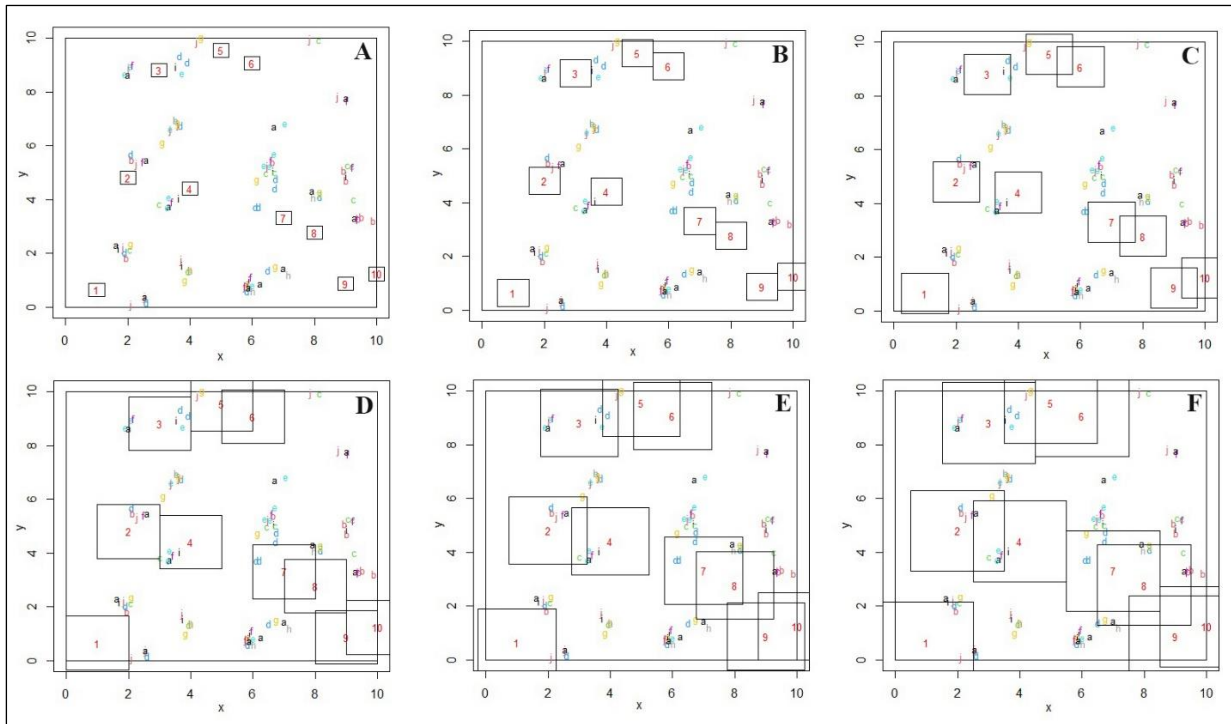


Fig.4. Random sampling from the clumped distribution pattern with plots of different sizes. A=0.5; B=1; C=1.5; D=2; E=2.5; F=3m²

3. Results

3.1. Relationship between the number of species and sampling area

Using a greater sampling area will result in having more species inside the plot. The

relationship between the area of the sampling plot and the number of species is illustrated in Fig. 5. In this Fig, it can be seen that as the number of sampling plots increases, so does the number of species observed in all three distribution patterns.

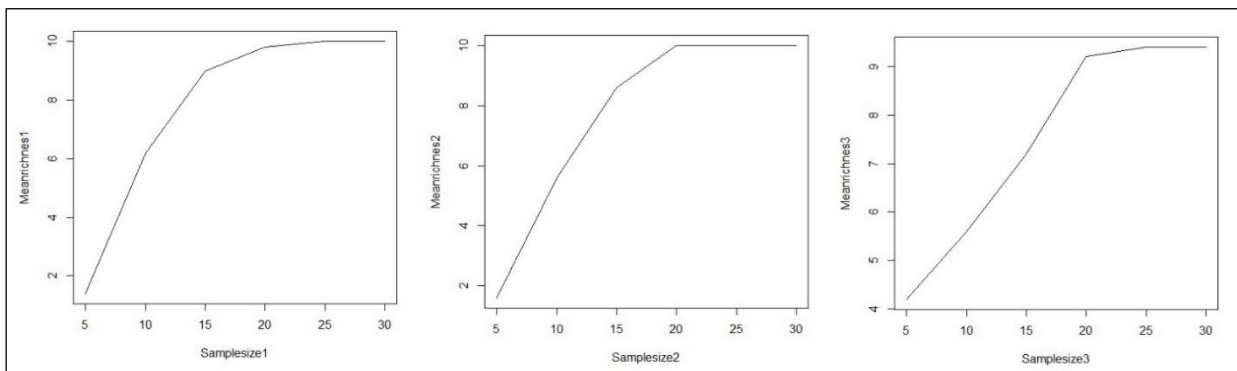


Fig. 5. Relationship between sampling area and species richness in different distribution patterns (right= random, center=clumped, left=uniform)

The results related to the species observed in the plot and their abundance are presented in Tables 1, 2, and 3. It should be noted that the frequency of species and other richness, diversity, and evenness indices were calculated only for 1m² plots, and the calculations done and

the diagrams drawn for other plots only intend to demonstrate the relationship between the area of the plot and the species.

Finally, the supply command was executed to determine the richness of all species and their abundance. Then, the richness and abundance of

species were calculated. In Tables 1, 2, and 3, species abundance was obtained from the sum of row values (rowSums) and species richness was

obtained from the sum of column values (colSums).

Table 1. Number of species and their abundance in the sampling plots for the random distribution

Species Plot No.	a	b	c	d	e	f	g	h	i	j	sum
Q1	0	0	0	0	0	0	0	1	0	0	1
Q2	0	0	0	0	0	0	0	0	0	0	0
Q3	0	0	0	0	0	0	0	0	0	0	0
Q4	0	0	0	0	0	0	0	0	0	0	0
Q5	0	0	1	0	0	0	0	0	0	0	1
Q6	0	0	1	0	0	0	0	0	0	0	1
Q7	0	0	0	0	1	0	1	0	0	0	2
Q8	0	0	1	0	0	0	0	0	0	0	1
Q9	0	0	1	1	0	0	0	0	0	0	2
Q10	0	0	0	0	0	1	0	0	0	0	1
sum	0	0	4	1	1	1	1	1	0	0	----

Table 2. Number of species and their abundance in the sampling plots for the uniform distribution

Species Plot No.	a	b	c	d	e	f	g	h	i	j	sum
Q1	0	0	0	0	0	0	1	0	0	0	1
Q2	0	0	0	0	1	0	0	0	0	0	1
Q3	0	0	0	0	0	0	0	0	0	1	1
Q4	0	0	0	0	1	0	0	0	0	0	1
Q5	0	1	0	0	0	0	0	0	0	0	1
Q6	0	0	0	0	0	0	0	1	0	0	1
Q7	0	0	0	1	0	0	0	0	0	0	1
Q8	0	0	1	0	0	0	0	0	0	0	1
Q9	0	0	1	0	0	0	0	0	0	0	1
Q10	0	0	0	0	0	0	0	0	0	0	0
sum	0	1	2	1	2	0	1	1	0	1	----

Table 3. Number of species and their abundance in the sampling plots for the clumped distribution

Species Plot No.	a	b	c	d	e	f	g	h	i	j	sum
Q1	0	0	0	0	0	0	0	0	0	0	0
Q2	0	0	0	0	0	0	0	0	0	0	0
Q3	0	0	0	0	0	0	0	0	0	0	0
Q4	0	0	0	0	0	0	0	0	0	0	0
Q5	0	0	0	0	0	0	0	0	0	0	0
Q6	0	0	0	0	0	0	0	0	0	0	0
Q7	0	0	0	0	1	0	0	0	1	0	2
Q8	0	0	0	0	0	0	0	0	0	0	0
Q9	0	0	0	0	0	0	0	0	0	0	0
Q10	0	0	0	0	0	0	0	0	0	0	0
sum	0	0	0	0	1	0	0	0	1	0	----

3.2. Normality test and statistical comparison of indices

After the rarefaction of data, their normality was tested and the boxplots for the three richness indices were drawn (Fig. 6). In this step, Bartlett's test for the homogeneity of variances was also performed. There are several functions including qqnorm and shapiro.test for testing the normality of data. In this study, shapiro.test and boxplot were used for this purpose. Considering the box plots and the heterogeneity of variances, it was concluded that the data related to the richness index are not normal ($p < 0.05$) and therefore a non-parametric statistics should be used for statistical comparison. The non-parametric statistical method chosen for this

purpose was the Friedman test. In this study, the statistical comparison of indices was performed using the agricolae package (De Mendiburu, 2009).

The statistical comparison of richness indices showed significant differences between richness indices computed for each distribution pattern ($p < 0.05$). Naturally, the richness indices obtained for the clumped distribution pattern can be expected to vary from those obtained for the random and uniform distribution pattern. This is because, in the random sampling of the clumped distribution pattern, the sampling plot may be placed right on a cluster, leading to overestimation of richness, or may be placed far away from any cluster, leading to underestimation of species richness.

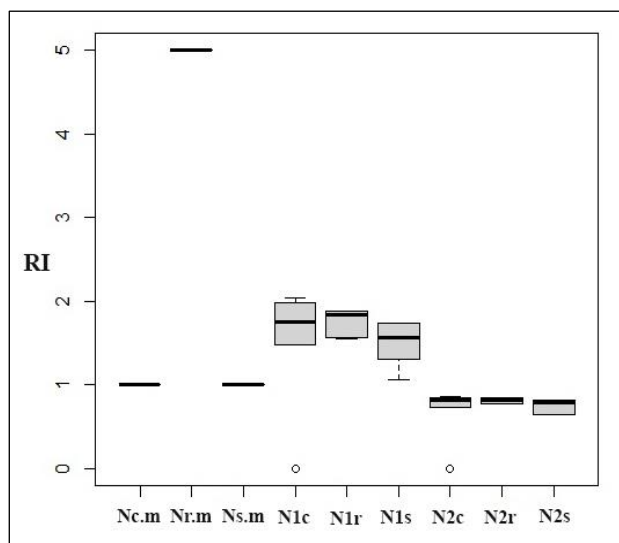


Fig. 6. Boxplots of richness indices divided by plots and distribution pattern. RI= richness index, Nc.m= the number of species in clumped distribution, Nr.m= the number of species in random distribution, Ns.m= the number of species in uniform distribution, N1c= Margalef index in clumped distribution, N1r= Margalef index in random distribution, N1s= Margalef index in uniform distribution, N2c= Menhinick index in clumped distribution, N2r= Menhinick index in random distribution, N2s= Menhinick index in uniform distribution

For the diversity indices, again the boxplots of the indices for all three distribution patterns were drawn and the normality of the data was investigated (Fig. 7). Here, too, the obtained box plots and the heterogeneity of variances showed

that the data related to the diversity indices are not normal ($p < 0.05$). Therefore, these indices were also compared using the Friedman test, which is a non-parametric test for randomized complete block design (De Mendiburu, 2009).

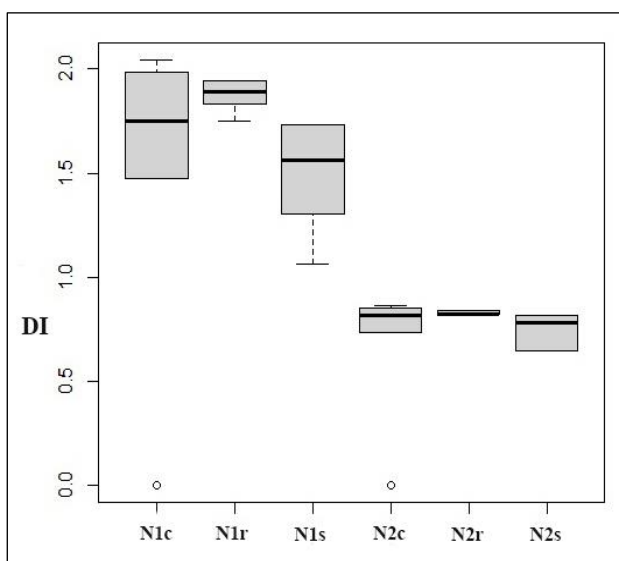


Fig.7. Boxplots of diversity indices divided by plots and distribution pattern. DI= diversity index, N1c=Shannon index in clumped distribution, N1r= Shannon index in random distribution, N1s= Shannon index in uniform distribution, N2c= Simpson index in clumped distribution, N2r= Simpson index in random distribution, N2s= Simpson index in uniform distribution

After running the commands in R software for the statistical comparison of indices, the results of the Friedman test showed significant differences between diversity indices of the three distribution patterns ($p < 0.05$). This means that the distribution pattern has a significant effect on the choice of diversity indices. As shown in

Table 4, the values obtained for the Simpson diversity index are close to 1, which is indicative of high species diversity in the area.

The next statistical comparison was for evenness indices. Similar to the steps followed for diversity indices, first the normality of the data and their boxplot were investigated (Fig. 8).

As shown in Fig. 8, the boxplots showed heterogeneity and the existence of outliers and the normality test showed that the data are not normal ($p < 0.05$). Hence, again the non-parametric Friedman test was used to compare

the evenness indices. As Table 4 illustrates, like diversity indices, evenness indices also showed significant differences, which means they are significantly influenced by the distribution pattern.

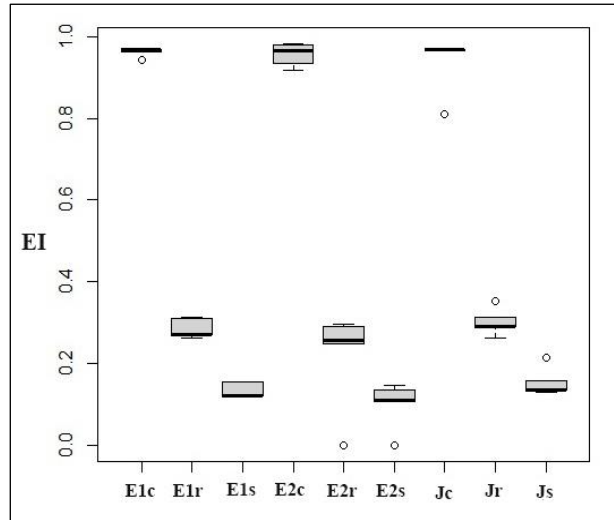


Fig. 8. Boxplots of evenness indices divided by plots and distribution pattern. EI= evenness index, E1c=Shannon index in clumped distribution, E1r= Shannon index in random distribution, E1s= Shannon index in uniform distribution, E2c= Simpson index in clumped distribution, E2r= Simpson index in random distribution, E2s= Simpson index in uniform distribution, Jc= Pielou index in clumped distribution, Jr= Pielou index in random distribution, Js= Pielou index in uniform distribution

Table 4. Values of richness, diversity, and evenness indices for the random, clumped, uniform distribution patterns.

P-value	The value of the index in each sampling	Distribution pattern	Formula	Index	Reference
Richness					
*0.013	7-5-7-5-7	Random Clumped Regular	$N_0 = S$	Species diversity	Mesdaghi 2005
	1-5-8-8-6				
	3-5-5-6-6				
	2.23- 2.60- 2.60- 2.05- 2.60		$\frac{s-1}{\ln N}$	Margalef	Margalef 1958
	0- 2.05- 2.47- 3.18- 2.56				
	0.91- 1.82- 1.92- 2.27- 2.27				
	2.1- 1.88- 2.21- 2.04- 2.21				
1-1.88- 1.94- 2.66- 2.66					
1-1.66-1.76-2-2	$\frac{s}{\sqrt{N}}$	Menhenic	Menhenic 1964		
Diversity					
*0.005	0.82- 0.77- 0.84- 0.77- 0.84	Random Clumped Regular	$1-D=1-\sum_{i=1}^s p_i^2$	Simpson	Simpson 1949
	0- 0.73- 0.85- 0.86- 0.81				
	0.64- 0.64- 0.78- 0.81- 0.81		$H = -\sum_{i=1}^s (p_i \ln p_i)$	Shannon-Wiener	Shannon & Weaver, 1949
	1.83- 1.54- 1.88- 1.56- 1.88				
	0- 1.47- 1.98- 2.04- 1.74				
1.06- 1.30- 1.55- 1.73- 1.73					
Evenness					
1.554e ^{-8*}	0.79- 0.89- 0.89- 0.90- 0.89	Random Clumped Regular	$E = \frac{1/D}{s}$	Simpson	Simpson 1949
	1- 0.75- 0.84- 0.92- 0.90				
	0.93- 0.55- 0.91- 0.90- 0.90		$J = \frac{\sum_{i=1}^s (p_i \ln p_i)}{\ln s}$	Shannon Wiener	Shannon & Weaver, 1949
	0.89- 0.94- 0.94- 0.95- 0.94				
	1- 0.87- 0.91- 0.96- 0.95				
	0.96- 0.73- 0.95- 0.94- 0.94				
	0.94- 0.96- 0.96- 0.96- 0.96				
	0- 0.91- 0.95- 0.98- 0.97				
0.95- 0.80- 0.96- 0.96- 0.96	$E = H' / \ln(s)$	Pielou	Pielou 1975		

4. Discussion and Conclusion

This study tried to compare multiple indices of diversity, richness, and evenness in three distribution patterns and with different plot sizes. As the results show (Table 4), the values obtained for Simpson and Shannon-Wiener indices indicated high species diversity. The study found significant differences between the values of diversity, richness, and evenness indices, which shows that the distribution pattern has an impact on the estimation of these indices. This is consistent with the results of Lepretre (1999), Eshaghi *et al.* (2009), Jahantab *et al.* (2010), Bahmany *et al.* (2013), Bidarnamani (2019), Talal and Santelmann (2019), and Heidari and Bayat (2019), which reported a significant difference between the studied indices (Mouillot and Lepretre, 1999; Eshaghi *et al.*, 2009; Jahantab *et al.*, 2010; Bahmany *et al.*, 2014; Bidarnamani and shabanipour, 2019; Heidari and Bayat, 2019; Talal and Santelmann, 2019). Morris *et al.* (2014) tested several diversity indices in a range of simple to complex statistical analyses in order to determine whether some were better suited for certain analyses than others. The researchers concluded if dominant species are expected to be more important, then Simpson's diversity, Simpson's dominance would be more appropriate. Shannon's diversity could be used in situations where rare and abundant species are expected to be equally important. Comparison of a few carefully chosen indices could greatly enhance understanding of the complex components driving diversity (Morris *et al.*, 2014).

However, it is inconsistent with the results of other studies including Kooch *et al.* (2010) and Omidzadeh *et al.* (2013). This is because these two studies have only used 1m² sampling plots, which has led to using similar samples for different indices.

The results of this study suggest that the investigated indices are all sensitive to the distribution pattern of species. In general, the highest richness and diversity values were obtained for the random distribution pattern (Table 4). The mean value of the Simpson diversity index for the random distribution pattern was 0.80, which is quite high (this index can vary from 0 to 1) and indicates higher diversity compared to clumped and uniform distribution patterns. In some other studies, too, the values obtained for this index were as high as 0.86 and 0.85 (Kindt and Coe, 2005). In the present study, the mean value of the Shannon-Wiener index for the random distribution pattern was 1.73 (this index can vary from 0 to 3.5). For

this index, too, the diversity value obtained for the random distribution pattern was higher than the one obtained for the two other distribution patterns. This is because, in the random distribution, species may concentrate in one area, which if captured by a sampling plot, will lead to a significant overestimation of species in that sample (Baddeley, 2008). In this study, a simulation tool was used to investigate how different richness, evenness, and diversity indices can be influenced by the distribution of species, which could be an example of how this can be done for plant species in natural habitats. For natural habitats, after determining the coordinates of each plant by GPS, one can draw the distribution map of plant species in R software, choose the appropriate sampling method (random, systematic, or a combination of both), and continue the rest of the data analysis process in the software.

The novelty of this study was in the use of extensively repeated sampling and drawing all three distribution patterns i.e. uniform, random, and clumped. It should be noted that although the uniform distribution is rarely seen in natural landscapes, it is possible to simulate this distribution pattern in software. Also, the sheer size of many natural habitats makes it extremely expensive, time-consuming, and sometimes impossible to survey the whole area, whereas, in this study, the study area was a 10×10 m² frame and sampling could be done by executing sampling commands with sampling plots of any size and even using rectangular plots and also using other non-random sampling methods. The results of this study showed that the pattern of distribution and abundance of species has an impact on the values of the studied indices. The vast number and variety of available diversity indices allows researchers to be flexible in their choice of index, with the key stipulation that the underlying definition of the index should first be considered carefully to ensure that it is appropriate for the particular application, and will not lead to misinterpretations. To avoid confusion and misinterpretation, researchers should first define their objectives and then choose the appropriate indices for the specific problem (Daly *et al.*, 2018). Considering that the studied indices are sensitive to the distribution pattern, the suitable index can be chosen based on the species present in the region (dominant and rare species). For example, if the management objective is focused on the dominant species, it is recommended to use the Simpson index, but if the management objective is more concerned with rare species, it is better to use the Shannon-Wiener index.

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