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A New Species Richness Measure Improved from Margalef and Menhinick Indices

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Highlights

- A new species richness calculator was proposed as an alternative to Margalef and Menhinick indices.
- Results indicated that the proposed estimator presented better performance.
- New estimator likely yields lower values if species vastly outnumber individuals.

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Abstract

In the present study, a new estimator $\left({}^{\alpha^*}D_{MM}\right)$ is proposed to measure species richness. Its' essential inputs are alfa (α) scale parameters of Margalef (D_{MG}) and Menhinick (D_{MN}) indices. To evaluate the performance of ${}^{\alpha^*}D_{MM}$, both hypothetical and natural community datasets were used. The computations were performed using a spreadsheet program created for ${}^{\alpha^*}D_{MM}$. The new proposed estimator is also integrated into the BİÇEB software. According to estimation results, ${}^{\alpha^*}D_{MM}$ seems to be a better form rather than D_{MG} and D_{MN}. Therefore it may be employed for comparing species richness of the natural communities. To better understand the performance of ${}^{\alpha^*}D_{MM}$, further studies should be generated using various types of real ecological data.

1. INTRODUCTION

Biodiversity plays a vital role for ecosystem productivity, stability, health and dynamism. It is therefore the main issue in conservation biology, environmental ecology and biogeography [1-2].

As stated by Peet 1974, biodiversity, in essence, has always been defined by using the measures. Various 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 [3]. To estimate species diversity using heterogeneity indices and species abundance models, the main inputs are the number of species and their abundance or incidence data. Among those measures, Shannon entropy [4], Simpson diversity index [5] and log-normal [6] are the most popular ones.

In comparison with heterogeneity indices and species abundance models, species richness indices have simpler forms. The core members of species richness indices are species richness (S) [7], Woodwell index (R_W) [8], Menhinick index (D_{MN}) [9] and Margalef index (D_{MG}) [10], a small modification of Odum index (R_o) [11]. Those indices estimate species richness without using species abundance or incidence data. Among them, the oldest, simplest and still most commonly used measure is species richness (S). It refers to the number of species present in an area or an assemblage without regard to number of individuals [3]. Unlike S, the other richness indices $(R_W, D_{MN}$ and $D_{MG})$ assume that there is a relationship between S and total number of individuals (N). Even though R_W, D_{MN} and D_{MG} have the same structural characteristics,

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*Corresponding author, e-mail: serkanozdemir@isparta.edu.tr the importance degrees to N given by them are different. The weight of N is equal to N in R_w whereas it corresponds to $\sqrt{N}$ in D_{MN} and, $\ln N$ in D_{MG} respectively.

R_w has been scarcely preferred in estimation of species richness. However, D_{MN} and D_{MG} have frequently used since they are intuitively much more favorable measures compared to R_w.

Regarding to D_{MN} and D_{MG}, there is no consensus about which one should be used to compare species richness. Therefore, researchers generally use both of those indices instead of selection one of them [12-17]. Nevertheless employment both of them may cause conflicting results in comparisons of species richness among communities. For instance, suppose that 2 communities, A and B. Community A includes 15 species and totally of 45 individuals and, Community B is composed of 20 species and 150 individuals. A is richer than B according to D_{MN} results $(D_{MN}(A) = 2.24, D_{MN}(B) = 1.63)$ whereas D_{MG} results indicate that B is richer than A $(D_{MG}(A) = 3.68, D_{MG}(B) = 3.79)$. As can be understood from this comparative example, selecting both of the indices or one of them is not a solution. The solution may be produced an index from both of them. To the best of our knowledge, there is no such an estimator produced or derived from D_{MN} or D_{MG} in the literature.

The present study offers a species richness measure derived from D_{MN} and D_{MG} and explains how to employ this measure in estimation of species richness using hypothetical and natural community data.

2. MATERIAL AND METHOD

As mentioned in the introduction, the following equations are the core members of species richness measures

$$S = \sum_{i=1}^{S} i^0 \tag{1}$$

$$D_{MG} = \frac{S-1}{\ln(N)} \tag{2}$$

$$D_{MN} = \frac{S}{\sqrt{N}} \tag{3}$$

$$R_w = S/N \tag{4}$$

where S, D_{MG}, D_{MN} and R_w are species richness [7], Margalef index [10], Menhinick index [9], and Woodwell index [8] respectively. In the equations, N represents total number of individuals.

By using a scale parameter (α) Equation (1), Equation (3) and Equation (4) can be combined into one formula $({}^{\alpha}DS)$.

$${}^{\alpha}DS = \frac{S}{N^{\alpha}},\ 1 \geq \alpha \geq 0 \tag{5}$$

Where the formula reduces $S\left(\frac{\sum_{i=1}^{S} i^0}{N^0}\right)$ at $\alpha = 0$, D_{MN} at $\alpha = 0.5$ $\left(\alpha_{D_{MN}} = 0.5\right)$ and R_w at $\alpha = 1$. Suppose that a community includes a total of 8 species $(S = 8)$ and 27 individuals $(N = 27)$. Equation (5) allows us to create a curve (Figure 1).

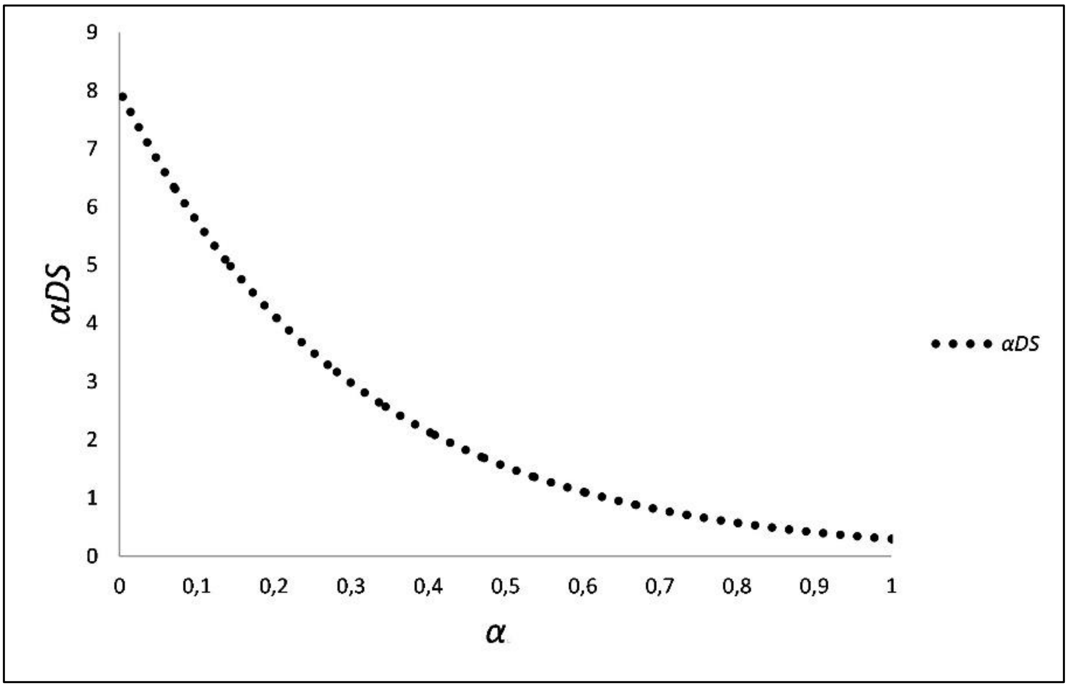


Figure 1. *The profile of* ${}^{\alpha}DS$ *for* $S = 8$ *and* $N = 27$ $(S = 8\ (\alpha = 0)$ *and* $R_w = 0.296\ (\alpha = 1))$

This curve may be called species richness profile. That is however not the issue focused on. The focal issue is related to D_{MG}. D_{MG} has not a fixed α value because it contains $\ln(N)$. Its α value $\left(\alpha_{D_{MG}}\right)$ generally changes from 0 to 0.5 depending on S and N values. Herein the value of D_{MG} (2.12) corresponds to $\alpha = 0.4024$ for $S = 8$ and $N = 27$ (Figure 2).

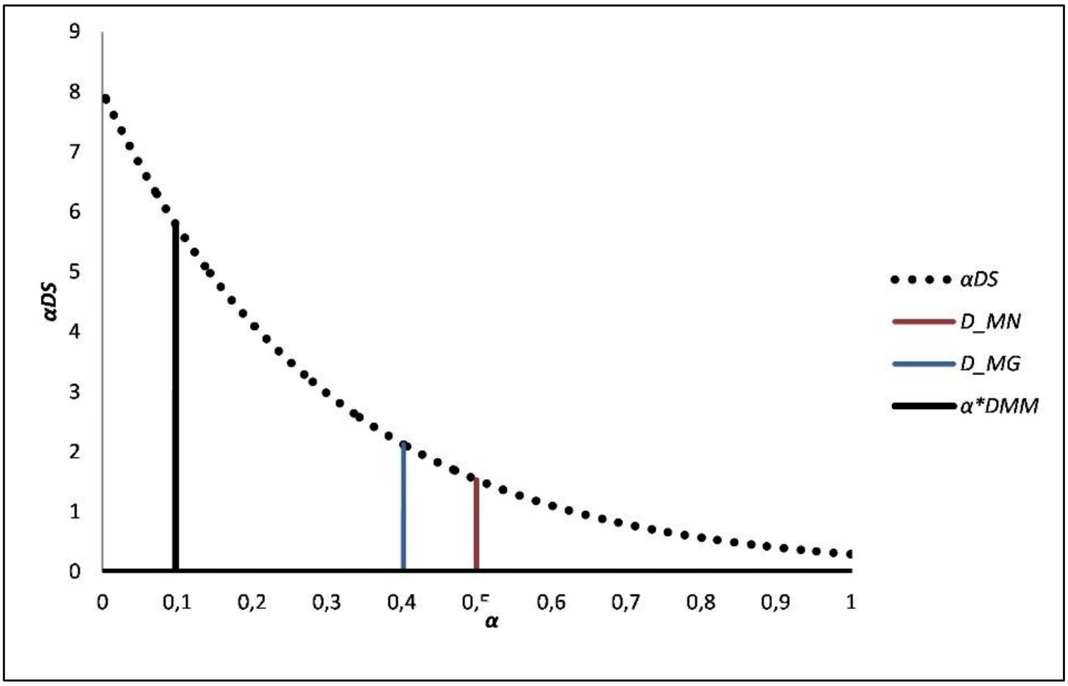


Figure 2. *The results of Margalef index* $\left(D_{MG} = 2.12,\ \alpha_{D_{MG}} = 0.4024\right)$, *Menhinick index* $\left(D_{MN} = 1.54,\ \alpha_{D_{MN}} = 0.5\right)$ *and the proposed estimator* $\left({}^{\alpha^*}D_{MM} = 5.80,\ \alpha^* = 0.0976\right)$ *for* $S = 8$ *and* $N = 27$

The proposed estimator $\left({}^{\alpha^*}D_{MM}\right)$ is based on α values of D_{MN} and D_{MG}

$$ {}^{\alpha^*}D_{MM} = c_{2S}\frac{S}{N^{\alpha*}} \tag{6} $$

where,

$$ \alpha^* = \alpha_{D_{MN}} - \alpha_{D_{MG}}c_{1S} = 0.5 - \alpha_{D_{MG}}c_{1S} \ . \tag{7} $$

c_{1S} and c_{2S} are the correction coefficients. c_{2S} gets the fixed values which are 1, 1.208, 1.258, 1.202, 1.150, 1.080 and 1.016 from $S = 1$ to $S = 7$. The fixed values of c_{1S} are 0.4, 0.42, 0.54, 0.7, 0.8, 0.9 and 0.98 from $S = 1$ to 7. If $S > 7$, then $c_{2S} = c_{1S} = 1$. Note that if there is only one species and one individual in a community($S = N = 1$), it is assumed that ${}^{\alpha^*}D_{MM} = 1$. That constraint is due to D_{MG} numerator (If $S = 1$, $S - 1 = 0$). For $S = 8$ and $N = 27$, all the computed values are given in Figure 2. A dataset composed of 10 hypothetical communities was created and used to evaluate the performance of the proposed estimator (Table 1).

Table 1. *S and N values of the hypothetical communities*

Communities	C_1	C_2	C_3	C_4	C_5	C_6	C_7	C_8	C_9	C_{10}
S	15	15	15	15	20	20	20	20	15	25
N	15	30	45	930	20	150	1800	70000	20	150

The natural community data obtained from the Sütçüler District of Isparta province in the Mediterranean Region were used to evaluate the new proposed estimator [18]. In the mentioned study, plant cover data were recorded using Braun-Blanquet cover-abundance scale. Then, the plant cover data were transformed according to Westhoff and Maarel [19] so that each corresponding to a value between 1 and 9. Estimations were performed for the data obtained from 10 sample areas. S, N and the transformed values are given in Table 2. As can be seen in Table 2, a total of 26 taxa were observed in 10 sample plots.

Table 2. *Transformed abundance values of natural community data*

	rC_1	rC_2	rC_3	rC_4	rC_5	rC_6	rC_7	rC_8	rC_9	rC_{10}
Berberis crataegina DC.	3	3	0	0	0	0	0	2	1	2
Cistus salviifolius L.	2	2	5	3	2	3	1	3	3	5
Colutea cilicica Boiss. & Balansa	0	0	2	2	0	0	0	0	0	0
Crataegus orientalis Pallas ex Bieb.	3	2	0	0	0	0	0	0	0	0
Daphne gnidioides Jaub. & Spach	0	0	0	2	0	0	0	0	0	0
Daphne sericea Vahl.	0	0	3	3	2	2	2	3	3	0
Fontanesia phillyreoides Labill.	0	0	1	2	3	3	2	2	0	0
Jasminium fructicans L.	0	0	1	2	2	2	0	0	2	2
Juniperus excelsa Bieb.	0	0	0	0	0	0	5	5	7	5
Juniperus oxycedrus L.	2	1	5	5	5	3	0	0	0	0
Origanum minutiflorum Schwrd et Davis.	0	2	0	0	0	0	0	0	0	0
Origanum onites L.	0	0	0	0	0	0	0	0	0	0
Osyris alba L.	0	0	0	0	0	0	1	0	0	0
Paliurus spina-christi Mill.	0	0	0	0	0	0	0	0	0	0
Phillyrea latifolia L.	0	0	5	5	5	5	5	5	5	5
Phlomis grandiflora H.S. Thompson.	0	0	0	0	0	0	0	0	0	2
Pinus brutia var. *brutia* Ten.	0	0	7	7	5	7	8	7	5	5
Pinus nigra J.F.Arnold	8	8	0	0	0	0	0	0	0	0
Pistacia terebinthus L.	0	0	3	2	3	2	5	5	5	5
Quercus cercis L.	2	2	0	0	1	2	0	0	0	0
Quercus coccifera L.	0	0	8	5	5	5	7	7	3	5
Rosa canina L.	2	3	0	0	0	0	0	0	0	0
Ruscus aculeatus L.	0	0	0	0	1	2	0	0	0	0
Styrax officinalis L.	0	0	1	0	0	3	3	3	0	2
Teucrium chamaedrys L.	0	0	0	0	0	0	0	0	0	0
Teucrium polium L.	0	0	2	1	0	2	0	0	0	0

3. RESULTS AND DISCUSSION

As can be seen in Table 1, the first four communities $(C_1: C_4)$ have the same S value $(S = 15)$ but different N values changing from 15 to 930. From C_1 to C_4, with decreasing D_{MN} and D_{MG}, ${}^{\alpha^*}D_{MM}$ decreases. D_{MN}, D_{MG} and ${}^{\alpha^*}D_{MM}$ have similar trends from C_5 to C_8 since they have the same number of species $(S = 20)$ with different N values ranging from 20 to 70000. Parallel trends of D_{MN}, D_{MG} and ${}^{\alpha^*}D_{MM}$ are in line with expectation for a fixed S value agains changing N values. As a result of comparisons within group 1 $(C_1: C_4)$ and within group 2$(C_5: C_8)$, the difference of ${}^{\alpha^*}D_{MM}$ from D_{MN} and D_{MG} is invisible.

The difference of ${}^{\alpha^*}D_{MM}$ can however be understood by comparing C_9 with C_{10} and C_4 with C_7. C_{10} contains more species and much more individuals than C_9 (Table 3). According to D_{MN} results, C_9 is richer than C_{10}. However, D_{MG} results indicate that C_{10} is a richer community than C_9. As expected, the decision of ${}^{\alpha^*}D_{MM}$ is in favor of D_{MN} because the occurrence probability of the number of rare species in particular singletons is likely to be much bigger in C_9 rather than C_{10}.

Table 3. *The species richness results of hypothetical communities* $\left(\alpha_{D_{MN}} = 0.5\right)$

Communities	$\alpha_{D_{MG}}$	α^*	D_{MN}	D_{MG}	${}^{\alpha^*}D_{MM}$
C_1	0.3934	0.1066	3.8730	5.1698	11.2388
C_2	0.3802	0.1198	2.7386	4.1162	9.98003
C_3	0.3693	0.1307	2.2361	3.6778	9.12045
C_4	0.2913	0.2087	0.4919	2.0482	3.60221
C_5	0.3834	0.1166	4.4721	6.3424	14.1036
C_6	0.3319	0.1681	1.6330	3.7919	8.61448
C_7	0.2756	0.2244	0.4714	2.5348	3.72003
C_8	0.2208	0.2792	0.0756	1.7031	0.88773
C_9	0.3893	0.1107	3.3541	4.6733	10.7663
C_{10}	0.3298	0.1702	2.0412	4.7898	10.6554

When comparing C_4 to C_7, we see that there is no agreement between D_{MN} and D_{MG} once again. ${}^{\alpha^*}D_{MM}$ supports D_{MG} results this time. The decision of ${}^{\alpha^*}D_{MM}$ is intuitively accurate since both C_4 and C_7 have a great number of total individuals comparing to their number of species. This means that none of them is most likely to include a notable negative bias. Consequently, ${}^{\alpha^*}D_{MM}$ seems to reduce to the effect of negative bias originated from occurrences of rare species in a community. However, it does not mean that the results of ${}^{\alpha^*}D_{MM}$ correspond to true species richness because true species richness is equal or larger than the observed number of species.

S and N values estimated for the natural community data of 10 sample plots obtained from Sütçüler District are given in Table 3. To avoid confusion with the hypothetical data, the sample plots in the natural community data were named $rC_1 \ldots rC_{10}$ from 1 to 10.

Table 4. *S and N values of natural community data*

Communities	rC_1	rC_2	rC_3	rC_4	rC_5	rC_6	rC_7	rC_8	rC_9	rC_{10}
S	7	8	12	12	11	13	10	10	9	10
N	22	23	43	39	34	41	39	42	34	38

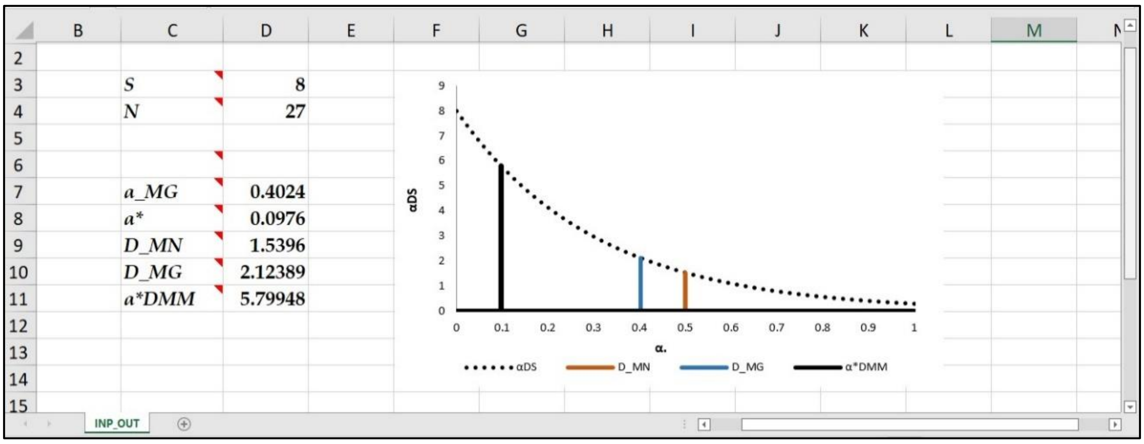
After obtaining S and N values, $\alpha_{D_{MG}}$, α^*, D_{MN}, D_{MG} and ${}^{\alpha^*}D_{MM}$ estimations were performed (Table 5).

Table 5. *The species richness results of natural community data* $\left(\alpha_{D_{MN}} = 0.5\right)$

Communities	$\alpha_{D_{MG}}$	α^*	D_{MN}	D_{MG}	${}^{\alpha^*}D_{MM}$
rC_1	0.415	1.4924	0.0933	1.941	5.3327
rC_2	0.4071	1.6681	0.0929	2.2325	5.9784
rC_3	0.3743	1.83	0.1247	2.9246	7.5074
rC_4	0.3782	1.9215	0.1218	3.0025	7.6805
rC_5	0.3844	1.8865	0.1156	2.8358	7.3173
rC_6	0.3749	2.0303	0.1251	3.2314	8.1693
rC_7	0.3832	1.6013	0.1168	2.4566	6.5187
rC_8	0.3809	1.543	0.1191	2.4008	6.4072
rC_9	0.3908	1.5435	0.1092	2.2686	6.1236
rC_{10}	0.384	1.6222	0.116	2.4762	6.5576

When the values in Tables 4 and 5 are examined, it is seen that the S values of rC_3 and rC_4 are the same. However, the N value of rC_3 (43) is higher than the N value of rC_4 (39). Nevertheless, in terms of D_{MN} , the value of rC_3 is higher than that of rC_4, while for D_{MG} the value of rC_4 is higher. ${}^{\alpha^*}D_{MM}$ is higher in rC_4, which has a lower N value. Similar results are also observed for rC_7 and rC_8. Özkan [3] obtained different results for D_{MN} and D_{MG} in his calculations based on hypothetical data. However, it is thought that these results alone cannot be an indicator. Since, Süel et al. [20] estimated higher values for DMG in all 43 sample areas in their study. Mulya et al. [21] also compared species richness and diversity estimations in their study. Researchers stated that D_{MG} produced different results and performed better than Shannon, Simpson, D_{MN} in terms of their data. In contrast to this study, Davari et al. [13] found that D_{MN} performed better than D_{MG}. Both the aforementioned studies and our study shown that non-overlapping results can be observed in different data in terms of D_{MN} and D_{MG}. Therefore, ${}^{\alpha^*}D_{MM}$ is suggested as a useful option.

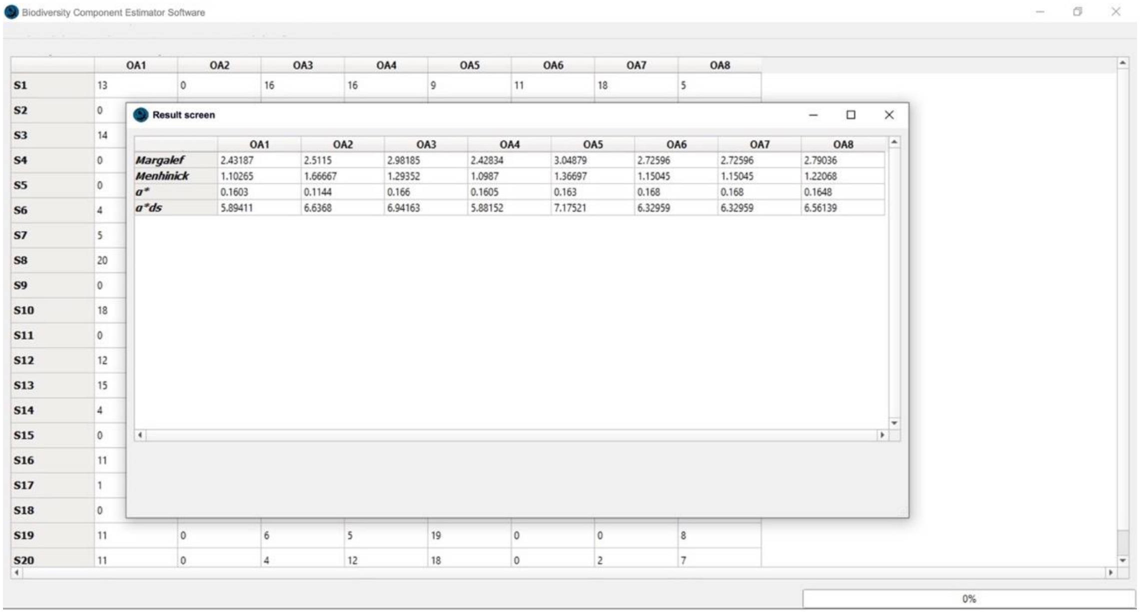
Lastly, it is worth mentioning here that ${}^{\alpha^*}D_{MM}$ may take a smaller value than D_{MG} as can be seen the values of C_8 in Table 2. The lower limit ${}^{\alpha^*}DS$ goes to the value of D_{MN} and, S draws the line of its' upper limit. The spreadsheet program (DMM_macro_v1) that calculates the parameters in Table 2 is available on the website at https://kantitatifekoloji.net/takdivozkan. Application of the spreadsheet program is simple. Enter the values of S and N into D3 and D4 cells, respectively. The outputs ($\alpha_{D_{MG}}$, α^*, D_{MN}, D_{MG} and ${}^{\alpha^*}D_{MM}$) appear in D7-D11 cells (Figure 3).



S 8
N 27
a_MG 0.4024
a* 0.0976
D_MN 1.5396
D_MG 2.12389
a*DMM 5.79948

Figure 3. *The menu of the spreadsheet program for computation of* ${}^{\alpha^*}D_{MM}$

In addition, related calculations are integrated into the BİÇEB software [22] for the calculation of the parameter. BİÇEB is based on python and a version suitable for different operating systems (Mac, Windows, and Linux) that can be downloaded free of charge from the https://kantitatifekoloji.net/biceb (Figure 4). BİÇEB is a software developed using Python programming language within the scope of TÜBİTAK 1005 grant. It can be downloaded free of charge from the link provided. Since it is developed in open code, it can be used free of charge on all operating systems (Windows, Mac OS and Linux). When the program is downloaded, it has the potential to be easily used by researchers since it comes with a download and user manual.



	OA1	OA2	OA3	OA4	OA5	OA6	OA7	OA8
S1	13	0	16	16	9	11	18	5
S2	0							
S3	14							
S4	0							
S5	0							
S6	4							
S7	5							
S8	20							
S9	0							
S10	18							
S11	0							
S12	12							
S13	15							
S14	4							
S15	0							
S16	11							
S17	1							
S18	0							
S19	11	0	6	5	19	0	0	8
S20	11	0	4	12	18	0	2	7

	OA1	OA2	OA3	OA4	OA5	OA6	OA7	OA8
Margalef	2.43187	2.5115	2.98185	2.42834	3.04879	2.72596	2.72596	2.79036
Menhinick	1.10265	1.66667	1.29352	1.0987	1.36697	1.15045	1.15045	1.22068
α*	0.1603	0.1144	0.166	0.1605	0.163	0.168	0.168	0.1648
α*ds	5.89411	6.6368	6.94163	5.88152	7.17521	6.32959	6.32959	6.56139

Figure 4. *BİÇEB software for computation of* ${}^{\alpha^*}D_{MM}$

4. CONCLUSIONS

The present study offers a new richness estimator $\left({}^{\alpha^*}D_{MM}\right)$. $\alpha_{D_{MG}}$ and $\alpha_{D_{MN}}$ are the scale values forming the basis of ${}^{\alpha^*}D_{MM}$ (Equation (6)). With increasing proportional differences between S and N, ${}^{\alpha^*}D_{MM}$ value decreases. If there is an enormous difference between S and N, it is very likely that ${}^{\alpha^*}D_{MM}$ takes a less value than D_{MG}. The essential difference of ${}^{\alpha^*}D_{MM}$ arises by comparing community pairs such as C_9 with C_{10} or C_4 with C_7 given in Table 1.

The results obtained from the data of the hypothetical and natural communities indicate that the new proposed index have the ability to represent both of D_MG and D_MN. That is why it seems to promising to estimate species richness. However, to better understand strengths and weaknesses of the proposed estimator, further studies should be performed using natural community data. In addition, it is thought that the new estimator can be preferred by researchers due to both the development of MS Excel Macro and the possibility of free use through the BİÇEB software.

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CONFLICTS OF INTEREST

No conflict of interest was declared by the authors.

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