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Pülümür ve Munzur Nehirlerindeki Bentik Alglerin Deng Entropi Tabanlı Taksonomik Çeşitlilik Ölçümleri

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Öz

Son yıllarda Deng entropisi büyük ilgi çekmiş ve çeşitli alanlarda uygulama alanı bulmuştur. Deng Entropisi, Dempster-Shafer Kanıt Teorisi çerçevesinde geliştirilen ve temel olasılık atamasına dayanan entropik bir denklemdir. Bu çalışmada, Deng entropisine dayalı yeni bir taksonomik çeşitlilik indeksi kullanılmıştır. Çalışmada Tunceli'deki Munzur ve Pülümür nehirlerinin bentik alg florası, Ekim 2016 ve Eylül 2017 tarihleri arasında toplanan altı örnek alandan elde edilen veriler kullanılarak incelenmiştir. Sonuçlar, önerilen yeni indeksin taksonomik çeşitliliği hesaplamak için uygulanabilir olduğunu göstermektedir. Bununla birlikte, bu yeni indeksin performansını daha iyi anlamak için, geniş bir ekolojik veri yelpazesi kullanarak diğer geleneksel ve taksonomik çeşitlilik indeksleriyle karşılaştıran daha fazla çalışmaya ihtiyaç vardır.

Deng Entropy Based Taxonomic Diversity of Benthic Algae of Pülümür and Munzur Streams

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Abstract

In recent years, Deng entropy has attracted considerable interest and found applications in various fields. Deng Entropy is an entropic equation developed within the framework of the Dempster-Shafer Theory of Evidence and is based on basic probability assignment. In this study, a new taxonomic diversity index based on Deng entropy was used. The study investigated the benthic algal flora of Munzur and Pülümür rivers in Tunceli, using data from six sample sites collected between October 2016 and September 2017. The results indicate that the proposed new index is applicable for calculating taxonomic diversity. However, to better understand the performance of this new index, further studies comparing it with other traditional and taxonomic diversity indices using a wide range of ecological data are needed.

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INTRODUCTION

Various indices are used to assess biodiversity. Among them, species richness (Peet, 1974), the Simpson index (Simpson, 1949) and Shannon entropy (Shannon, 1948) are the most preferred. Species richness, Simpson index, and Shannon entropy fall into the category of traditional diversity indices, which are calculated based on presence-absence, abundance, or frequency data of species (Özkan, 2016). Unlike traditional diversity indices, taxonomic diversity indices use character-based presence-absence, abundance, or frequency data of species. Therefore, taxonomic diversity indices do not only rely on numerical data of species, but also provide direct or indirect information on the genetic, functional, and structural characteristics of species.

Another method proposed to calculate taxonomic diversity is the quadratic entropy developed by Rao (1982). This entropy is based on the measurement of distances between pairs of species. These distances can be determined according to the morphological and functional characters of the species or according to the Linnean taxonomy. Another measure of taxonomic diversity developed by Ricotta and Avena (2003) takes into account the abundance values and taxonomic distinctions of species. However, unlike Rao's quadratic entropy, this information-theoretic measure does not rely on the distances between pairs of species.

The most well-known and widely used methods in the field of taxonomic diversity and taxonomic distance indices were developed by Warwick and Clarke (1995). These indices calculate weighted taxonomic differences between species.

This study proposes a new measure (*pTO*) for assessing taxonomic diversity and/or taxonomic distance. This new measure is based on the Deng entropy, which is one of the entropic measures in the Dempster-Shafer theory. Deng Entropy is a generalized version of Shannon Entropy and was first proposed by Deng (2016). Deng Entropy has become increasingly popular and has been widely applied in various fields such as model definition, risk assessment, and decision-making processes. Unlike entropic measures in information theory, Deng Entropy focuses on measuring uncertainty in fundamental probability assessments. Therefore, the taxonomic diversity measure proposed in this study for the first time differs in conceptual and formulaic structure from the taxonomic diversity measures developed by Pielou (1975), Vane-Wright et al. (1991), Faith (1992), Rao (1982), Warwick and Clarke (1995), and Ricotta and Avena (2003).

The objectives of this study are as follows Calculate Özkan's taxonomic species diversity index for biological species indices at 6 points identified in Pülümür and Munzur stations and compare their performance with Shannon Weaver.

MATERIAL AND METHOD

The benthic algae and seasonal variations in the Munzur and Pülümür Rivers were examined through samples collected from 6 stations. These stations are as follows: Station 1 (St1): (39°19'52.6"N 39°03'18.5"E) Located approximately 75 km away from Tunceli in Ziyaret Village; Munzur Gözeler locality (source point of the Munzur River). During spring and summer, the number of springs where water emerges increases, leading to higher flow and velocity. In autumn and winter, the decrease in spring numbers significantly reduces river flow and velocity. The ground consists mainly of stones and gravel. Station 2 (St2): (39°18'02.8"N 39°22'12.4"E) Located in the Munzur Valley, approximately 53 km away from Tunceli, in Aşağı Torunoba village where livestock activities take place. During spring and summer, due to rain and melting snow, the water flow and velocity are high. The ground is composed of stones and fine sand. This point also experiences noticeable discharge of animal manure into the water. Additionally, there is no wastewater treatment algae between stations I and II, including Ovacık town center, leading to domestic wastewater being discharged into the Munzur River. Station 3 (St3): (39°08'03.4"N 39°29'41.0"E) Located in the Munzur Valley, approximately 8 km away from Tunceli, at the Anafatma locality. The ground is gravel and fine sandy. Due to rain and melting snow during spring and summer, and because the river is mainly fed by streams and the channel is narrower and steeper compared to the first two stations, the water flow and velocity are higher. Station 4 (St4): (39°11'35.5"N 39°41'33.8"E) Located in the Pülümür Valley, approximately 18 km away from Tunceli, at the Kutudere locality. The ground is gravel and fine sandy. During spring and summer, rain and melting snow increase the water volume, and due to the steeper and narrower riverbed, the flow rate is occasionally high. There is no wastewater treatment algae in Pülümür town center, leading to domestic wastewater mixing with the Pülümür River. Station 5 (St5): (39°06'23.5"N 39°36'53.0"E) Located in the Pülümür Valley, about 6 km away from Tunceli, in Kocakoç village at Pah Bridge locality. The ground is fine sandy. Due to the influence of rain and melting snow during spring and summer, and more streams joining, the water flow is higher compared to station 4. The ground is flatter and wider, resulting in lower water velocity. Station 6 (St6): (39°06'07.1"N 39°33'36.0"E) Located in the Pülümür Valley, approximately 1 km away from Tunceli, beneath the Batman Bridge (before the confluence of Munzur and Pülümür Rivers). The ground is fine sandy. Due to the influence of rain and melting snow during spring and summer, and more streams joining, the water flow is higher compared to the first two stations. However, due to pollution from wastewater mixing, the water is occasionally turbid. Additionally, near this station, municipal waste is disposed of in an area without modern storage facilities, leading to wastewater and rainwater being carried to streams and from there to the Pülümür River. The study investigated the benthic algal flora of Munzur and Pülümür rivers in Tunceli, using data from six sample sites collected between October 2016 and September 2017. At the bottom of Munzur and Pülümür creeks, samples were taken from 6 points designated to study

epiphytic algae living by attaching to the sediment surface, preferably in the coastal areas where the water flow velocity is lower. A glass tube with a diameter of 1 cm and a length of 100 cm was used. During sampling, one end of the glass pipe was closed with the thumb, the other end was gently touched to the bottom of the water, the closed end was then opened, and the glass pipe was gently moved in a radial direction on the bottom. After filling the glass tube with a thin layer of muddy water taken from the ground, the outer end of the tube was closed again with the finger and the muddy water was poured into 500 ml plastic bottles. Some water was then added to the muddy water (the same amount was used in each process). At the end of the process, the container was labelled with the date, station number and type of sample. The pipe water samples were kept in a dark and cold environment for a while to allow the sludge to settle. The water on top of the settled sludge was then carefully removed without clouding; the sludge remaining at the bottom of the container was thoroughly shaken and spread in petri dishes of 10 cm diameter and 1 cm thickness so that it was evenly distributed throughout the container. After completely removing the settled sludge in the petri dishes with a dropper, the remaining wet sludge was rinsed with a dropper to remove the algae that appeared on the surface of the sludge due to phototaxis. The system of Round (1984) was taken as a basis for the ranking of the algae identified in Munzur and Pülümür streams. Bourelly (1968, 1970), Cox (1996), Hustedt (1930), Krammer, Lange- Bertalot (19786), Prescott (1973), Patrick and Raimer (1975) were taken into consideration for species identification.

Shannon Entropy

$$S = \sum_{i=1}^s S_i$$

$$H = -\sum_{i=1}^n p_i \log_b p_i$$

The proposed measures by Warwick and Clarke (1995) and Clarke and Warwick (1998) taxonomic diversity (Δ), taxonomic distinctness (Δ^*), and average taxonomic distinctness (Δ^+) are computed by following equations

$$\Delta = \frac{\sum_{i < j} w_{ij} X_i X_j + \sum_i 0.5 X_i (X_i - 1) / 2}{\sum_{i < j} X_i X_j + \sum_i X_i (X_i - 1) / 2}$$

$$\Delta^+ = \frac{\sum_{i < j} w_{ij}}{[S(S-1)]/S}$$

Where S is the number of species, w_{ij} is the distinctness weight given to the path length linking species i and j according to Linnean taxonomic classification, and X_i and X_j are numerical values of i-th species and j-th species respectively.

The results of all measures were defined for each of the 107 sample plots. UTo, To, uTo+ and To+ were then compared to taxonomic diversity indices Species richness (S), Shannon entropy (H) and Simpson's diversity (1-D) using correlation analysis (CoA) and principal component analysis (PCA). S, H and 1-V were computed by using the BİÇEB (A software for estimating Biodiversity Components) program (Özkan et al, 2020). In calculations of Δ , Δ^* , and Δ^+ Paleontological Statistics (PAST) software version 1.89 was used (Hammer et al., 2001). Notice that Δ^+ is not found in PAST. However, it is possible to compute it from PAST since taxonomic diversity (Δ , Δ^* , Δ^+ values of the sample plots in this way. Software version Where N is the number of basic states is the probability of state i and p_i satisfied and b is the basis of the logarithm which accounts for the scaling of H. Although b is arbitrary, b is usually chosen to be 2, and the unit of information entropy is bit. If b is the nature base, then the unit of information entropy will be Nat.

Deng entropy, introduced by Deng in 2015 and 2016 (Deng, 2016), has found application in numerous real-world scenarios. Deng entropy is defined as:

$$Ed = \sum m(Q_i) \ln \frac{m(Q_i)}{2^{Q_i} - 1} = - \sum m(Q_i) \ln m(Q_i)$$

$$M(F1) = (m(F1))^0 / \sum m(Fi)^0$$

Regarding the application of the new proposed measure, the Deng Entropy is calculated for each level according to the Linnean taxonomic system. In this case, Eds, EDg, Edf, Edo, Edo, Edc, Edp and Edk represent the Deng Entropy values at the species (S), genus (G), family (F) order (O) class (C), branch (P) and kingdom (K) levels respectively. It is naturally equal to Shannon Entropy (Eds=H). This is because at the species level the opinion is assigned only to single elements or to each species. In other words, the proportional or numerical values of all elements (species) are known at the species level.

The newly proposed taxonomic diversity (pTo) based on Deng Entropy is calculated as shown below.

$$pTo = \left(\frac{\sum_{nk=0}^{ns} (ns - nk) (w1(e^{Eds} + 1) (w2(\frac{e^{Eds}^2}{e^{Edg}} + 1)) \dots (w6(\frac{e^{Eds}^2}{e^{Edg}} + 1)) (w7(\frac{e^{Eds}^2}{e^{Edg}} + 1)))}{n_s + \sum nk} \right)$$

Computation of $m(Fi)$ is based on the following equation, since Deng entropy-based taxonomic diversity measure only uses sliced data (Özkan, 2018a)

$$m(Fi) = m(Fk)^0 / \sum m(Fk)^0$$

Where $m(Fk)^0 = 1$ and $m(Fk)^0$ is the number of remaining species at the k-th step. $\sum m(Fk)^0 = S$ (the number of species) at the first step ($nk=0$).

The proposed measure by Warwick and Clarke (1995) and Clarke and Warwick (1998), taxonomic diversity.

$$\Delta = \frac{\sum_{i < j} w_{ij} x_i x_j + \sum_{i < j} o_{ij} x_i (x_j - 1) / 2}{\sum \sum i}$$

$$\Delta^* = \frac{\sum_{i < j} w_{ij} x_i x_j}{\sum_{i < j} x_i x_j} = \frac{\sum w_{kfk}}{\sum f_k}$$

$$\Delta^+ = \frac{\sum_{i < j} w_{ij}}{[s(s-1)/2]}$$

RESULT AND DISCUSSION

Deng entropy is a generalization of Shannon entropy. When the basic probability assignment degenerates into a probability distribution, it is the same as Shannon entropy (Deng, 2016). Deng entropy is the fundamental equation for the taxonomic diversity estimator (pTO) proposed by Özkan (2018a, 2018b). The Deng entropy-based taxonomic diversity (pTO) estimators derived from Özkan's pTO have been applied using species presence and turnover data from six sample sites in the Pülümür and Munzur Rivers in the Eastern Anatolia Region of Turkey.

The descriptive statistics for the diversity measures are presented in Table 1. In this table, uTO, TO, uTO+, and TO+ represent the estimators derived from Özkan's taxonomic diversity measure (pTO). The mean values of Shannon entropy (H) were found to be 2.57 ± 0.38 and 1.635 ± 0.03 , respectively. The average values for Δ and Δ^* were determined to be 4.12 ± 0.17 (ranging from 3.43 to 4.46) and 4.33 ± 0.13 (ranging from 3.82 to 4.76), respectively. The mean value of Δ^+ was 4.36 ± 0.13 , with a range of 3.87 to 4.73. The minimum and maximum ranges of the values for uTO, TO, uTO+, and TO+ were determined to be 5.61–7.44, 8.88–12.23, 5.61–7.44, and 8.88–12.23, respectively. The mean values were calculated as 6.02 ± 0.70 for uTO, 15.97 ± 1.09 for TO, 6.02 ± 0.70 for uTO+, and 10.54 ± 1.09 for TO+ (Table 1).

Table 1. Descriptive statistics of the Diversity Measure (n=133)

Determining taxonomic diversity, especially based on presence-absence data of species, is of great importance for conservation purposes. As noted by Vane-Wright and colleagues (1991), taxonomic diversity measurements based on proportional values, frequencies, or abundance values of species may not fully provide the information needed to meet conservation objectives. Therefore, taxonomic diversity should be calculated without considering these proportional values, frequencies, or abundances of species. In other words, taxonomic distance measurements based on the presence-absence data of species are a more appropriate approach for conservation purposes, rather than taxonomic diversity measurements based on abundance values of species (Özkan, 2018).

Contrary to the approach of Ricotta and Avena (2003), if we consider the levels in taxonomic trees independently and use Shannon Entropy (H) on this basis, we achieve a value of $A_{HS}=1.63$ at the species level in the community. However, in the community at the station, we obtain values of $B_{HS}=1.7917$ and $B_{HG}=1.0986$ at the species and genus levels, respectively. Since there is only one node at the family level in both communities, the Shannon Entropy values at this level are zero ($A_{HF}=0$; $B_{HF}=0$).

Table 2. Results of the To components of the complexes

The results of TO, uTO, uTO+, and TO+ for the complexes are presented in Table 2. As expected, the obtained results for all complexes are in the order of $TO+ \geq uTO$, $uTO+ \geq uTO$, $TO \geq uTO$, and $TO+ \geq uTO+$.

Therefore, weighted or unweighted taxonomic diversity measurements (uTO+ and TO+) based on Deng Entropy, calculated from presence-absence data of species, can be referred to as taxonomic distance measurements. To evaluate the appropriateness of this naming for uTO+ and TO+, Clarke and Warwick's (1998) method, developed to explain taxonomic distance (Δ^+), is used.

Table 3. Numerical distribution of algae in the complexes according to taxonomic levels

In all complexes, there are a total of 132 different species. The highest number of species is found in St3 (83). The species in K3 are distributed across 28 genera, 19 families, 19 orders, 2 classes, and 1 phylum. St1 is the complex with the lowest numerical values (46) at the taxonomic levels. The species in St1 are distributed across 19 genera, 15 families, 12 orders, 2 classes, and 1 phylum (Table 3).(Table 4)

Figure 1. Principal Component Analysis (PCA) Results of the Diversity Measures

Principal Component Analysis (PCA) also confirmed the correlation results. The first and second axes of the applied PCA explained almost the entire variance, at 82.72%, respectively. As shown in Figure 1, PCA revealed that UT0max, uT0max, To+max, Tomax, and S Warwick-Clarke behave similarly. Traditional diversity indices (S) are located in the lower regions of the ordination diagram, while uT0max, uT0max+, To+max, and Tomax are located in the upper regions of the ordination diagram (Table).

Table 4 . Correlation Analysis Results Among the Diversity Measures

CONCLUSION

One of the most well-known equations of this theory, which has become quite popular in recent years, is Deng Entropy. As previously mentioned, Deng Entropy is a suitable unit of measurement that can be used particularly in risk assessment and decision-making processes. It is specifically designed to cater to these areas of expertise. In these fields, a high entropy value generally indicates a high level of risk and/or difficulty in the decision-making processes (the accuracy of decisions might be low). In other words, Deng Entropy directly provides information about uncertainty; high entropy means high uncertainty.

For complex ecological examples, it has been determined that the components of the newly proposed measurement (*pTO*) have both the ability to define each other and their differences. In this context, the components of *pTO*, namely *TO*, *uTO*, *TO+*, and *uTO+*, have been named respectively as weighted taxonomic diversity measurement, unweighted taxonomic diversity measurement, weighted taxonomic distance measurement, and unweighted taxonomic distance measurement.

COMPLIANCE WITH ETHICAL STANDARDS

a) Authors' Contributions

Each of the authors contributed 50%.

b) Conflict of Interest

The authors declare that there is no conflict of interest.

c) Statement of Human Rights

Work does not require a legal permit.

d) Statement of Human Rights

This study does not involve human participants.

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Tables

Table 1. Descriptive statistics of the Diversity Measure (n=133)

	Min	Max.	Mean	Standard Deviation
To ⁺	8.80	12.23	10.54	1.09
UT ₀	5.61	7.44	6.02	0.70
T ₀	8.80	12.23	10.54	1.09
uT ₀ ^{+max}	11.94	10.59	11.28	0.46
T ₀ ^{+max}	14.29	16.73	15.80	0.86
uT ₀ ^{max}	10.59	11.94	11.28	0.46
T ₀ ^{max}	14.29	16.73	15.80	0.86
Δ	3.47	3.62	3.56	0.12
Δ*	3.34	3.42	3.38	0.11
Δ+	3.66	3.72	3.68	0.12
S	1.63	2.71	2.20	0.13

Table 2. Results of the To components of the complexes

Station	uT ₀	T ₀	uT ₀ ⁺	T ₀ ⁺
St1	7.44	12.23	11.61	16.40
St2	5.78	10.57	11.17	15.95
St3	5.73	10.51	11.59	16.73

St4	5.61	10.39	10.59	15.38
St5	5.96	10.75	11.24	16.03
St6	5.62	8.80	11.11	14.29

Table 3. Numerical distribution of algae in the complexes according to taxonomic levels.

Std Dev	St1	St2	St3	St4	St5	St6
Species	0	0	0	0	0	0
Genus	2.71	4.01	4.06	4.03	3.55	3.62
Family	3.26	5.38	5.42	5.73	5.15	5.23
Order	5.06	8.20	8.52	9.42	8.15	8.40
Class	31.11	50.91	57.27	51.61	47.37	0
Phylum	0	0	0	0	0	0
Kingdom	0	0	0	0	0	0

Table 4. List of Epiphytic Diatoms

			Cod
BACILLARIOPHYTA	Cod	<i>Denticula elegans</i> Kütz.	dnel
<i>Aulacoseira islandica</i> (Otto müller) Simonsen	aulis	<i>Denticula tenuis</i> Kützing	dnt
<i>Camplydiscus noricus</i> Ehrenberg ex Kützing	cnor	<i>Diatoma ehrenbergii</i> Kützing	dieh
<i>Ellerbeckia arenaria</i> Crawford	elar	<i>Diatoma hyemalis</i> (Roth) Heiberg	dihy
<i>Melosira moniliformis</i> (O.F. Müll.) C.Agardh	melmf	<i>Diatoma meseodon</i> (Ehrenberg) Kützing	dimes
<i>Melosira undulata</i> (Ehrenberg) Kützing	melun	<i>Diatoma moniliformis</i> Kütz.	dimo
<i>Meridion circulare</i> var. <i>constricta</i> f.obliquecostata	mcir	<i>D. vulgare</i> Bory	divul
<i>Achnanthes lanceolata</i> var. <i>hynaldii</i> Breb.	achl	<i>Didymosphenia geminata</i> (Lyngbye) Mart.Schmidt	didg
<i>Achantes minutissima</i> Kützing	achm	<i>Diploneis subovalis</i> (Hilse) Cleve	dips
<i>Achnanthes semiaperta</i> Hustedt	achs	<i>Epithemia adnata</i> (Kütz.)	ead
<i>Amphora ovalis</i> Kützing	amo	<i>Epithemia argus</i> (Ehrenberg) Kützing	ear
<i>Asterionella formosa</i> Hassall	asfor	<i>Epithemia frickei</i> Krammer	efri
<i>Caloneis amphisbaena</i> (Bory) Cleve	calam	<i>Epithemia geoppertiana</i> Hilse	egeo
<i>Caloneis alpestris</i> (Grunow) Cleve	calal	<i>E.sorex</i> Kütz.	esor
<i>Caloneis schumanniana</i> (Grunow)Cleve	calsc	<i>Eunatia veneris</i> (Kütz.)De Toni	euv
<i>Caloneis silicula</i> var. <i>tenuis</i> Hustedt	calsi	<i>Fragilaria construens</i> var. <i>binodis</i>	fcons
<i>Caloneis ventricosa</i> (Ehr.) Meister	calve	(Ehrenberg) Grunow	

<i>Cocconeis placentula</i> Ehr.	cocpl	<i>Fragilaria germainii</i> E.Reichardt & Lange-Bertalot	fger
<i>Cymatopleura elliptica</i> Breb. W Smith	ctpe	<i>Fragilaria leptostauron</i> var. <i>martyi</i>	flept
<i>Cymatopleura solea</i> (Breb.)W.Smith	ctps	(Ehrenberg) Hustedt	
<i>Cymbella affinis</i> Kützing	camp	<i>Fragilaria virescens</i> Ralfs	fvir
<i>Cymbella amphisephala</i> var. <i>heroynica</i> Naegeli in Kützing	ccis	<i>Frustulia rhomboides</i> var. <i>saxonica</i> (Robenhorst) De Toni	frur
<i>Cymbella cistula</i> (Ehrenberg)	ccos	<i>Gomphonema angustum</i> C.Agardh	gang
<i>Cymbella cosleyi</i> L.Bahls	ccos	<i>Gomphonema clavatum</i> Ehrenberg	gcla
<i>Cymbella cuspidata</i> Kützing	ccus	<i>Gomphonema constrictum</i> var. <i>capitata</i> (Ehr.)Cleve	gcon
<i>Cymbella hebridica</i> (Grunow ex Cleve) Cleve	cheb	<i>Gomphonema gracile</i> Ehrenberg	ggr
<i>Cymbella helvetica</i> Kützing	chel	<i>Gomphonema minutum</i> (C.Agardh) C.Agardh	gmin
<i>Cymbella excisiformis</i> Krammer	cecx	<i>Gomphonema olivaceum</i> (Hornemann) <i>Olivaceum</i> var.	gol
<i>Cymbella lanceolata</i> (C.Agardh) Kirchner	clan	<i>Gomphonema parvulum</i> Kützing	gpar
<i>Cymbella lata</i> Grunow ex Cleve	clata	<i>Gomphonema tergestinum</i> (Grunow) Fricke	gter
<i>Cymbella minuta</i> Hilse ex Rabenhorst	cmin	<i>Gomphonema truncatum</i> Ehrenberg	gtru
<i>Cymbella naviculiformis</i> Auerswald ex Heiberg	cnav	<i>Gyrosigma acuminatum</i> (Kützing) Rabenhorst	grac
<i>Cymbella obscura</i> Krasske	cobs	<i>Gyrosigma attenatum</i> (Kützing) Robenhorst	grat
<i>Cymbella obtusiuscula</i> (Kütz.)Grun.	cobt	<i>Gyrosigma nodiferum</i> (Grunow) Reimer	gmod
<i>Cymbella proxima</i> Reimer	cpro	<i>Navicula plicata</i> Donkin	napli
<i>Navicula proctata</i> (W.Smith) Ralfs	napro		
<i>Navicula menisculus</i> Schumann	name		
<i>Navicula plicata</i> Donkin	napli		
<i>Navicula proctata</i> (W.Smith) Ralfs	napro		
<i>Navicula pupula</i> Kützing var.	napu		
<i>Navicula radiosa</i> Kützing	nara		
<i>Navicula salinarum</i> Grunow	nasa		
<i>Navicula schoenfeldii</i> Hustedt	nasho		
<i>Navicula similis</i> Krasske	nasi		
<i>Navicula trivialis</i> Lange-Bertalot	natri		
<i>Navicula viridula</i> var. <i>linearis</i> (Kütz.)	navi		
<i>Neidium ampliutum</i> (Ehrenberg) Krammer	neam		
<i>Neidium binodiformis</i> (Krammer) Lange-Bertalot&N.Angeli	nebi		
<i>Neidium dubium</i> (Ehrenberg) Cleve	nedu		

<i>Neidium productum</i> (W.Sm.) Cleve	nepro
<i>Nitzschia amphibia</i> Grunow	niam
<i>Nitzschia brevissima</i> Grunow	nibr
<i>Nitzschia constricta</i> Kützing	nicon
<i>Nitzschia flexa</i> Schumann	nifx
<i>Nitzschia flexoides</i> Geitler	niflx
<i>Nitzschia heufleriana</i> Grunow	nihf
<i>Nitzschia incognita</i> Legler&Krasske	ninc
<i>Nitzschia intermedia</i> Hantzsch	nint
<i>Neidium ampliatus</i> (Ehrenberg) Krammer	neam
<i>Neidium binodiformis</i> (Krammer) Lange-Bertalot&N.Angeli	nebi
<i>Neidium dubium</i> (Ehrenberg) Cleve	nedu
<i>Neidium productum</i> (W.Sm.) Cleve	nepro
<i>Nitzschia amphibia</i> Grunow	niam
<i>Nitzschia brevissima</i> Grunow	nibr
<i>Nitzschia constricta</i> Kützing	nicon
<i>Nitzschia flexa</i> Schumann	nifx
<i>Nitzschia flexoides</i> Geitler	niflx
<i>Nitzschia heufleriana</i> Grunow	nihf
<i>Nitzschia incognita</i> Legler&Krasske	ninc
<i>Nitzschia intermedia</i> Hantzsch	nint

Table 4. Correlation Analysis Results Among the Diversity Measures

	uTo	To	uTo+max	To+max	uTomax	Warwick clark	S	
uTo								
To	0.40	0.36						
uTo+max	0.42	0.78	0.66					
uTomax	0.40	0.36	1.00	0.66				
Tomax	0.42	0.78	0.66	1.00	0.66			
Warwick clark	0.20	0.60	0.89	0.58	0.94	0.58		
S	0.22	0.45	0.36	0.58	0.36	0.58	0.72	1

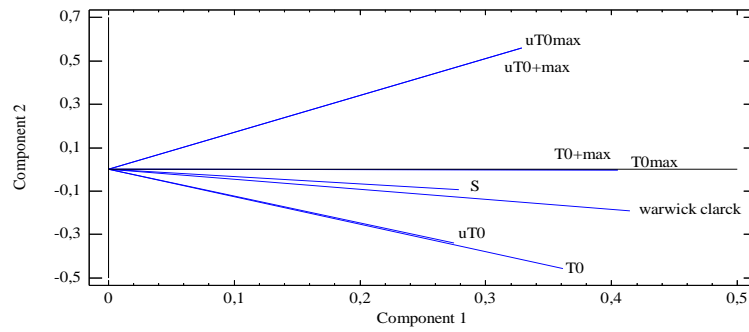
Figures

Figure 1. Principal Component Analysis (PCA) Results of the Diversity Measures