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## METHODS FOR MEASUREMENT AND VISUALIZATION OF CHANGES IN BIODIVERSITY

### METODY POMIARU I WIZUALIZACJI ZMIAN BIORÓŻNORODNOŚCI

**Abstract:** Biodiversity can be evaluated basing on the species numbers or numbers of chosen taxa ( $S$ ). The biodiversity assessment is also enabled using the Shannon index ( $H$ ) that includes numbers of taxa and their relative abundances (or relative biomass likely relative degrees of covering). The proper description of biological or statistically significant differences (or their absence) between the compared taxocenosis of identical or subjectively different values of  $S$  and  $H$ , is not possible by use of both methods mentioned. Thus, the aim of our work was to present the manners for solving these problems basing on the example of three hypothetical organism communities. Two of the communities mentioned were characterized by the same values of  $S$  (taxon richness) and different values of  $H$  (the Shannon index) and two ones had similar  $H$  values and different values of  $S$ . To obtain the complete description of biological differences between compared communities the following indices were calculated:  $H_{\max}$  (a maximum value of Shannon index for the richness of taxa represented by the same number of individuals),  $V_d$  (a percentage value of covering structural capacity of community, "evenness deficiency"),  $E$  (MacArthur index - a taxon number ( $S$ ) in a community for which the observed value of  $H$  equals  $H_{\max}$ ) and  $P_s$  (taxon richness shortage in percents). Moreover, graphical method of  $\Delta_\beta$  profiles was used for comparing community diversities. Instead, to obtain information about statistically significant differences in biodiversity between analyzed communities, the rarefaction curves were applied. The curves are based on the zero models and the Monte Carlo method.

**Keywords:** biodiversity, Shannon index, rarefaction curves, profile method

While undertaking the 'strategy of protection and rational usage of biological diversity' [1], an ideal solution would be the formation of conditions enabling the 'control of strategy to be realized', where the monitoring, ie systematic measurements, would be performed, therefore the results of the measurements reliably compared. Biodiversity (biological diversity  $\alpha$ ,  $\beta$ , and  $\gamma$ ) may be evaluated based on the *richness of species*  $S$ , or taxa selected at own preference [2]. It may also be assessed with consideration of the number of taxa and their relative abundance (or relative biomass, or relative coverage degree) by calculating *Shannon's index of diversity*  $H'$ . While applying both methods, it is not possible to determine correctly the biological or statistically significant differences (or the lack of such differences) between the compared taxocenoses of identical or subjectively different  $S$  and  $H'$  values. Hence, the objective of the presented study is to demonstrate methods of solving this problem, which can possibly be adopted.

### Materials and methods

The material used for the study were three hypothetical communities, two of which had the same values  $S$  (species richness), but differed with respect to the  $H'$  values (Shannon's index), and two possessed similar  $H'$  values but differed by  $S$  values; for better illustration of the problem - they had the same number of individuals  $N = 20$  (Tab. 1).

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Table 1

Taxonomic-biocenotic characteristics of three hypothetical communities A, B and C

Taxa	Community		
	A	B	C
$s_i$	$n_i$	$n_i$	$n_i$
a	4	10	3
b	4	1	6
c	4	3	-
d	4	2	4
e	4	4	7

The below-mentioned formulas were applied to perform measurements and comparisons of biological diversity of the communities (objects) characterised [3-5]:

$$S = \sum_{i=1}^s s_i \quad (1)$$

$$N = \sum_{i=1}^s n_i \quad (2)$$

$$\Pi_i = \frac{n_i}{N} \quad (3)$$

$$H' = -\sum_{i=1}^s \Pi_i \lg_2 \Pi_i \quad (4)$$

$$H'_{\max} = \lg_2 S \quad (5)$$

$$V_d = \left(1 - \frac{H'}{H'_{\max}}\right) \cdot 100 \quad (6)$$

$$E = 2^{H'} \quad (7)$$

$$P_s = \left(1 - \frac{E}{S}\right) \cdot 100 \quad (8)$$

where:  $S$  - species richness, number of taxa;  $s_i$  - distinguished taxon;  $N$  - total number of individuals in the sample (total number of individuals in taxocenosis);  $n_i$  - number of individuals of  $i^{\text{th}}$  taxon;  $\Pi_i$  - relative abundance of the  $i^{\text{th}}$  taxon;  $H'$  - Shannon's index of biodiversity;  $H'_{\max}$  - maximum  $H'$  value for a given richness  $S$ , which would occur if all taxa were equally abundant;  $V_d$  - a percentage value of implementation of community capacity (evenness deficiency),  $E$  - species richness of community, for which the observed  $H'$  is  $H'_{\max}$  value;  $P_s$  - expressed in percent species shortage.

Moreover, in order to compare the biodiversity of communities, a graphic profile method of  $\Delta_\beta$  was applied [4]. The  $\Delta_\beta$  profiles were plotted based on the points on the coordinate axes ( $\beta$ ,  $\Delta_\beta$ ), where  $\beta > -1$  and  $\Delta_\beta$  is described by the following formula:

$$\Delta_\beta = \sum_{i=1}^s \left\{ \frac{1 - \Pi_i^\beta}{\beta} \right\} \Pi_i = \frac{1 - \sum_{i=1}^s \Pi_i^{\beta+1}}{\beta} \quad (9)$$

To obtain information concerning the statistically significant differences between the communities analysed from the aspect of diversity of the taxa, null models were applied, which are based on the Monte Carlo method [6, 7]. For the analysed communities A, B and C calculations were performed by means of the Eco Sim 7.0 software [6, 7], obtaining data necessary for plotting rarefaction curves.

## Results and discussion

Table 2 presents the results of calculations performed according to the formulas (1)-(4).

Table 2  
Taxa richness, total abundance and Shannon's index for communities A, B, and C

Index	Community		
	A	B	C
S	5	5	4
N	20	20	20
H'	2.3219281	1.9232196	1.9261206

Based on the above-presented results, it is not possible to state unequivocally if the communities compared, especially B and C, vary with respect to the biological differences. However, based on the data contained in Table 3, it may be presumed that in the biological sense community C is poorer with respect to biodiversity than community A, but richer than community B because it is characterised by a lower evenness deficiency  $V_d$  and a lower species shortage  $P_s$ .

Table 3  
Values of indices  $H'_{max}$ ,  $V_d$ , E and  $P_s$  for communities A, B and C

Index	Community		
	A	B	C
$H'_{max}$	2.3219281	2.3219281	2.0
$V_d$	0.0%	17.2%	3.7%
E	5.0	3.7926851	3.8003192
$P_s$	0.0%	24.2%	5%

Figure 1 present the results of the application of the profile method. It is worth explaining that  $\Delta_\beta$  profiles plotted for compared communities show their ranking according to three indices: 'species count'  $\Delta_{Si} = S - 1$ , Shannon's index and Simpson's index

$$\Delta_{Si} = 1 - \sum_{i=1}^s \Pi_i^2.$$

For the communities considered, based on the  $\Delta_\beta$  profiles it may be presumed that taxocenosis A is more diverse than taxocenoses B and C, while the taxocenoses B and C cannot be compared due to the crossing courses of the profiles (Fig. 1).

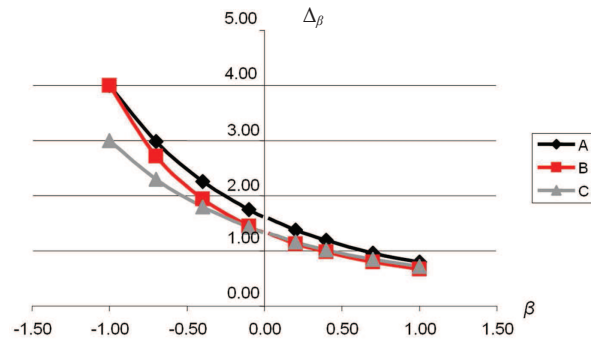


Fig. 1. The  $\Delta_\beta$  profiles for communities A, B and C

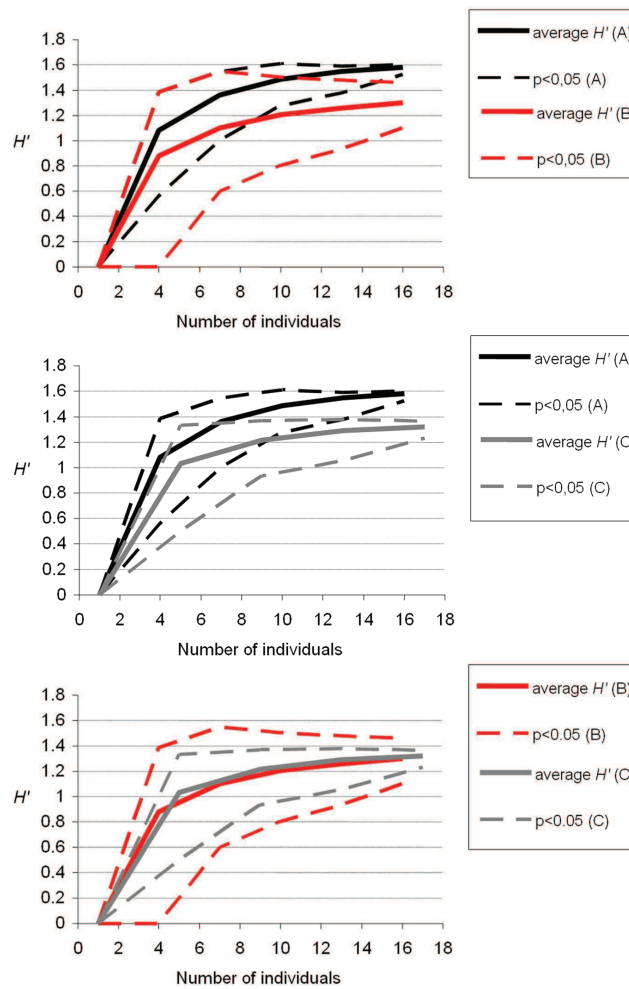


Fig. 2. Rarefaction curves of Shannon's index  $H'$  for communities A, B and C

The above-presented methods do not allow making judgements concerning neither statistical significance of the differences nor confidence intervals - the latter, when they do not overlap, decide about the significance of the differences between the communities compared. The problem discussed may be solved based on the multiple sampling methods. Using these methods, the rarefaction curves were obtained for the compared communities A, B and C (Fig. 2). A low number of taxa and individuals causes a certain 'angularity' of the graphs obtained, which should disappear with regard to more abundant samples  $N > 50$ .

The  $H'$  values obtained with the use of the EcoSim 7.0 software differ from those listed in Table 2, because the EcoSim software calculates Shannon's index using a natural logarithm, while the base-2 logarithm is commonly applied in the theory of computer science. Hence,  $H'(A)$  value is 1.61, and  $H'(B)$  and  $H'(C)$  obtains the value of 1.33.

The present graphs were plotted with the use of MS Excel 2007 software. The authors of the EcoSim software suggest the application of the SigmaPlot or S-Plus software, which enable more desired effects to be obtained with respect to the graphic illustration of the calculations performed [6-8]. The application of Excel also provides opportunities of interpretation of the results; therefore, based on the results, it may be presumed that in the case of Shannon's species diversity, taxocenosis A significantly differs from taxocenoses B and C, which do not differ by the parameter discussed.

### Summary and conclusions

Analysis of the results allows for the following conclusions:

- Biodiversity may be expressed quantitatively, and after performing its measurements it is possible to compare taxocenoses and their changes in time function with respect to this parameter.
- The rarefaction methods enable determination of the statistical significance of the differences, or statistical lack of the differences, between Shannon's index values for the compared communities.
- Elaborate indices - derivatives of the  $H'$  index (especially  $V_d$  and  $P_s$ ) allow concluding about the significance of the biological differences, even when the values of the Shannon's  $H'$  indices are numerically similar.
- The  $\Delta_\beta$  profiles serving the comparison of the values of species richness, Shannon's and Simpson's indices in the investigated taxocenoses, have a basic shortcoming - the  $\beta$  values in the denominator of the fraction have to pass by 0 value, which from the point of view of arithmetic is inadmissible.

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### References

- [1] Andrzejewski R. and Weigle A.: Biological diversity of Poland. Narodowy Fundusz Ochrony Środowiska, Warszawa 2003 (in Polish).
- [2] Whitaker R.H.: *Evolutional measurements of species diversity*. Taxonomy, 1972, **21**, 213-251.
- [3] MacArthur R.H.: *Patterns of diversity*. Biol. Rev., 1965, **40**, 510-533.

- [4] Gove I.H., Patil G.P., Swindel B.F. and Taille C.: *Ecological diversity and forest management*. [In:] Handbook of Statistic 12, Eds. G.P. Patil and C.R. Rao. Elsevier Science B.V., Amsterdam, London, New York, Tokyo 1994, 409-462.
- [5] Łagód G., Malicki J., Chomczyńska M. and Montusiewicz A.: *Interpretation of the results of wastewater quality biomonitoring using saprobes*. Environ. Eng. Sci., 2007, **24**(7), 873-879.
- [6] Błędzki L.A.: *Method for comparing species richness and species diversity. Part I*. Bioskop, 2007, **1**, 18-22, (in Polish).
- [7] Błędzki L.A.: *Method for comparing species richness and species diversity. Part II*. Bioskop, 2007, **2**, 20-23, (in Polish).
- [8] Gotelli N.J. and Entsminger G.L.: *EcoSim: Null models software for ecology. Version 7.0*, Jericho: Ackuiret Intelligence Inc. and Kesey-Bear, USA, 2006.

## METODY POMIARU I WIZUALIZACJI ZMIAN BIORÓŻNORODNOŚCI

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**Abstrakt:** Bioróżnorodność można oceniać na podstawie liczby gatunków lub liczby dowolnie wybranych taksonów (S). Ocenę bioróżnorodności można również przeprowadzić za pomocą indeksu Shannona (H), do obliczeń którego wykorzystuje się liczbę taksonów oraz ich względne liczebności (lub względne biomasy ewentualnie relatywne stopnie pokrycia). Przy użyciu obu wymienionych metod nie można poprawnie określić statystycznie istotnych czy też biologicznych różnic (lub ich braku) pomiędzy porównywanymi taksocenozami o identycznych lub subiektywnie różnych wartościach S i H. Stąd celem prezentowanej pracy było przedstawienie sposobów rozwiązania tego problemu na przykładzie trzech hipotetycznych zbiorowisk żywych organizmów. Wśród tych taksocenoz dwie charakteryzowały się takimi samymi wartościami S (bogactwa taksonów) i różnymi wartościami H (indeksu Shannona), a dwie miały zbliżone wartości H, a różne wartości S. Dla pełnego określenia różnic biologicznych pomiędzy porównywanymi zbiorowiskami obliczono wskaźniki:  $H_{max}$  (maksymalna wartość indeksu Shannona dla danego bogactwa taksonów charakteryzujących się takimi samymi liczebnościami),  $V_d$  (wyrażona w % wartość wypełnienia strukturalnych możliwości zbiorowiska; niedostatek „równomierności”), E (indeks MacArthura, czyli liczba taksonów S w zbiorowisku, dla którego dany indeks H przyjąłby wartość maksymalną) oraz  $P_s$  (wyrażony w % niedostatek bogactwa taksonów). Dodatkowo, dla porównania bioróżnorodności zbiorowisk użyto graficznej metody profili  $\Delta_B$ . W celu uzyskania informacji o statystycznie istotnych różnicach między analizowanymi zbiorowiskami pod względem bioróżnorodności wykreślono krzywe rarefakcji, bazujące na modelach zerowych i metodzie Monte Carlo.

**Słowa kluczowe:** bioróżnorodność, indeks Shannona, krzywe rarefakcji, metoda profili