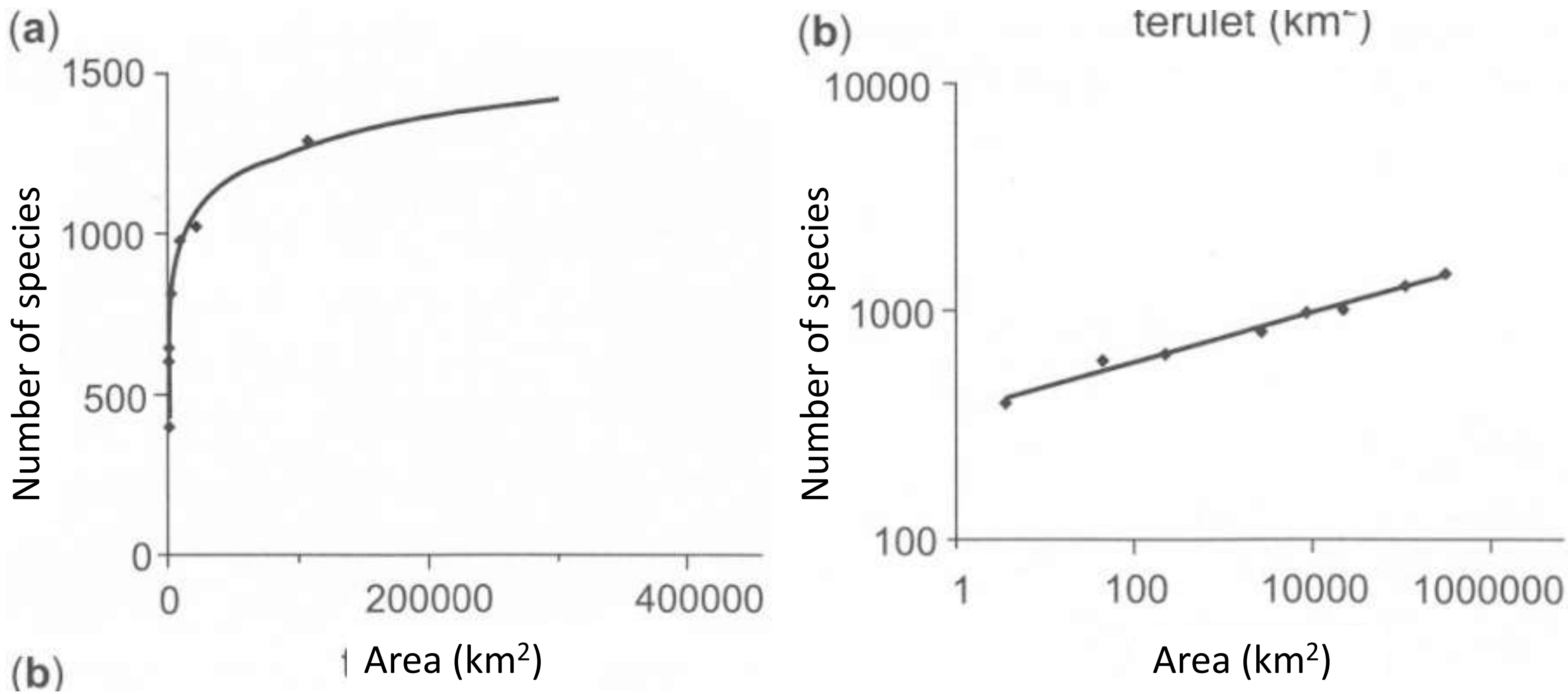
DESCRIPTION OF THE STRUCTURE OF COMMUNITIES USING QUANTITATIVE METHODS

The study and understanding of associations begins with field sampling.

Sampling

- aims to understand the area as thoroughly and without distortion as possible.
- its accuracy is proportional to the proportion of the area examined. (Ideally, there is a relationship between the size of the sampling unit and the number of species found in it that can be described with a saturation curve.)

The species–area relationship



The data come from the plant species of Great Britain. The smallest survey area is about 3 km² and hosts around 400 species. In a larger area—the South Thames district, which spans several tens of thousands of square kilometers—around 1,000 species are found. Across the whole of Great Britain, which covers 350,000 km², approximately 1,600 species are present.

In graph a), both axes are linear.

In graph b), the same data set is used, but the axis scaling has been changed: a log-log scale is applied. It is apparent that in this representation, the data form a straight line, indicating a good fit to the Arrhenius model.

Minimum / Minimi **area**

- In sampling aimed at characterizing a plant community, it is expected that nearly all characteristic species will be present within the quadrat (typically a square sampling unit—or a shape adapted to the form of the community).This area size is referred to as the minimum area (area minima).

- Based on previous studies, the following quadrat sizes are generally acceptable in Hungary:
  - in woody (forest) communities: 20×20 m
  - in shrublands: 10×10 m
  - in grasslands: 2×2 m
  - for animal species using large areas, larger units are used (e.g., 100×100 m, 1×1 km, 2.5×2.5 km, etc.)

TÁRSULÁSOK SZERKEZETÉNEK JELLEMZÉSE KVANTITATÍV MÓDSZEREKKEL

Establishing sampling quadrats

In the field minutes/logbook, the following data must be recorded for each surveyed sampling quadrat:

- the date of sampling
- the name(s) of the surveyor(s)
- the precise geographic location of the sampling site (coordinates)
- the sampling ID (e.g., quadrat number or identifier)
- the (approximate) name of the surveyed community
- the altitude above sea level
- slope inclination and aspect (cardinal direction)
- information about the bedrock and soil

For vegetation, the following should be estimated within the quadrat:

- the total percentage cover for the different vertical layers(canopy, shrub, herb/grass, moss layer)
- the height of the distinct vegetation layers
- the age of trees, and average trunk diameter (measured at 1.3 meters above ground)a list of the number of trees (i.e., number of trunks) within the quadrat

During surveys conducted in the sampling areas (after establishing the quadrat), the following tasks must be carried out (steps 1–3):

1 – Compilation of a species list

2 – Determination of species abundance

This can be done using one of the following methods:

a – Based on individual counts

Abundance = number of individuals: Ni

where Ni is the number of individuals of the ith species within the area

b – Based on biomass estimation

Biomass: Bi

where Bi is the total biomass (combined weight) of individuals of the ith species in the area

c – Based on cover estimation

Cover: Di

where Di is the percentage cover of the ith species within the surveyed area (%)

3 – Calculation of relative species proportions

A much more accurate description of plant community composition can be achieved by taking into account the relative proportions of species. This leads to the determination of the species texture, which expresses the share of each species within the community (often in percentages).

Traditionally used formulas:

Relative abundance (pi):This value can be calculated by expressing the Ni, Bi, or Di values of a species as a proportion of the total values for all species:

$$p_i = \frac{N_i}{\sum N}, \quad \frac{B_i}{\sum B}, \quad \text{or} \quad \frac{D_i}{\sum D}$$

Where:

Ni = number of individuals of species I

Bi = biomass of species I

Di = cover of species I

ΣN, ΣB, ΣD = total number of individuals, total biomass, or total cover across all species

Each of the three methods presents specific challenges:

- Determining the number of individuals is not feasible for clonal (vegetatively reproducing) plants.

- Estimating cover and biomass can involve subjective errors.

- When using data on above-ground plant parts (e.g., for calculating relative abundance based on number or cover), the role of a species within a community may be misrepresented. To obtain a more accurate picture, it would be important to also consider below-ground proportions (i.e., relative abundance based on biomass including root mass).

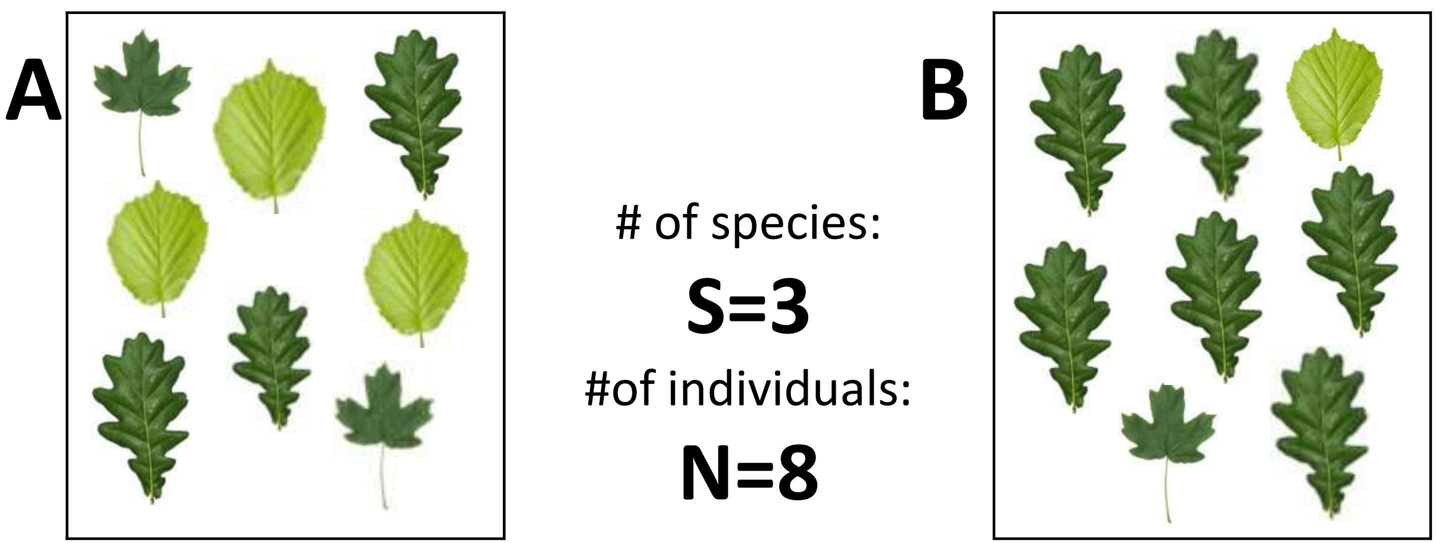
Measuring Biological Diversity

(species richness, species texture, diversity index, evenness, mosaic structure)

Species Richness (S)

The most basic way to characterize the richness of a community is by the number of its components, that is, the species count (S).

A well-known limitation of this metric is that it does not account for differences in species abundance



Species texture

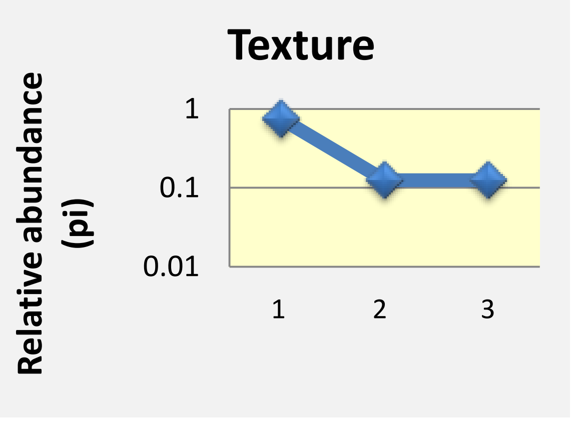
How even is the distribution of species abundance

For each species, we determine what fraction of the total count (or biomass/coverage) they represent (Relative abundance ,pi), and then we plot the species' frequency from the most common to the rarest. To do this, we arrange the species in order of their frequency, and then represent their frequencies along the y-axis, using the logarithm of the frequency values

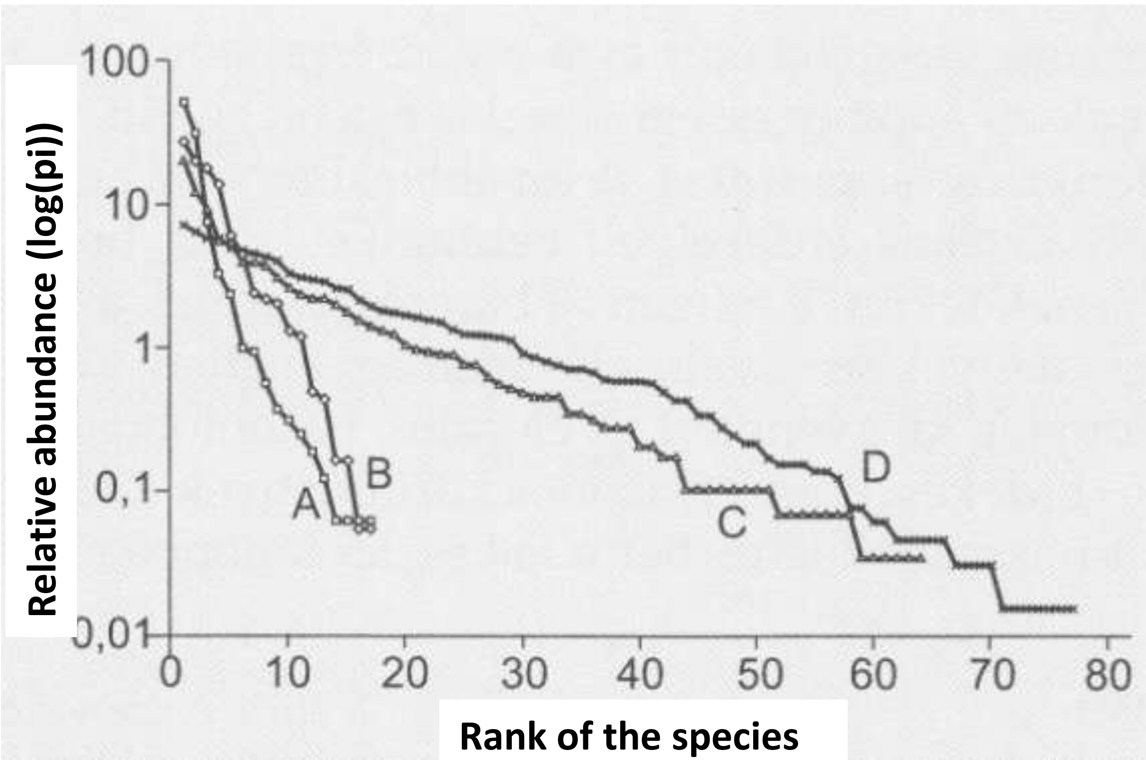
B area

i	Species	N_i	$N_i/N=p_i$	$p_i(\%)$
1	oak	6	0.75	75
2	hasel	1	0.125	12.5
3	f.maple	1	0.125	12.5
	Sum:	8	1	100

N = 8



Species texture in four communities



A – Open Sand Grassland (Fülöpháza, Kiskunság)B – Saline Steppe (Hortobágy)C – Forest-Steppe Meadow (Belsőbáránd, Mezőföld)D – Loess Steppe Grassland (Virágosvölgy, Erdélyi Mezőség)

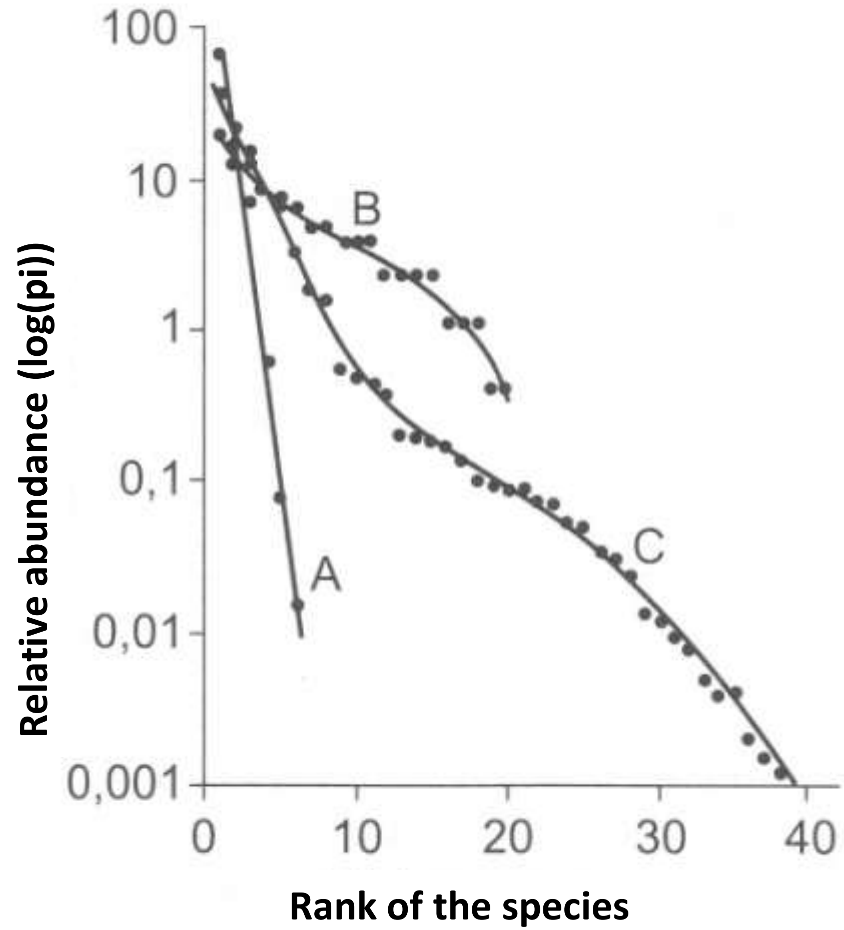
The vertical axis is logarithmic, meaning that there are significant differences in the abundance between the species. The horizontal axis shows the rank in decreasing order of abundance. In the sand grassland and saline vegetation, the number of species is not very high (less than 20, as shown on the horizontal axis). The distribution of abundance is highly hierarchical: one or two species are very common, while the rest are rare. In contrast, the loess steppe grassland and forest-steppe meadow communities are composed of many more species. There are many moderately common species. The overall picture suggests that the power dynamics between species are much more balanced. The A and B communities' habitats are characterized by strong abiotic stress: water scarcity, high soil salinity, and strongly alkaline pH. The C and D communities developed under more favorable living conditions, with relatively good water availability

Three Basic Models:

A: Geometric SequenceEarly stages of succession.In the dominance hierarchy, the consumption of resources by the species above limits the abundance of the species below.

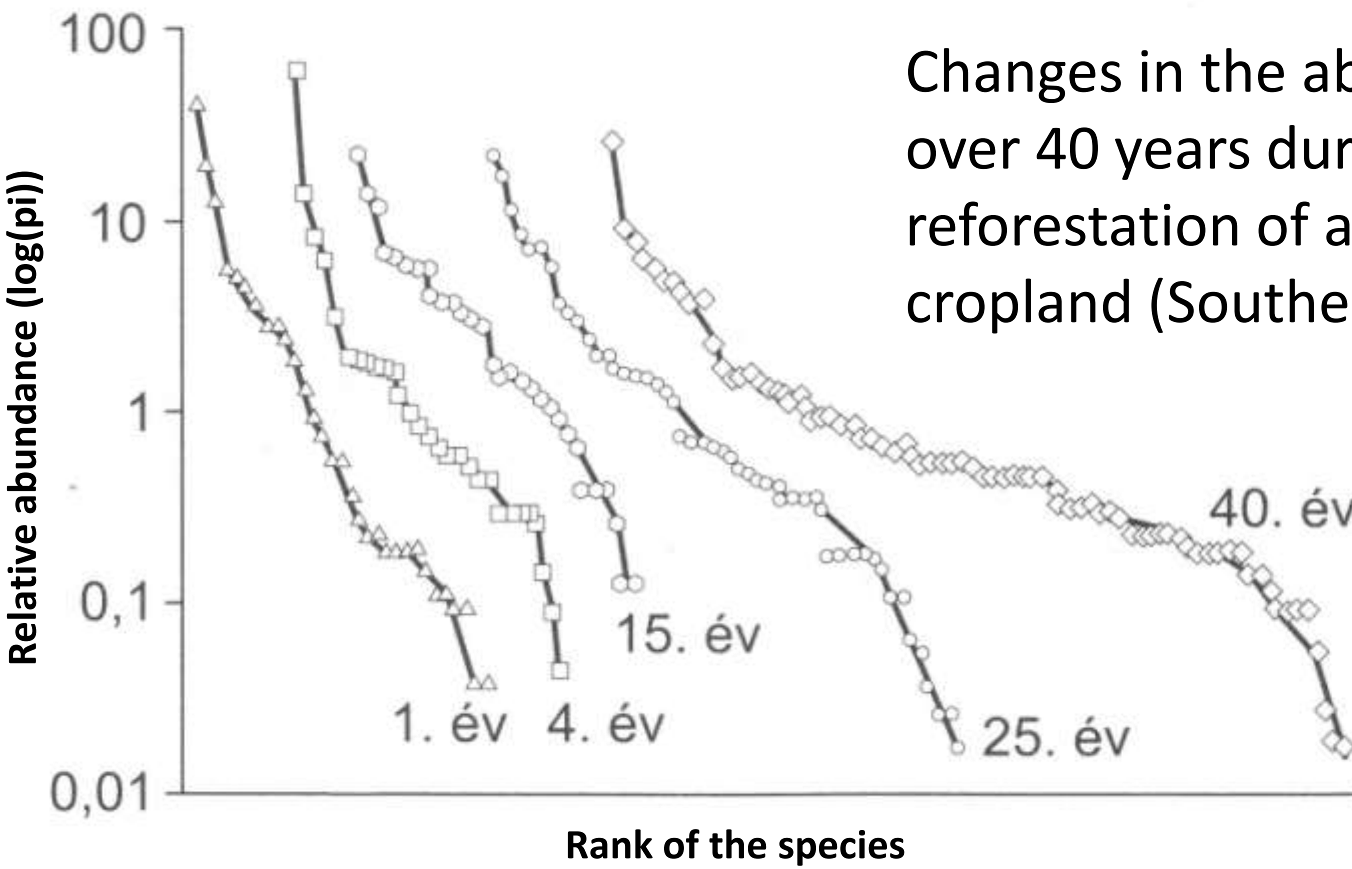
B: Broken StickPrimarily in animal communities.Species randomly divide the resources among themselves.

C: LognormalLate stages of succession.Hierarchical resource distribution occurs at the group level, not the species level.



Some examples of the fit between theoretical and empirical data:(
A) Geometric Sequence Model: plant species of a subalpine spruce forest (Tennessee, USA)(B) Broken Stick Model: species of a low-diversity bird community (West Virginia, USA)(C) Lognormal Model: vegetation of a temperate deciduous forest

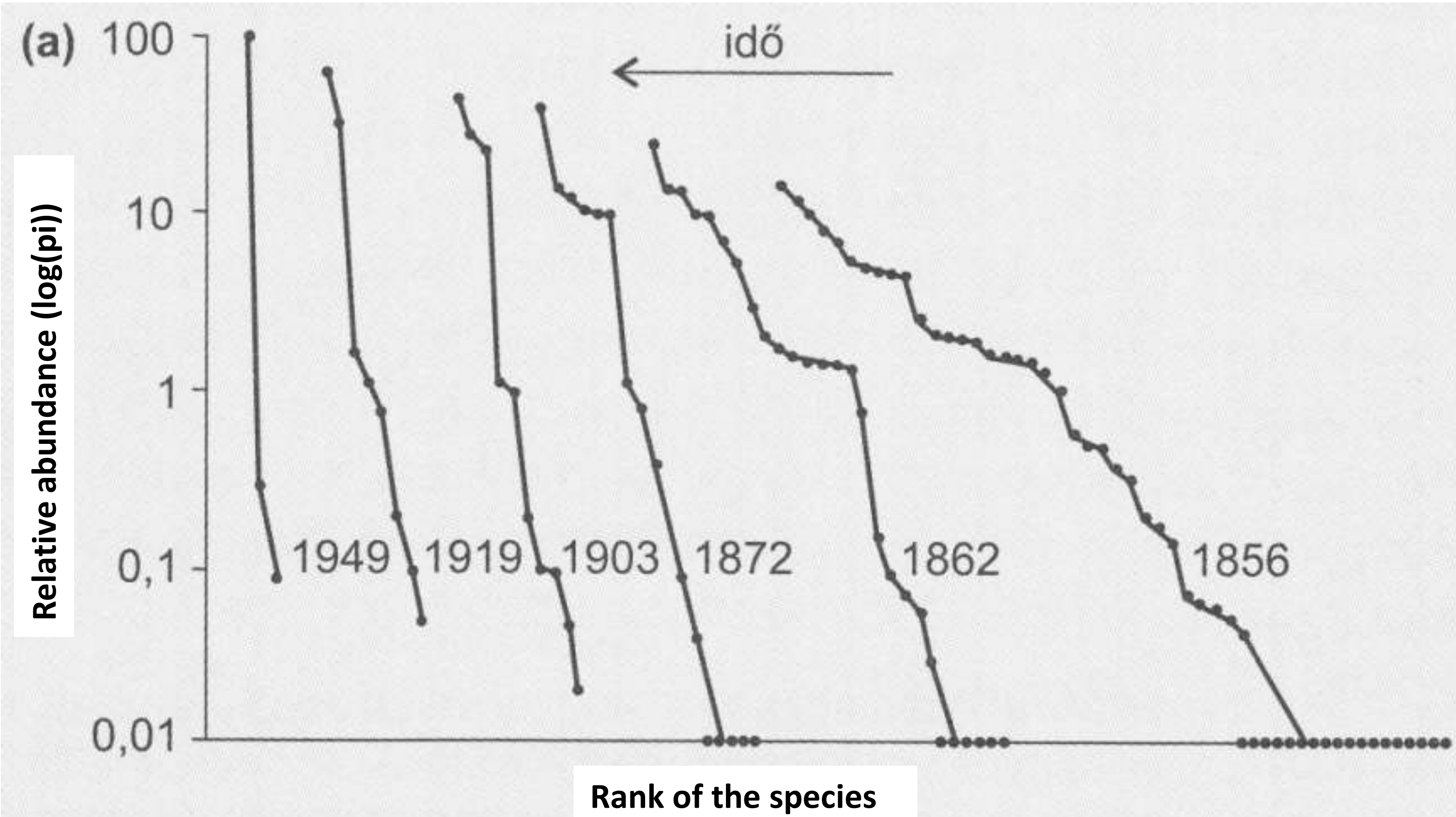
The change in texture indicates the change in the given community



Changes in the abundance ranking over 40 years during the reforestation of an abandoned cropland (Southern Illinois, USA)

The vertical axis shows coverage data on a logarithmic scale. It is evident that during the succession of the fallow land, the number of species increases, and the abundance ratios between species become more balanced. In the early stage (the first year), the distribution follows a geometric sequence. After 40 years of fallow, a lognormal distribution is observed.

The change in texture indicates the change in the given community



Fertilization experiment in a grassland in England: The experimental plots were continuously treated with fertilizers containing nitrogen, phosphorus, and potassium. As a result, the number of species drastically decreased.

- Diversity Index

Diversity indices based on the ratio of species and individual numbers provide a more adequate characterization than species richness alone. These are calculated using diversity functions, which are characterized by the fact that their values increase with both species richness and evenness. The most commonly used diversity index is the Shannon-Wiener index**.**

Shannon-Wiener diversity index:

$$H = -\sum_{i=1}^{S}(p_i * \ln p_i)$$

where ***H*** *:* diversity index

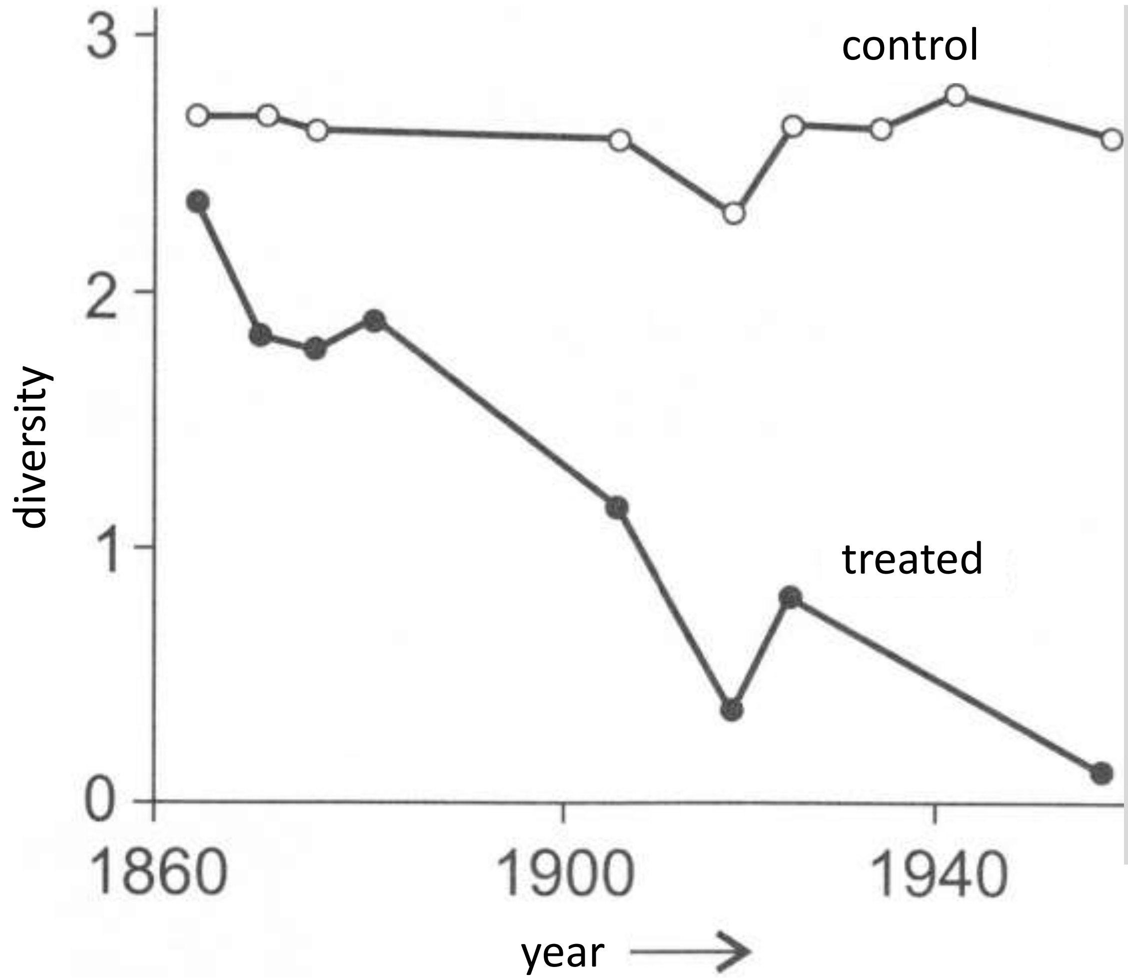
S *:* # of species in the community

$\boldsymbol{p_i}$*:* relative abundance of the *ith*-species ($p_i=N_i/N$)

$\boldsymbol{\ln p_i}$*:* natural logarithm of the *pi*. (ln pi is has negative value)

The negative sign ensures that the value of H is positive

Species texture and diversity index



Change in Shannon diversity during the grassland degradation shown earlier.
It can be seen that in the treated, over-fertilized grassland, diversity decreases significantly over time: the grassland becomes impoverished.
In contrast, on the control plots, the initial diversity – with minor fluctuations – is maintained.

- **Evenness**

Evenness (E) it expresses how evenly the total number of individuals (or cover, biomass) is distributed among the species in the community. Its value always ranges between 0 and 1

Calculation: $$E = H/H_{max}$$

where H : actual diversity,
H_{max} : maximum diversity at the given number of species.

$$H_{\max} = -\sum_{i=1}^{S} (1/S) * \ln(1/S)$$

where S : number of species in the community,
$ln(1/S)$: natural logarithm of the $1/S$.
$H_{max} \geq H$

Among communities with the same number of species, the one with greater evenness is more diverse.

- Mosaic structure

It describes how evenly or mosaic-like the spatial distribution of species is across the area.

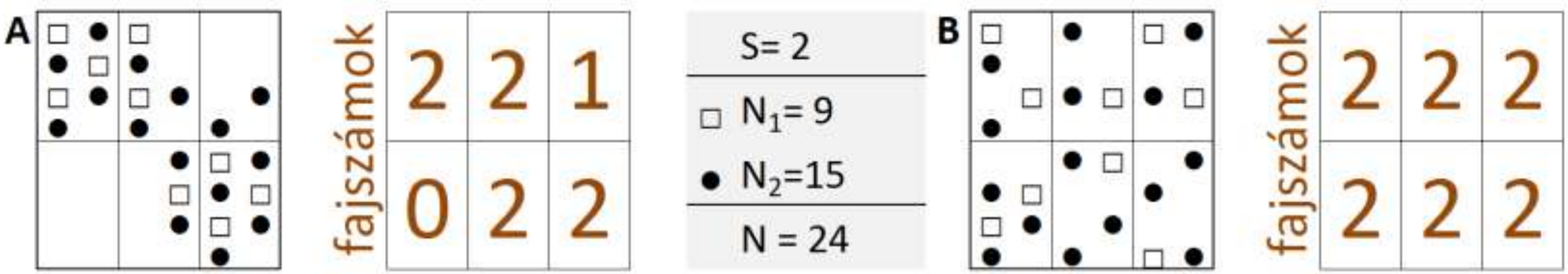
Whittaker index : $$\beta w = \frac{S}{\text{mean } (S_{kvad})} - 1$$

ahol S : # of species in the area,

mean (S_{kvad}) : mean number of species in the sampling quadrats

The more mosaic-like an area is, the higher its βw value (with the same number of species and the same number of individuals per species).

β_w Its value can range between 0 and (r-1), where r is the number of sampled quadrats.



S=2 **mean** (S_{kv})=9/6= **1,5**

β_W= 2/1,5-1=**0,333**

S=2 **mean** (S_{kv})=12/6= **2**

β_W= 2/2-1=**0**

IMPORTANT:

When analyzing and comparing the diversity of communities, it is crucial to proceed carefully with the results obtained from the calculations.

The significance of the species forming the community varies, which greatly influences the assessment of the natural diversity of the given community.

For example, non-native and invasive species increase the species count, but are unfavorable from the perspective of the community's natural diversity, a factor that must be considered when analyzing and comparing communities.

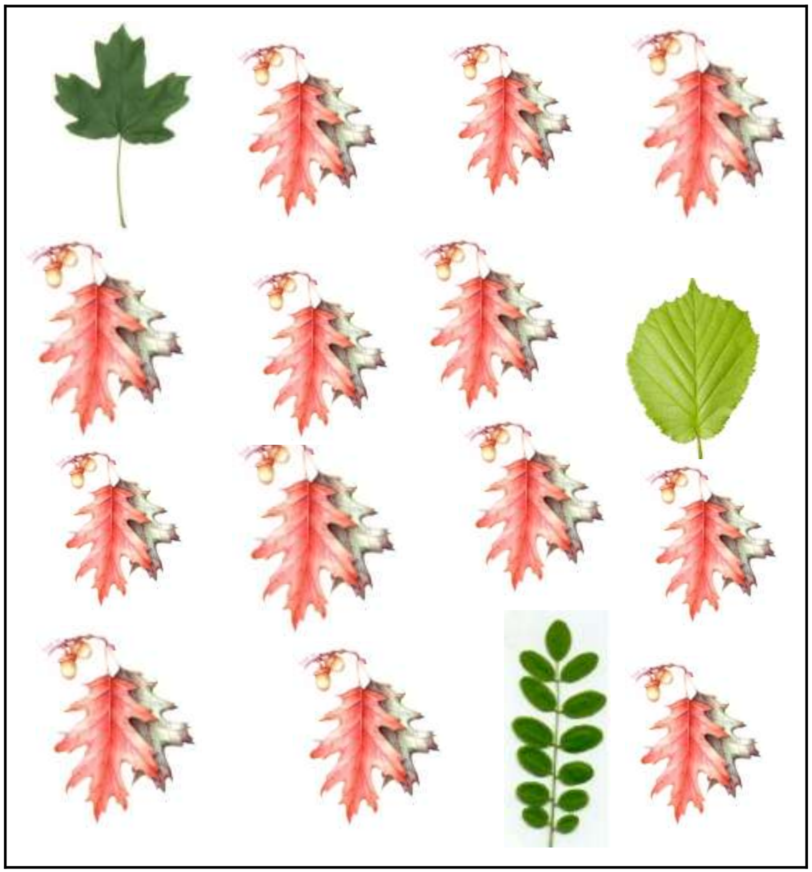
When assessing the naturalness of forests, other criteria should also be taken into account (e.g., composition and structure of the tree layer, shrub layer, herb layer, and regeneration, dead wood, soil, and wildlife impacts).

The most common shrub and tree species occurring in the Sóstó Forest, along with their characteristics. Species marked with an X are non-native (introduced), invasive, or nitrophilous species in Hungary

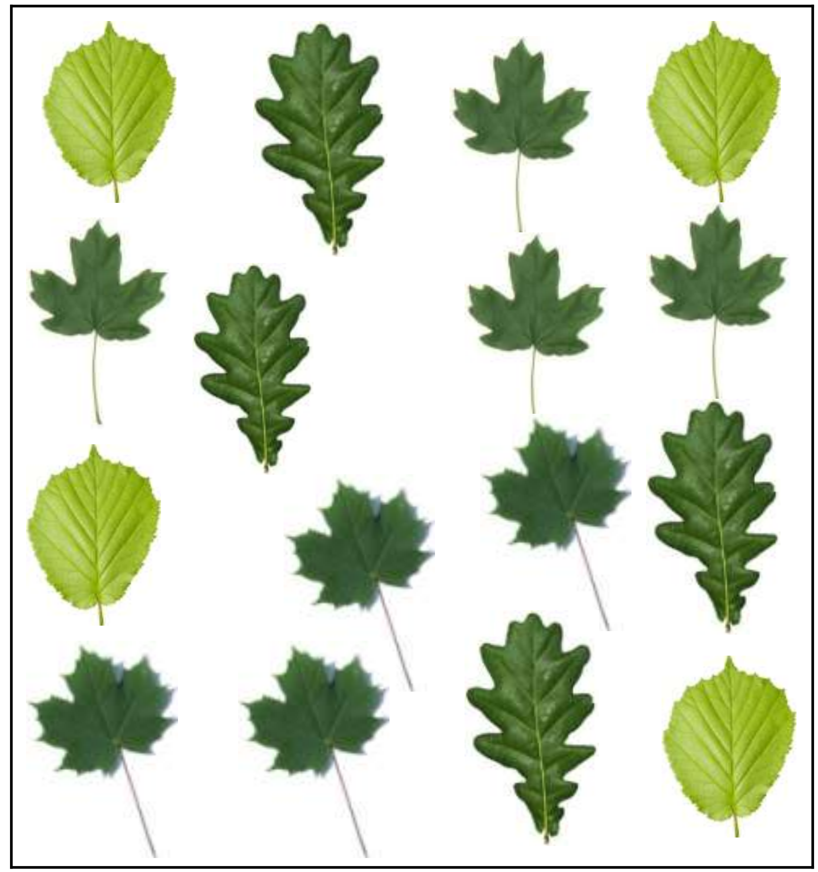
English name	Latin name	Non natív	Invasive	nitrophil
Black elder	Sambucus nigra			X
Black locust	Robinia pseudoacacia	X	X	X
Boxelder	Acer negundo	X	X	
Common hackberry	Celtis occidentalis	X	X	
Common hazel	Corylus avellana			
Common Oak	Quercus robur			
Dog rose	Rosa canina			
Elm	Ulmus sp.			
Field maple	Acer campestre			
Ivy	Hedera helix			
Late cherry	Padus serotina	X	X	
Linden	Tilia sp.			
Maple-leaved plane tree	Platanus hybrida	X		
Norway maple	Acer platanoides			
Red oak	Quercus rubra	X		
Scotch pine	Pinus sylvestris	X		
Silver birch	Betula pendula			
Single-seed hawthorn	Crataegus monogyna			
Spindle	Euonymus europaeus			
Sycamore maple	Acer pseudoplatanus			
Tatarian maple	Acer tataricum			
Tree of Heaven	Ailanthus altissima	X	X	
White poplar	Populus alba			
Wild cherry	Cerasus avium			

1. Example : Which area is more diverse? Let's confirm our hypothesis through calculation! (species count: S, diversity index: H, evenness: E)

A) area

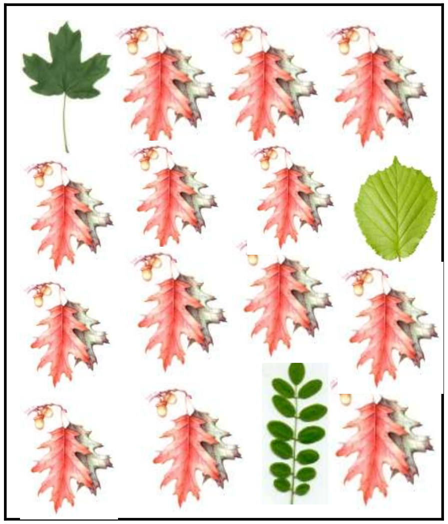


B) area



1. Calculation:

$$p_i = N_i / N \qquad H = -\sum_{i=1}^{S} (p_i * \ln p_i) \qquad H_{max} = -\sum_{i=1}^{S} (1/S) * \ln(1/S)$$

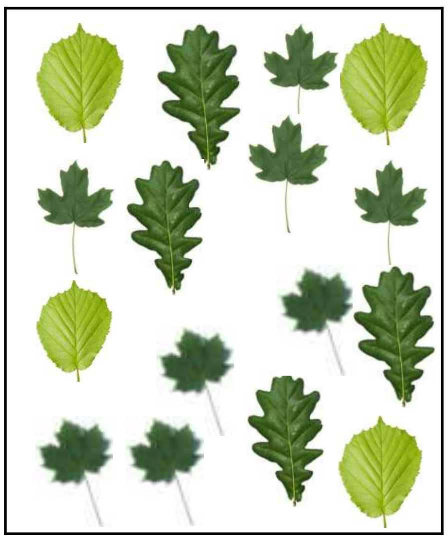


A) area

i	Faj	N_i	p_i	$\ln p_i$	$p_i * \ln p_i$	$1/S$	$\ln 1/S$	$1/S * \ln 1/S$
			H calculation			H_{max} calculation		
1	**field maple**	1	0.0625	-2.77	-0.173	0.25	-1.39	-0.346574
2	**red oak**	13	0.8125	-0.21	-0.169	0.25	-1.39	-0.346574
3	**hasel**	1	0.0625	-2.77	-0.173	0.25	-1.39	-0.346574
4	**black locust**	1	0.0625	-2.77	-0.173	0.25	-1.39	-0.346574
	SUM	16	1		-0.689	1		-1.386294

S = 4 **H = 0.689** **H_{max} = 1.386294**

N = 16 **E = 0.496696**



B) area

i	Faj	N_i	p_i	$\ln p_i$	$p_i * \ln p_i$	$1/S$	$\ln 1/S$	$1/S * \ln 1/S$
			H calculation			H_{max} calculation		
1	**hasel**	4	0.25	-1.39	-0.347	0.25	-1.39	-0.346574
2	**field maple**	4	0.25	-1.39	-0.347	0.25	-1.39	-0.346574
3	**common oak**	4	0.25	-1.39	-0.347	0.25	-1.39	-0.346574
4	**Norway maple**	4	0.25	-1.39	-0.347	0.25	-1.39	-0.346574
	SUM	16	1		-1.386	1		-1.386294

S = 4 **H = 1.386** **H_{max} = 1.386294**

N = 16 **E = 1**

1. Example - Comparison of the two forest plots

	A)		B)
# of species:	$S_A = 4$	=	$S_B = 4$
# of individuals:	$N_A = 16$	=	$N_B = 16$
diversity index:	$H_A = 0.689$	<	$H_B = 1.386$
evenness:	$E_A = 0.497$	<	$E_B = 1.000$
# of invasive species:	1		0
# of invasive individuals:	1		0
Ratio of invasive individuals (%):	6.25%		0%
# of non-nativ species:	1		0
# of non-native individuals:	13		0
Ratio of non-nativeindividuals (%):	81.25%		0%

Both areas have the same number of species and individuals. However, the diversity index and evenness are much higher in area B). Only native tree species are found in area B), while in area A), 81.25% of the species are non-native and 6.25% are invasive species. Based on this, area B) is more diverse and natural.

2. example The table contains the aggregated species list and individual counts from the tree survey conducted in 6 quadrats of the forest plot. Based on this data, let's calculate the patchiness (**Mosaic structure**) of this area!

Species	**1.kv**	**2.kv**	**3.kv**	**4.kv**	**5.kv**	**6.kv**	**N_i**
black elder	5	3	7	23	1		**39**
red oak	6	6		1	8	1	**22**
linden	1	1			1	4	**7**
elm			5		1		**6**
tataria maple	3		2				**5**
Sycamore maple		3	1			1	**5**
common hasel			2		1	1	**4**
singel-seed hawthorn	1					3	**4**
spindle				4			**4**
wildcherry			1			1	**2**
norway maple	1						**1**
white poplar						1	**1**
sum number : N							**100**
S_{kvad}, S	6	4	6	3	5	7	

Whittaker index:

$$\beta w = \frac{S}{\text{mean } (S_{kvad})} - 1$$

$\boldsymbol{S}$=

mean $\boldsymbol{S_{kvad}}$ =

$\boldsymbol{\beta_W}$ =

2. Example The table contains the aggregated species list and individual counts from the tree survey conducted in 6 quadrats of the forest plot. Based on this data, let's calculate the patchiness (Mosaic structure) of this area!

Species	1.kv	2.kv	3.kv	4.kv	5.kv	6.kv	N_i
black elder	5	3	7	23	1		**39**
red oak	6	6		1	8	1	**22**
linden	1	1			1	4	**7**
elm			5		1		**6**
tataria maple	3		2				**5**
Sycamore maple		3	1			1	**5**
common hasel			2		1	1	**4**
singel-seed hawthorn	1					3	**4**
spindle				4			**4**
wildcherry			1			1	**2**
norway maple	1						**1**
white poplar						1	**1**
sum number : N							**100**
S_{kvad}, S	**6**	**4**	**6**	**3**	**5**	**7**	**12**

Whittaker index:

$$\beta w = \frac{S}{\text{mean }(S_{kvad})} - 1$$

S=12

mean S_{kvad} = (6+4+6+3+5+7) / 6 = 5,1667

β_W = 12/5.1667 – 1 = 1.3225