Supplementary Material 1.

Distribution of fine-scale species richness in 5 x 5cm micro-quadrats (Figure S1).

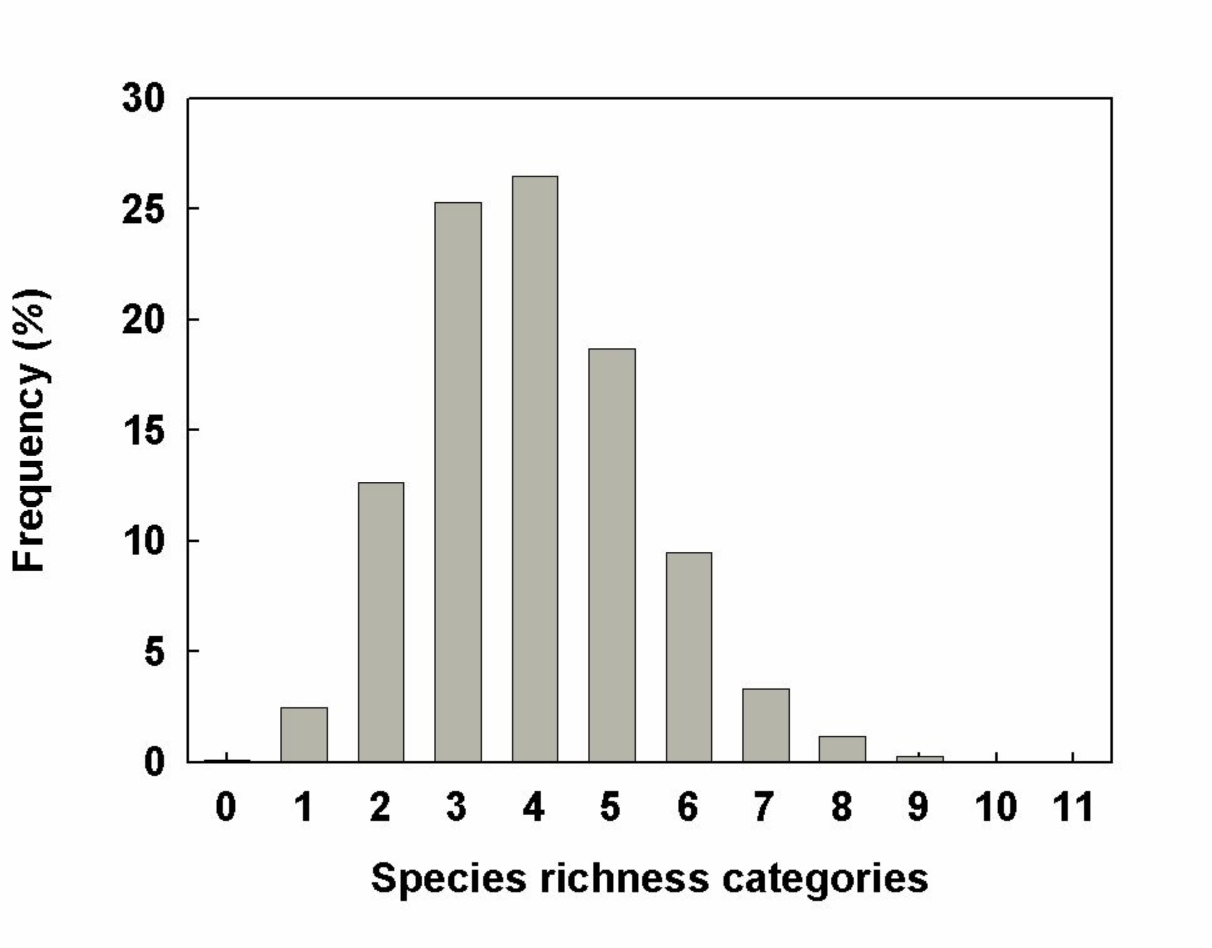


Figure S1 Distribution of fine-scale species richness in 5 x 5cm micro-quadrats (all species were considered and all data merged). Data represent the 12 transects (each 5m long) that was monitored over 5 years. The median species richness was 4 species (Q1=3 Q3=5 species). Species richness categories refers to the number of species found in a micro-quadrat.

Supplementary Material 2.

Diversity of species combinations and spatial scaling

Plant species form various species combinations in nature. For assessing within-stand spatial patterns of species combinations we used a diversity measure from a family of information theory models developed by Juhász-Nagy (Juhász-Nagy and Podani 1983, Juhász-Nagy 1993). We chose this model because it appeared to be especially sensitive detecting fine-scale changes in coexisting relationships within communities and could be used successfuly to describe vegetation changes during succession or degradation (Juhász-Nagy and Podani, 1983; Margóczi, 1993; Gosz, 2000; Bartha et al., 1995, 1998, 2004, 2011, 2020; Virágh 2008; Bakacsy, 2019). Using this model we expect to detect some early signals of vegetation changes due to changing the management regimes.

Spatial scaling is an inherent part of the methodology (Juhász-Nagy, 1993; Podani et al., 1993; Bartha et al., 1998) and the biological interpretation of models linked directly to the assembly dynamics (Bartha et al., 1995, 1998; Bartha et al., 2020). Traditional diversity indices often assessed at a single scale or at few arbitrarily chosen scales and they are often estimated from small samples. In contrast, Juhász-Nagy's models are assessed at a series of gradually increasing sampling units sizes (spatial scaling process) (Podani, 1987; Podani et al., 1993). The transect sampling design we used in this study was specifically developed and optimized for estimating these models (Bartha et al., 2004). Compositional Diversity (CD) is the diversity of realized (observed) species combinations at a given scale; which is calculated as the Shannon entropy of the frequency distribution of species combinations observed within the sampling units:

$$CD = -\sum_{k=1}^{\omega} p_k \log_2 p_{\mathbf{k}} \quad ,$$

where $\boldsymbol{\omega} = \mathbf{2}^{\mathbf{S}}$ is the number of possible species combinations, S is the number of species and p_k is the relative frequency of the **k**th species combinations in the sample. To estimate CD large sample sizes are required (100 units or more) and it is calculated at a series of increasing sampling unit sizes (gradually merging 2, 3, 4, etc. adjacent micro-quadrats along transect (Figure S2., S3). Spatial scaling used to be performed by computerized resampling of the base-line transects (Podani, 1987; Podani et al., 1993) with gradually increasing sampling unit sizes.

Illustration of how CD (the Shannon diversity of species combinations) differs from the traditional Shannon diversity calculated from species abundances is shown in Figure S4.

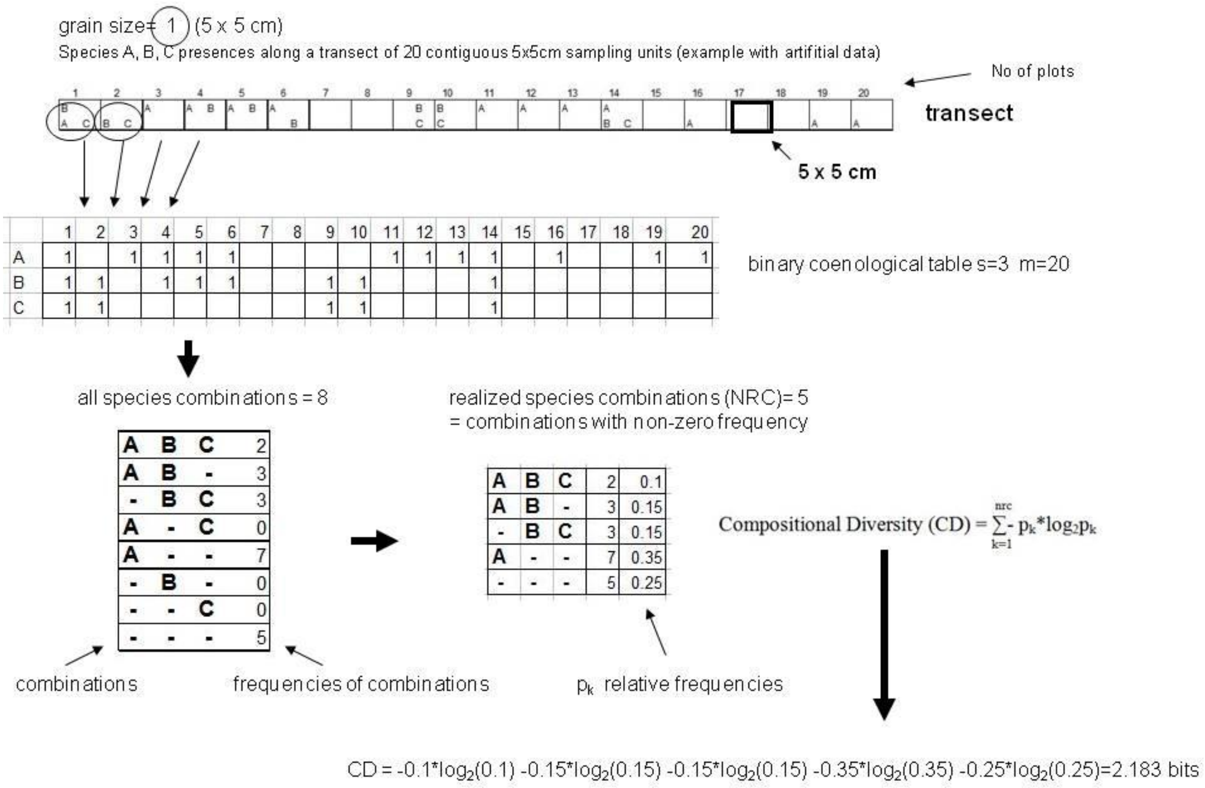


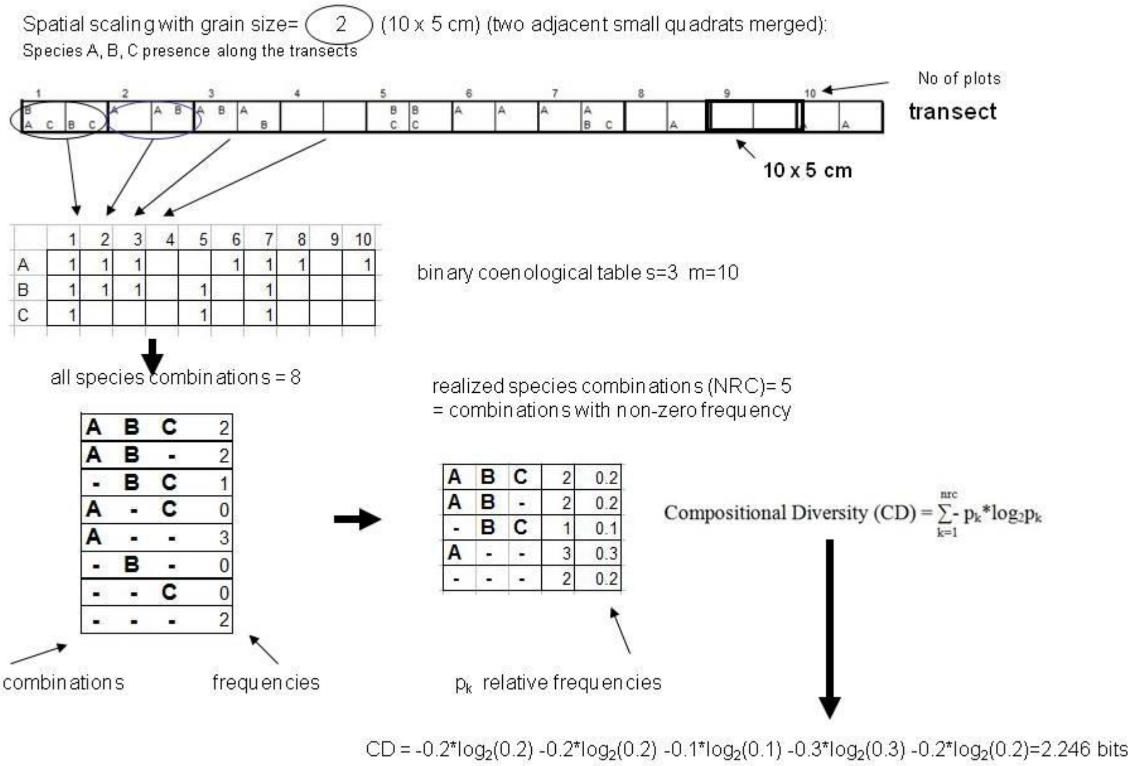
Figure S2. Illustration of the computerized sampling from the base-line transect data and the calculation of Compositional Diversity using artificial data Example for calculating Compositional Diversity with grain size=1

1, The baseline transect (20 units long with 3 species) resampled with computer (with grain size =1) and a binary coenological table is created.

2, Species combinations calculated from the binary coenological table.

3, Number of realized species combinations (NRC) are the number of combinations with non-zero frequency (from 3 species the potential maximum number of combinations would be 8, however, only 5 had non-zero frequency in our example (NRC=5).

4, Compositional Diversity (CD), i.e. the diversity of species combinations, which is calculated based on the relative frequency of species combinations.



	1	2	3	4	5	6	7	8	9	10
A	1	1	1			1	1	1		1
B	1	1	1		1		1			
C	1				1		1			

A	B	C	2
A	B	-	2
-	B	C	1
A	-	C	0
A	-	-	3
-	B	-	0
-	-	C	0
-	-	-	2

A	B	C	2	0.2
A	B	-	2	0.2
-	B	C	1	0.1
A	-	-	3	0.3
-	-	-	2	0.2

Compositional Diversity (CD) = $\sum_{k=1}^{nrc} -p_k * \log_2 p_k$

CD = $-0.2*\log_2(0.2) -0.2*\log_2(0.2) -0.1*\log_2(0.1) -0.3*\log_2(0.3) -0.2*\log_2(0.2)=2.246$ bits

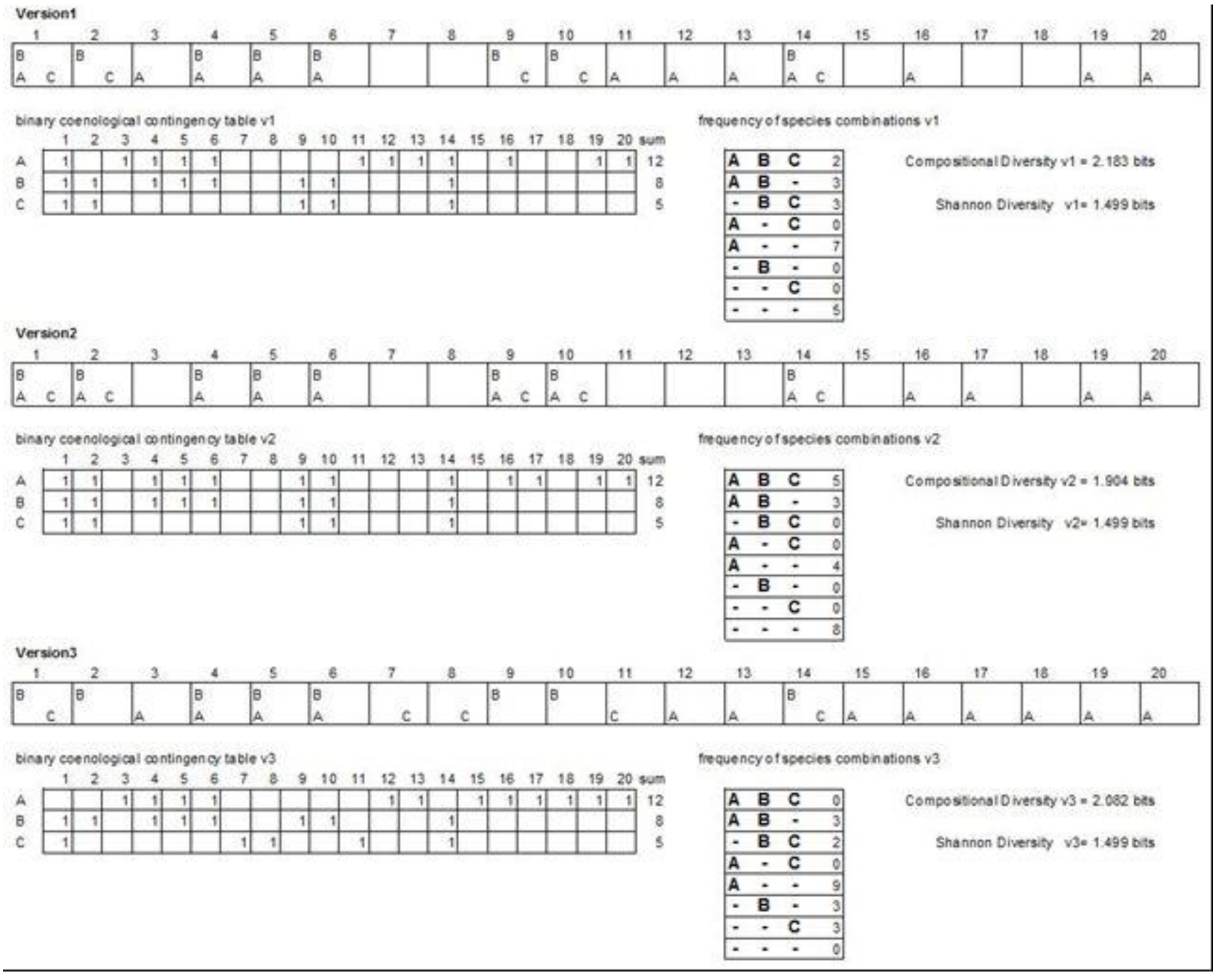
Figure S3. Example for calculating Compositional Diversity with grain size=2

1, The baseline transect (20 units long with 3 species) resampled with computer (with grain size =2) and a binary coenological table is created.

2, Species combinations calculated from the binary coenological table.

3, Number of realized species combinations (NRC) are the number of combinations with non-zero frequency (from 3 species the potential maximum number of combinations would be 8, however, only 5 had non-zero frequency in our example (NRC=5).

4, Compositional Diversity (CD), i.e. the diversity of species combinations is calculated based on the relative frequency of species combinations.



Version1

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
B A C	B C	A	B A	B A	B A			B C	B C	A	A	A	B A C		A			A	A

binary coenological contingency table v1

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	sum
A	1		1	1	1	1					1	1	1	1		1			1	1	12
B	1	1		1	1	1			1	1				1							8
C	1	1							1	1				1							5

frequency of species combinations v1

A	B	C	2
A	B	-	3
-	B	C	3
A	-	C	0
A	-	-	7
-	B	-	0
-	-	C	0
-	-	-	5

Compositional Diversity v1 = 2.183 bits

Shannon Diversity v1= 1.499 bits

Version2

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
B A C	B A C		B A	B A	B A			B A C	B A C				B A C		A	A		A	A

binary coenological contingency table v2

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	sum
A	1	1		1	1	1			1	1				1		1	1		1	1	12
B	1	1		1	1	1			1	1				1							8
C	1	1							1	1				1							5

frequency of species combinations v2

A	B	C	5
A	B	-	3
-	B	C	0
A	-	C	0
A	-	-	4
-	B	-	0
-	-	C	0
-	-	-	8

Compositional Diversity v2 = 1.904 bits

Shannon Diversity v2= 1.499 bits

Version3

1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20
B C	B	A	B A	B A	B A	C	C	B	B	C	A	A	B C	A	A	A	A	A	A

binary coenological contingency table v3

	1	2	3	4	5	6	7	8	9	10	11	12	13	14	15	16	17	18	19	20	sum
A			1	1	1	1						1	1		1	1	1	1	1	1	12
B	1	1		1	1	1			1	1				1							8
C	1						1	1			1			1							5

frequency of species combinations v3

A	B	C	0
A	B	-	3
-	B	C	2
A	-	C	0
A	-	-	9
-	B	-	3
-	-	C	3
-	-	-	0

Compositional Diversity v3 = 2.082 bits

Shannon Diversity v3= 1.499 bits

Figure S4. Illustration of how CD (the Shannon diversity of species combinations) differs from the traditional Shannon diversity calculated from species abundances. In the example we show three different communities with the same abundance of species but with different patterns of species co-occurrences (different combinations of species). The traditional abundance diversity estimates do not differ between these communities. In contrast, Compositional Diversity (CD) is able to detect the fine changes in coexistence relationships.

Illustration for the importance of estimating Compositional diversity (CD) at many different grain sizes. At very small grain sizes many of the sampling units are empty or contain only one species (consequently we have relatively few species combinations). At very large grain size it can appear that all sampling units have all species (i.e. we have only one species combinations). The largest number of realized species combinations tends to appear in intermediate grain sizes. Consequently, CD shows a unimodal maximum curve if it is plotted against the grain size. (Figure S5, S6)

The maximum Compositional Diversity is usually different in different communities and it can change also due to stress, disturbance or succession (Juhász-Nagy and Podani, 1983; Margóczi, 1993; Bartha et al., 2004, 2011; Virágh et al., 2008; Bartha et al., 2020). Careful spatial scaling is necessary to find precisely the resolution where the function maximum appears. In this paper 23 different grain sizes were tested. (Figure S5, S6).

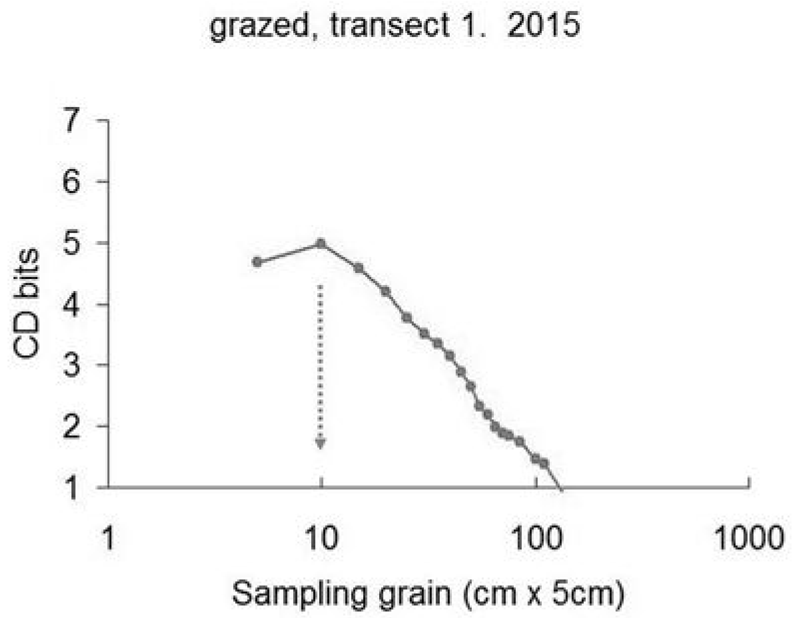


Figure S5. Spatial scaling of Compositional diversity with real data (one transects in 2015 at the grazed site). The arrow shows the spatial scale where the function maximum was detected.

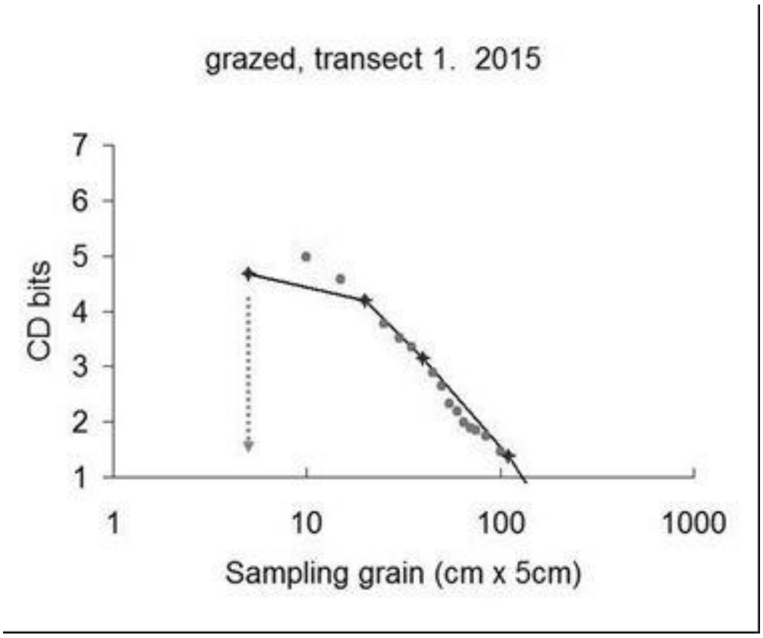


Figure S6. Illustration of improper scaling. Biased results for curve and for maximum scale because few grain sizes were tested (real data, the same transect in 2015 at the grazed site). Arrow shows the spatial scale where the function maximum was detected (10cm was the proper scale but 5cm was detected due to improper spatial scaling).

Illustration of choosing the right number of species in the analyses.

The number of potential species combinations of **s** species is $\mathbf{2^s}$, i.e. the number of potential species combinations increases exponentially when we increase the number of species in the analyses (Figure S7). Selecting too many species in the analyses might results in biased estimates because it would require very large sample sizes that usually cannot be collected in practice. Therefore, we usually focus on a reasonable subset of species (usually the most important dominant species forming the vegetation matrix).

The number of species combinations found in an analysis is constrained by the maximum number of sampling units. The sample size was 100 in our case that allow 6-7 species (if $s=6$ $2^s=64$ if $s=7$ $2^s=128$) to be considered (Figure S7). However, during analyses we do not prefer to fix the number of species considered because the number of species playing an important role tends to change during vegetation dynamics. Instead, we fix the maximum number of species that can be analysed. Setting an abundance threshold (larger or equal to 20 presences per transect) was an optimal choice in our study resulting in 6-8 species and in 6-96 species combinations. We assume here that species appearing in less than 20% of sampling units might not be so important functionally.

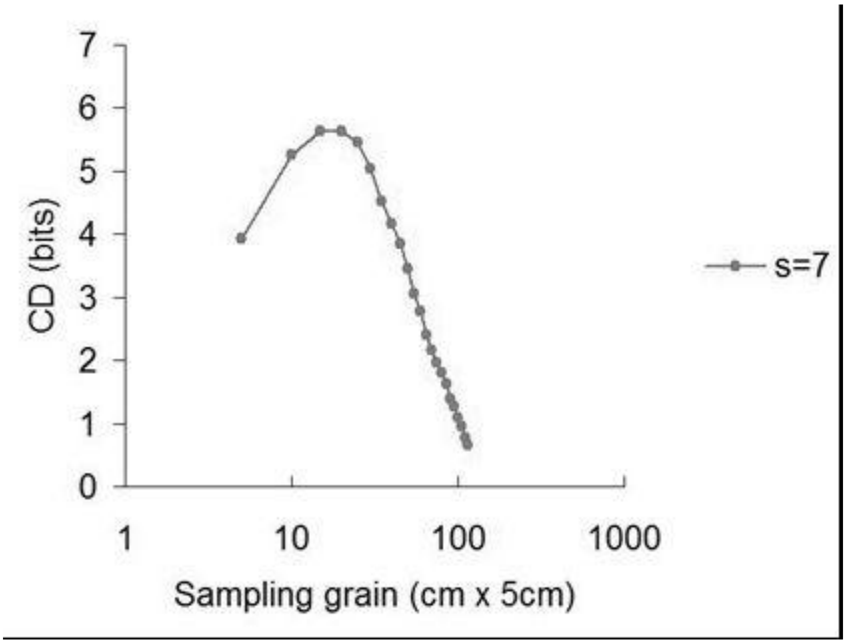


Figure S7. Illustration of properly estimated curve of Compositional Diversity.

However, compositional diversity curves appear in truncated forms if it is calculated from too many species (Figure S8). Maximum values and the spatial scale of maxima cannot be detected precisely from these truncated curves. For 15, 35 or 45 species the max. CD would be larger than 7 bits. However, due to the limited sample size (m=100) we reached a threshold where all microquadrats had different species combinations and all combinations were equally frequent, this is 6.643 bits in our case. Larger CD values cannot be detected.

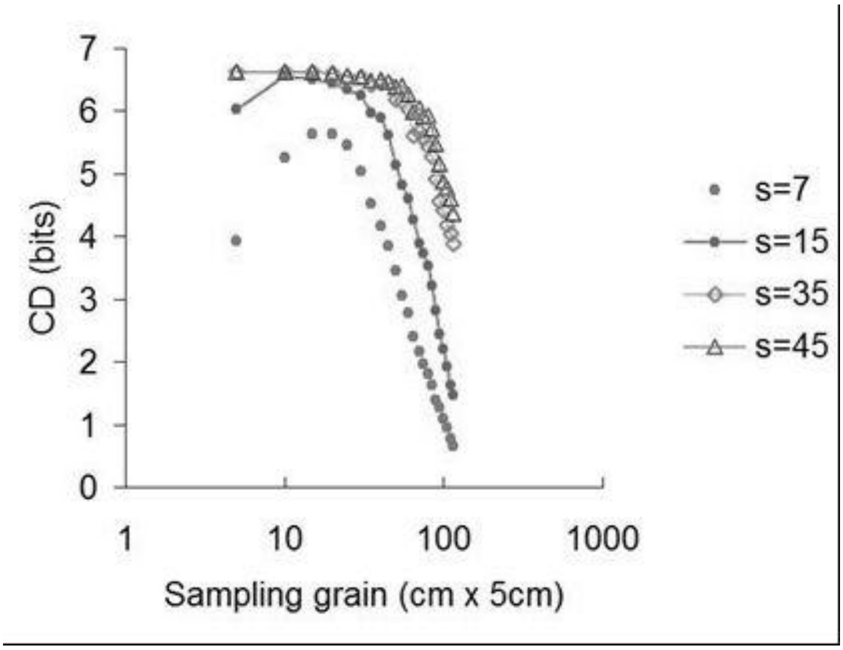


Figure S8. Ccompositional diversity curves appear in truncated forms if it is calculated from too many species (maximum values and the spatial scale of maxima cannot be detected precisely from these truncated curves. For 15, 35 or 45 species the max. CD would be larger than 7 bits.)

In this study we used an abundance threshold (minimum 20 presence in a 100 units (5m long) transect. This threshold resulted in 6-8 species per transects and represented the most important dominant (matrix forming) species of the grassland.

Characteristic scales detected in this study

After careful scaling and careful selection of proper abundance threshold, the detected maximum scales did not differ between the grazed (transects G1-G6) and mowed (transects M1-M6) vegetation patches (Figure S9). All maximum data appeared at 5 x 5 cm (or rarely at 5 x 10 cm) (Figure S9). In contrast to the heterogeneity in species composition (spatial heterogeneity) and the compositional variability due to fluctuating weather conditions (temporal heterogeneity), the estimated scales of maximum Compositional Diversity appeared at very fine scales and remained stable in our study.

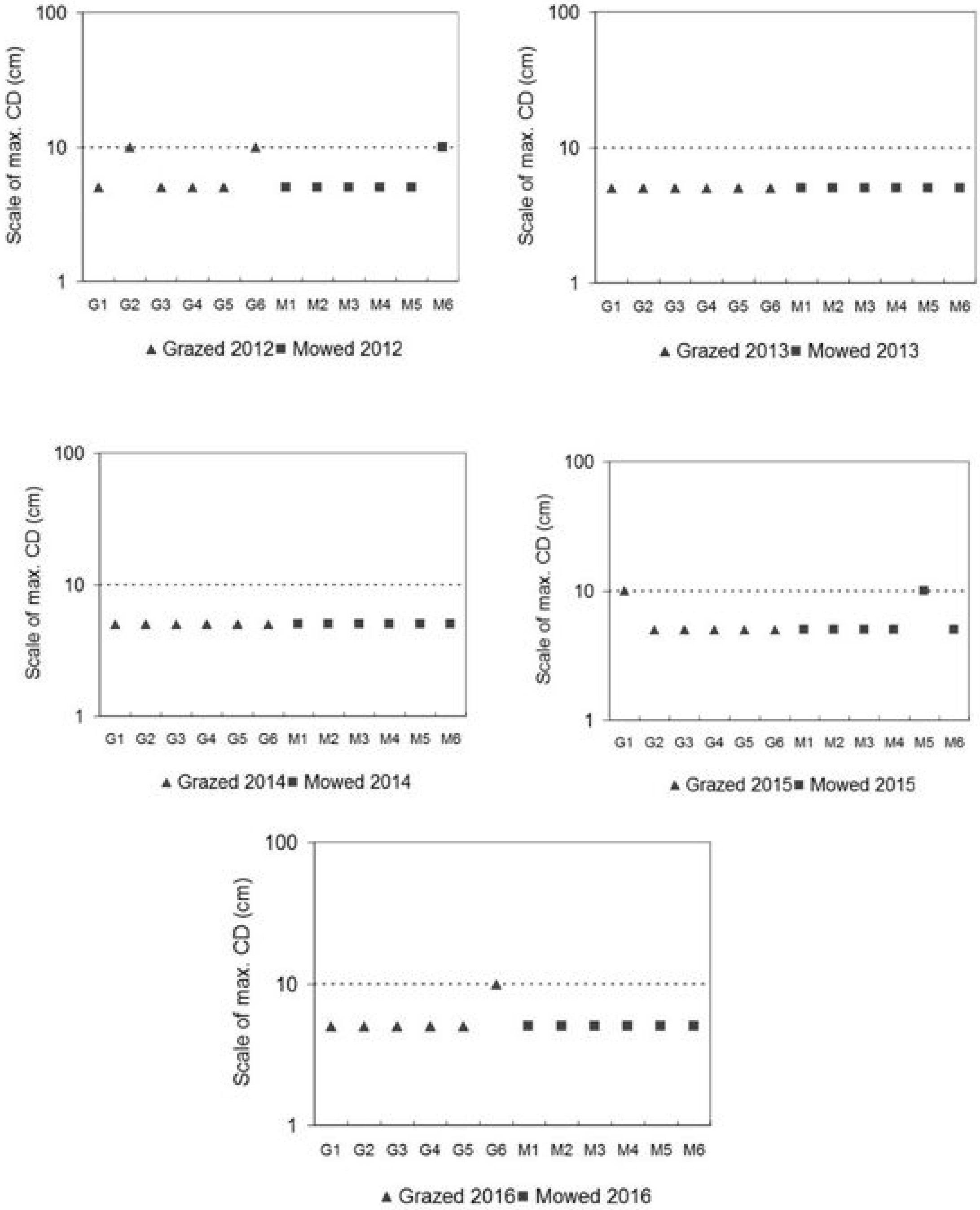


Figure S9. Characteristic scales detected in this study (grazed transects G1-G6, mowed transects M1-M6). All maximum data appeared at 5 x 5 cm (or rarely at 5 x 10 cm).

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