Plot size – a skeleton in the cupboard of phytosociologists

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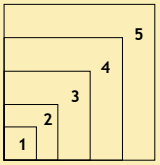
The size of plots used for sampling belongs to the primary topics in vegetation science. Plot sizes utilised by phytosociologists may differ considerably even within a vegetation type and the full range of plot sizes routinely used in phytosociology ranges from 0.1 to 2500 m^2. The effects of discrepant plot sizes on the results of vegetation classification remains however unknown. This is especially painful nowadays, when large databases are compiled and analysed. Our aim was to test the effect of plot size on classification of vegetation, using species-rich grasslands as a model. Besides the plot size, we also considered the effect of transformations of plant cover data on the results of classification.

METHODS

Dry, species-rich grasslands, dominated by *Carex humilis* and *Brachypodium pinnatum*, were sampled in nature reserves in the southeastern part of the Czech Republic. Data from 21 plots, each consisting of 5 nested subplots of increasing size, were used in the analysis. The range of our plot sizes corresponds to plot sizes commonly used in grasslands by European phytosociologists.

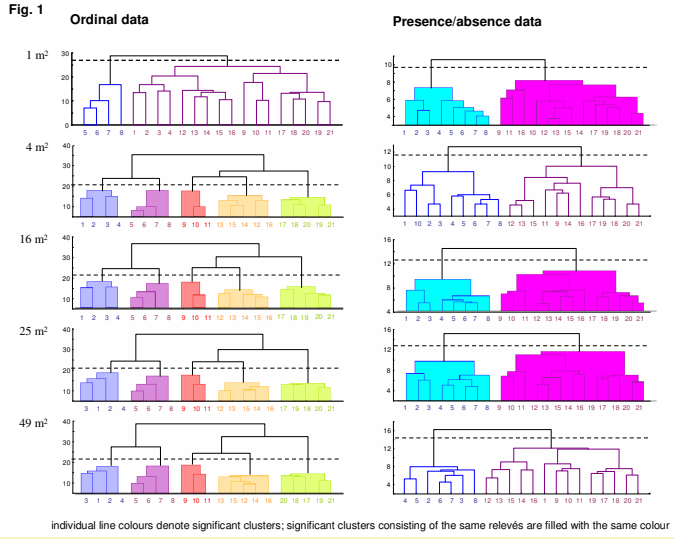


1 - 1 m^2
2 - 4 m^2
3 - 16 m^2
4 - 25 m^2
5 - 49 m^2

We classified the relevés using Ward´s method of clustering and Euclidean distance as a measure of dissimilarity between plots, for each individual plot size. Two transformations of species cover-abundances (presence/absence and cover values on a 9-grade ordinal scale) were used. Significance of the resulting clusters was evaluated by bootstrap resampling (at p = 0.1), developed by Pillar (1999). This method examines the stability of the partition at a given level by resampling the original data. Unstable partitions at particular levels of partition indicate a fuzzy group structure of the data. Additionally, resulting classifications were compared for diagnostic species (Chytrý et al. 2002; here defined as species with fidelity u_{hyp} >0.49), in the program JUICE (Tichý 2001). Their number was counted for each cluster and plot size separately (Figs. 2A and B) and their relative number was calculated as the ratio between the number of diagnostic species shared by pairs of corresponding clusters (in Fig. 1) calculated for plot sizes X and Y_i, and total number of diagnostic species shared by those pairs of clusters at the same plot sizes, multiplied by 100 (Figs. 2C and D). X denotes plots 4 m^2 in size for ordinal data and 1 m^2 for presence/absence data, Y_i denotes plots with sizes larger than 4 m^2 and 1 m^2 for ordinal and presence/absence data, respectively.

RESULTS

Fig. 1

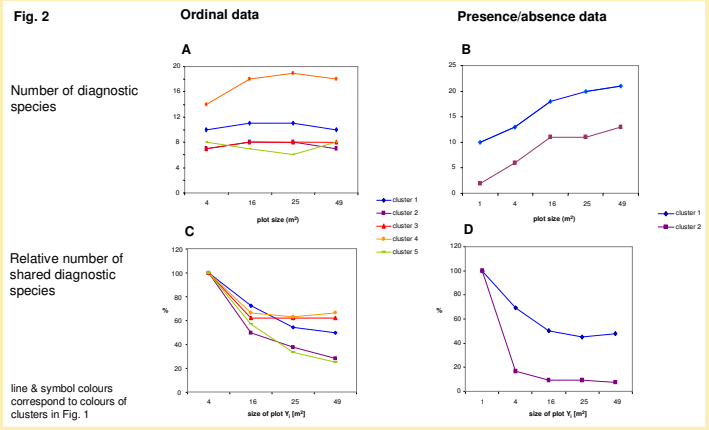


individual line colours denote significant clusters; significant clusters consisting of the same relevés are filled with the same colour

When ordinal data were used, five significant clusters were obtained for plots 4 to 49 m^2 in size, with the same assignment of relevés to individual clusters between classifications, but only two clusters were obtained at the smallest plot size. In contrast, only two clusters were significant, independently of plot size, when presence/absence data were used. In this case, assignment of relevés to clusters was affected by plot size (Fig. 1).

The effect of plot size was more profound with diagnostic species. While changes in absolute numbers of diagnostic species did not show a consistent trend across plot sizes for ordinal data (Fig. 2A), it markedly increased for plots from 1 to 16 m^2 in size for presence/absence data (Fig. 2B). On the other hand, the relative number of shared diagnostic species decreased with plot size for all clusters and for both transformations of cover data (Fig. 2C and D). Relative numbers of shared diagnostic species dropped down to about 30 % in some clusters. This implies a high turnover of diagnostic species across plot sizes and indicates that diagnostic species are highly dependent on the scale used. The composition of diagnostic species was similar between larger plots, while it changed considerably towards the smallest plots.

Fig. 2



CONCLUSION

Number of significant clusters and assignment of individual relevés to the clusters were independent of plot size, except for the smallest plot (1 m^2), but were affected by transformations of plant cover data. The low proportion of diagnostic species shared by corresponding clusters calculated for different plot sizes indicates that combining plots with very different sizes may result in unexpected biases in vegetation classification, especially if very small plots are included. Plot sizes within one order of magnitude should be used to avoid unintentional effects of plot size.

REFERENCES

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