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Presenter Information

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New approaches to measuring the functional value of biodiversity in plant communities

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Introduction The weight of evidence across a wide range of organisms points to a positive relationship between diversity and ecosystem function. The methods used to analyse biodiversity experiments have been largely based on ANOVA or graphical representation (e.g. Figure 1). We propose a framework based on biologically meaningful coefficients that quantify the separate contribution of each species and various interactions among species to the functional response. Recent work (Kirwan et al., 2007) and preliminary analysis suggest that diversity-function (DF) relationships can largely be described in terms of the identity of species and low order species interactions. The difficulties attending DF research are further compounded as the size of the species pool from which communities can be assembled increases. We propose a quantitative approach based on a small number of biologically meaningful coefficients.

Materials and methods In general the functional response (y) for a community of t species selected from a pool of s species can be characterised as the sum of five terms, $y = ID_m + ID_p + D_m + D_p + \epsilon$, where Average Identity effect (ID_{av}) = mean average monoculture effect over all s species and Particular identity effect (ID_p) for the t species selected, Average diversity effect (D_{av}) = Mean difference between response and ID ($= ID_m + ID_p$), averaged over all t -species selections (solid line Figure 1), Particular diversity effect (D_p) = extra diversity effect due to the particular species selected (Range bars Figure 1) and Random error. The diversity effect is $D = D_m + D_p$. We used data of 206 experimental plots and 100 different plant assemblages of grassland species that varied in species richness (1, 2, 3, 4, 6 and 9 species, Roscher et al., (2004), data supplied courtesy of Dr Christiane Roscher, Max-Planck-Institute for Biogeochemistry in Jena, Germany) to test our models.

Results and discussion We propose a range of models to quantify the terms in [1] to provide a description of the functional response. We fitted several of these models to the data. We estimated 5 coefficients for a simple version of the model (all estimates in $g\ m^{-2}$): ID_m (estimate of coefficient 312), the standard deviation among monoculture yields (212), D_m (926), the standard deviation of pairwise interaction coefficients (385) and the residual standard deviation (123). ID_p and D_p are related to the first two standard deviations estimated. The model describes the data as well as the 99 degrees of freedom between all assemblages.

The model can be used to address a wide range of theoretical questions about diversity-function relationships including:

- Does the diversity effect saturate with increasing richness and is there a simple characterisation/explanation of this effect?
- What is the relative importance of the average diversity effect, the sampling and selection effects in contributing to the DF relationship?
- What is the relative importance of the identity and diversity effects?
- Is there evidence for transgressive overyielding (do mixtures perform better than the best monoculture)?

In addition, the model is flexible enough to explore changes in DF relations through time and the effect of functional types and species traits.

References

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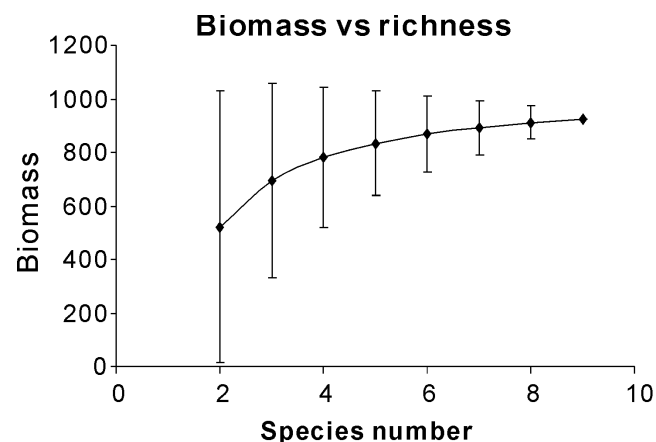


Figure 1 Idealized relationship between diversity effect (D) and species richness. The solid line shows the average diversity effect over all species selections and the bars the range of deviations for particular species selections.