Oikos

O18411

Mokany, K. and Roxburgh, S. H. 2010. The importance of spatial scale for trait-abundance relations. – Oikos 119: 1504–1514.

Appendix 1

Single trait simulation exercise

We examined the capacity of both the MaxEnt and correlation approaches to detect underlying relationships between species abundances and their trait values through a simulation exercise. Relative abundance data from the landscape scale (where all 76 species have non-zero abundances) were applied in combination with simulated trait data for a single trait. We generated six types of relationships between the abundances of species and their trait values, by allocating species abundances to five equal sections of the trait axis (Table A1 – rows). Species abundances were allocated to trait values so as to represent strong trait-based environmental filters, with all the most abundant species having a narrow range of trait values. The trait values applied (range 0 to 1) were generated randomly (once only) from five different trait value distributions: central mean (0.5) normally distributed; mean shifted to the low or high end (0.3 or 0.7) with a slightly skewed distribution; mean at the low or high extreme (0.2 or 0.8) with a more skewed distribution (Table A1 – columns).

For each of the six trait-abundance distributions, we randomised (n = 100) the abundances of species within each of the five sections of the trait axis, such that the basic relationship between relative abundance and trait value was retained. For each randomisation we determined the correlation coefficient between trait values and abundance (Pearson's r), correlation significance, predictive accuracy of MaxEnt ($\text{RMSE}_{\text{sqrt}}$), and significance of MaxEnt predictions of species abundances (generated from one set of 2000 randomisations of species abundances across the entire trait axis for each combination of trait-abundance relation and trait value distribution).

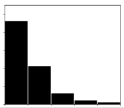
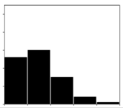
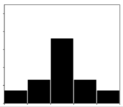
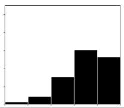
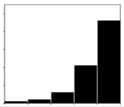
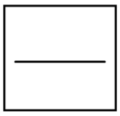
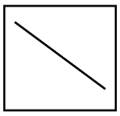
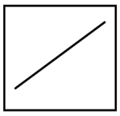
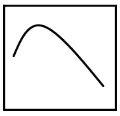
Our simulation exercise revealed that the potential of both MaxEnt and correlation analysis to identify a strong underlying trait-abundance relationship depended on the nature of the trait-abundance relationship and the distribution of trait values along the trait axis. For the linear relationships between trait values and abundance, both correlation analysis and MaxEnt identified significant trait-abundance relations regardless of the underlying distribution of trait values (Table A1). However, correlation strength (Pearson's r) and fit of the MaxEnt predicted abundances ($\text{RMSE}_{\text{sqrt}}$) were greater when fewer trait values occurred at the end of the trait axis associated with higher abundances of species. For the three unimodal curve functions, the ability of both simple correlation analysis and MaxEnt to significantly identify underlying trait-abundance relations depended strongly on the distribution of trait values along the trait axis (Table A1). For both MaxEnt and correlation analysis, trait-abundance relations were only significant when the highest abundances were associated with sections of the trait axis where few species occurred (e.g. the central unimodal curve with trait values skewed to the high or low end) (Table A1).

The dependence of MaxEnt's predictive accuracy on the underlying distribution of trait values (Table A1) is of some concern in its practical application for identifying key traits which influence abundance. All traits identified by MaxEnt are important, but some important traits may be missed. Transforming trait values whose distributions are skewed is not necessarily a solution to this issue, as normalising the distribution of trait values may result in loss of predictive accuracy for some types of trait-abundance relationships (Table A1). The inherent distribution of trait values along a trait axis may also contain valuable information on community assembly processes (Cornwell and Ackerly 2009), so transforming the distribution of trait values would require strong justification.

References

Cornwell, W. K. and Ackerly, D. D. 2009. Community assembly and shifts in plant trait distributions across an environmental gradient in coastal California. – Ecol. Monogr. 79: 109–126.

Table A1. Mean correlation coefficient (r), correlation significance (P_r), fit of MaxEnt predicted abundances ($RMSE_{sqrt}$), and significance of MaxEnt predictions (P_{RMSEs}) for the five simulated trait value distributions (columns) applied to each of the six simulated trait-abundance relations (rows). For the trait-abundance relations (rows), stylised figures depict abundance (y-axis) as a function of trait value (x-axis). For the trait value distributions (columns), figures show the frequency of species (y-axis) within five trait value categories (x-axis).

			Trait value distribution				
			low / skew	int.low / skew	int. / normal	int.high / skew	high / skew
Trait-abundance relation							
No relation		r	-0.0078	-0.0197	-0.0079	0.0017	0.0123
		P_r	0.5157	0.4943	0.5259	0.4917	0.5179
		$RMSE_{sqrt}$	0.0932	0.0933	0.0930	0.0930	0.0933
		P_{RMSEs}	0.5218	0.5338	0.5168	0.4878	0.5364
Negative linear		r	-0.6188	-0.7559	-0.8674	-0.9138	-0.8952
		P_r	0.0000	0.0000	0.0000	0.0000	0.0000
		$RMSE_{sqrt}$	0.0801	0.0670	0.0463	0.0338	0.0337
		P_{RMSEs}	0.0009	0.0001	0.0000	0.0000	0.0000
Positive linear		r	0.8938	0.9166	0.8657	0.7551	0.6185
		P_r	0.0000	0.0000	0.0000	0.0000	0.0000
		$RMSE_{sqrt}$	0.0340	0.0330	0.0471	0.0667	0.0806
		P_{RMSEs}	0.0000	0.0000	0.0000	0.0000	0.0012
Low unimodal curve		r	0.1568	-0.1000	-0.6234	-0.8642	-0.8555
		P_r	0.1811	0.3958	0.0000	0.0000	0.0000
		$RMSE_{sqrt}$	0.0928	0.0937	0.0825	0.0609	0.0567
		P_{RMSEs}	0.2258	0.6231	0.0012	0.0000	0.0000
Central unimodal curve		r	0.6511	0.6119	0.0187	-0.5929	-0.7125
		P_r	0.0000	0.0000	0.8591	0.0000	0.0000
		$RMSE_{sqrt}$	0.0806	0.0837	0.0938	0.0807	0.0766
		P_{RMSEs}	0.0001	0.0048	0.7572	0.0002	0.0010
High unimodal curve		r	0.8729	0.8667	0.5800	0.1794	-0.1420
		P_r	0.0000	0.0000	0.0000	0.1245	0.2266
		$RMSE_{sqrt}$	0.0509	0.0604	0.0856	0.0935	0.0930
		P_{RMSEs}	0.0000	0.0000	0.0045	0.5329	0.2586

int. = intermediate
low, int.low, int., int.high, high = the relative position of the mean along the trait axis
skew = the frequency distribution is skewed along the trait axis
normal = the frequency distribution is normally distributed along the trait axis

Appendix 2

Environmental variation for habitats and micro-habitats

In this study, the environmental variables have not been quantified extensively enough to test which environmental factors are most important in influencing community assembly through trait based environmental filtering at different scales. Indeed, one of the key environmental variables structuring the communities studied is likely to be subtle differences in grazing management practices applied over long time periods, which would be challenging to quantify adequately. However, the environmental factors which were measured demonstrate the potential for trait-based environmental filtering at the habitat and micro-habitat scales. For example, there is substantial variation in soil nutrient concentrations at the habitat level (Fig. A1) within the small landscape area examined. At the finer micro-habitat scale, attributes such as soil depth and soil stoniness also show substantial levels of variation (Fig. A2), indicating the potential for fine-scale environmental variation to influence community assembly through trait-based filtering.

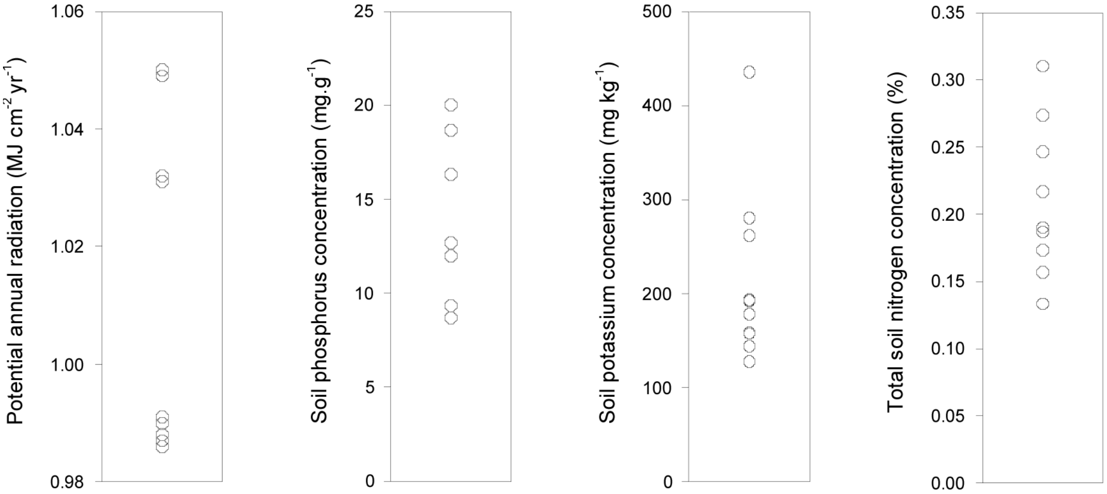


Figure A1. Selected environmental attributes for the ten habitats examined.

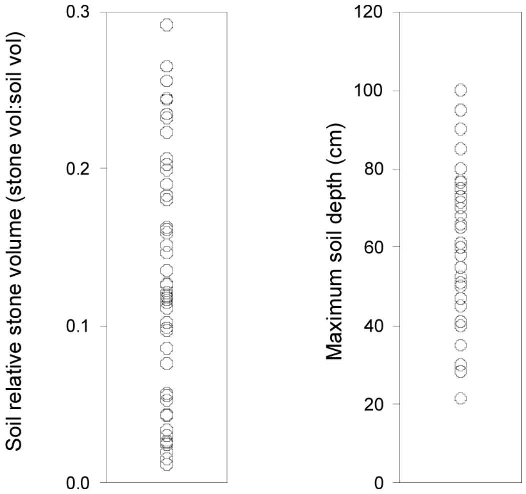


Figure A2. Two important soil attributes for the 50 habitats examined: soil stoniness and soil depth.