CERF biodiversity analysis using Rank Abundance Distributions

Biodiversity is an important topic of current ecological research. However, it is generally ambiguously defined and usually quantified by single metrics that vary with multiple aspects of biodiversity. This approach is likely to obscure real patterns seen in observed data. We consider that the abundance, species richness, and the species' relative frequency (evenness) to be central for considering biodiversity.

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Rank Abundance Distributions

The three central aspects of biodiversity (abundance, richness and evenness) are attributes of the rank abundance distribution (RAD) of a sample, see Figure 1. The RAD is a representation of the data that omits species identification. This omission allows comparison of sites with a disparit set of species. Of particular interest is when the sites cover an environmental gradient and the RADs can be used to delineate the effect of the environment on biodiversity.

Modelling RADs

Let N_i be the abundance, S_i be the richness, and n_i be the proportions of each of these species. The joint distribution of N_i , S_i , and n_i is factorised into three (conditional)

Figure 1



Example RADs: note that these data have different abundances, richness, and evenness.

West Australian data

A series of 120 samples from as many sites were taken during a large scale sampling effort in 2007 (the Voyage of Discovery; Figures 2 & 3).

Biodiversity was modelled, using the RAD approach, as a function of oceanographic variables and resulted in a rich description of the way that biodiversity changes with the environment. Predictions were made at a fine grid of locations spanning the area and depths of interest (Figures 4, 5 & 6). These predictions indicate that large and small scale oceanographic features (e.g. the Leeuwin Current and its under-current) may have substantial impact on biodiversity.

Figure 4



Figure 2



Voyage of Discovery target area.

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univariate distributions that can be separately modelled as functions of environmental variables. The factorisation is

 $\Pr(S_i, N_i, \boldsymbol{n}_i) = \Pr(N_i) \Pr(S_i | N_i) \Pr(\boldsymbol{n}_i | N_i, S_i)$

where the probability distribution functions are defined by their arguments.

Model specifics

We model each of the three univariate distributions using variations on common models. In particular, we use the following set of models:

 N_i : A negative binomial model.

 $S_i | N_i$: A truncated negative binomial. The truncation is needed as $S_i \leq N_i$.

 $n_i | N_i, S_i$: A novel modified Dirichlet-multinomial model. Note that n_i is the partition of N_i individuals into S_i species. The modification is required as these types of data typically exhibit a specific type of over-dispersion.

The model for $n_i | N_i, S_i$ provides a natural measure for evenness: the slope of the modelled probabilities at the most abundant species.

Predictions

Once the model has been specified and estimated it can be used to make predictions at new sites, marginal to the other aspects of biodiversity.

Predicted total abundance and prediction coefficient of variation.



Predicted species richness and prediction coefficient of variation.



Figure 5



Measures of uncertainty, due to sampling and estimation, can be incorporated using a parametric bootstrap routine.

Predicted evenness and prediction coefficient of variation.

References

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Conclusion

We have proposed a statistical framework for modelling three important aspects of biodiversity. Application to the West Australian data demonstrates that the method provides a rich description of biodiversity. Interestingly, the spatial patterns of biodiversity appear to follow important oceanographic features.



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