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Empirical relationships in species abundance relationships

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Summary

Assembly patterns for communities have been mostly described in terms of assembly rules based on permitted and un-allowed (niche) overlaps or with respect to power law relationships and fractal dimensions. Accumulation curves instead are often applied to analyze species-area relationships, which can be easily translated into species-abundance relationships (SAD). SADs in terms of Coleman curves from 73 marine faunal assemblages from deep sea to semi-terrestrial salt marshes were analyzed by means of a semi-log model (Gleason model). The semi-log model refers to the log-series distribution of species and resembles patterns predicted by the zero-sum multinomial distribution model in the neutral theory of biodiversity. The zero-sum model relies on certain preconditions such as near-equilibrium conditions and dependence on logistic growth, but the sampling model also applies to non-equilibrium conditions. As a results, the semi-log curves described by their inclination and offset can be arranged along a linear gradient ranging from oligotrophic deep-sea conditions to mesotrophic communities in shallow oceanic waters. Departures from the general figure can be explained as increases in disturbance and trophic status of the system. These coherent cross-system assembly patterns allow to define rules of change of diversity in a 2-dimensional panel.

Introduction

Hubbell's (2001) 'unified neutral theory of biodiversity and biogeography' makes very simple assumptions on processes assembling species into communities, but has to a remarkable degree been able to reproduce patterns in diversity. One of the basic assumptions is that species are ecologically identical, at least in terms of their contribution to community and regional diversity. One facet of the theory that has, however, received little critical attention is that the prediction of equality of local and regional species richness, species abundances in local communities will reflect the structure of the metacommunity. However, observations on saturation in local communities are in contradiction to this assumption (Fock, 2009). This leads to the formulation of a 2-step hypothesis, i.e. that general patterns exist but are locally modified.

Methods

Species–abundance relationships or species accumulation curves (SAD) and species–area relationships (SAR) differ in that SNR shows how species are assembled into a community across specimens whereas SAR indicates how this relationship is transposed into the physical sampling unit space. SNR based on individual-based rarefaction (Coleman curves) and linearized as S ~ log (N) puts emphasis on the log-normal component in an assemblage, whereas the rarer components (in particular singletons) are better represented by a log-series approach (Magurran and Henderson, 2003). SAD slopes allow separation between species rich and species poor assemblages (Gotelli and Colwell, 2001). As opposed to indices dependent on sample size (e.g. Hills family of diversity measures), SNR slopes and intercepts are independent of sample size and thus applied in this analysis. All calculations were done with EstimateS software (Colwell, 2006).

Results and Discussion

Based on Coleman curves exemplified for fish assemblages from the German Bight (left panel, Fig.1), parameters slope and intercept are plotted for 73 faunal assemblages.

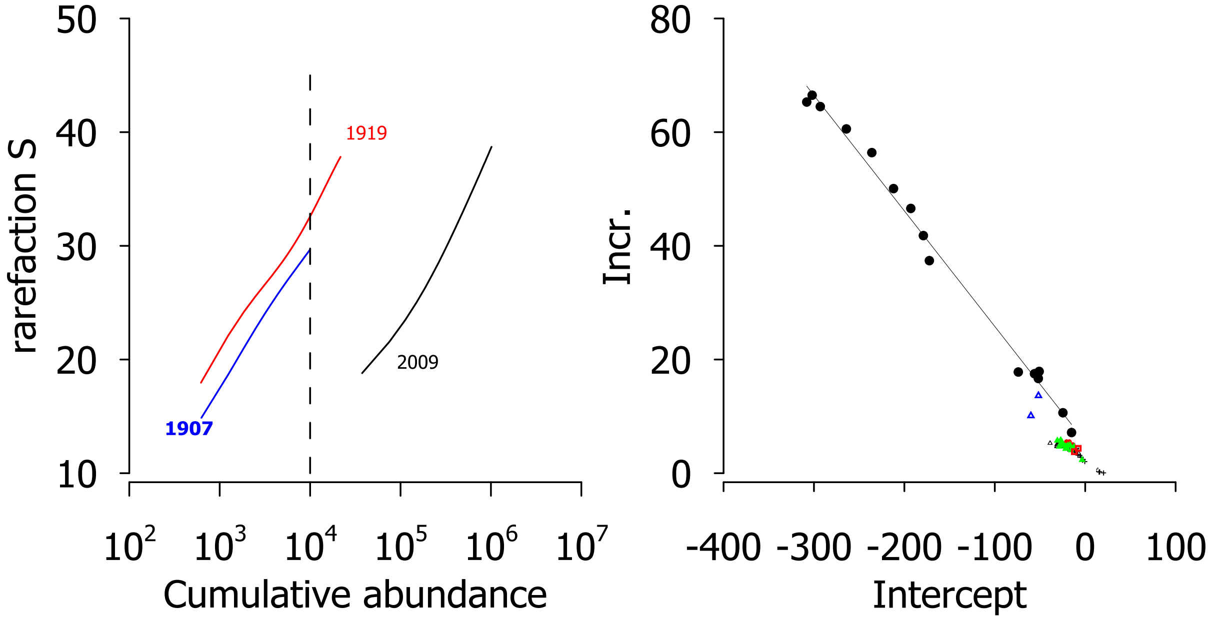

Fig. 1 Coleman curves — species accumulation curves (SAD) after individual-based rarefaction. Left panel : Semi log graph for years 1907, 1919 and 2009 for demersal fish assembalges in the german Bight, right panel - increment vs. intercept for all semi log relationships.

References

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