Received: 29 August 2017 | Revised: 21 September 2017 | Accepted: 8 October 2017

DOI: 10.1002/ece3.3570

ORIGINAL RESEARCH

WILEY Ecology and Evolution Open Access

An approach based on the total-species accumulation curve and higher taxon richness to estimate realistic upper limits in regional species richness

Stanislao Bevilacqua[1,6] | **Karl Inne Ugland**[2] | **Adriana Plicanti**[1] | **Danilo Scuderi**[3] | **Antonio Terlizzi**[4,5,6]

[1]Laboratory of Zoology and Marine Biology, Department of Biological and Environmental Sciences and Technologies, University of Salento, Lecce, Italy

[2]Department of Marine Biology, University of Oslo, Oslo, Norway

[3]I.I.S.S. "Ettore Majorana", Catania, Italy

[4]Department of Life Sciences, University of Trieste, Trieste, Italy

[5]Stazione Zoologica Anton Dohrn, Napoli, Italy

[6]CoNiSMa, Piazzale Flaminio, 9, Roma, Italy

Correspondence
Stanislao Bevilacqua, Department of Biological and Environmental Sciences and Technologies, University of Salento, Lecce, Italy.
Email: stanislao.bevilacqua@unisalento.it

Abstract

Most of accumulation curves tend to underestimate species richness, as they do not consider spatial heterogeneity in species distribution, or are structured to provide lower bound estimates and limited extrapolations. The total-species (T–S) curve allows extrapolations over large areas while taking into account spatial heterogeneity, making this estimator more prone to attempt upper bound estimates of regional species richness. However, the T–S curve may overestimate species richness due to (1) the mismatch among the spatial units used in the accumulation model and the actual units of variation in β-diversity across the region, (2) small-scale patchiness, and/or (3) patterns of rarity of species. We propose a new framework allowing the T–S curve to limit overestimation and give an application to a large dataset of marine mollusks spanning over 11 km^2 of subtidal bottom (W Mediterranean). As accumulation patterns are closely related across the taxonomic hierarchy up to family level, improvements of the T–S curve leading to more realistic estimates of family richness, that is, not exceeding the maximum number of known families potentially present in the area, can be considered as conducive to more realistic estimates of species richness. Results on real data showed that improvements of the T–S curve to accounts for true variations in β-diversity within the sampled areas, small-scale patchiness, and rarity of families led to the most plausible richness when all aspects were considered in the model. Data on simulated communities indicated that in the presence of high heterogeneity, and when the proportion of rare species was not excessive (>2/3), the procedure led to almost unbiased estimates. Our findings highlighted the central role of variations in β-diversity within the region when attempting to estimate species richness, providing a general framework exploiting the properties of the T–S curve and known family richness to estimate plausible upper bounds in γ-diversity.

KEYWORDS

β-diversity, habitat mapping, higher taxa, Mollusca, multivariate dispersion, species-accumulation curves

---