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Uniquity: A general metric for biotic uniqueness of sites

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ABSTRACT

1. Species richness is unrivalled as the most reported biodiversity metric in ecological and conservation research. Unfortunately, species richness ignores the scale-dependency of biodiversity.
2. We propose the metric *uniquity*, a quantitative and spatially scalable measure of uniqueness of a site based on a species-by-site matrix and a site-by-habitat type classification with area weights for habitat types correcting for sampling biases.
3. An example of *uniquity* is presented using vascular plant data from 130 sites representing a larger region (Denmark). We demonstrate the importance of the scale parameter of *uniquity* for the prediction of independent uniqueness indices calculated from species distribution data and the number of recorded red listed species.
4. We compare the performance of *uniquity* with the performance of the indices Local Contribution to Beta Diversity (LCBD) and Range Rarity Richness (RRR), and we investigate its sensitivity to small sample size and poorly resolved habitat classification.
5. We assess the performance of the *uniquity* metric applied to DNA metabarcoding data for plants, fungi and eukaryotes from the same set of study sites.
6. *Uniquity* is a strong predictor of site uniqueness based on national distribution data and also correlates neatly with the observed number of red listed species. *Uniquity* based on DNA metabarcoding corresponds well with the number of red listed species observed.
7. Perspective: *Uniquity* is generally applicable to biotas sampled with comparable effort, including field inventories, trap sampling, and DNA metabarcoding data. To our knowledge *uniquity* is the first index of uniqueness that explicitly considers spatial scale and sampling biases, while simultaneously accepting non-annotated DNA-data as input. Based on our study we offer general recommendations for further use and testing of *uniquity* as conservation value metric.

1. Introduction

The selection and designation of areas for protection or management is essential to biodiversity conservation (Brooks et al., 2006). State of the art in systematic conservation planning is a complementarity approach ensuring an optimal selection of reserve networks, implying a cost-effective conservation of the largest possible set of species (Margules and Pressey, 2000; Moilanen et al., 2009). Despite a fast development of methods and software for optimal reserve selection, there are still constraints to systematic conservation planning. First, incomplete biodiversity mapping restricts reserve selection to operate at coarse spatial resolution and for the few taxonomic groups for which adequate distribution data exists, such as birds, mammals or vascular plants. Second, ecosystems and their biotas are dynamic and change in response to natural processes and human pressures (Pressey et al., 2007), implying a demand for monitoring of temporal changes. In practice conservation planning rarely works entirely top-down; in most cases local managers and landowners make decisions that shape actual conservation efforts bottom-up. The local emphasis in practical conservation management creates a demand for tools to support local conservation prioritization. In other words: what is the unique conservation value of the local site irrespective of the whole set of

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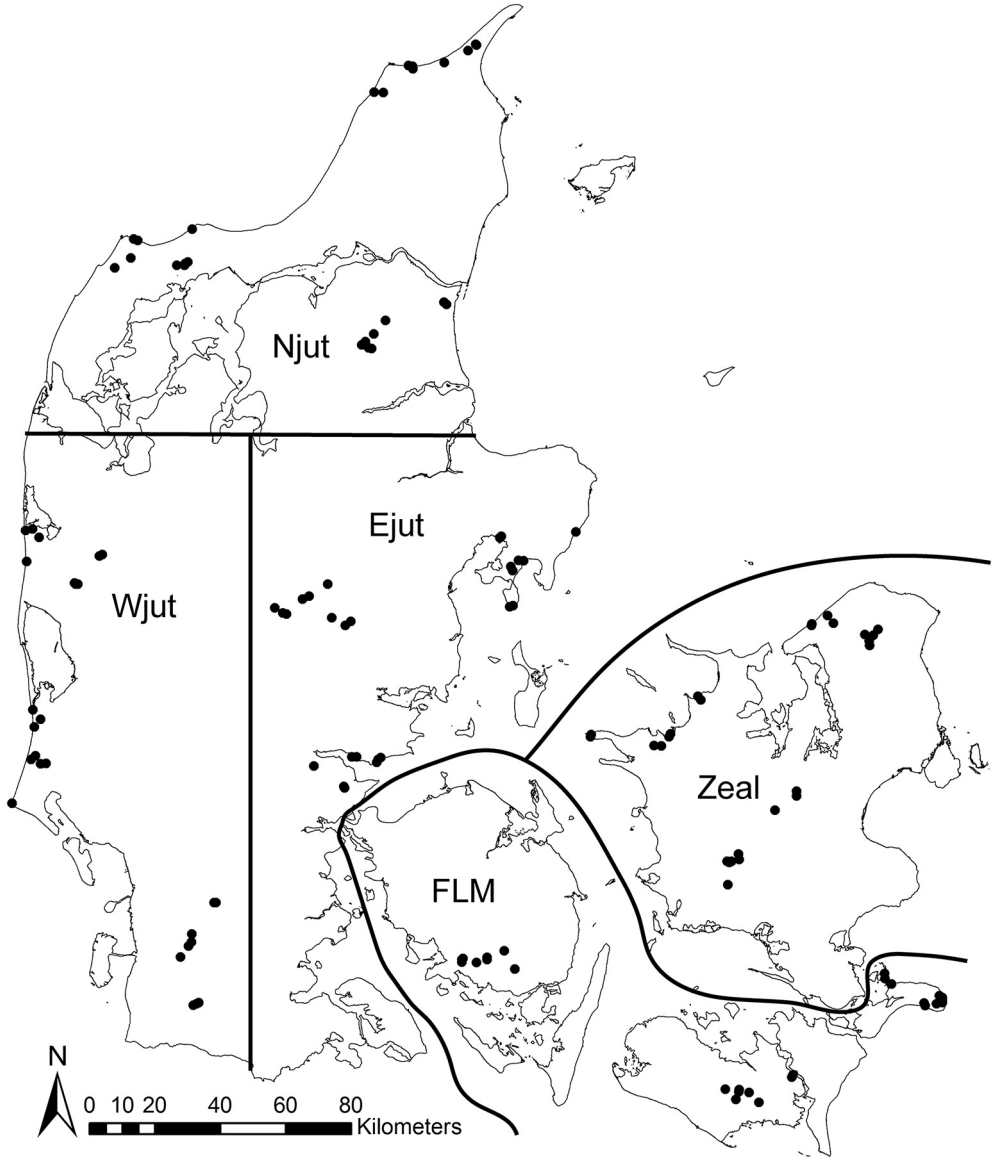

Fig. 1. Map of Denmark showing the location of the 130 sites grouped into 15 clusters within five regions (Njut: Northern Jutland, Wjut: Western Jutland, Ejut: Eastern Jutland, FLM: Funen, Lolland, Møn, Zeal: Zealand).

designated areas?

Species richness or alpha-diversity is by far the most often used indicator for local biodiversity. This is problematic when local species do not contribute appreciably to larger scale diversity. The alternative hotspot approach emphasizes species-rich sites or sites which host rare or threatened species (Reid, 1998). While the hotspot approach may be suitable for datasets with large spatial extent (Myers et al., 2000), distribution data for most taxa is not available at sufficiently high resolution for practical conservation planning. Consequently, reliable information regarding which resident species are regionally rare or threatened is often lacking. For most areas, even in well-studied western countries, most species in the local biota, have likely not yet been recorded. These obstacles are by no means trivial, as many species from megadiverse groups, such as fungi and insects, are notoriously difficult to record and identify. Even in cases where proper resources have ensured a broad taxonomic inventory, the study sites or monitoring quadrats are of limited spatial extent resulting in low coverage of species known to be rare or threatened in the surrounding geographic region.

The immediate motivation for the present study came from the research project Biowide ("Biodiversity in width and depth", 2014–2017), in which we studied variation in biodiversity by conducting a multitaxon biodiversity survey of 130 sites, selected by stratified random sampling across the major environmental gradients in the terrestrial landscape of Denmark (Brunbjerg et al., 2017). While well established procedures could be applied to estimate the species richness of vascular plants, bryophytes, carabid beetles, hoverflies, spiders, molluscs, macrofungi and lichens, we found no widely accepted way of estimating the biotic uniqueness of sites. We considered counting the number of rare or threatened species, but this would only apply to species assessed in the national red list or species with known distribution ranges. In addition, our small study sites cannot adequately represent the rare species potentially belonging to a surveyed habitat. We also applied metabarcoding of soil DNA to assess the biodiversity of e.g. fungi and eukaryotes. Only a small fraction of such data come with trustworthy taxonomic annotation and we know of no current approach for inclusion of DNA-data in uniqueness assessment. It cannot be justified to use the empirical frequency of species within the 130 sites as input for a calculation of uniqueness, given the identical sample size for rare habitats, such as ancient swamp forest, and ubiquitous habitats,