

# Characterizing the diversity of biological communities

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Nowadays, 'biodiversity' is generally regarded as an important indicator of ecosystem health. However, no general agreement exists on what exactly is meant with the diversity of a biological community and how it should be measured. Classical diversity indices give only a limited summary of the community of interest, while other more-informative measures are often community-specific, difficult to interpret, or not very concise. We combined these measures into a new index that contains all of their good properties.

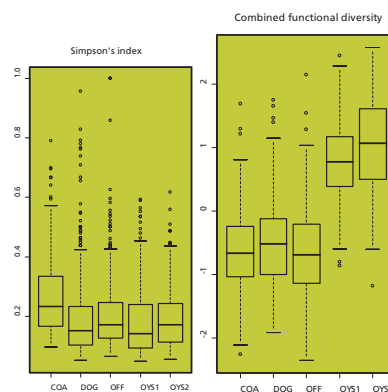
Classical diversity indices such as Simpson's index are often used to characterize the diversity of a community. These indices focus on the number of species ('species richness') and their relative abundance ('evenness') and do not take into account how much these species actually differ from each other ('species distinctiveness'). Therefore, they give only a limited summary of the community of interest, and totally different assemblages may be characterized by similar index values. To better capture the diversity of a system, ordination methods such as 'principal components analysis' or 'correspondence' analysis are used. A disadvantage of these methods is that they are difficult to interpret and that their results cannot be compared between communities that do not share the same species.

We propose to solve the above problems by extending Simpson's index with species distinctiveness. We quantify 'distinctiveness'

by means of species properties or traits that are linked to their functioning or to their effect on the system's energy flow, such as for example body size or feeding mode. For this, we combine multiple traits, as together these will give a more complete and general picture of the communities' functional diversity than a single trait. Furthermore, we make use of an ordination method. Apart from the fact that this ordination method solves the problems related to combining multiple traits, it also optimizes the functional diversity index in such a way that it will show the differences between communities with maximum clarity.

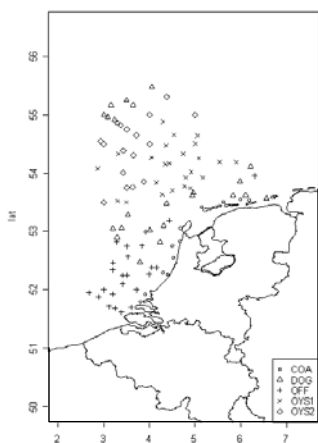
The resulting 'canonical index' provides a concise, general and unambiguous measure to characterize the differences and similarities of biological communities with respect to their functional diversity. The measure is interpretable in terms of (relative importance of) species traits, and may thus form a first step towards a better understanding of biodiversity. Furthermore, the index is optimized to clearly show differences in diversity, but it may also be optimized with respect to one or a few variables of interest. As such it may be used to study how functional diversity responds to for example environmental gradients or human disturbances.

The canonical index was successfully tested using a dataset on organisms living in and on the bottom of the Dutch part of the North Sea. In this area, five regions are recognized that are known to vary distinctly with regard to species assemblages. As expected, the canonical index performed better at characterizing



Simpson's index, does not show any distinction between the zones (left panel), whereas the newly developed canonical index (right panel) clearly separates the Oysterground from the rest.

these communities than the classical diversity indices. A second case study on oil contamination illustrated that the canonical index can indeed help to provide more insight in the effects of pollution (or other factors) on functional diversity.



Five faunistically distinct regions on the Dutch part of the continental shelf. The Oysterground is split in two regions (OYS1 and OYS2).

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