

## Explanation

This indicator measures local biodiversity by dividing the total number of unique species by the surface area, representing the number of unique species found per square kilometre. For maps, the value is calculated for each spatial cell. For time-series analyses, species richness density is obtained by dividing the total number of unique species per year by the surface area of the entire cube.

 **High value:** The grid cell contains a high concentration of unique species.

 **Low value:** The area contains a low concentration of unique species.

## Applicability for policy

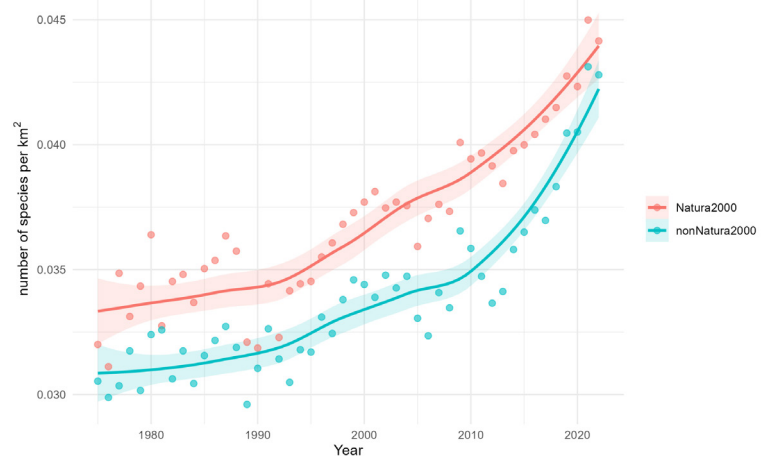
 Allowing comparison across scales: cubes with different grid sizes can easily be compared.

 Identifying hotspots of biodiversity.

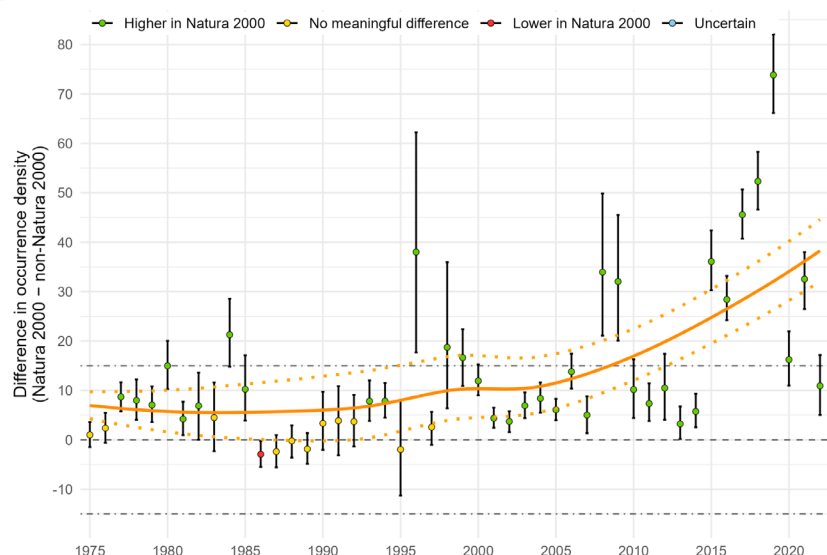
By including a filter at a higher taxonomic rank, richness can be compared between different orders or kingdoms.

## Limitations

Observed richness is highly dependent on the comprehensiveness of the dataset it is being applied to. If some regions are more intensively, carefully or systematically sampled than others, this will likely reflect as higher observed richness. Observed richness also depends on the relative abundance and spatial aggregation of each species, with less abundant and less aggregated species less likely to be discovered during surveys (Hillebrand et al., 2018), as well as the detectability of each species.

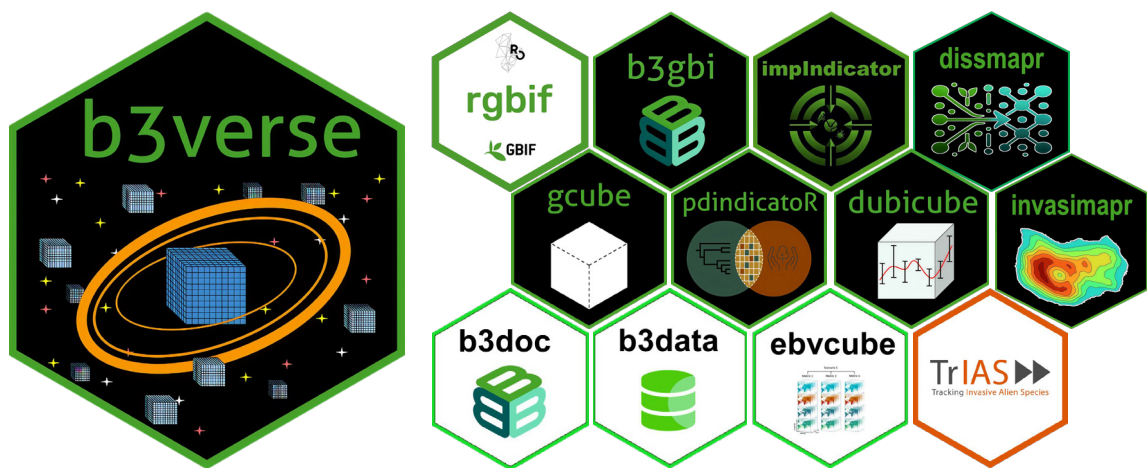
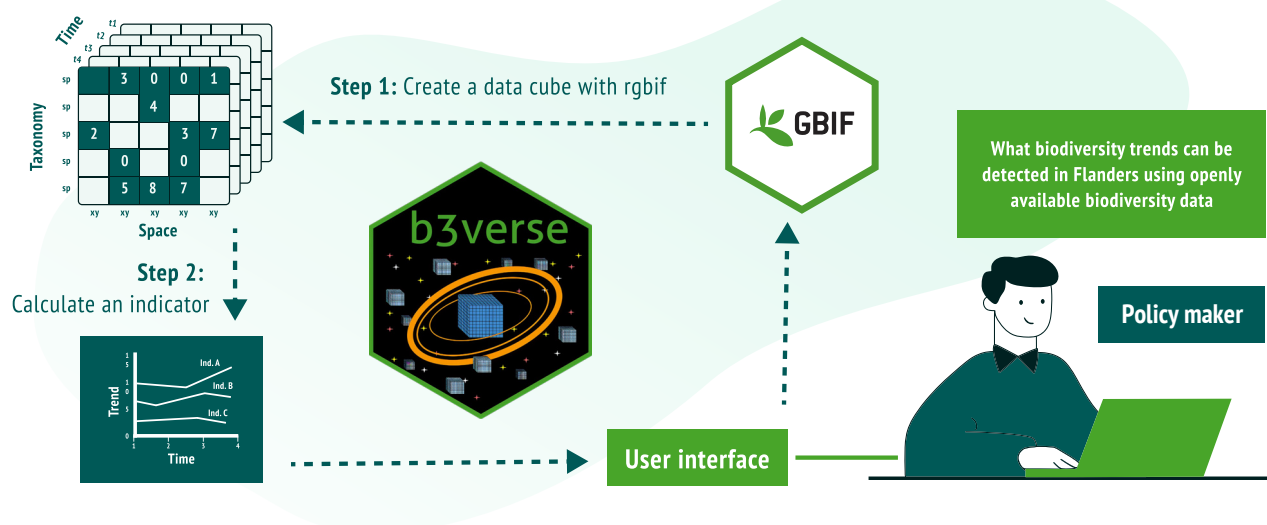


**Figure 1:** Calculating species richness density allows comparisons of species richness between areas of different sizes. In this example, the species richness density of native flowering plants recorded since 1975 is compared between Natura 2000 and non-Natura 2000 areas in Flanders. GBIF Occurrence Download <https://doi.org/10.15468/dLknsn44> Accessed from R via rgbif (<https://github.com/ropensci/rgbif>) on 2026-03-16.



**Figure 2:** Difference in species richness density between Natura 2000 and non-Natura 2000 areas. Percentile confidence intervals (95 %) were obtained by bootstrapping grid cells per year. Effect classification is done with reference 0 and a threshold of 5 differences in species per km<sup>2</sup>. GBIF Occurrence Download <https://doi.org/10.15468/dLknsn44> Accessed from R via rgbif (<https://github.com/ropensci/rgbif>) on 2026-03-16.

The B-Cubed workflow supports the creation and analysis of a data cube based on GBIF data. Further documentation is available at <https://docs.b-cubed.eu/>. Overview of all available packages at <https://b-cubed-eu.r-universe.dev/builds>.



[b-cubed.eu](https://b-cubed.eu)

B-Cubed aimed to standardise access to biodiversity data, helping transform fragmented biodiversity records into timely, policy-relevant indicators. This was achieved by developing a service to create "species occurrence cubes", which then served as the basis for models and indicator of past, current and future biodiversity. To ensure its results can be reused, the project created exemplary workflows for modelling and indicator calculation, as well as a suite of guides, tutorials and hands-on training sessions. The application and usefulness of B-Cubed's algorithms and software are demonstrated through the project's four case studies.

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