

Explanation

This indicator estimates how complete our knowledge of an ecological community is by calculating "Sample Coverage" (a concept originally developed by Turing and Good (1953), and popularised by Chao and Jost (2012)). Instead of just counting the raw number of observations, it estimates the proportion of all individuals in the actual community that belong to the species we have already detected in our sample. For maps, the value is calculated for each spatial cell using all historical data for that cell. For time-series analyses, the value is calculated independently for each time step over the complete data cube.

-  **High value (Value of 1.0 or 100%):** The sample is almost complete, suggesting that further fieldwork or additional searches are unlikely to reveal many new species. Although other species might be present, they are likely very rare and/or have extremely low detectability.
-  **Low value (Value of 0.2 or 20%, for example):** The sample is incomplete. This suggests that while you have found some species, an estimated 80% of all individuals in that community belong to species that have not yet been detected or logged in the database.

Applicability for policy

-  An important indicator of data quality: This indicator is an absolute prerequisite for reliable, data-driven policymaking. If completeness is high, it ensures that any differences are real ecological trends rather than just reflections of uneven sampling sizes.
-  Tracing "blind spots": This indicator allows environmental agencies to identify gaps in data coverage. A low completeness score in a given region signals the need for increased monitoring efforts.

Limitations

Completeness is a statistical correction tool calculated behind the scenes via the iNEXT package. It measures the reliability and maturity of the dataset, not the actual nature quality of the habitat. As species turnover occurs, and some species are highly mobile, a completeness of 1 is rarely, if ever, achieved.

References

- Chao A, Jost L. (2012). Coverage-based rarefaction and extrapolation: standardizing samples by completeness rather than size. *Ecology*. 93(12):2533-47. doi: 10.1890/11-1952.1. PMID: 23431585.
- Hsieh, T.C., Ma, K.H. and Chao, A. (2016), iNEXT: an R package for rarefaction and extrapolation of species diversity (Hill numbers). *Methods Ecol Evol*, 7: 1451-1456. <https://doi.org/10.1111/2041-210X.1261>

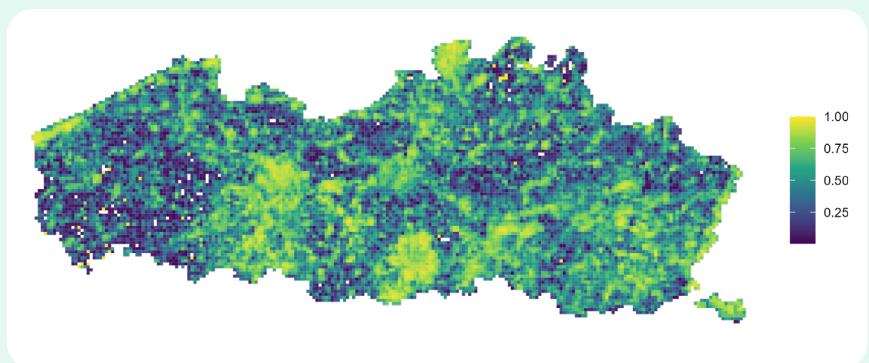


Figure 1: This figure illustrates the completeness of GBIF data for representing flowering plant communities in Flanders from 1975 to the present. GBIF Occurrence Download <https://doi.org/10.15468/dl.knsn44> Accessed from R via rgbif (<https://github.com/ropensci/rgbif>) on 2026-03-16.

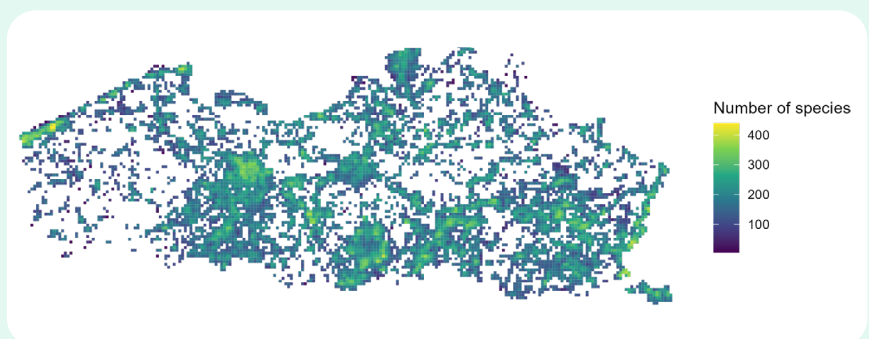
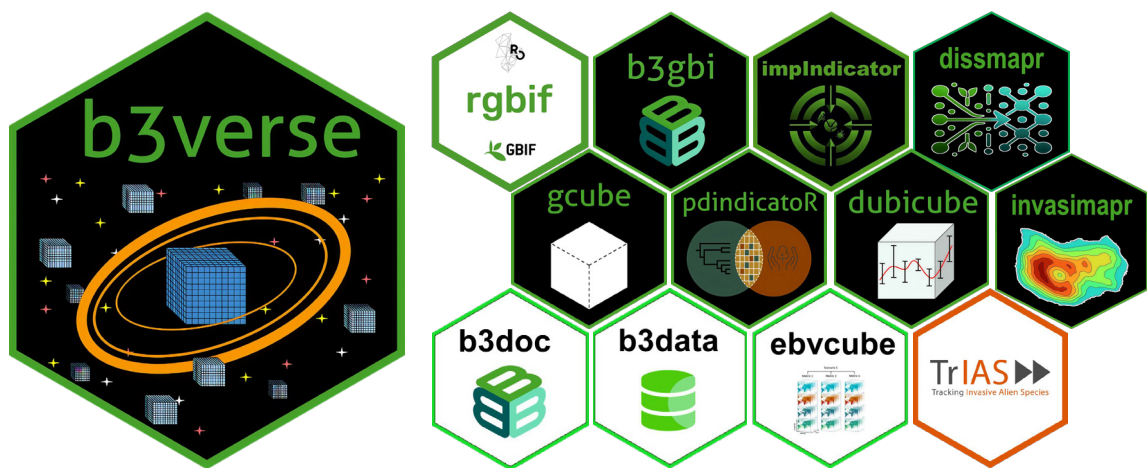
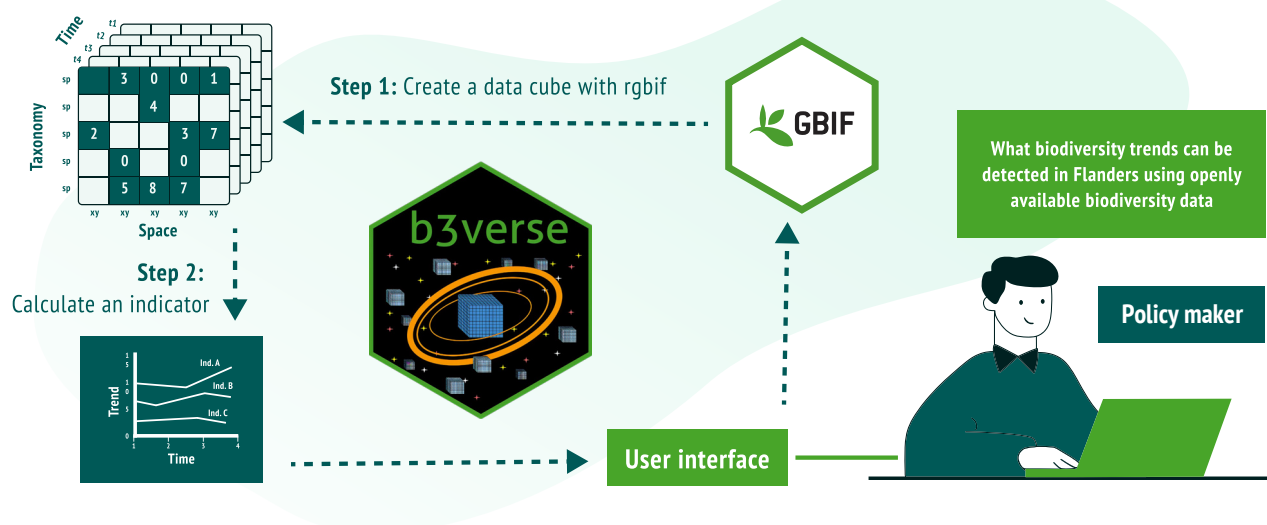


Figure 2: This figure demonstrates how completeness can be used as a mask when displaying other indicators. Here, the number of flowering plant species in Flanders since 1975 is shown, restricted to locations with completeness greater than 0.5. GBIF Occurrence Download <https://doi.org/10.15468/dl.knsn44> 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

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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