

Explanation

This indicator takes into account the evolutionary relatedness of species by calculating the sum of the branch lengths (representing the accumulated genetic changes) of the evolutionary tree of life that connect all the species found in a specific area. Instead of just counting the number of different species (species richness), it calculates the minimum path length needed to span across those species on a phylogenetic tree.

- 🌿 **High value:** The area contains species that are far apart on the tree of life (for example, it includes species of ancient lineages that have evolved separately from most other modern species). This means a wide variety of evolutionary features and distinct genetic traits are probably present in that ecosystem.
- 🌿 **Low value:** The species in the area are very closely related and clumped together on the same or a few related branches of the tree of life, meaning the ecosystem has a comparatively low variety of distinct evolutionary features.

Applicability for policy

This metric is highly valuable for long-term conservation planning and climate change adaptation policies. Because we can only guess which biological traits and features will be crucial for species survival in changing future environments, protecting a wide variety of features (rather than just the number of species) maximizes the overall adaptability and resilience of the ecosystem.

Limitations

The indicator is highly dependent on having an accurate and complete phylogenetic tree with reliable branch lengths for the taxonomic group being analyzed. If the evolutionary relationships are poorly mapped behind the scenes, the calculated tree-spanning path can become skewed, potentially over- or underestimating the true evolutionary value of the area.

References

Faith, D.P. (1992). Conservation evaluation and phylogenetic diversity. *Biological Conservation*, 61,1:1-10, ISSN 0006-3207, [https://doi.org/10.1016/0006-3207\(92\)91201-3](https://doi.org/10.1016/0006-3207(92)91201-3).

Robuchon, M., da Silva, J., Dubois, G., Gumbs, R., Hoban, S., Laikre, L., Owen, N. R., & Perino, A. (2023). Conserving species' evolutionary potential and history: Opportunities under the Kunming–Montreal Global Biodiversity Framework. *Conservation Science and Practice*, 5(6), e12929. <https://doi.org/10.1111/csp2.12929>

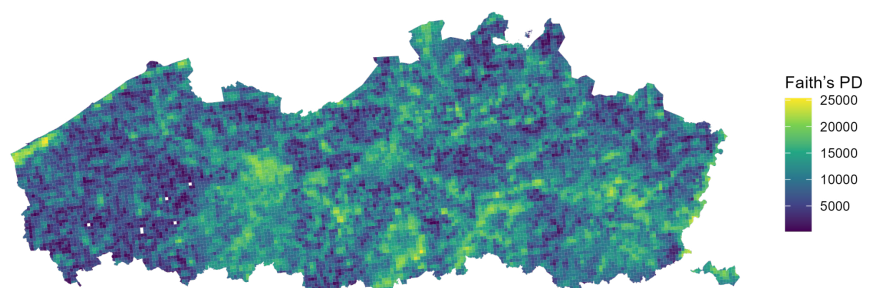
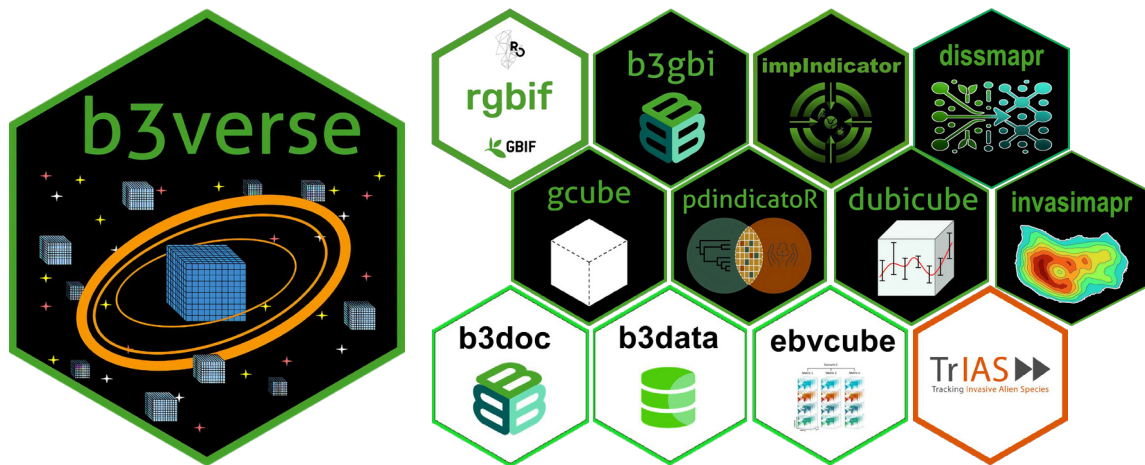
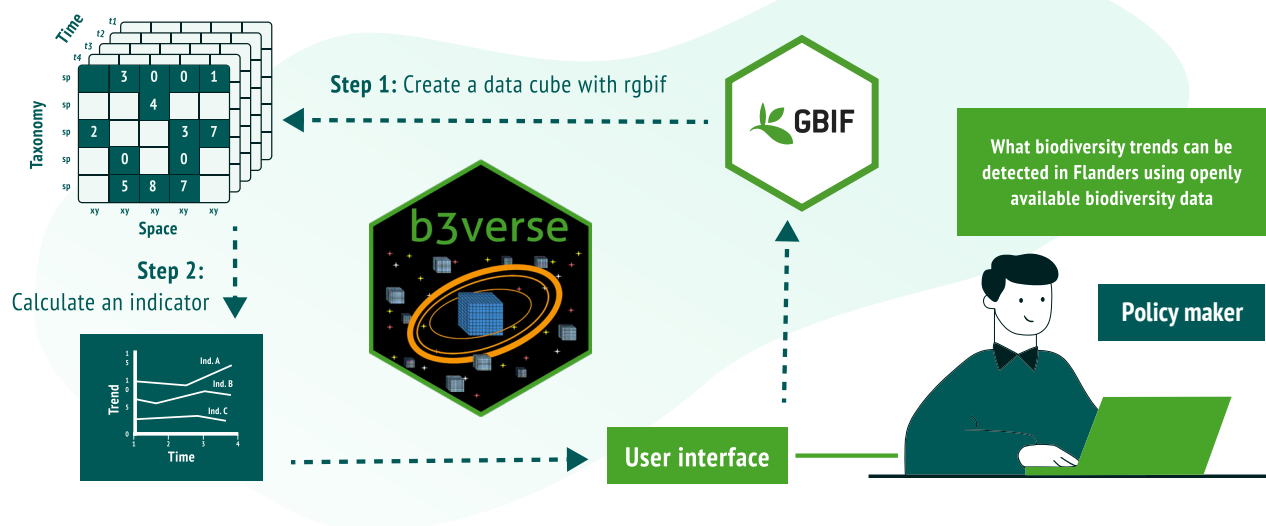


Figure 1: This map shows the spatial distribution of phylogenetic diversity among native flowering plants in Flanders, based on records collected since 1975. GBIF Occurrence Download <https://doi.org/10.15468/dLknsn44> Accessed from R via rgbif (<https://github.com/ropensci/rgbif>) on 2026-03-16.

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>.





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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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