

Explanation

This indicator calculates exactly how much evolutionary history we stand to lose if threatened species disappear from a specific grid cell. Species are considered 'threatened' when classified as Critically Endangered (CR), Endangered (EN) or Vulnerable (VU) according to the local IUCN Red List. The total Phylogenetic Diversity is then once calculated with all species present; and second, without the threatened species. The difference between these two scores equals the Expected PD Loss.

-  **High value (High Expected Loss):** If the threatened species in this grid cell go extinct, a substantial chunk of the evolutionary tree of life and the feature diversity associated with it for this region will vanish. This happens because these endangered species have no close relatives in these cells that share their evolutionary history and evolved traits.
-  **Low value (Low Expected Loss):** The threatened species in this cell are either close cousins to other common species (meaning their disappearance won't completely delete that branch of the tree of life) or there are few threatened species present in the area.

Applicability for policy

This indicator provides a "triage map" for policymakers and conservation agencies that highlights the areas where the loss of evolutionary heritage is expected to be greatest. Rather than just looking at the decline in species richness alone, it also considers the variety of features across the evolutionary tree of life. Resources can then be allocated towards high-priority areas, for example, to expand protected areas to include hotspots of evolutionary heritage.

Limitations

This indicator treats all "threatened" categories (CR, EN, VU) with equal weight when calculating the expected loss, and therefore, it does not differentiate between a species that is on the brink of extinction versus one that is vulnerable. Furthermore, it relies on the up-to-date accuracy of regional Red Lists, and therefore, the potential loss of a species that has become threatened but is not officially assessed yet will not be factored in.

References

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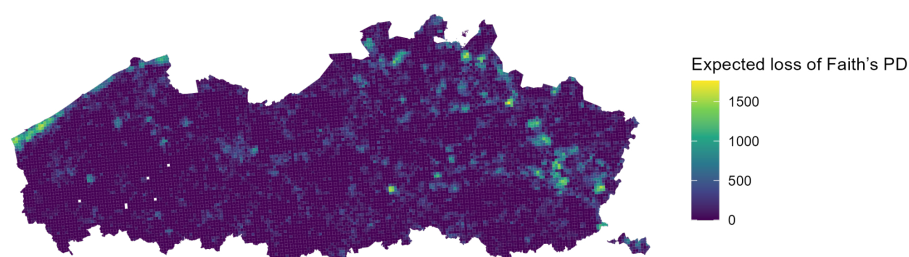
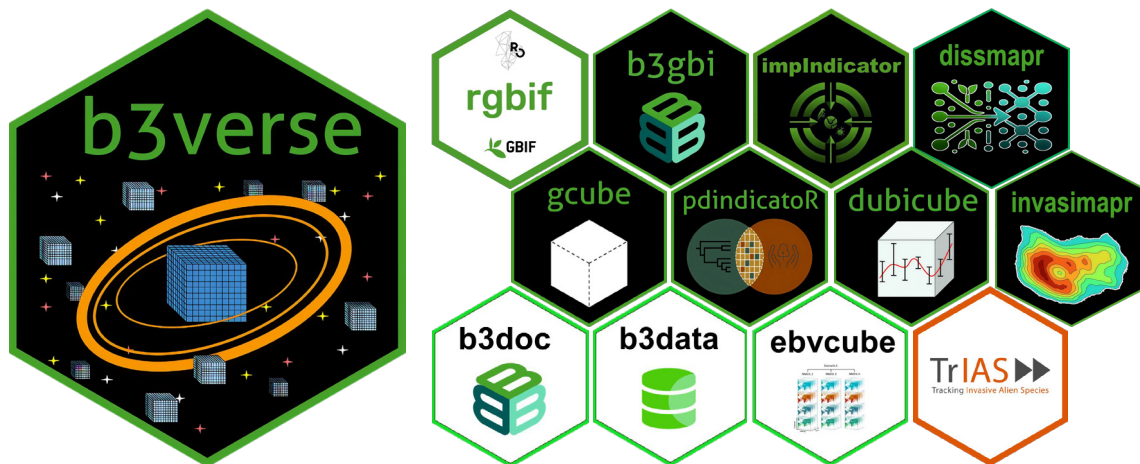
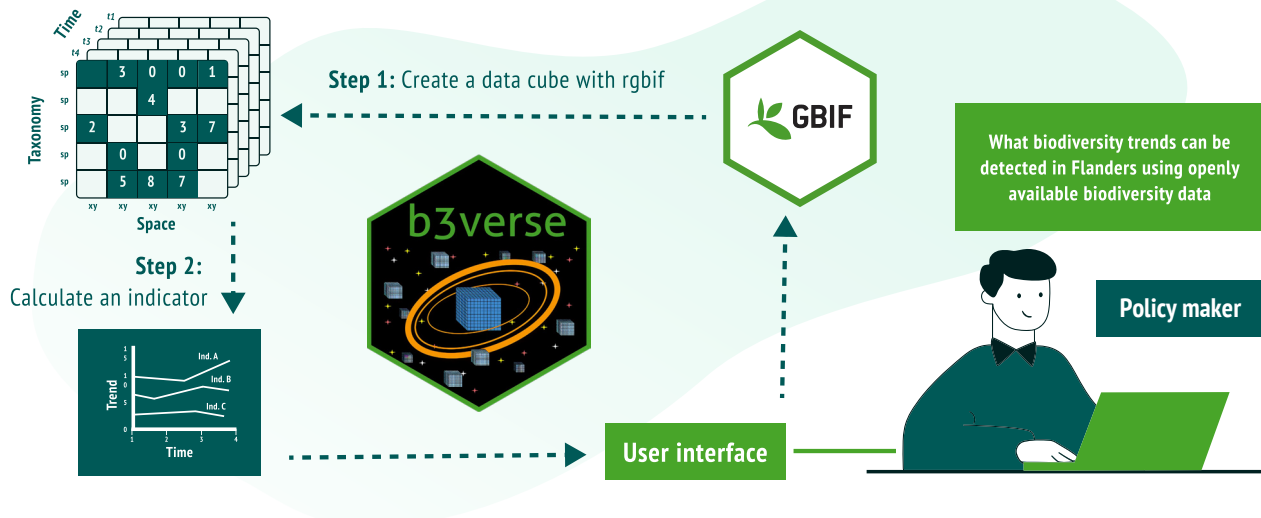


Figure 1: This map represents the 'Expected Phylogenetic Diversity (PD) Loss Map' of native flowering plants in Flanders, based on records collected since 1975. GBIF Occurrence Download <https://doi.org/10.15468/dl.knsn44> Accessed from R via rgbif (<https://github.com/ropensci/rgbif>) on 2026-03-16.

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>.



**BIODIVERSITY
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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.

PROJECT COORDINATOR

Dr Quentin Groom
Meise Botanic Garden
quentin.groom@plantentuinmeise.be

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