

BIODIVERSITY BUILDING BLOCKS FOR POLICY

M28 Design of R packages for indicator calculation

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Summary

This document outlines the integration and maintenance of R package software for calculating biodiversity indicators from occurrence cubes within the B3 project. We propose the **b3verse**, which is not an R package but the name for a collection of related R packages that streamline indicator calculation, organize code, and simplify package management. Currently, six packages are included in the **b3verse**:

- 1. **rgbif:** Download occurrence cubes (data generation)
- 2. gcube: Simulation of occurrence cubes (data generation)
- 3. **b3gbi**: Calculate general biodiversity indicators from occurrence cubes (indicator calculation)
- 4. **pdindicatoR**: Calculate phylogenetic indicators from occurrence cubes (indicator calculation)
- 5. **impIndicator**: Calculate alien impact indicators from occurrence cubes (indicator calculation)
- 6. **dubicube**: Calculation of robustness measures for occurrence cubes and uncertainty calculation for indicators (uncertainty estimation)

All packages will be accessible and maintained via an R-universe platform, ensuring continuous updates, easy distribution, and efficient installation.

An indicator calculation workflow is proposed, integrating the different **b3verse** packages. Occurrence cubes can be downloaded from GBIF data with **rgbif** or simulated using **gcube**, then processed with **b3gbi** to standardize input data. Indicator calculations follow using specialized packages (**b3gbi**, **pdindicator** or **impIndicator**), with **dubicube** supporting uncertainty estimation.





1 Introduction

The B3 project uses the concept of data cubes to standardise access to biodiversity data. These occurrence cubes are the basis for models and indicators of biodiversity (<u>https://b-cubed.eu/</u>). Multiple indicators are being developed in work package 5 (WP5) of the project. In this report, we describe the organisation of all related software code within a single framework, and how a potential indicator calculation workflow could be structured.

The software packages are developed using the R programming language (R Core Team, 2024). R provides an environment for data analysis, modelling, and visualisation and is widely used in ecological and biodiversity research (Lai et al., 2019, 2023). By structuring our work as R packages, we ensure that functions, datasets, tests and documentation are well-organized, easily accessible, and reusable (Wickham & Bryan, 2023).

2 Software availability, accessibility and maintenance

2.1 Software availability

Three types of indicators are currently being developed for occurrence cubes: (1) general biodiversity indicators (Dove, 2024), (2) phylogenetic indicators (Breugelmans et al., 2024), and (3) indicators on the impact of invasive alien species (Yahaya et al., 2025). Additional software includes robustness measures for occurrence cubes and uncertainty calculation for indicators via bootstrapping (Langeraert & Van Daele, 2025). Close collaboration within WP5 during software development, along with adherence to the B3 software development guidelines (Huybrechts et al., 2024), has resulted in a well-aligned suite of R packages for each of these four topics. Collectively, we refer to this assemblage as the **b3verse** (Fig. <u>1</u>).



Figure 1: The logo of the b3verse.

While not directly involved in indicator calculation, the **rgbif** and **gcube** packages are also part of the **b3verse** (Table <u>1</u>). The **rgbif** package facilitates downloading occurrence cubes in R (Chamberlain et al., 2025), while **gcube** provides a simulation framework for generating occurrence cubes (Langeraert, 2024), supporting applications such as sensitivity analysis. All packages originated under the B3 project, with the exception of **rgbif** which existed before.





Table 1: Overview of software that needs to be integrated for indicator calculation. The tasks relate to the tasks of the B3 project.

Package	Description	Task	GitHub link
b3gbi	Calculate general biodiversity indicators from occurrence cubes	T5.1	https://github.com/b-cubed-eu/b3gbi
pdindicatoR	Calculate phylogenetic indicators from occurrence cubes	T5.2	https://github.com/b-cubed-eu/pdindicatoR
impIndicator	Calculate alien impact indicators from occurrence cubes	T5.3	https://github.com/b-cubed-eu/impIndicator
dubicube	Calculation of robustness measures for occurrence cubes and uncertainty calculation for indicators	T5.4	https://github.com/b-cubed-eu/dubicube
rgbif	Download occurrence cubes	T2.3	https://github.com/ropensci/rgbif
gcube	Simulation of occurrence cubes	T4.5	https://github.com/b-cubed-eu/gcube

2.2 Improving publication and discovery via the R-universe platform

To assist in the accessibility and maintenance of the R packages developed within the B3 project, we set up an R-universe at <u>https://b-cubed-eu.r-universe.dev</u>. R-universe is an open





platform developed by rOpenSci (Boettiger et al., 2015) that allows organisations to publish and distribute their R packages. In addition to the **b3verse** packages, software not available in mainstream repositories will be included in the B3 R-universe platform. The platform offers more flexibility to distribute R packages than the Comprehensive R Archive Network (CRAN), while still making them easily installable using base R functionality, e.g.:

```
Unset
install.packages("gcube", repos = "https://b-cubed-eu.r-universe.dev")
```

Development versions can still be installed from GitHub, for example using the **remotes** package (Csárdi et al., 2024):

```
Unset
install.packages("remotes")
remotes::install_github("b-cubed-eu/gcube@v1.0.0")
```

A key advantage of the platform is its continuous build system, which automatically updates and compiles packages when changes are pushed to GitHub. This eliminates the need for manual submissions and allows for faster deployment of updates. R-universe offers a web interface where users can browse packages, check build statuses, view download metrics, and access documentation. The platform also supports binary package distribution, which accelerates installation across different operating systems, such as Windows and macOS, by offering precompiled versions (Fig. 2).



Figure 2: Screenshot of the R-universe web interface displaying R packages hosted by the B3 project (<u>https://b-cubed-eu.r-universe.dev</u>).





3 The b3verse and indicator calculation workflow

The **b3verse** is not a separate package but a concept that encompasses all R packages related to the indicator calculation workflow. A dedicated webpage on the B3 documentation website will be created at <u>https://docs.b-cubed.eu/guides/b3verse/</u> containing:

• A simple base R command to install all R packages of the **b3verse**, e.g.

```
Unset
pkgs <- available.packages(
    repos = "https://b-cubed-eu.r-universe.dev")[, "Package"]
install.packages(pkgs, repos = "https://b-cubed-eu.r-universe.dev")</pre>
```

- Short overview of the packages within the **b3verse** (cf. Table <u>1</u>)
- Description of the indicator calculation workflow within the **b3verse** (see below)
- The logo
- Links to relevant pages (e.g., GitHub and R-universe)

A visualisation of the indicator calculation workflow is proposed in Figure <u>3</u>. Occurrence cubes can be derived from GBIF data using the **rgbif** package or simulated using the **gcube** package. They are then processed using the process_cube() function from the **b3gbi** package. This ensures standardised input data across all indicator packages and verifies that the data format is correct. After cube processing, indicators can be calculated using the software developed in tasks 5.1-5.3. The software from task 5.4 can be used as a dependency for the packages from 5.1-5.3 for uncertainty calculation via bootstrapping.



Figure 3: Indicator calculation workflow within the b3verse.





Seamless integration and cooperation among the **b3verse** packages, supported by the dedicated R-universe platform, will also facilitate cloud computing. Streamlining the deployment and management of multiple related packages reduces setup complexity. In a cloud environment, this enables efficient use of the **b3verse** workflow on large biodiversity datasets and facilitates its integration into a user interface (Fig. <u>4</u>) or into existing pipelines, such as BON in a Box (<u>https://boninabox.geobon.org/</u>). The first author attended the workshop "BON in a Box: bring your own pipelines" on 12/03/2025. This platform shows high potential for publishing and sharing **b3verse** workflows.



Figure 4: Cloud computing used for indicator calculation workflow from an undefined user interface. WP2 and WP5 relate to the work packages of the B3 project.

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