BIODIVERSITY
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POLICY

MS29 Version 0.1 of the b3verse R package suite publicly available

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Summary

This milestone report presents version 0.1 of the **b3verse**, a suite of R packages developed to support biodiversity analysis workflows based on occurrence cubes within the B3 project. The **b3verse** provides a coherent, modular, and reproducible software ecosystem for data acquisition, cube simulation, processing, indicator calculation, and uncertainty assessment. It is designed for ecological researchers, developers, and policy-oriented users who work with biodiversity data.

The current version of the **b3verse** includes eleven R packages, available through a dedicated R-universe platform, with individual GitHub repositories for collaborative development and issue tracking. To ensure accessibility and sustainability, snapshot versions are archived on Zenodo. The platform also includes the **b3data** data package, providing example datasets in the Frictionless Data Package format, directly accessible via R.

This milestone documents:

- the current structure and installation of the **b3verse**;
- ongoing development and quality assurance, including code reviews and testing;
- future goals, such as migrating additional packages, enhancing tutorials, and broadening the data resource base;
- and recommendations for improving usability and reproducibility, focussing on tutorials, unit testing, and formal archiving.

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 (https://b-cubed.eu/). The **b3verse** was developed to organise all R software code related to the B3 project within a coherent framework (Langeraert et al., 2025b). The **b3verse** is not a single software package itself, but rather a name for a collection of related R packages designed to streamline indicator calculation, organise code, and simplify package management (Fig. 1). This suite of packages supports the entire workflow of working with occurrence cubes, which includes data retrieval, cube simulation, data processing, exploration, indicator calculation, and uncertainty estimation.

> *"The software packages are developed using the R programming language (R Core Team, 2025). 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)." (Langeraert et al., 2025b)*

The milestone report serves to summarise the current state of the platform, including its documentation hub and installation procedures, lists the included packages, and details the approach to publication and archiving. Additionally, it provides an overview of ongoing developments and future plans, such as planned package integrations, pending reviews, quality checks, and targeted package developments. Finally, it addresses the data resources that are added to the **b3verse**, covering current and future data additions.

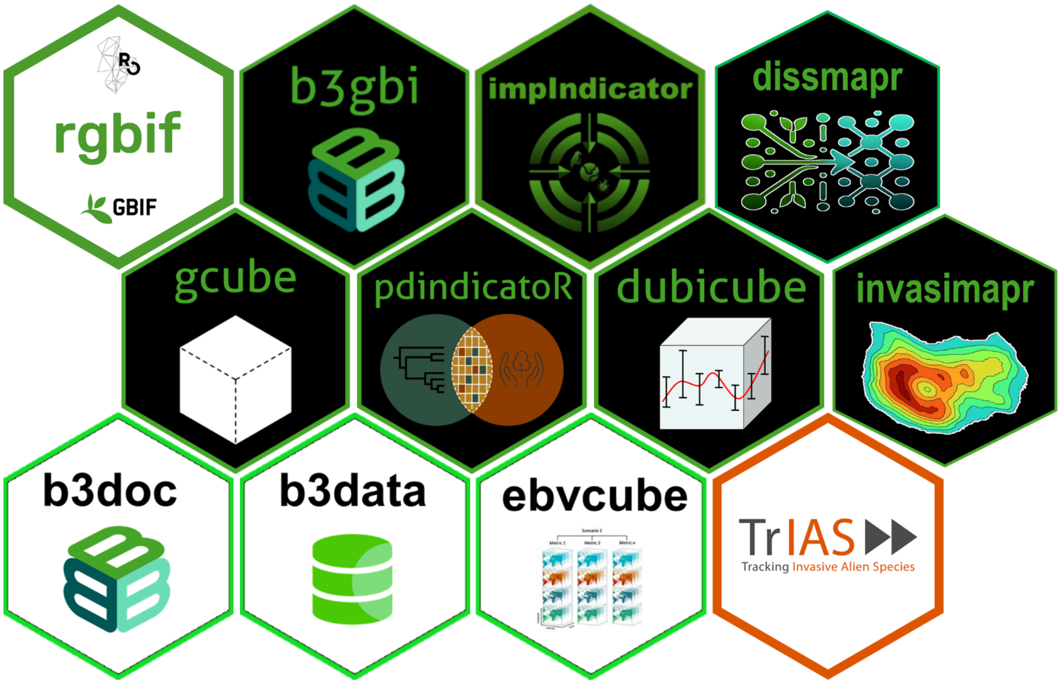

Figure 1: Packages of the b3verse.

2 The b3verse platform

2.1 Current state of the platform

The B3 project documentation website contains a guide on the **b3verse** which is actively maintained to stay up-to-date with new packages, workflows, and installation procedures (Table 2) (Langeraert et al., 2025a). It contains an introduction and overview of included packages, installation guidelines, contributing guidelines, and an indicator calculation workflow example.

Initially, the **b3verse** comprised six core packages: **rgbif** for downloading occurrence cubes from GBIF data (Chamberlain et al., 2025), **gcube** for simulating occurrence cubes (Langeraert, 2025b), **b3gbi** for calculating general biodiversity indicators (Dove, 2025), **pdindicatoR** for phylogenetic diversity indicators (Breugelmans et al., 2024), **impIndicator** for alien impact indicators (Yahaya et al., 2025), and **dubicube** for data quality measures and uncertainty calculation (Langeraert & Van Daele, 2025c). This collection has since expanded to include **b3doc** (Govaert et al., 2025), **ebvcube** (Quoss et al., 2024), **trias** (Oldoni et al., 2025), **dissmapr** (MacFadyen & Hui, 2025), and **invasimapr** (MacFadyen et al., 2025) (Table 1). Furthermore, the **b3verse** now also includes a dedicated data package, **b3data** (Langeraert & Van Daele, 2025a) (see Chapter 3). The scope of the **b3verse** has therefore been broadened from R packages for an indicator calculation workflow based on occurrence cubes to all R and data packages related to occurrence and modelled cubes. Finally, any R package dependencies not available in mainstream repositories are also added to the R-universe platform. These dependencies will be installed automatically, but are not discussed here.

Table 1: Progress in development and versioning of R packages in the b3verse. Visit https://www.repostatus.org/ for status descriptions. *(continues on next page)*

Package	Short description	Version	Status	GitHub repository
b3doc	Create Markdown pages for the B3 documentation website	0.2.0	Active	https://github.com/b-cubed-eu/b3doc
b3gbi	Calculate general biodiversity indicators from occurrence cubes	0.6.3	WIP	https://github.com/b-cubed-eu/b3gbi
dissmapr	Analyse and map multi-site compositional dissimilarity (ζ-diversity)	0.1.0	Active	https://github.com/b-cubed-eu/dissmapr
dubicube	Data exploration for occurrence cubes and uncertainty calculation for indicators	0.9.5	Active	https://github.com/b-cubed-eu/dubicube
ebvcube	Access and visualise datacubes of Essential Biodiversity Variables (EBV)	0.5.2	Active	https://github.com/EBVcube/ebvcube
gcube	Simulation of occurrence cubes	1.3.7	Active	https://github.com/b-cubed-eu/gcube

Package	Short description	Version	Status	GitHub repository
impIndicator	Calculate alien impact indicators from occurrence cubes	0.2.0	WIP	https://github.com/b-cubed-eu/impIndicator
invasimapr	Estimate and map invasion fitness (λ)	0.1.0	Active	https://github.com/b-cubed-eu/invasimapr
pdindicatoR	Calculate phylogenetic indicators from occurrence cubes	0.1.0	WIP	https://github.com/b-cubed-eu/pdindicatoR
rgbif	Download occurrence cubes	3.8.2	Active	https://github.com/ropensci/rgbif
trias	Functionality for the TrIAS and LIFE RIPARIAS projects	3.1.0	Active	https://github.com/trias-project/trias

To ensure accessibility, maintenance, continuous updates, easy distribution, and efficient installation of the R packages, all **b3verse** packages are made available and maintained through a dedicated R-universe platform (Table 2).

All packages of the **b3verse** can be installed or updated using this command in R:

```
pkgs <- rownames(available.packages(repos =
"https://b-cubed-eu.r-universe.dev"))
install.packages(pkgs, repos = c("https://b-cubed-eu.r-universe.dev",
"https://cloud.r-project.org", "https://bioc.r-universe.dev"))
```

If you only want to install the **b3verse** packages you do not have yet, you can install them via:

```
pkgs <- rownames(available.packages(repos =
"https://b-cubed-eu.r-universe.dev"))
pkgs_to_install <- setdiff(pkgs, rownames(installed.packages()))
if (length(pkgs_to_install) > 0) {
  install.packages(pkgs_to_install, repos =
c("https://b-cubed-eu.r-universe.dev", "https://cloud.r-project.org",
"https://bioc.r-universe.dev"))
}
```

Single packages can be installed via:

```
install.packages("dubicube", repos = c("https://b-cubed-eu.r-universe.dev",
"https://cloud.r-project.org"))
```

If the package has Bioconductor dependencies, add the Bioconductor repo:

```
install.packages("ebvcube", repos = c("https://b-cubed-eu.r-universe.dev",
"https://cloud.r-project.org", "https://bioc.r-universe.dev"))
```

Each R package in the collection has its own GitHub repository, where you can find contributing guidelines and report issues. Before contributing, please consult the Contributing Guidelines in the relevant repository. Contributions may include bug fixes, feature requests, documentation improvements, or new functionality. If you encounter a problem or would like to suggest an improvement, open an issue in the corresponding package repository and provide as much detail as possible, including R session information, error messages, and reproducible examples where applicable. To propose adding or removing packages, open an issue and/or pull request in the **b3verse** development repository (Table 2), clearly describing the purpose of the package and how it integrates with the existing b3verse. New packages will be reviewed in accordance with the B3 software development guidelines (Huybrechts et al., 2024).

b3verse R-universe snapshots are published and archived on Zenodo for long-term reproducibility (Table 2) (Langeraert et al., 2025c).

Table 2: Important references to online resources of the b3verse.

Source	Use	Link
Documentation website	Practical user guide with description, installation guidelines, contributing guidelines, and an indicator calculation workflow example using multiple packages of the **b3verse**.	https://docs.b-cubed.eu/guides/b3verse
R-universe platform	Web interface where users can browse packages, check build statuses, view download metrics, and access documentation. This is a more technical platform than the user guide on the documentation website.	https://b-cubed-eu.r-universe.dev
GitHub development repository	GitHub repository that keeps track of packages to include in the R-universe. Mainly used by developers of the **b3verse**.	https://github.com/b-cubed-eu/b-cubed-eu.r-universe.dev
Zenodo archive	Repository containing R-universe snapshots for long-term archiving.	https://doi.org/10.5281/zenodo.15781060

2.2 Future developments

All R packages of the B3 project were identified and are now hosted in the B3 repository and integrated into the **b3verse**. The packages **ebvcube**, **rgbif** and **trias** are part of the **b3verse** but are hosted outside the B3 GitHub organisation as they are part of different initiatives. These packages will remain in their current locations and do not require migration for continued integration (Table 3).

Although several packages have already undergone formal review, others have only received informal evaluations: **b3doc**, **dissmapr**, **dubicube**, **impIndicator**, **invasimapr**, and **pdindicatoR**. These packages will receive a formal code review in accordance with B3 software development guidelines (Huybrechts et al., 2024) during the second quality assessment report of B3 software (MS8, due 27 Feb. 2026).

As the B3 project approaches its final phase, the focus is now gradually shifting from adding new features to improving the robustness, usability, and reproducibility of existing software. We therefore propose three areas to prioritise for all **b3verse** packages: (1) implementation of unit tests, (2) development of user tutorials, and (3) archiving releases on Zenodo for citation and long-term availability.

Most packages already include basic unit tests. When it comes to tutorials, there remains room for improvement. Several packages lack dedicated tutorials, though in some cases the README provides sufficient guidance for basic use. Finally, most packages have already been archived on Zenodo, enabling citation and versioned references in publications and reports (Table 3).

Table 3: Assessment across b3verse packages. All packages have received an (internal) informal review. ebvcube, rgbif and trias do not require do not require migration to the B3 GitHub organisation as they are part of different initiatives. ***(continues on next page)***

Package	B3 repo	B3 review	Unit tests	Tutorials	Zenodo	Comment
b3doc	✅ yes	❌ no	✅ yes	❌ no	✅ yes	README can serve as tutorial
b3gbi	✅ yes	✅ yes	✅ yes	✅ yes	❌ no	Rather limited tutorials
dissmapr	✅ yes	❌ no	❌ no	✅ yes	❌ no	
dubicube	✅ yes	❌ no	✅ yes	✅ yes	✅ yes	
ebvcube	❌ no	✅ yes	✅ yes	❌ no	❌ no	README can serve as tutorial
gcube	✅ yes	✅ yes	✅ yes	✅ yes	✅ yes	
impIndicator	✅ yes	❌ no	✅ yes	✅ yes	✅ yes	Rather limited tutorials
invasimapr	✅ yes	❌ no	❌ no	✅ yes	❌ no	
pdindicatoR	✅ yes	❌ no	❌ no	❌ no	✅ yes	
rgbif	❌ no	✅ yes	✅ yes	✅ yes	✅ yes	

Package	B3 repo	B3 review	Unit tests	Tutorials	Zenodo	Comment
trias	❌ no	✅ yes	✅ yes	❌ no	✅ yes	Tutorials will be added in 2026 in the context of the GuardIAS project

Future development efforts will therefore focus on (1) validating the recent migration of **dissmapr** and **invasimapr** to the B3 GitHub organisation for quality control (repository cleanup, continuous integration, unit tests and coverage, documentation, vignettes, code style linting, tagged releases), (2) completing reviews for **b3doc**, **dissmapr**, **dubicube**, **impIndicator**, **invasimapr**, and **pdindicatoR**, (3) continuing development of existing software with focus on unit tests, tutorials and Zenodo archiving, and (4) continuing integration to ensure all relevant B3 packages are documented, tested, and accessible via the **b3verse** platform.

3 Data resources for the b3verse

3.1 Current data resources

In addition to the R packages, the **b3verse** also includes a dedicated data package, **b3data** (Langeraert & Van Daele, 2025a), published in the Frictionless Data Package format (https://frictionlessdata.io/). This package aims to provide datasets that can be used directly with the **b3verse** software, including example occurrence cubes and spatial reference layers. The documentation website of the B3 project contains a guide on the **b3data** with a description of the package, an example on how to extract the data in R, and contributing guidelines (Table 5) (Langeraert, 2025a).

Data resources can be downloaded from the Zenodo repository (Table 5), but can also be accessed directly in R using the **frictionless** R package (Desmet et al., 2025):

Step 1 — Load the frictionless R package

```
# install.packages("frictionless")
library(frictionless)
```

Step 2 — Read the package descriptor from Zenodo

```
b3data_package <- read_package(
  "https://zenodo.org/records/15211029/files/datapackage.json"
)
b3data_package
#> A Data Package with 2 resources:
#> • bird_cube_belgium_mgrs10
#> • mgrs10_refgrid_belgium
#> For more information, see <https://doi.org/10.5281/zenodo.15211029>.
#> Use `unclass()` to print the Data Package as a list.
```

This object contains metadata and references to all the resources included in the data package. There are currently two resources available in **b3data**:

- bird_cube_belgium_mgrs10: occurrence cube of birds in Belgium using the MGRS grid on a 10 km scale
- mgrs10_refgrid_belgium: MGRS 10 km grid for Belgium

Step 3 — Import a resource (dataset)

Tabular datasets (such as occurrence cubes) can be loaded using `read_resource()`.

```
bird_cube_belgium <- read_resource(
  b3data_package,
  "bird_cube_belgium_mgrs10"
)
head(bird_cube_belgium)
#> # A tibble: 6 × 8
#>    year mgrscode specieskey species          family     n
mincoordinateuncerta...¹
#>   <dbl> <chr>         <dbl> <chr>            <chr>  <dbl>
<dbl>
#> 1  2000 31UDS65     2473958 Perdix perdix    Phasi...     1
3536
#> 2  2000 31UDS65     2474156 Coturnix coturn... Phasi...     1
3536
#> 3  2000 31UDS65     2474377 Fulica atra      Ralli...     5
1000
#> 4  2000 31UDS65     2475443 Merops apiaster  Merop...     6
1000
#> 5  2000 31UDS65     2480242 Vanellus vanell... Chara...     1
3536
#> 6  2000 31UDS65     2480637 Accipiter nisus  Accip...     1
3536
#> # ℹ abbreviated name: ¹mincoordinateuncertaintyinmeters
#> # ℹ 1 more variable: familycount <dbl>
```

For non-tabular resources such as spatial or raster files, use specialised packages such as **sf** (Pebesma, 2018; Pebesma & Bivand, 2023) or **terra** (Hijmans, 2025) directly.

```
# Load package sf
library(sf)

# Read data from repository
mgrs10_belgium <- st_read(
  "https://zenodo.org/records/15211029/files/mgrs10_refgrid_belgium.gpkg",
  quiet = TRUE
)
head(mgrs10_belgium)
#> Simple feature collection with 6 features and 1 field
#> Geometry type: POLYGON
#> Dimension:     XY
#> Bounding box:  xmin: 460000.1 ymin: 5620000 xmax: 480000.1 ymax: 5670000
#> Projected CRS: WGS 84 / UTM zone 31N
```

```
#>   mgrscode                           geom
#> 1  31UDS65 POLYGON ((470000.1 5651000,...
#> 2  31UDS66 POLYGON ((470000.1 5661000,...
#> 3  31UDS72 POLYGON ((480000 5621000, 4...
#> 4  31UDS73 POLYGON ((480000.1 5631000,...
#> 5  31UDS74 POLYGON ((480000.1 5641000,...
#> 6  31UDS75 POLYGON ((480000.1 5651000,...
```

Once loaded, resources can be filtered, joined, or passed into **b3verse** indicator functions.

We welcome contributions to the **b3data** resources. Before contributing, please consult the ‘Contributing Guidelines’ in the b3data-scripts repository (Table 5) (Langeraert & Van Daele, 2025b). To propose changes, start by forking the repository and follow the instructions in the README to set up your local workflow. Once your changes are ready, submit a pull request. If you prefer not to make changes directly, you can also suggest the addition of one or more resources by opening an issue in the repository; the maintainers can then evaluate and include your contribution in the data package. For reporting bugs or suggesting improvements, open an issue in the same repository and describe the problem as clearly and completely as possible. Please include relevant information about the R session, any error messages, and, if applicable, a reproducible example.

Table 5: Important references to online resources of b3data.

Source	Use	Link
Documentation website	Practical user guide with description, ‘getting started’ tutorial, and contributing guidelines.	https://docs.b-cubed.eu/guides/b3data
GitHub development repository	Scripts to create the **b3data** frictionless data package. Mostly used by developers.	https://github.com/b-cubed-eu/b3data-scripts
Zenodo archive	Repository containing **b3data** data resources.	https://doi.org/10.5281/zenodo.15181097

3.2 Future data additions

We plan to add more data resources to **b3data**. Currently, only a small-scale (10 km) dataset is included. On a large scale (e.g. 100 km), we propose adding an occurrence cube of mammals in Europe using the EEA reference grid (and also including the grid itself). On a medium scale (30x30 minutes), we propose adding an occurrence cube of plants in South Africa using Extended Quarter Degree Grid Cells (and also including the grid itself). Finally, datasets related to specific **b3verse** R packages will be included.

4 Acknowledgements

The authors thank Damiano Oldoni for his input regarding the **trias** package.

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