BIODIVERSITY
BUILDING
BLOCKS FOR
POLICY

D5.5 R Package and Documentation (Vignettes) for the Calculation of the Indicators

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Key takeaway messages

- The **b3verse** R package suite was successfully delivered, integrating all biodiversity indicator calculation workflows (T5.1-T5.4) into a single, open-source framework (guide).
- The **b3verse** provides a standardized, reproducible pipeline for converting occurrence cube data into policy-relevant indicators.
- The software is hosted on the R-universe platform for continuous distribution (URL) and archived on Zenodo for long-term sustainability and citation (DOI).
- Robust quality assurance, including automated unit tests and formal code reviews, ensures calculation efficiency and stability.
- Comprehensive documentation, vignettes, and the dedicated **b3data** data package maximize user accessibility and facilitate reproducible analysis.

Executive summary

This report outlines the design, implementation, and public release of the complete R package ecosystem, the **b3verse**, developed under Work Package 5 of the B3 project. The **b3verse** consists of eleven software packages and one dedicated data package (**b3data**). Together, these packages consolidate biodiversity indicator calculation into a single coherent and reproducible open-source framework, covering general biodiversity indicators, phylogenetic diversity indicators, alien species impact indicators, and bootstrap-based uncertainty estimation.

The ecosystem includes core indicator packages (**b3gbi**, **pdindicatoR**, **impIndicator**, and **dubicube**), as well as modelling-oriented cube packages (**dissmapr** for compositional turnover modelling, and **invasimapr** for invasion risk assessment based on occurrence and trait-derived invasion fitness and community invasibility). Supporting packages provide data access, simulation utilities, workflow infrastructure, and documentation, complemented by the example dataset package **b3data** to enable reproducible demonstrations and testing.

Quality and sustainability are core principles of current and future development. The software adheres to B3 development guidelines, utilizes automated integration workflows via a dedicated R-universe platform for continuous distribution, and employs automated unit tests to guarantee the efficiency and stability of results against a variety of data inputs. Furthermore, the entire suite is permanently archived on Zenodo to ensure long-term reproducibility and stable citation.

The **b3verse** delivers comprehensive documentation, including detailed R package documentation, vignettes, and tutorials, maximizing user accessibility. The robust automation capabilities lay the necessary groundwork for generating simple dashboards in Work Package 6 to facilitate cloud computing and direct accessibility for policymakers. Future efforts will focus on finalizing formal code reviews, expanding unit test coverage, and ensuring the continued maintenance and evolution of the packages.

Non-technical summary

The B3 project aims to transform complex biodiversity data into clear and trustworthy information that supports policy decisions. This report presents the **b3verse**, a unified toolkit consisting of twelve free and open-source software packages developed for the R programming language.

The **b3verse** offers a standardized and automated workflow that converts openly available biodiversity data (e.g., GBIF 'occurrences cubes', IUCN EICAT data) into policy-relevant indicators, such as changes in species richness or the impact of alien species. By formalizing and automating the calculation process, the toolkit ensures that results are consistent, reproducible, and transparent across datasets and reporting contexts.

List of abbreviations

B3	Biodiversity Building Blocks for Policy
Dx.x	Deliverable report x.x of the B3 project
EBV	Essential Biodiversity Variables
EICAT	Environmental Impact Classification for Alien Taxa
EU	European Union
GBIF	Global Biodiversity Information Facility
IUCN	International Union for Conservation of Nature
Mx	Milestone report x of the B3 project
R	R programming language
Tx.x	Task x.x of the B3 project
WPx	Work Package x of the B3 project

1. Introduction

The B3 project (Biodiversity Building Blocks for Policy, https://b-cubed.eu/) is dedicated to transforming raw biodiversity data into standardized, actionable information for ecological modelling and policy support. Central to this mission is the concept of occurrence cubes, which standardize access to heterogeneous biodiversity data, making them the foundational input for models and indicators across the project. This deliverable report outlines the design, implementation, and public release of the complete R package ecosystem, the **b3verse**, developed under Task 5.5 (T5.5) of Work Package 5 (WP5).

The primary objective of T5.5 was to consolidate the various R software tools developed throughout WP5, covering general biodiversity indicators, phylogenetic indicators, alien species impact indicators, and uncertainty estimation, into a single, coherent, modular, and reproducible framework. The result is the **b3verse**: a collection of robust R packages specifically engineered to streamline the entire biodiversity data analysis workflow, from initial data retrieval to the final calculation and uncertainty assessment of policy-relevant indicators (Fig. 1).

Figure 1: b3verse logo.

The software packages for the B3 project are developed using the R programming language (R Core Team, 2025), a widely adopted environment for data analysis, modelling, and visualisation in ecological and biodiversity research (Lai et al., 2019, 2023). By structuring the work as R packages, the project ensures that functions, datasets, tests, and documentation are well-organized, easily accessible, and reusable (Wickham & Bryan, 2023).

The **b3verse** is not a single software package but a concept unifying several functionally distinct yet interconnected R packages (Langeraert, Desmet, et al., 2025b). The suite supports the entire data-to-indicator pipeline, structured around five core processes: (1) data generation (**rgbif** and **gcube**), (2) data processing (**b3gbi**'s processing functions), (3) data exploration (**dubicube**'s quality measures), (4) indicator calculation (**b3gbi**, **pdindicatoR**, and **impIndicator**), and (5) indicator uncertainty and interpretation (**dubicube**). This structure ensures standardized data input and smooth interoperability, enabling users to reliably execute complex indicator calculations.

The successful public release of 'Version 0.1 of the b3verse suite' (Langeraert, Desmet, et al., 2025c) represents the key achievement of this task. All packages are hosted and maintained on a dedicated, continuous-build R-universe platform, which ensures easy accessibility, efficient installation via base R functionality, and continuous updates (Langeraert, Breugelmans, et al., 2025). The initial six core packages have expanded to twelve, including utilities for documentation (**b3doc**), advanced analysis (**dissmapr**, **invasimapr, trias**), and working with Essential Biodiversity Variables (**ebvcube**). Furthermore, the suite includes the **b3data** data package, providing archived, example occurrence cubes and reference grids in the Frictionless Data Package format, thereby enhancing reproducibility and lowering the barrier to entry for new users (Fig. 2).

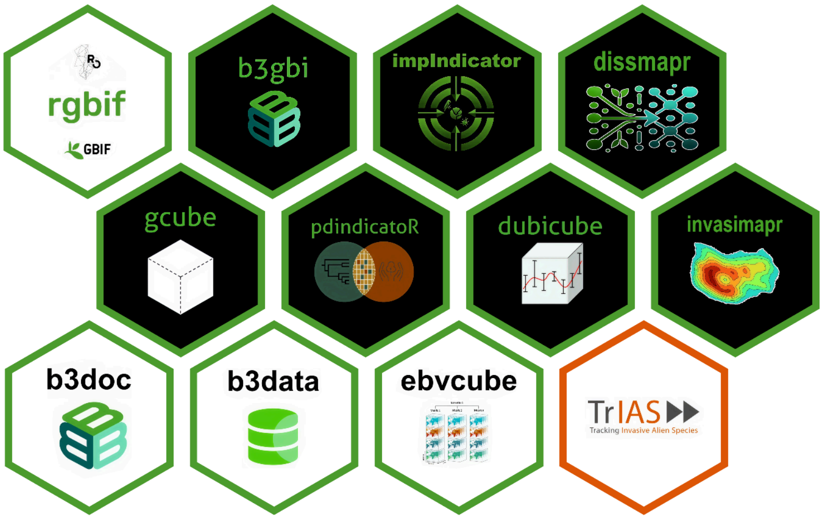


Figure 2: Visual overview of the b3verse packages.

In fulfilling the requirements of the B3 project, we have focused on quality assurance, including internal reviews, the implementation of unit tests for robustness, and the creation of user tutorials to maximize usability. This report serves as the comprehensive final documentation for T5.5, detailing the architecture of the **b3verse**, the status of its component packages, the steps taken to ensure its sustainability and long-term reproducibility (including archiving on Zenodo), and the future roadmap for continuous improvement and potential integration with broader biodiversity data platforms.

2. Integration of indicator calculation into R Packages

2.1. The b3verse R-Universe and its packages

The **b3verse** is designed to support the entire workflow related to occurrence cubes. While initially comprising six core packages focused strictly on the indicator calculation workflow, the suite has expanded to eleven software packages (Table 1), alongside a dedicated data resource package (detailed in Section 3.2), to cover all R-related software within the B3 project.

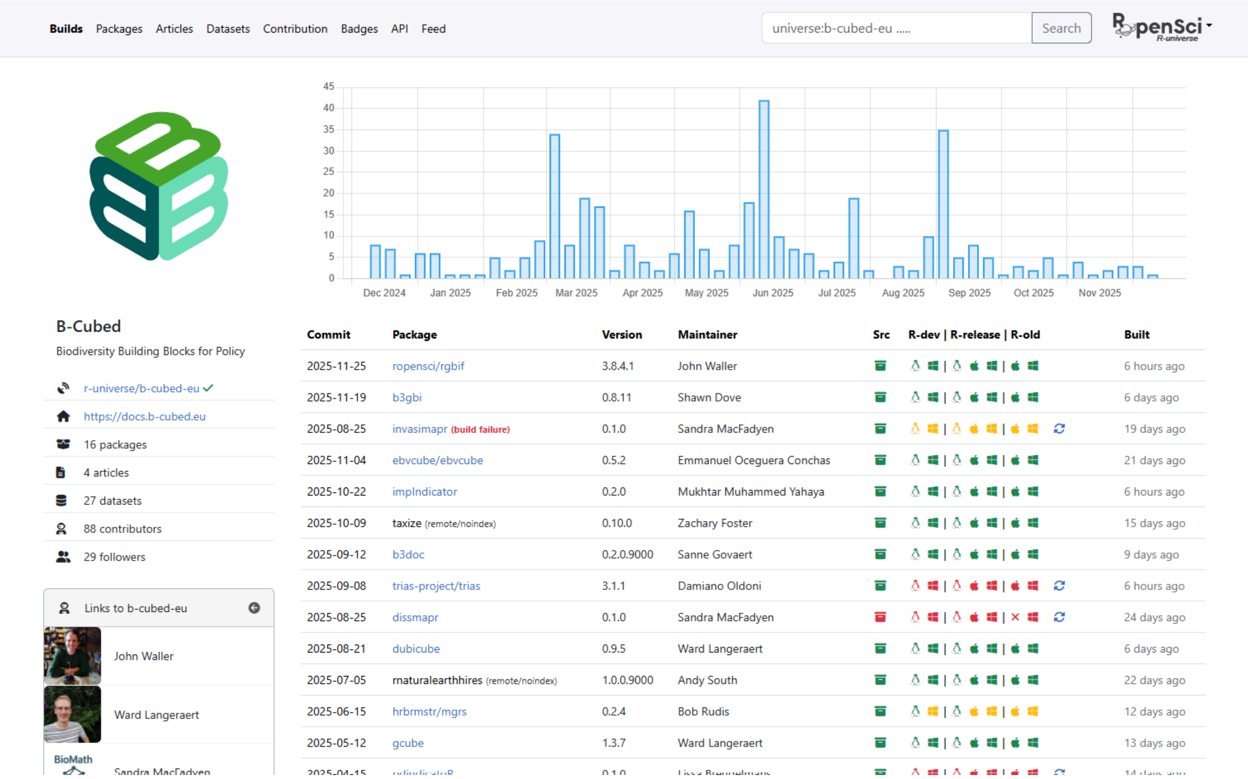
Table 1: Overview of the b3verse packages (software-only), including the latest version and development status. Status values according to https://www.repostatus.org/: Active – The project has reached a stable, usable state and is being actively developed. WIP – Initial development is in progress, but there has not yet been a stable, usable release suitable for the public.

Package	Short description	Version	Status	Reference
b3doc	Create Markdown pages for the B3 documentation website	0.2.0	Active	(Govaert et al., 2025)
b3gbi	Calculate general biodiversity indicators from occurrence cubes	0.8.14	WIP	(Dove, 2026)
dissmapr	Analyse and map multi-site compositional dissimilarity (ζ-diversity)	0.1.0	Active	(MacFadyen & Hui, 2025)
dubicube	Data exploration for occurrence cubes and uncertainty calculation for indicators	0.11.1	Active	(Langeraert & Van Daele, 2026)
ebvcube	Access and visualise data cubes of Essential Biodiversity Variables (EBV)	0.5.2	Active	(Quoss et al., 2024)
gcube	Simulation of occurrence cubes	1.4.4	Active	(Langeraert, 2026)
impIndicator	Calculate alien impact indicators from occurrence cubes	0.6.0	WIP	(Yahaya et al., 2026)
invasimapr	Estimate and map invasion fitness (λ)	0.1.0	Active	(MacFadyen et al., 2025)
pdindicatoR	Calculate phylogenetic indicators from occurrence cubes	0.1.0	WIP	(Breugelmans et al., 2025)

rgbif	Download occurrence cubes	3.8.4	Active	(Chamberlain et al., 2025)
trias	Functionality for the TrIAS and LIFE RIPARIAS projects	3.2.3	Active	(Oldoni et al., 2026)

2.2. Installation, availability, and archiving

To assist in the accessibility, maintenance, and distribution of the software, all **b3verse** packages are made available through a dedicated R-universe platform (Fig. 3). The R-universe platform is crucial for continuous build and distribution (https://b-cubed-eu.r-universe.dev/). It automatically updates and compiles packages whenever changes are pushed to GitHub, offering more flexibility than mainstream repositories (Boettiger et al., 2015), including continuous builds triggered by code updates, automatic generation of platform-specific binaries, and the ability to host additional package dependencies outside standard repositories. It also supports binary package distribution, accelerating installation for users on Windows and macOS. This platform ensures that the development version of the **b3verse** is always easily installable using base R functionality and up to date. 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 in this report.



B-Cubed

Biodiversity Building Blocks for Policy

r-universe/b-cubed-eu ✓

https://docs.b-cubed.eu

16 packages

4 articles

27 datasets

88 contributors

29 followers

John Waller

Ward Langeraert

Sandra MacFadyen

Commit	Package	Version	Maintainer	Src	R-dev | R-release | R-old		Built
2025-11-25	ropensci/rgbif	3.8.4.1	John Waller	🟩	🟩🟩 | 🟩🟩🟩 | 🟩🟩		6 hours ago
2025-11-19	b3gbi	0.8.11	Shawn Dove	🟩	🟩🟩 | 🟩🟩🟩 | 🟩🟩		6 days ago
2025-08-25	invasimapr (build failure)	0.1.0	Sandra MacFadyen	🟩	🟨🟨 | 🟨🟨🟨 | 🟨🟨	↻	19 days ago
2025-11-04	ebvcube/ebvcube	0.5.2	Emmanuel Oceguera Conchas	🟩	🟩🟩 | 🟩🟩🟩 | 🟩🟩		21 days ago
2025-10-22	impIndicator	0.2.0	Mukhtar Muhammed Yahaya	🟩	🟩🟩 | 🟩🟩🟩 | 🟩🟩		6 hours ago
2025-10-09	taxize (remote/noindex)	0.10.0	Zachary Foster	🟩	🟩🟩 | 🟩🟩🟩 | 🟩🟩		15 days ago
2025-09-12	b3doc	0.2.0.9000	Sanne Govaert	🟩	🟩🟩 | 🟩🟩🟩 | 🟩🟩		9 days ago
2025-09-08	trias-project/trias	3.1.1	Damiano Oldoni	🟩	🟥🟥 | 🟥🟥🟥 | 🟥🟥	↻	6 hours ago
2025-08-25	dissmapr	0.1.0	Sandra MacFadyen	🟥	🟥🟥 | 🟥🟥🟥 | ✕🟥	↻	24 days ago
2025-08-21	dubicube	0.9.5	Ward Langeraert	🟩	🟩🟩 | 🟩🟩🟩 | 🟩🟩		6 days ago
2025-07-05	rnaturalearthhires (remote/noindex)	1.0.0.9000	Andy South	🟩	🟩🟩 | 🟩🟩🟩 | 🟩🟩		22 days ago
2025-06-15	hrbrmstr/mgrs	0.2.4	Bob Rudis	🟩	🟩🟨 | 🟩🟨🟨 | 🟨🟨		12 days ago
2025-05-12	gcube	1.3.7	Ward Langeraert	🟩	🟩🟩 | 🟩🟩🟩 | 🟩🟩		13 days ago

Figure 3: Screenshot of the R-universe web interface displaying R packages hosted by the B3 project (https://b-cubed-eu.r-universe.dev).

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

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

To install only those **b3verse** packages that are not yet present in the local R environment, the following approach can be used:

```
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"))
}
```

Individual packages can be installed separately, for example:

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

For packages with Bioconductor dependencies, the Bioconductor repository must be included:

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

For long-term reproducibility and citation, snapshot versions of the **b3verse** R-universe and the associated data resources (more info on data resources in Section 3.2) are published and archived on Zenodo (https://zenodo.org/), ensuring that the released software versions remain permanently available and citable, providing a stable foundation for external research and policy work (Table 3 in Section 3.1).

2.3. Software development and quality assurance

Development followed the B3 software development guidelines (Huybrechts et al., 2024), ensuring a well-aligned and high-quality suite of R packages. As the B3 project nears its final phase, the focus is shifted from adding new features to enhancing robustness, usability, and reproducibility (Table 2).

All packages have received at least one internal, informal evaluation. The packages **b3gbi**, **gcube**, **ebvcube**, **rgbif**, and **trias** have undergone formal quality assessment reviews (Desmet et al., 2024). The other packages (**b3doc**, **dissmapr**, **dubicube**, **impIndicator**, **invasimapr**, and **pdindicatoR**) will receive a formal code review in accordance with B3 software during the second quality assessment report of B3 software (MS8, due 27 Feb. 2026).

To guarantee code robustness and reliability, we prioritized the implementation of unit tests across all packages to validate functionality, with continuous efforts focused on improving test coverage to meet B3 quality standards (75 %). Furthermore, significant effort was dedicated to improving user accessibility by developing comprehensive tutorials and vignettes, which are discussed further in Chapter 3. Continuous work is also underway to ensure all packages are formally archived on Zenodo for long-term stability, proper academic citation, and versioned referencing.

Each R package in the collection has its own GitHub repository, where contributing guidelines are provided and issues can be reported. Prior to contributing, users are requested to consult the Contributing Guidelines. Contributions may include bug fixes, feature requests, documentation improvements, or new functionality. Problems or suggestions for improvement can be reported by opening an issue in the corresponding package repository, providing as much detail as possible, including R session information, error messages, and reproducible examples where applicable. Proposals to add or remove packages should be submitted via an issue and/or pull request in the **b3verse** development repository (Table 3), with a clear description of the package purpose and its integration within the existing **b3verse**. New packages are reviewed in accordance with the B3 software development guidelines.

Table 2: Quality assessment across b3verse packages. All packages have received an (internal) informal review. (*) ebvcube, rgbif and trias do not require migration to the B3 GitHub organisation as they are maintained as part of other initiatives than B3.

Package	B3 repo	Quality assessment	Unit tests	Tutorials	Zenodo	Comment
b3doc	✅ yes	🔄 in review	✅ yes	❌ no	✅ yes	README can serve as tutorial
b3gbi	✅ yes	✅ yes	✅ yes	✅ yes	❌ no	Rather limited tutorials
dissmapr	✅ yes	🔄 in review	❌ no	✅ yes	❌ no	
dubicube	✅ yes	🔄 in review	✅ yes	✅ yes	✅ yes	
ebvcube	❌ no*	✅ yes	✅ yes	❌ no	❌ no	README can serve as tutorial
gcube	✅ yes	✅ yes	✅ yes	✅ yes	✅ yes	
impIndicator	✅ yes	🔄 in review	✅ yes	✅ yes	✅ yes	Rather limited tutorials
invasimapr	✅ yes	🔄 in review	❌ no	✅ yes	❌ no	
pdindicatoR	✅ yes	🔄 in review	❌ no	❌ no	✅ yes	
rgbif	❌ no*	✅ yes	✅ yes	✅ yes	✅ yes	
trias	❌ no*	✅ yes	✅ yes	❌ no	✅ yes	Tutorials will be added in 2026 in the context of the GuardIAS project

3. Documentation and vignettes

3.1. User documentation, vignettes and articles

The primary entry point for users is the dedicated B3 project documentation website (https://docs.b-cubed.eu/), which features a guide on the **b3verse** (Langeraert, Desmet, et al., 2025a) (Table 3). This guide is actively maintained and serves as a practical resource, providing:

- An introduction and overview of all included packages.
- Installation guidelines and procedures for the entire **b3verse** suite.
- Guidelines for contributing to the software.
- A step-by-step example of an indicator calculation workflow using multiple packages (= example of Section 4.2).

The website also contains all relevant vignettes and articles from the packages themselves harvested by the **b3doc** R package. Vignettes are also collected at the R-universe platform but not articles (vignettes are tutorials or extra documentation included in a package; articles are the same in content but are not included in the R package itself).

For developers and technical users, the R-universe platform offers a complementary resource to the B3 documentation website. This platform allows users to browse packages, check build statuses, view download metrics, and access more technical documentation (Table 3).

Table 3: 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	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	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	Repository containing R-universe snapshots for long-term archiving.	https://doi.org/10.5281/zenodo.15781060

A critical component of the **b3verse**'s usability strategy is the development of robust vignettes and tutorials. While packages are continuously assessed for quality assurance, there is a commitment to expanding user resources:

- **Current status:** Most packages include basic documentation, and, in some cases, the README file provides sufficient guidance for basic use. Packages like **b3gbi** and **impIndicator** currently feature limited tutorials, while others are actively developing theirs.
- **Future focus:** Future development efforts are focused on creating dedicated, comprehensive user tutorials for all packages to simplify complex workflows and ensure proper usage. These tutorials will also be available on the B3 project documentation website.
- **Archiving for reference:** To ensure reproducibility, all package releases (including documentation and tutorials) are archived on Zenodo (at least from version 1.0), allowing users to cite and reference specific, stable versions used in their publications or reports.

3.2. Data resources for the b3verse

The **b3data** package is a dedicated data resource included in the **b3verse** to ensure that users have direct access to stable example datasets for testing, demonstrations, and reproducible code examples (Langeraert & Van Daele, 2025a).

3.2.1. b3data package and frictionless data format

The **b3data** data package is published in the Frictionless Data Package format (https://frictionlessdata.io/), providing publicly accessible 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 4) (Langeraert, 2025).

Currently, two key resources are available via the package, archived on Zenodo:

- **bird_cube_belgium_mgrs10:** An example occurrence cube of birds in Belgium using the MGRS grid at a 10 km scale.
- **mgrs10_refgrid_belgium:** The corresponding MGRS 10 km reference grid for Belgium.

All data resources and the scripts used to create the **b3data** package are maintained in a dedicated GitHub development repository (Langeraert & Van Daele, 2025b), with versioned snapshots archived on Zenodo for long-term availability (Table 4) (Langeraert & Van Daele, 2025a). Data resources can be downloaded from the Zenodo repository, but can also be accessed directly in R using the **frictionless** R package (Desmet et al., 2025) (Section 3.2.2).

Table 4: 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	Scripts to create the **b3data** frictionless data package. Mostly used by developers.	https://github.com/b-cubed-eu/b3data-scripts
Zenodo	Repository containing **b3data** data resources.	https://doi.org/10.5281/zenodo.15181097

3.2.2. Example: accessing and processing cube data in R

The structure of the **b3data** package allows for easy data import and immediate integration into the indicator workflow. The following example demonstrates the use of the **b3data** resources and is not intended as an example of rigorous ecological analysis. The spatial and temporal patterns shown in the outputs below primarily reflect the data coverage in GBIF and may not reflect actual biodiversity patterns.

Step 1 — Load the frictionless R package

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

Step 2 — Read the package descriptor from Zenodo

```r
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.

```
# install.packages("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,...
```

Step 4 — Post-processing
Once loaded, resources can be filtered, joined, or passed into **b3verse** indicator functions.

```
# Install b3gbi package from b3verse:
# install.packages("b3gbi", repos = c("https://b-cubed-eu.r-universe.dev",
"https://cloud.r-project.org"))

# Load packages
library(b3gbi)   # General biodiversity indicators for occurrence cubes
library(dplyr)   # Data wrangling
library(ggplot2) # Data visualisation
```

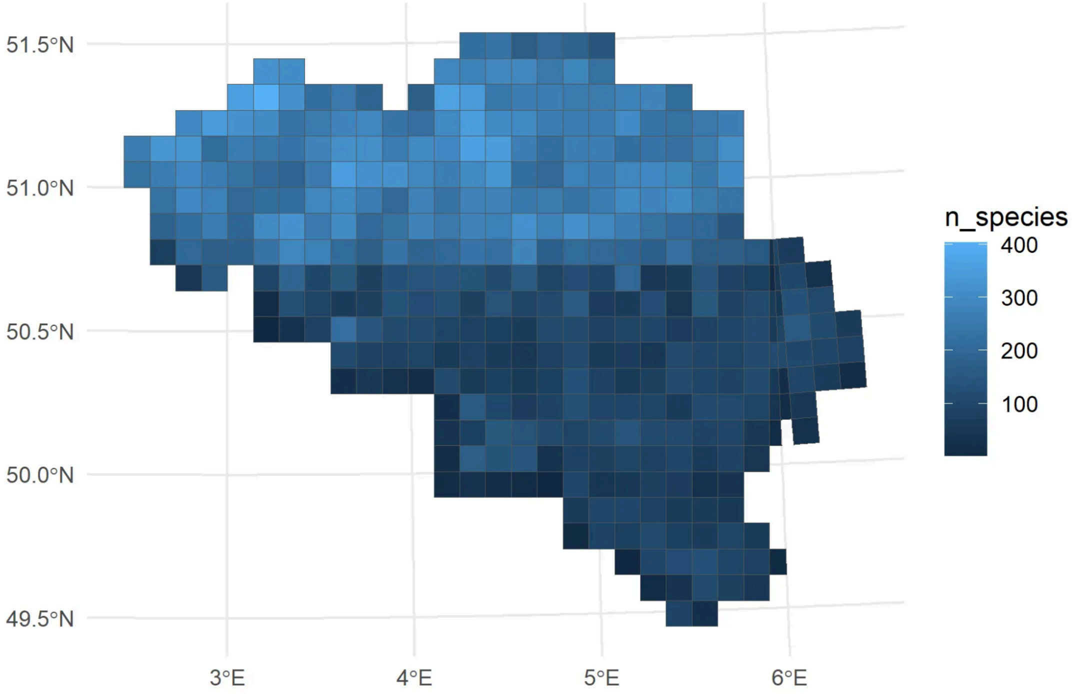
We filter out any data with a minimal coordinate uncertainty larger than 10 km.

```
bird_cube_belgium_clean <- bird_cube_belgium %>%
  dplyr::filter(mincoordinateuncertaintyinmeters <= 10 * 10^3)
```

We join the loaded resources together and visualise the number of species per grid cell.

```
bird_cube_belgium_clean %>%
  # Count number of species
  summarise(
    n_species = n_distinct(species),
    .by = mgrscode
  ) %>%
  # Add MGRS grid
  left_join(mgrs10_belgium, by = join_by(mgrscode)) %>%
```

```
  st_sf(sf_column_name = "geom", crs = st_crs(mgrs10_belgium)) %>%
  # Visualise result
  ggplot() +
    geom_sf(aes(fill = n_species)) +
    theme_minimal()
```



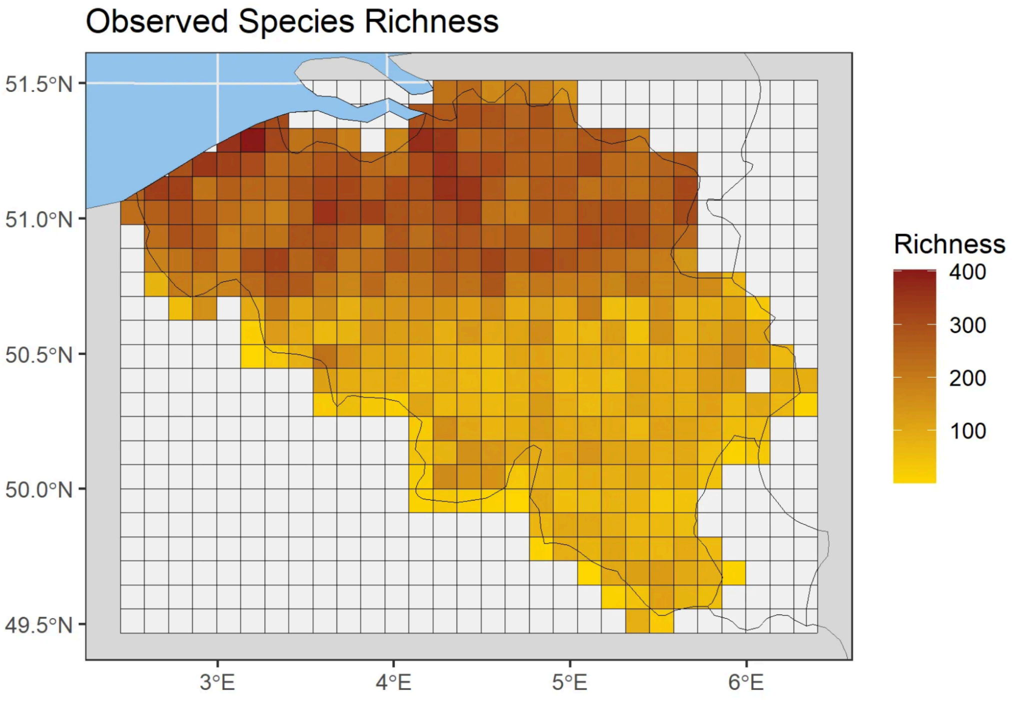
We now process the cleaned data cube using the **b3gbi** package (v0.4.0), which prepares the data for indicator calculations.

```
bird_cube_processed <- process_cube(
  bird_cube_belgium_clean,
  cols_occurrences = "n"
)
bird_cube_processed
#>
#> Processed data cube for calculating biodiversity indicators
#>
#> Date Range: 2000 - 2024
#> Single-resolution cube with cell size 10km ^2
#> Number of cells: 379
#> Grid reference system: mgrs
#> Coordinate range:
```

```
#>       xmin      xmax      ymin      ymax
#>   2.428844  6.334746 49.445981 51.444030
#>
#> Total number of observations: 17609047
#> Number of species represented: 733
#> Number of families represented: 95
#>
#> Kingdoms represented: Data not present
#>
#> First 10 rows of data (use n = to show more):
#>
#> # A tibble: 557,608 × 11
#>     year cellCode taxonKey scientificName    family   obs
minCoordinateUncerta...¹
#>    <dbl> <chr>       <dbl> <chr>             <chr>  <dbl>
<dbl>
#>  1  2000 31UDS65   2473958 Perdix perdix     Phasi...     1
3536
#>  2  2000 31UDS65   2474156 Coturnix coturnix 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 vanellus Chara...     1
3536
#>  6  2000 31UDS65   2480637 Accipiter nisus   Accip...     1
3536
#>  7  2000 31UDS65   2481172 Larus marinus     Larid...     1
3536
#>  8  2000 31UDS65   2481174 Larus fuscus      Larid...     1
3536
#>  9  2000 31UDS65   2481890 Phalacrocorax ca... Phala...     2
1000
#> 10  2000 31UDS65   2482054 Podiceps cristat... Podic...     5
1000
#> # ℹ 557,598 more rows
#> # ℹ abbreviated name: ¹minCoordinateUncertaintyInMeters
#> # ℹ 4 more variables: familyCount <dbl>, xcoord <dbl>, ycoord <dbl>,
#> #   resolution <chr>
```

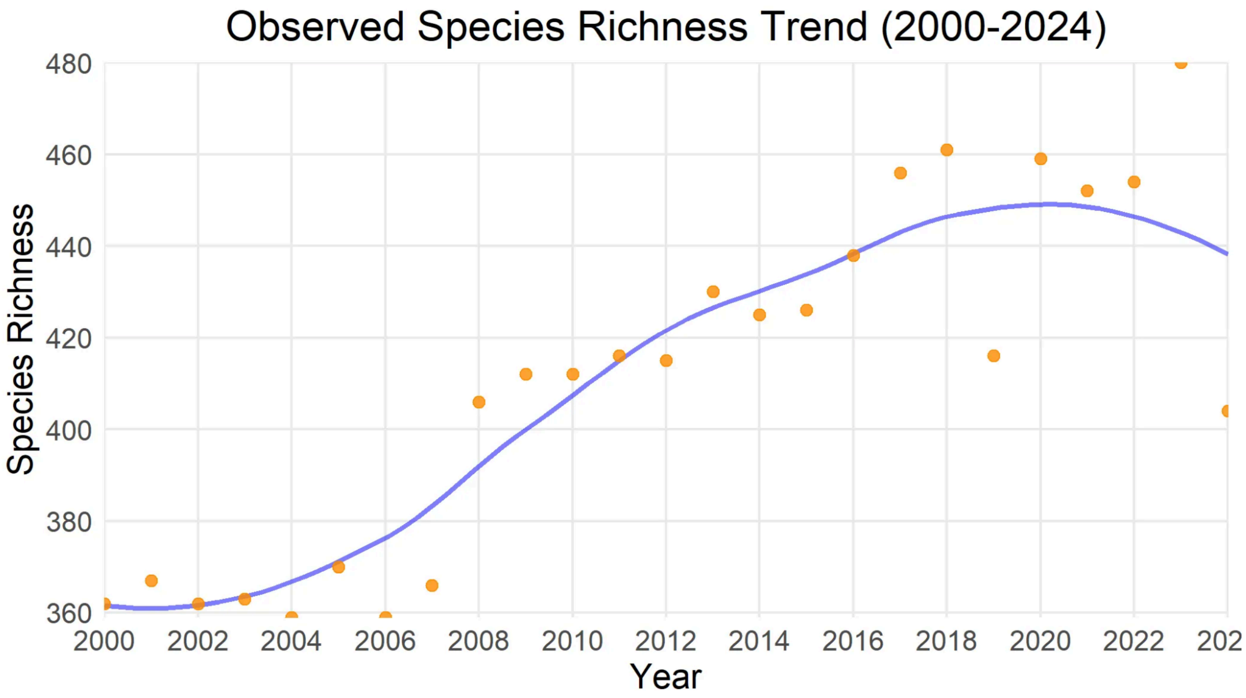
With the processed cube, we can reproduce a species richness map similar to the one created earlier.

```
bird_cube_richness_map <- obs_richness_map(bird_cube_processed)
plot(bird_cube_richness_map)
```



We can also calculate other biodiversity indicators. In the example below, we generate a time series of observed species richness. Confidence intervals are omitted here to reduce computation time.

```
bird_cube_richness_ts <- obs_richness_ts(
  bird_cube_processed,
  ci_type = "none"
)
plot(bird_cube_richness_ts)
```



3.2.3. Future data additions and contribution guidelines

To broaden the utility of the data package and demonstrate the **b3verse**'s capabilities across different spatial scales and taxa, the following data additions are proposed for **b3data** for the future:

- **Large Scale (e.g., 100 km):** An occurrence cube of mammals in Europe using the EEA reference grid, along with the grid itself.
- **Medium Scale (e.g., 30x30 minutes):** An occurrence cube of plants in South Africa using Extended Quarter Degree Grid Cells, along with the corresponding grid.
- **Specific Package Data:** Datasets specifically related to the functionality of other specialized **b3verse** R packages will also be integrated.

Contributions to the **b3data** resources are welcomed. Prior to contributing, users are requested to consult the Contributing Guidelines in the b3data-scripts repository (Table 4). Proposed changes should be submitted by forking the repository and following the instructions in the README to set up a local workflow, after which a pull request can be opened. Alternatively, suggestions for adding one or more resources can be made by opening an issue in the repository, allowing the maintainers to evaluate and potentially include the contribution in the data package. Bugs or suggestions for improvement can likewise be reported by opening an issue in the same repository, with a clear and complete description of the problem. Where applicable, reports should include relevant R session information, error messages, and reproducible examples.

4. Indicator calculation workflow

4.1. Workflow overview

The primary purpose of the **b3verse** is to provide a standardized workflow for translating raw biodiversity data into indicators suitable for policy-making, based on the occurrence cube data structure. This process integrates the core packages of the suite to ensure seamless data flow and standardized output (Fig. 4).

1. **Data Generation:** The process begins with the creation of an occurrence cube, either by downloading real-world data from GBIF using the **rgbif** package (T2.3) or by simulating cubes for sensitivity analysis, testing, or development using the **gcube** package (T4.5).
2. **Data Processing and Standardization:** The generated occurrence cube is then passed to the `process_cube()` function from the **b3gbi** package. This critical step ensures data standardization and verifies that the cube's format is correct and aligned for use across all specialized indicator packages.
3. **Data Exploration and Filtering:** Data exploration steps can be performed using the **dubicube** package (T5.4), after which the data might potentially be filtered.
4. **Indicator Calculation:** Following standardization and exploration, specialized packages handle the calculation of specific indicator types:
    - **b3gbi** (T5.1): Calculates general biodiversity indicators.
    - **pdindicatoR** (T5.2): Calculates phylogenetic diversity indicators.
    - **impIndicator** (T5.3): Calculates alien species impact indicators.
5. **Indicator Uncertainty and Interpretation:** The **dubicube** package can be used to calculate the uncertainty of the calculated indicators via bootstrapping techniques (as a dependency for the indicator packages or separately). Furthermore, it includes functions and tutorials regarding effect classification and visualization.

This integrated workflow streamlines the entire process, minimizing manual data manipulation and ensuring consistency and reproducibility across different indicator types. While this current workflow captures the core indicator calculation process, further clarification is still needed regarding how the remaining packages within the b3verse integrate into this structure. In principle, all downstream analytical or modelling packages are intended to operate on occurrence cubes that have first been standardized and validated using the `process_cube()` function from the **b3gbi** package. This ensures a consistent entry point for analysis and maintains interoperability across the ecosystem.

The modular structure of the **b3verse** enables the construction of automated pipelines. The integration of these packages also facilitates deployment in cloud computing environments. Streamlining the deployment and management of multiple related packages reduces setup complexity, which is essential for processing large biodiversity datasets. This facilitates the integration of the **b3verse** workflow into existing pipelines, such as the BON in a Box platform (https://boninabox.geobon.org/), or into a user interface for direct access by policymakers (Fig. 5). While complex, third-party platform integration is beyond the scope of this project task, the underlying automated pipeline functionality is essential for the simple dashboards being developed in Work Package 6, which focus on implementing the software for specific use cases and facilitating direct access by policymakers.

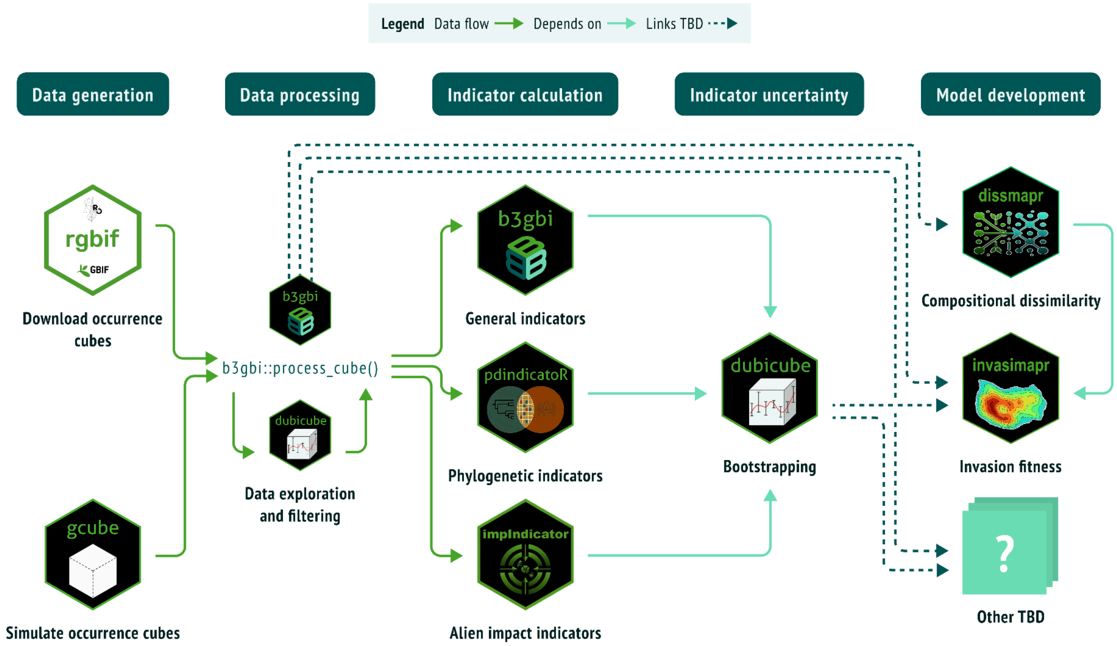


Figure 4: Workflows of indicator calculation and modelling from occurrence cubes within the b3verse. See text for explanation.

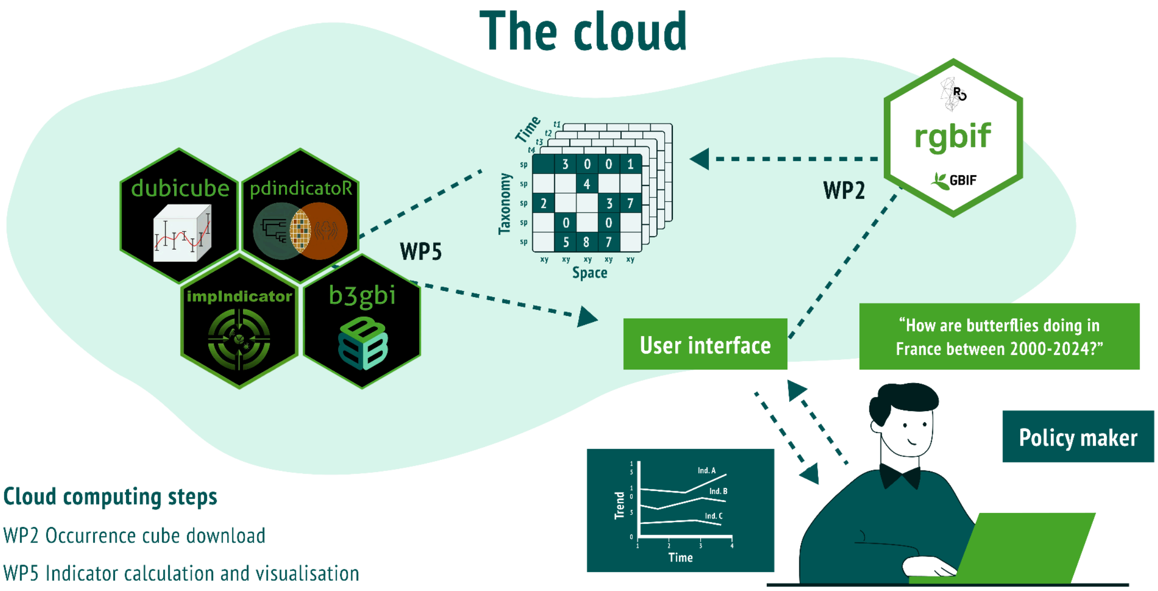


Figure 5: Conceptual visualisation of b3verse workflow integration into a cloud computing environment with user interface.

4.2. Example workflow using the b3verse

We provide a basic example of an analysis workflow using the **b3verse** packages. This example demonstrates the process but is not intended as a best-practice analysis. For more detailed guidance, refer to the package tutorials. This type of workflow could be done by individual researchers using the R packages directly or incorporated into the high-throughput, cloud-based pipelines for automated processing. In this workflow, we use **gcube** v1.4.1 to simulate an occurrence cube, **b3gbi** v0.6.3 to process the cube, and **dubicube** v0.11.0 to calculate uncertainty around indicator estimates.

```
# Load packages
library(gcube)     # simulate occurrence cubes
library(b3gbi)     # process occurrence cubes
library(dubicube)  # uncertainty calculation for occurrence cubes

library(sf)        # work with spatial objects
library(dplyr)     # data wrangling
library(ggplot2)   # data visualisation
```

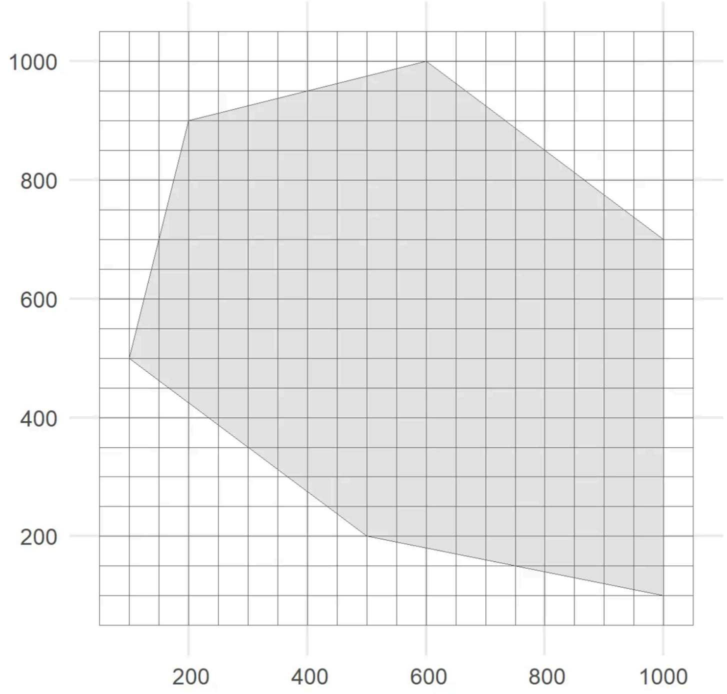
4.2.1. Simulate occurrence cube

As input, we create a polygon in which we simulate occurrences. It represents the spatial extent of the species. We also need a grid. Each observation will be designated to a grid cell.

```
# Create polygon
polygon <- st_polygon(list(cbind(c(500, 1000, 1000, 600, 200, 100, 500),
                                 c(200, 100, 700, 1000, 900, 500, 200))))

# Create grid
cube_grid <- st_make_grid(
  st_buffer(polygon, 50),
  n = c(20, 20),
  square = TRUE) %>%
  st_sf()

# Visualise
ggplot() +
  geom_sf(data = polygon) +
  geom_sf(data = cube_grid, alpha = 0) +
  theme_minimal()
```



We simulate three species for 5 time points where each species has a different average total number of occurrences at time point one and a different spatial clustering (see also this tutorial).

```
# Create dataframe with simulation function arguments
multi_species_args <- tibble(
  species = paste("species", 1:3, sep = "_"),
  species_key = 1:3,
  species_range = rep(list(polygon), 3),
  initial_average_occurrences = c(300, 400, 500),
  n_time_points = rep(5, 3),
  temporal_function = c(NA, simulate_random_walk, NA),
  sd_step = c(NA, 10, NA),
  spatial_pattern = c("random", "clustered", "clustered"),
  coords_uncertainty_meters = 25,
  grid = rep(list(cube_grid), 3),
  seed = 123
)

# How does this dataframe look like?
glimpse(multi_species_args)
#> Rows: 3
#> Columns: 11
#> $ species                    <chr> "species_1", "species_2",
"species_3"
```

```
#> $ species_key                   <int> 1, 2, 3
#> $ species_range                 <list> [POLYGON ((500 200, 1000 100...],
[POLYGON...
#> $ initial_average_occurrences <dbl> 300, 400, 500
#> $ n_time_points                 <dbl> 5, 5, 5
#> $ temporal_function             <list> NA, function
(initial_average_occurrences ...
#> $ sd_step                       <dbl> NA, 10, NA
#> $ spatial_pattern               <chr> "random", "clustered", "clustered"
#> $ coords_uncertainty_meters   <dbl> 25, 25, 25
#> $ grid                          <list> [<sf[400 x 1]>], [<sf[400 x 1]>],
[<sf[40...
#> $ seed                          <dbl> 123, 123, 123
```

We simulate the data cube with these arguments.

```
# Simulate occurrence cube
occurrence_cube_full <- multi_species_args %>%
  gcube::map_simulate_occurrences() %>%
  gcube::map_sample_observations() %>%
  gcube::map_filter_observations() %>%
  gcube::map_add_coordinate_uncertainty() %>%
  gcube::map_grid_designation(nested = FALSE)
#> [1] [using unconditional Gaussian simulation]
#> [2] [using unconditional Gaussian simulation]
#> [3] [using unconditional Gaussian simulation]

# Select relevant columns
occurrence_cube_df <- occurrence_cube_full %>%
  select("cell_code", "time_point", "species", "species_key", "n",
         "min_coord_uncertainty")

# Visualise
glimpse(occurrence_cube_df)
#> Rows: 6,000
#> Columns: 6
#> $ cell_code             <chr> "105", "108", "109", "110", "111", "112",
"113",...
#> $ time_point            <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, ...
#> $ species               <chr> "species_1", "species_1", "species_1",
"species_...
```

```
#> $ species_key             <int> 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1, 1,
1, 1, ...
#> $ n                       <int> 1, 1, 1, 1, 2, 3, 2, 2, 1, 1, 2, 2, 3, 2,
2, 2, ...
#> $ min_coord_uncertainty <dbl> 25, 25, 25, 25, 25, 25, 25, 25, 25, 25,
25, 25, ...
```

4.2.2. Process occurrence cube

We process our simulated cube using the `process_cube()` function from the **b3gbi** package. This ensures standardisation and verifies the data format complies with the b3verse specification.

```
# Process cube
processed_cube <- b3gbi::process_cube(
  cube_name = occurrence_cube_df,
  grid_type = "custom",
  cols_cellCode = "cell_code",
  cols_year = "time_point",
  cols_species = "species",
  cols_speciesKey = "species_key",
  cols_occurrences = "n",
  cols_minCoordinateUncertaintyInMeters = "min_coord_uncertainty"
)

processed_cube
#>
#> Simulated data cube for calculating biodiversity indicators
#>
#> Date Range: 1 - 5
#> Number of cells: 400
#> Grid reference system: custom
#> Coordinate range:
#> [1] "Coordinates not provided"
#>
#> Total number of observations: 6012
#> Number of species represented: 3
#> Number of families represented: Data not present
#>
#> Kingdoms represented: Data not present
#>
#> First 10 rows of data (use n = to show more):
```

```
#>
#> # A tibble: 6,000 × 6
#>    cellCode  year scientificName taxonKey   obs
minCoordinateUncertaintyInMeters
#>    <chr>    <dbl> <chr>             <dbl> <dbl>
<dbl>
#>  1 105          1 species_1             1     1
25
#>  2 108          1 species_1             1     1
25
#>  3 109          1 species_1             1     1
25
#>  4 110          1 species_1             1     1
25
#>  5 111          1 species_1             1     2
25
#>  6 112          1 species_1             1     3
25
#>  7 113          1 species_1             1     2
25
#>  8 117          1 species_1             1     2
25
#>  9 118          1 species_1             1     1
25
#> 10 119          1 species_1             1     1
25
#> # ℹ 5,990 more rows
```

4.2.3. Indicator calculation

Finally, we calculate a simple indicator: the total number of observations in the cube per year.

```
total_abundance <- function(cube) {
  cube %>%
    summarise(
      diversity_val = sum(obs),
      .by = "year"
    )
}
```

The values are calculated and added to a new column `diversity_val`.

```
total_abundance(processed_cube$data)
#> # A tibble: 5 × 2
#>    year diversity_val
#>   <dbl>         <dbl>
#> 1     1          1179
#> 2     2          1274
#> 3     3          1133
#> 4     4          1186
#> 5     5          1240
```

We use bootstrapping to calculate uncertainty around the estimates. We calculate the 95 % percentile interval for each estimate.

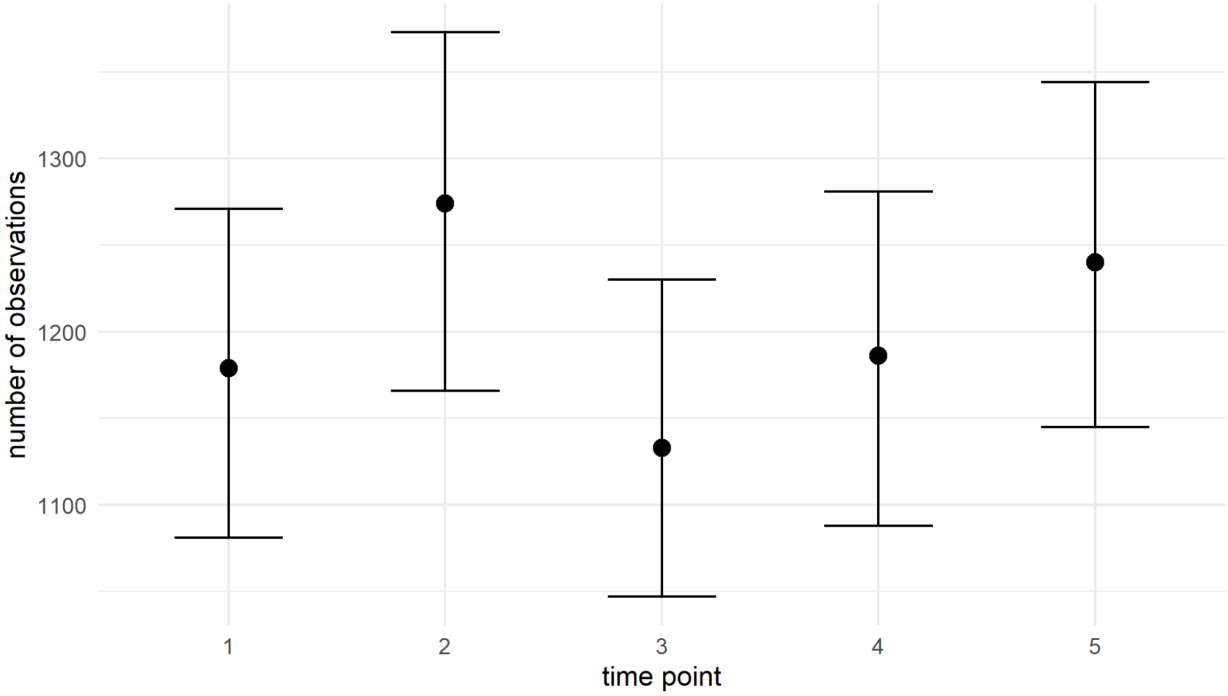
```
# Perform bootstrapping
bootstrap_observations <- dubicube::bootstrap_cube(
  data_cube = processed_cube,
  fun = total_abundance,
  grouping_var = "year",
  samples = 1000,
  seed = 123
)
#> [1] "Performing group-specific bootstrap with `boot::boot()`."

# Calculate percentile intervals
ci_observations <- dubicube::calculate_bootstrap_ci(
  bootstrap_results = bootstrap_observations,
  grouping_var = "year",
  type = "perc",
  conf = 0.95
)

ci_observations
#>   year est_original int_type       ll       ul conf
#> 1    1         1179     perc 1081.025 1271.000 0.95
#> 2    2         1274     perc 1166.051 1373.000 0.95
#> 3    3         1133     perc 1047.000 1229.949 0.95
#> 4    4         1186     perc 1088.025 1280.975 0.95
#> 5    5         1240     perc 1145.025 1344.000 0.95
```

We visualise the results.

```
ci_observations %>%
  ggplot(aes(x = year, y = est_original)) +
    geom_errorbar(aes(ymin = ll, ymax = ul), width = 0.5) +
    geom_point(size = 3, position = position_dodge(1)) +
    labs(y = "number of observations", x = "time point") +
    theme_minimal()
```



5. Conclusion and future outlook

5.1. Conclusion of project T5.5

Task 5.5 successfully achieved its primary goal: establishing a unified, reproducible, and public-facing R package ecosystem to standardize biodiversity indicator calculation within the B3 project.

The core objective of consolidating indicator workflows developed in tasks 5.1-5.4 was met through the establishment of the open-source **b3verse** suite. This collection of R packages provides the final, integrated functions necessary for indicator calculation, organized through a clear, standardized workflow.

The quality and efficiency of the software were checked through B3 software development guidelines and implementation of automated unit tests. The entire development process is anchored in open-source principles and utilizes integration workflows via an R-universe platform, ensuring continuous build, centralized documentation and easy installation using base R functionality.

Comprehensive documentation is currently available for most functions, packages, and workflows in the form of standard R package documentation (man pages), vignettes, and tutorials. Furthermore, a dedicated data package (**b3data**) was developed to provide essential example datasets and lower the barrier to reproducible analysis. This comprehensive documentation ensures that the final workflows are fully accessible and reproducible.

5.2. Future directions

As the project shifts its focus toward final quality assurance and broader integration, future development efforts for the **b3verse** will concentrate on ensuring long-term sustainability, reliability, and increased user adoption.

The highest priority is the formal validation of the entire suite, ensuring that the remaining six packages (**b3doc**, **dissmapr**, **dubicube**, **impIndicator**, **invasimapr**, and **pdindicatoR**) undergo formal code review as scheduled for the second quality assessment report. Beyond this formal milestone, the developers are committed to the continuous maintenance and evolution of the packages, including fixing issues reported by the community and releasing timely updates via the R-universe platform. This ongoing work will be supplemented by efforts to expand unit test coverage across all packages to enhance overall robustness and reliability.

To ensure the long-term sustainability and accessibility of the project's outputs, we aim to publish all package releases as well as snapshot versions of the entire **b3verse** on Zenodo, which provides stable, citable versions for all software and all versions of that software. The mechanisms for maintenance and continued development after the project ends are further detailed in the B3 sustainability report (Depecker et al., 2025).

To maximize the impact and adoption of the **b3verse**, efforts are focused on developing dedicated, comprehensive user tutorials and/or vignettes for all packages, both available via the R package repository and the B3 project documentation website. Furthermore, the robust automation capabilities developed in T5.5 lay the groundwork for seamless future integration into user interfaces, a requirement that will be demonstrated by the simple dashboards created in WP6 to facilitate cloud computing and direct accessibility for policymakers and other stakeholders.

6. Acknowledgements

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