



BIODIVERSITY  
BUILDING  
BLOCKS FOR  
POLICY

# The b3verse: an R package suite to process cubes and calculate indicators

Ward Langerært<sup>1</sup>, Shawn Dove<sup>2</sup> & Jasmijn Hillaert<sup>1</sup>

<sup>1</sup>Research Institute for Nature and Forest (INBO)

<sup>2</sup>Justus Liebig University Giessen (JLU)



Funded by  
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RESEARCH INSTITUTE  
NATURE AND FOREST



B-Cubed training session 6/27-03-2026/online

# Introduction

Ward



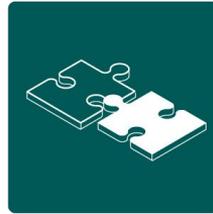
# Introduction

## Why occurrence cubes?



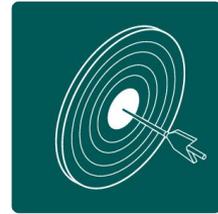
### Challenges

The global biodiversity crisis requires **rapid, reliable and repeatable biodiversity monitoring data** which decision makers can use to evaluate policy.



### Opportunities

Such information – from local to global level and within relevant timescales – calls for an **improved integration of data on biodiversity** from different sources.



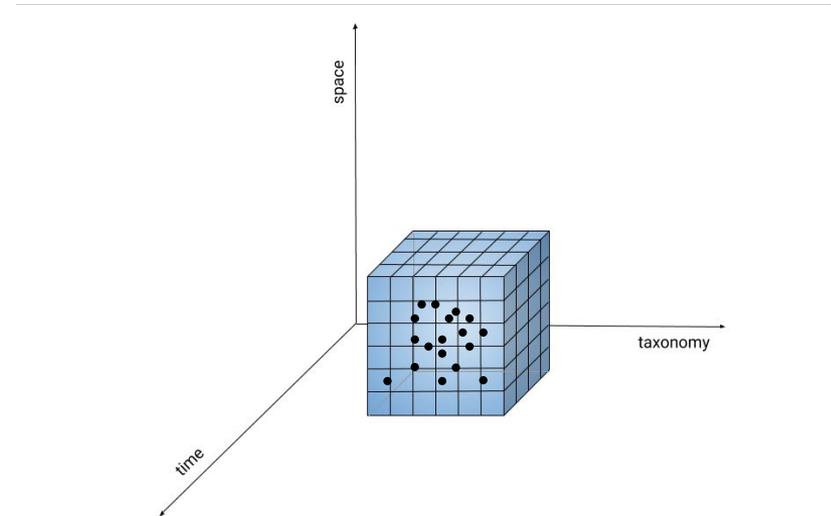
### Aim

B-Cubed is **standardising access to biodiversity data**, empowering policymakers to address the impacts of biodiversity change.

# Introduction

## What occurrence cubes?

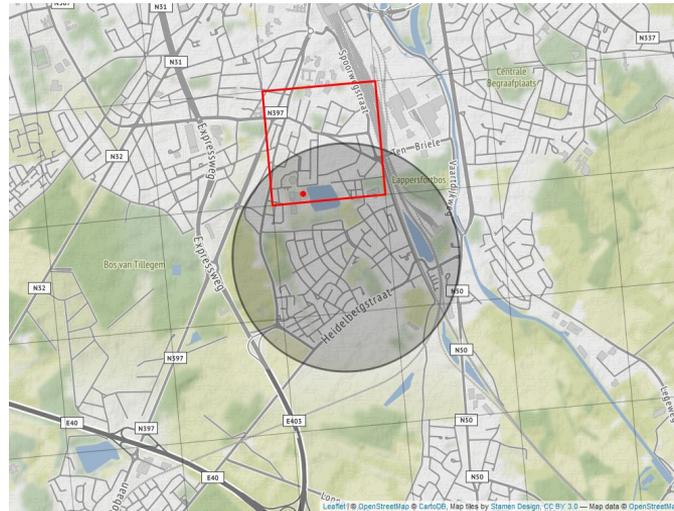
- The concept of **occurrence cubes** developed during the [TriAS project](#) to aggregate GBIF occurrences
  - **taxonomically**, e.g. species
  - **spatially**, e.g. EEA grid 1x1km
  - **temporally**, e.g. year
- Used for calculating emerging trends indicators
- Presented at TDWG2020 (see [slides](#), [abstract](#))
- Preprint ([PDF](#)) used in B-Cubed project proposal



# Introduction

## What occurrence cubes?

- What about **spatial uncertainty**?
  - Random assignment to grid within uncertainty circle



# Introduction

## What occurrence cubes?

- Aggregation
  - Number of occurrences of a specific **taxon** in a specific **cell** in a specific **time interval**

year	eea_cell_code	speciesKey	n	min_coord_uncertainty
2014	1kmE3886N3121	2889173	51	10
2014	1kmE3886N3122	2889173	109	10
...	...	...	...	...
2018	1kmE4047N3067	2889173	1	2828



# Introduction

## From cubes to indicators

- B-Cubed: create **reproducible** and **robust workflow**



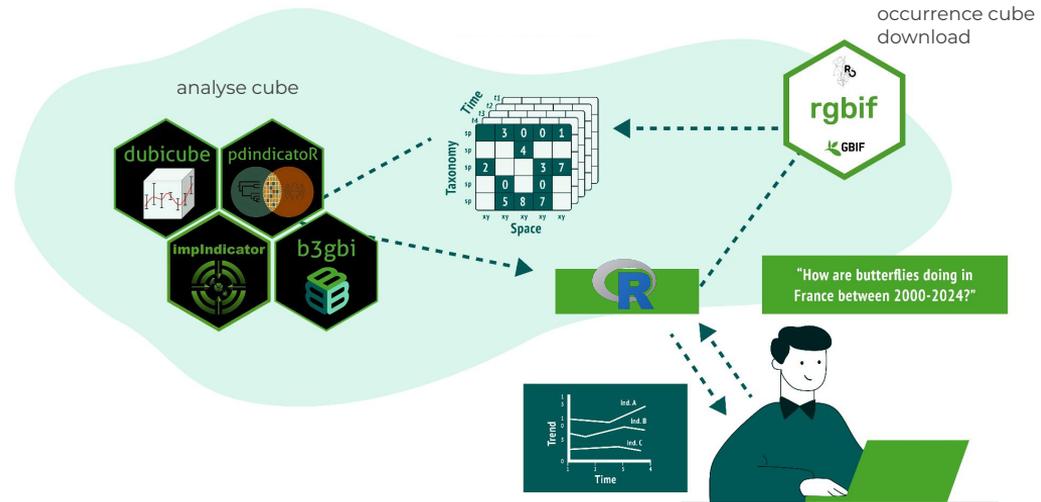
Generate cubes

Process cubes

Analyse cubes

- Statistical models
- Indicator calculation

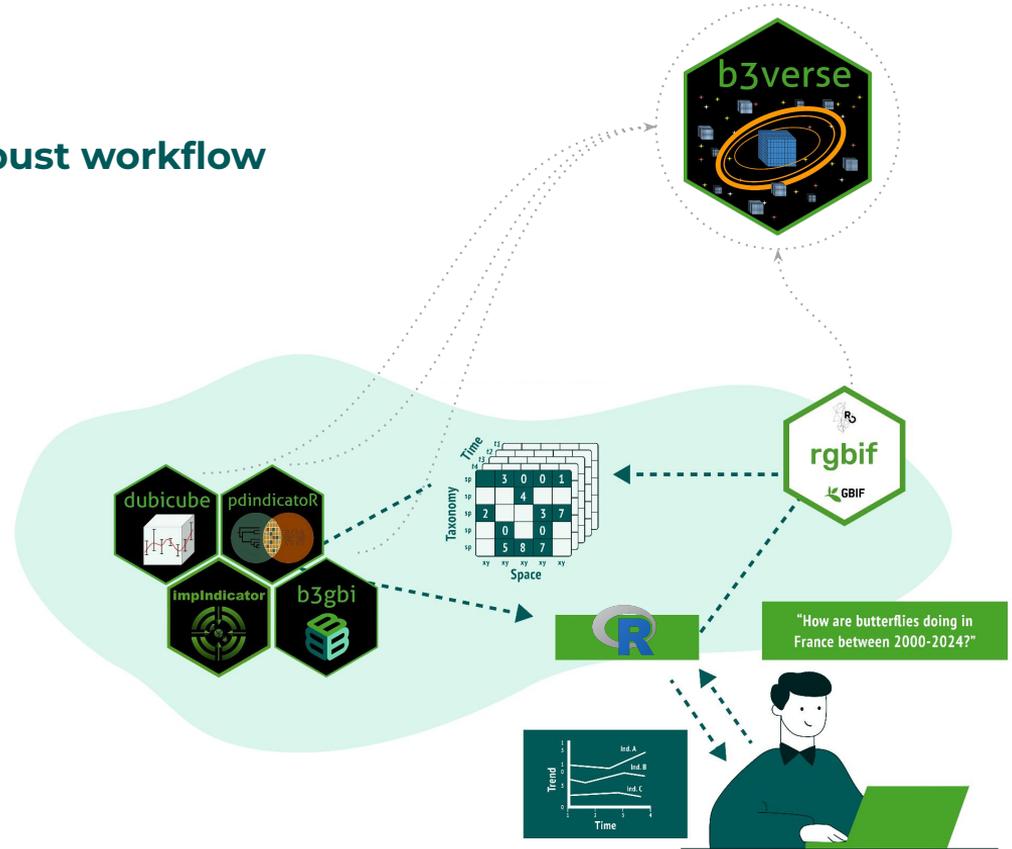
Visualise and interpret results



# Introduction

## From cubes to indicators

- B-Cubed: create **reproducible** and **robust workflow**
  - Generate cubes
  - Process cubes
  - Analyse cubes
    - Statistical models
    - Indicator calculation
  - Visualise and interpret results
- Approach: Group of interconnected R packages
  - **b3verse**



# b3verse, an ecosystem of R packages

Ward



# b3verse, an ecosystem of R packages

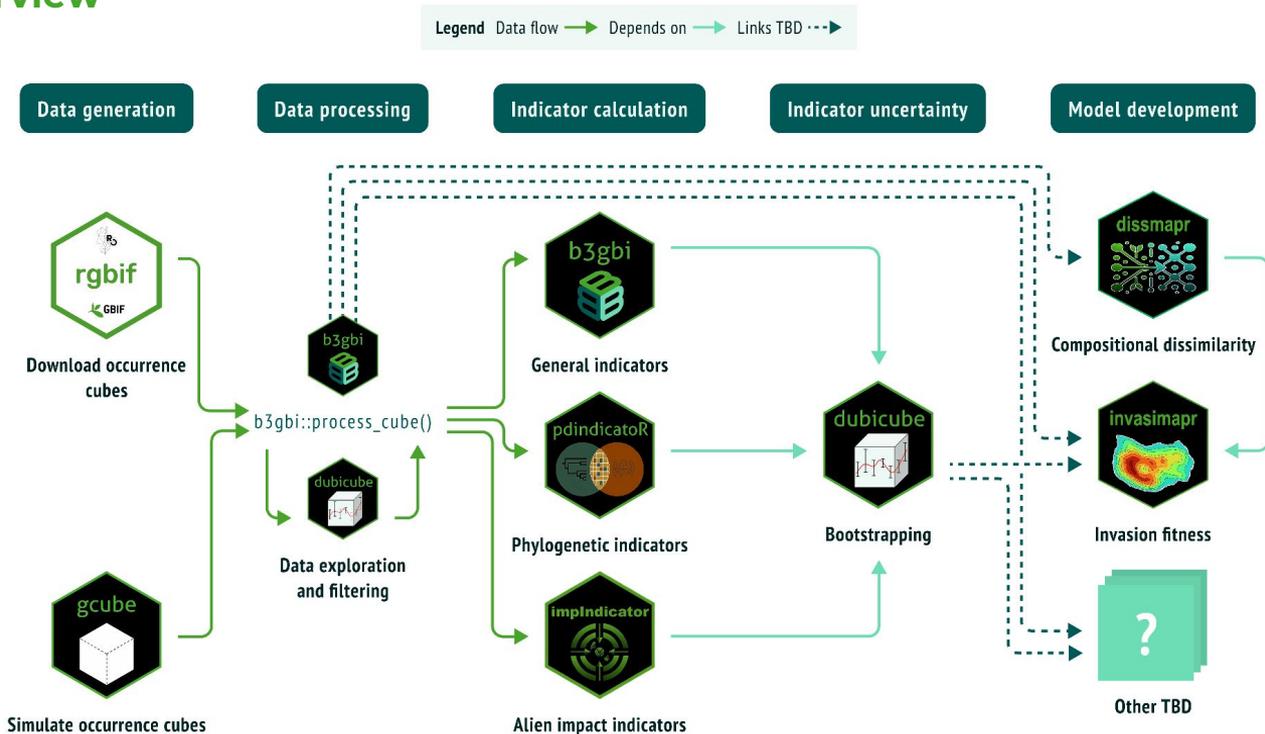
## General overview

- **b3verse** R package ecosystem
  - 11 R packages
  - 1 dedicated frictionless data package
- Maintained via R-Universe platform



# b3verse, an ecosystem of R packages

## General overview



# b3verse, an ecosystem of R packages

## Practical approach and technical implementation

The essentials

- Shared **software development guide**



B-Cubed software development | docs.b-cubed.eu/guides/software-development/

B-Cubed documentation

Search

Ctrl K

Auto

Guides

- Occurrence cube
- Software development**
- Suitability cube
- Dissimilarity cube
- Invasibility cube
- Data quality
- b3verse
- b3data

Software

Infrastructure

Tutorials

# B-Cubed software development guide

This guide specifies high-level requirements for software, computational tools and resources developed for B-Cubed (referred to in the sections as “software”) to ensure that the produced software meets the intended quality, openness, portability and reusability.

## How to cite

Huybrechts P, Trekels M, Abraham L, Desmet P (2024). B-Cubed software development guide. <https://docs.b-cubed.eu/guides/software-development/>

## Introduction

These requirements were carefully selected from numerous existing best practices and guidelines, and aim to promote a consistent **open source development** cycle that allows collaboration and reuse within and outside of the consortium. Emphasis is placed on standardized metadata (files) that make

On this page

- Overview
- How to cite
- Introduction
- Code repositories
  - Create a repository
  - Set the copyright holder
  - Ignore Mac .DS\_Store files
  - Add a CITATION.cff file
  - Add topics
  - Hide irrelevant tabs
  - Invite collaborators
  - Extend your README.md file
  - Setup your local environment, contribute code and collaborate
- The README file
  - Format
  - Title
  - Badges
  - Description
  - Installation instructions
  - Examples or usage instructions
  - README files for data
- Code collaboration
  - Add a Code of conduct
  - Enable notifications
  - Follow the GitHub flow

B-Cubed software development | docs.b-cubed.eu/guides/software-development/#r-analysis

B-Cubed documentation

Search [Ctrl K]

Guides

- Occurrence cube
- Software development**
- Suitability cube
- Dissimilarity cube
- Invasibility cube
- Data quality
- b3verse
- b3data

Software

Infrastructure

Tutorials

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## R analysis code

**B-Cubed software requirements**

- R analysis code **MUST** adhere to the proposed directory structure.
- Data files **MUST** be placed in the `data` directory in the applicable subdirectory `raw`, `interim` OR `processed`.
- Any included files **MUST** adhere to the tidyverse style guide [section on file names](#).
- R code meant as an analysis workflow **MUST** be stored in `.Rmd` OR `.R` format.

An important note is that most R analysis scripts could be wrapped as a package. This has many advantages:

- Packages provide a better structure.
- Packages are easier to install and use.
- Packages allow for better documentation.
- It is much easier for others to reuse your work.
- There are a lot of tools that can help you make your work more reproducible that work better in the context of an R package.
- Within B-Cubed and the wider R community there are people ready to help, so if you've been waiting for an opportunity to learn: this is it.

Code style

Testing

Check your R code

R functions

- How to split a script into functions
- Naming functions
- Function arguments
- Documenting functions

R packages

- Naming your package
- Creating metadata for your package
- Console messages
- README
- Documentation website
- DESCRIPTION and authorship
- CITATION
- LICENSE
- Examples
- Dependencies
- Code coverage

R analysis code

Python

- Repository structure
- Virtual environments
- Dependencies
- Code style
- Testing
- Packages

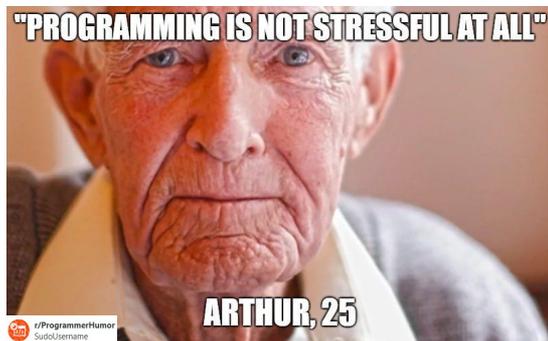
<https://docs.b-cubed.eu/guides/software-development/>

# b3verse, an ecosystem of R packages

## Practical approach and technical implementation

The essentials

- Shared **software development guide**
  - Including evaluation



### M8 Second quality assessment report of B3 software

23/02/2026

Author(s): Peter Desmet, Lissa Breugelmanns, Shawn Dove, Katelyn Faulkner, Sanne Govaert, Quentin Groom, Sandra MacFadyen, Luisa Machado, Damiano Oldoni, Lien Reyserhove, Duccio Rocchini, Maxime Ryckewaert, Hanno Seebens, Maarten Trekels, Toon Van Daele, Mukhtar Yahaya



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This project receives funding from the European Union's Horizon Europe Research and Innovation Programme (ID No 101059592). Views and opinions expressed are those of the author(s) only and do not necessarily reflect those of the European Union or the European Commission. Neither the EU nor the EC can be held responsible for them.

# b3verse, an ecosystem of R packages

## Practical approach and technical implementation

The essentials

- Shared **software development guide**
  - Including evaluation
  - Cooperation on GitHub + automated checks

Visualise uncertainty #70

Merged mmyahaya merged 9 commits into Prepare\_indicator\_bootstrap from visualise-uncertainty on Feb 18

Conversation 1 Commits 9 Checks 16 Files changed 19 +1,246 -864

wlangera commented on Feb 18 • edited

I have made some suggested changes:

- Reduce the number of arguments in `compute_impact_indicator`  
There were a lot of arguments which make it complicated for the user.  
Please revise the arguments to see if I did not make a mistake.

```
# Impact indicator
impactIndicator <- compute_impact_indicator(
  cube = acacia_cube,
  impact_data = eicat_acacia,
  method = "mean_cum",
  ci_type = "perc",
  boot_args = list(seed = 123)
)
```

- Improvement of the `plot` function  
I think it is better to visualise the indicators categorically since they are calculated per year.  
Line or smooth trends can be added:

Reviewers: mmyahaya

Assignees: No one—assign yourself

Labels: None yet

Projects: None yet

Milestone: No milestone

Development: Successfully merging this pull request may close these issues.

Implement data quality diagnostics for `processed_cube` objects #100  
wlangera wants to merge 50 commits into `main` from `implement-quality-diagnostics`

**This branch has not been deployed**  
No deployments

**Review required**  
At least 1 approving review is required by reviewers with write access.

**All checks have passed**  
7 successful checks

- check package with checklist / check package (push) Successful in 27m **Required**
- codecov/patch — 96.4% of diff hit (within 10.0% threshold of 99.5%)
- codecov/project — 98.6% (-1.0%) compared to 9cbf114
- R-CMD-check-OS / macOS-latest (release) (pull\_request) Successful in 3m
- R-CMD-check-OS / ubuntu-22.04 (devel) (pull\_request) Successful in 3m
- R-CMD-check-OS / ubuntu-22.04 (oldrel) (pull\_request) Successful in 3m
- R-CMD-check-OS / windows-latest (release) (pull\_request) Successful in 4m

**This pull request is still a work in progress**  
Draft pull requests cannot be merged. **Ready for review**

Merge pull request  You can also merge this with the command line. [View command line instructions.](#)

# b3verse, an ecosystem of R packages

## Practical approach and technical implementation

The essentials

- Shared **software development guide**
- **R-universe** platform:  
open platform for running personal CRAN-like package repositories ([more info](#))
  - **Searchable catalogue** for R software, articles, datasets
  - **Visible and accessible** to a big audience, easy installation
  - **Automatic updates and compilation** whenever changes are pushed to GitHub

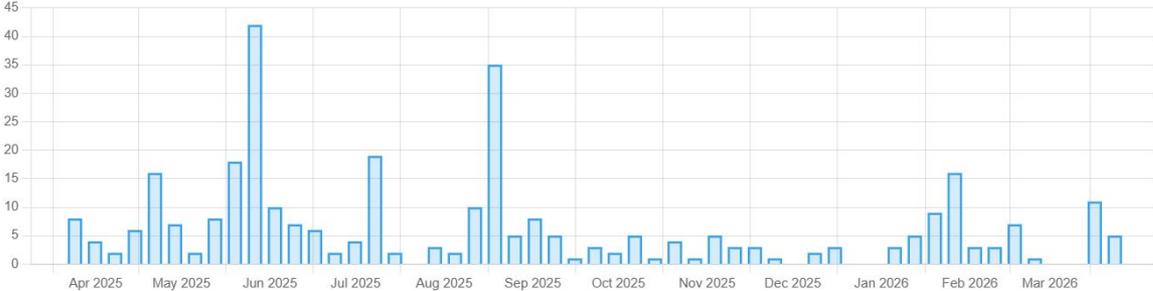


R packages by B-Cubed

b-cubed-eu.r-universe.dev/builds

Builds Packages Articles Datasets Contribution Badges API Feed

universe:b-cubed-eu ..... Search

**B-Cubed**  
Biodiversity Building Blocks for Policy

- r-universe/b-cubed-eu ✓
- https://docs.b-cubed.eu
- 12 packages (871.93MB)
- 10 articles
- 14 datasets
- 51 contributors
- 32 followers

Commit	Package	Version	Maintainer	Src	R-4.6   R-4.5	Built
2026-03-23	ebvcube/ebvcube	0.5.2	Emmanuel Oceguera Conchas			2 hours ago
2026-03-23	implIndicator	0.6.0	Mukhtar Muhammed Yahaya			4 hours ago
2026-03-23	pdindicatoR	0.1.0	Lissa Breugelmans			5 hours ago
2026-03-23	ropensci/rgbif	3.8.5	John Waller			6 hours ago
2026-03-19	b3gbi	0.8.16	Shawn Dove			4 days ago
2026-03-01	diissmapr	0.1.0	Sandra MacFadyen			22 days ago
2026-02-19	dubicube	0.11.1	Ward Langerært			2 days ago
2026-02-19	gcube	1.4.4	Ward Langerært			2 days ago

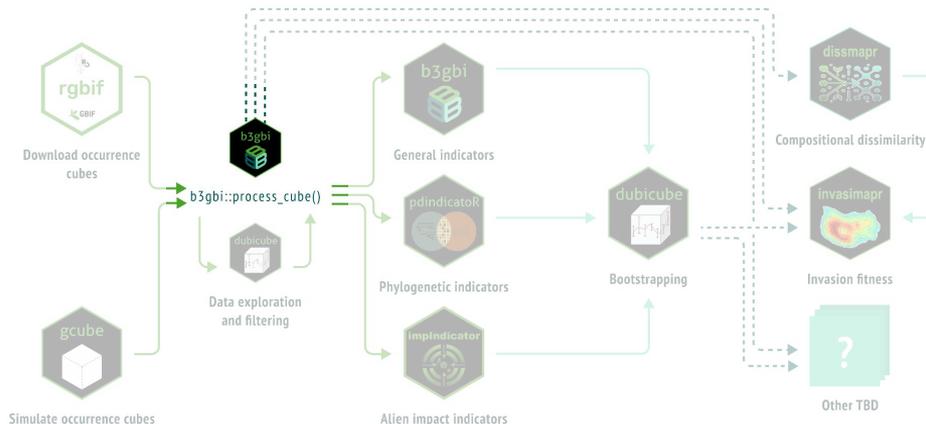
<https://b-cubed-eu.r-universe.dev/>

# b3verse, an ecosystem of R packages

## Practical approach and technical implementation

The essentials

- Shared **software development guide**
- **R-universe** platform
- Gatekeeper validation function **b3gbi::process\_cube()**
  - **Structural consistency and harmonization**
  - **Interoperability** across packages



# b3verse, an ecosystem of R packages

## Practical approach and technical implementation

The essentials

- Shared **software development guide**
- **R-universe** platform
- Gatekeeper validation function **b3gbi::process\_cube()**
- Visibility and outreach
  - Central documentation and tutorials



b3verse: A collection of R packages

docs.b-cubed.eu/guides/b3verse/

B-Cubed documentation

Q Search Ctrl K

Auto

Guides

- Occurrence cube
- Software development
- Suitability cube
- Dissimilarity cube
- Invasibility cube
- Data quality
- b3verse**
- b3data

Software

- b3doc
- b3gbi
- dubicube
- ebvcube
- gcube
- impIndicator
- pdindicatorR
- rgbif
- suitabilitycube
- trias
- vscube

Infrastructure

Tutorials

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# b3verse: A collection of R packages to work with occurrence cubes

Explore

Explore the [b3verse website](#).

r-universe [b-cubed-eu](#) Update universe [passing](#) r-universe [12 packages](#) r-universe [10 articles](#)

r-universe [14 datasets](#)

This guide provides an overview of the integration and maintenance of R packages designed for working with occurrence cubes.

## How to cite

Langerhaert W, Desmet P, Van Daele T (2026). b3verse: A collection of R packages to work with occurrence cubes. Version 1.0. <https://docs.b-cubed.eu/guides/b3verse/>

## What is the b3verse?

The **b3verse** is a collection of related R packages that support the entire workflow of working with occurrence cubes. This includes data retrieval, cube simulation, data processing, exploration, indicator calculation, and uncertainty estimation. These packages are accessible and maintained via a [dedicated R-universe platform](#), ensuring continuous updates, easy distribution, and efficient [installation](#).



### On this page

- Overview
- How to cite
- What is the b3verse?
- Installation
- Contributing and reporting issues
- Getting started
  - The b3verse indicator calculation workflow
  - Example workflow

<https://docs.b-cubed.eu/guides/b3verse/>

gcube: Simulating Biodiversity

docs.b-cubed.eu/software/gcube/readme/

B-Cubed documentation

Q Search Ctrl K

Auto

Software

- b3doc
- b3gbi
- dubicube
- ebvcube
- gcube**
  - Introduction**
  - Occurrence process
  - Detection process
  - Grid designation process
  - Multi-species approach
  - Cube for virtual species
  - Custom grid designation
- impIndicator
- pdindicatorR
- rgbif
- suitabilitycube
- trias
- vsucube

Infrastructure

Tutorials

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# gcube: Simulating Biodiversity Data Cubes

Source file Last updated: Jan 19, 2026

repo status: Active | release: v1.4.4 | r-universe: 1.4.4 | CRAN status

R-CMD-check-OS: passing | codecov: 100%

DOI: 10.5281/zenodo.14038996 | r-universe: b-cubed-eu

funder: European Union



The goal of **gcube** is to provide a simulation framework for biodiversity data cubes using the R programming language. This can start from simulating multiple species distributed in a landscape over a temporal scope. In a second phase, the simulation of a variety of observation processes and effort can generate actual occurrence datasets. Based on their (simulated) spatial uncertainty, occurrences can then be designated to a grid to form a data cube.

Simulation studies offer numerous benefits due to their ability to mimic real-world scenarios in controlled and customizable environments. Ecosystems and biodiversity data are very complex and involve a multitude of interacting factors. Simulations allow researchers to model and understand the complexity of ecological systems by varying parameters such as spatial and/or temporal clustering, species prevalence, etc.

## Installation

Install **gcube** in R:

<https://docs.b-cubed.eu/software/gcube/readme/>

On this page

- Overview
- Installation
- Package name rationale and origin story
- Example
  - Occurrence process
  - Detection process
  - Grid designation process
  - Cubes for multiple species

# b3verse, an ecosystem of R packages

## Practical approach and technical implementation

The essentials

- Shared **software development guide**
- **R-universe** platform
- Gatekeeper validation function **b3gbi::process\_cube()**
- Visibility and outreach
  - Central documentation and tutorials
    - Documentation helper package **b3doc**:



# b3verse, an ecosystem of R packages

## Practical approach and technical implementation

### The essentials

- Shared **software development guide**
- **R-universe** platform
- Gatekeeper validation function **b3gbi::process\_cube()**
- Visibility and outreach
  - Central documentation and tutorials
    - Documentation helper package **b3doc**
  - Training sessions and workshops



The screenshot shows a webpage from Biodiversity Building Blocks for Policy. The page title is "Fourth session of B-Cubed training series: Access the recording and materials". The date is "19 March 2026". The main text describes a training session on "Automating compositional dissimilarity and biodiversity turnover mapping with `dissmapr`". It mentions that the session was held on 13 March and focused on `dissmapr`, an open-source R framework. A list of links is provided: "Slides", "Recording", and "Q&A and R script". Below this, there is a paragraph about the application of `dissmapr` to butterfly assemblages in South Africa, highlighting its ability to reveal species-sharing patterns and produce heatmaps and delineations. At the bottom, it states that participants learned to use `dissmapr` and provides a GitHub link for installation: <https://github.com/b-cubed-eu/dissmapr>. On the right side of the page, there is a grid of four images showing presentation slides and a recording interface. The caption below the grid reads: "Training session on session on Automating compositional dissimilarity and biodiversity turnover mapping with `dissmapr`".

# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

Documentation

- **b3doc**

Indicator workflow

- **rgbif, gcube, b3gbi, pdindicatorR, implIndicator, dublicube**

Modelling cubes

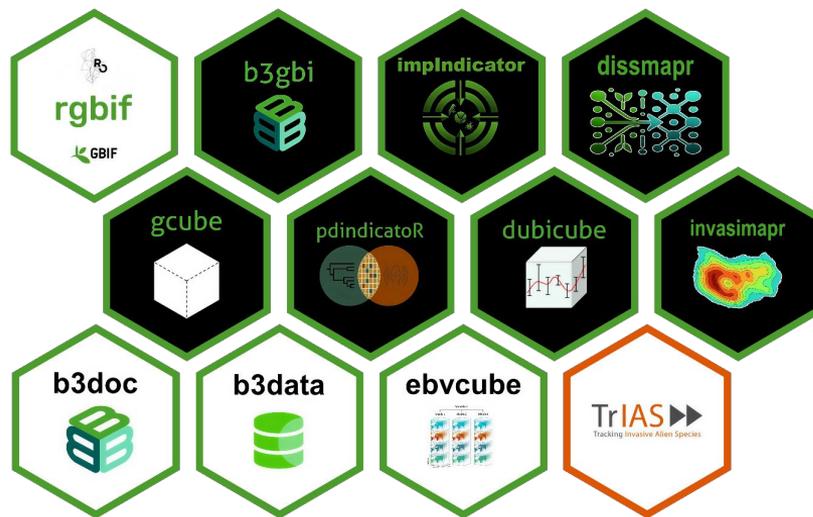
- **dissmapr, invasimapr**

Other projects

- **ebvcube, trias**

Data

- **b3data**



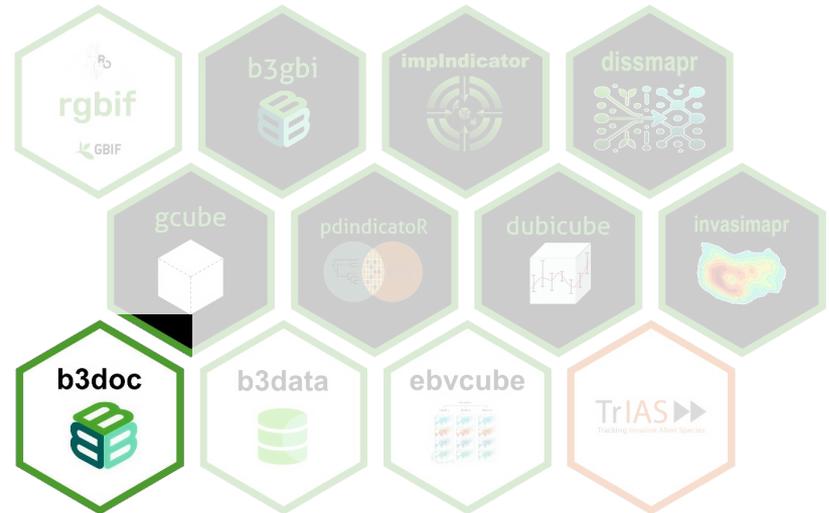
# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

Documentation

- **b3doc**
  - Create Markdown pages for the B-Cubed documentation website

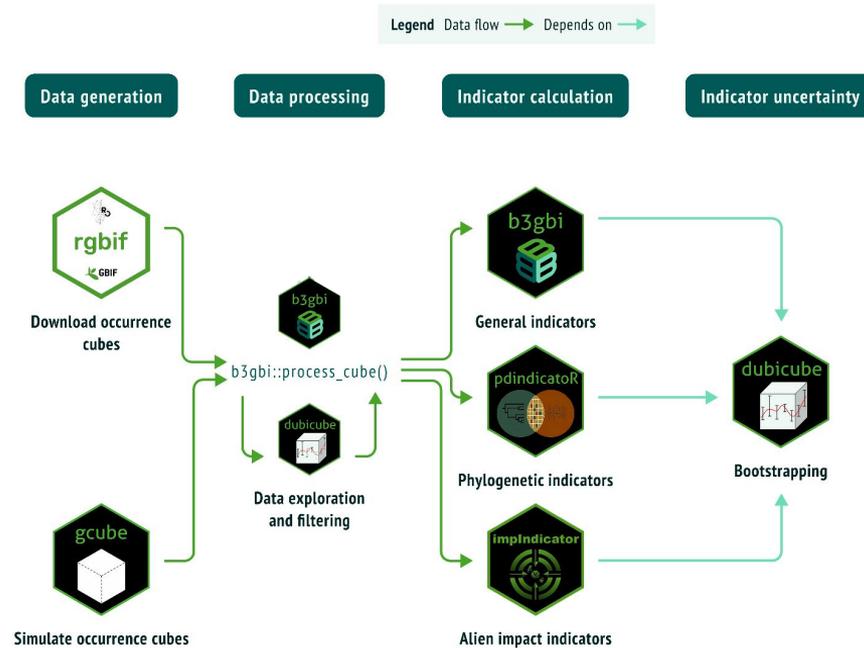
*See earlier*



# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

### Indicator workflow

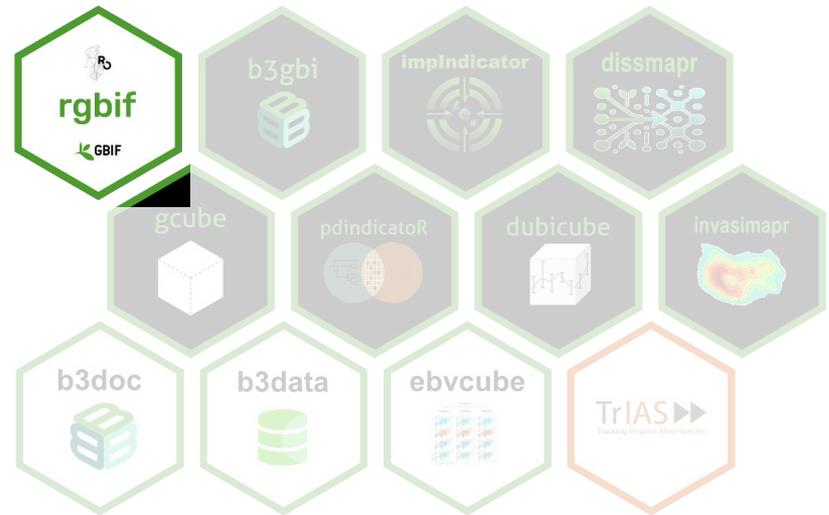


# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

Indicator workflow

- **rgbif**
  - Search and retrieve data from GBIF



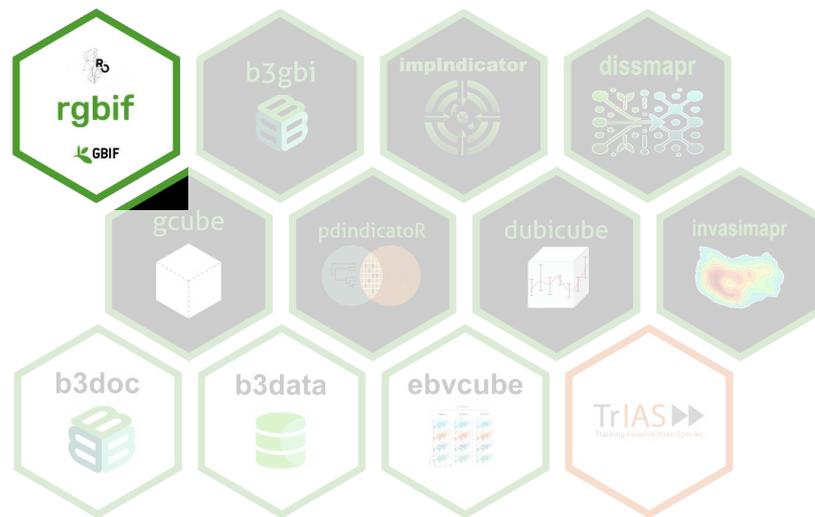
# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

Indicator workflow

- **rgbif**
  - Search and retrieve data from GBIF
  
- Download occurrences
- Match taxon names
- View dataset metadata
- ... download occurrence cubes :)

*See later*

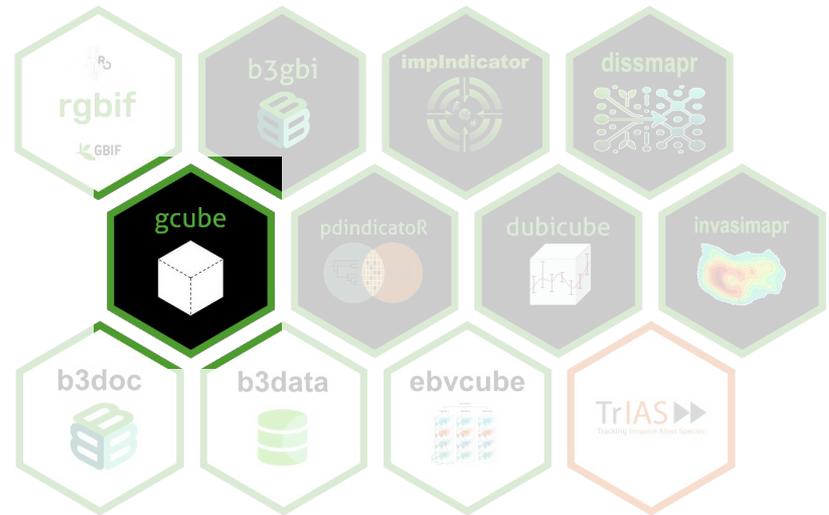


# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

Indicator workflow

- **gcube**
  - Simulation of occurrence cubes

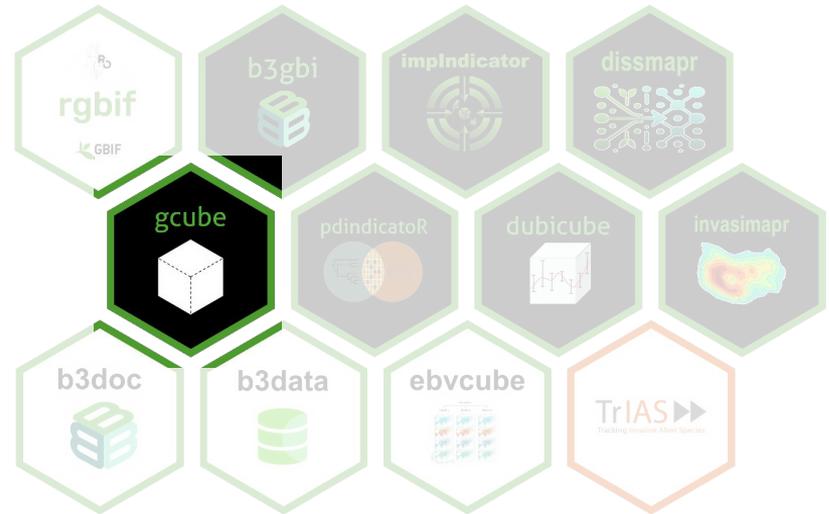


# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

### Indicator workflow

- **gcube**
  - Simulation of occurrence cubes
- Monte Carlo simulation
  - Occurrence process
  - Detection process
  - Grid designation process
- Virtual species
- Custom occurrence datasets



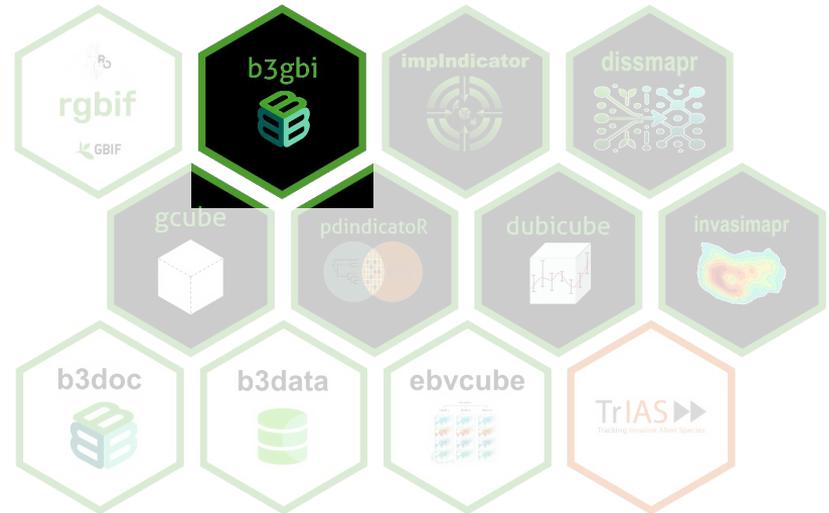
# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

Indicator workflow

- **b3gbi**
  - Calculate general biodiversity indicators from occurrence cubes

*See later*



# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

Indicator workflow

- **pdindicatorR**
  - Calculate phylogenetic indicators from occurrence cubes



# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

Indicator workflow

- **pdindicatorR**
  - Calculate phylogenetic indicators from occurrence cubes
  
- Input
  - Occurrence cube
  - Phylogenetic tree
  - (spatial grid for visualisation)

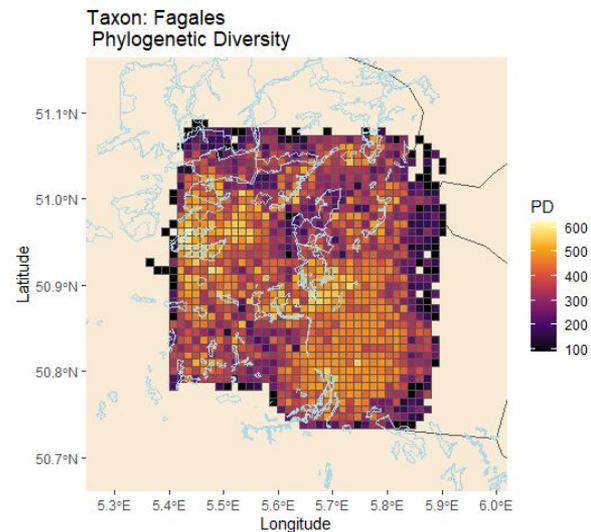


# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

### Indicator workflow

- **pdindicatorR**
  - Calculate phylogenetic indicators from occurrence cubes
- Input
  - Occurrence cube
  - Phylogenetic tree
  - (spatial grid for visualisation)
- Calculation of phylogenetic diversity
  - Sum of branch lengths

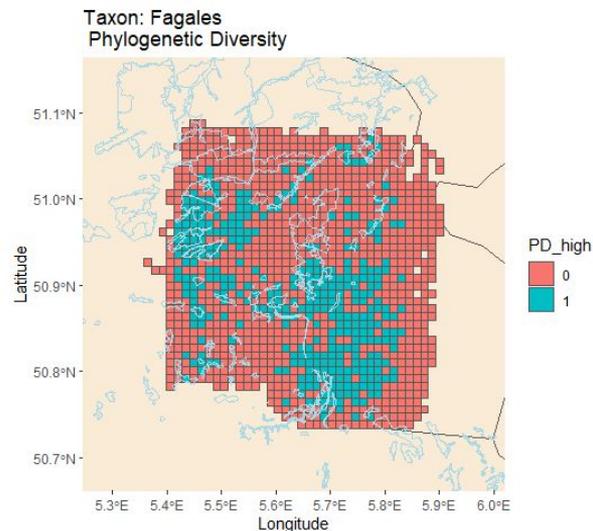


# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

### Indicator workflow

- **pdindicatorR**
  - Calculate phylogenetic indicators from occurrence cubes
- Input
  - Occurrence cube
  - Phylogenetic tree
  - (spatial grid for visualisation)
- Calculation of phylogenetic diversity
  - Sum of branch lengths
- Proportion high PD grid cells in protected areas
  - Cut-off value
  - Spatial grid with protected areas



# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

Indicator workflow

- **impIndicator**
  - Calculate alien impact indicators from occurrence cubes



# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

Indicator workflow

- **impIndicator**
  - Calculate alien impact indicators from occurrence cubes
  
- Input
  - Occurrence cube
  - EICAT assessment data
    - massive (MV), major (MR), moderate (MO), minor (MN), or minimal concern (MC)

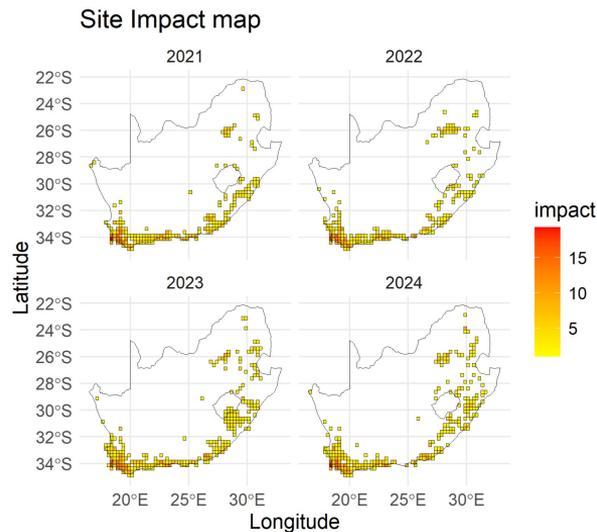


# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

### Indicator workflow

- **impIndicator**
  - Calculate alien impact indicators from occurrence cubes
- Input
  - Occurrence cube
  - EICAT assessment data
    - massive (MV), major (MR), moderate (MO), minor (MN), or minimal concern (MC)
- Calculation of impact of alien species
  - Site impact indicator

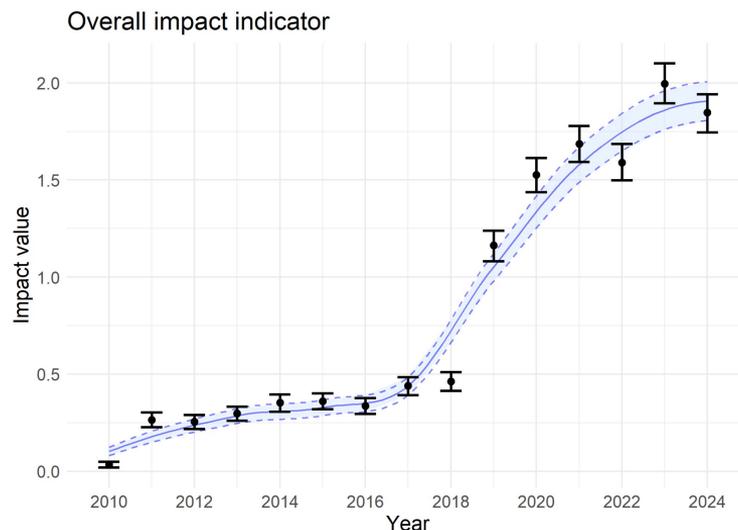


# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

### Indicator workflow

- **impIndicator**
  - Calculate alien impact indicators from occurrence cubes
- Input
  - Occurrence cube
  - EICAT assessment data
    - massive (MV), major (MR), moderate (MO), minor (MN), or minimal concern (MC)
- Calculation of impact of alien species
  - Site impact indicator
  - Overall impact indicator

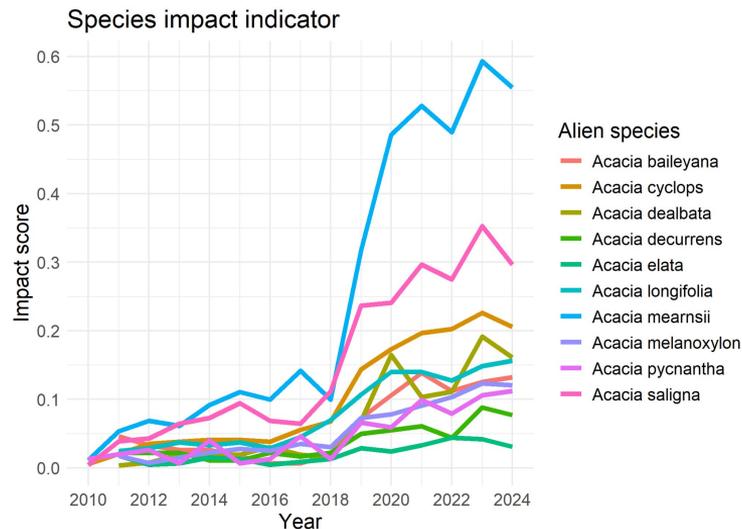


# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

### Indicator workflow

- **impIndicator**
  - Calculate alien impact indicators from occurrence cubes
- Input
  - Occurrence cube
  - EICAT assessment data
    - massive (MV), major (MR), moderate (MO), minor (MN), or minimal concern (MC)
- Calculation of impact of alien species
  - Site impact indicator
  - Overall impact indicator
  - Species impact indicator

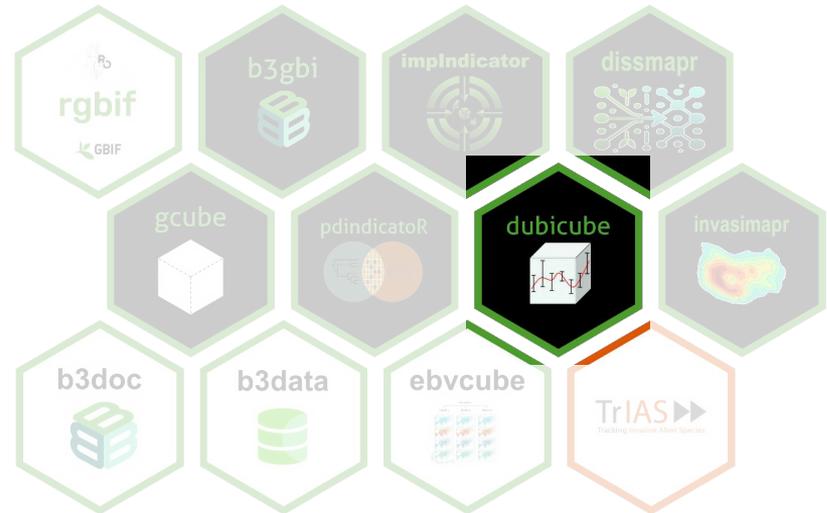


# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

Indicator workflow

- **dubicube**
  - Data exploration for occurrence cubes and uncertainty calculation for indicators



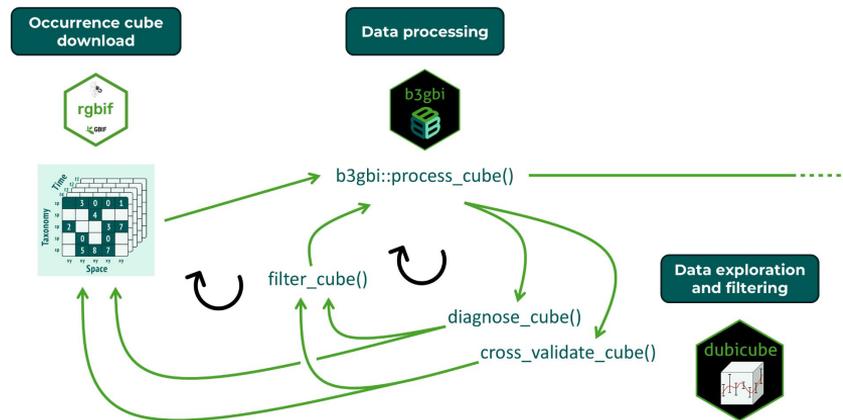
# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

### Indicator workflow

- **dubicube**
  - Data exploration for occurrence cubes and uncertainty calculation for indicators
  
- Data quality diagnostics

```
> diagnose_cube(cube)
Data cube diagnostics
-----
• OK - temporal_min_points
  Cube contains observations across 6 years.
• OK - temporal_missing_years
  Cube contains 0 missing years.
• OK - spatial_min_cells
  Cube contains observations across 5 grid cells.
• VERY_IMPORTANT - spatial_max_uncertainty
  Cube contains 90 records where the coordinate uncertainty is larger than the grid cell resolution.
• OK - spatial_miss_uncertainty
  Cube contains 0 records with missing coordinate uncertainty.
• NOTE - taxon_min_taxa
  Cube contains observations across 3 taxon keys.
• OK - obs_min_records
  Cube contains 90 observation records (rows).
• OK - obs_min_total
  Cube contains a total of 90 observations.
```

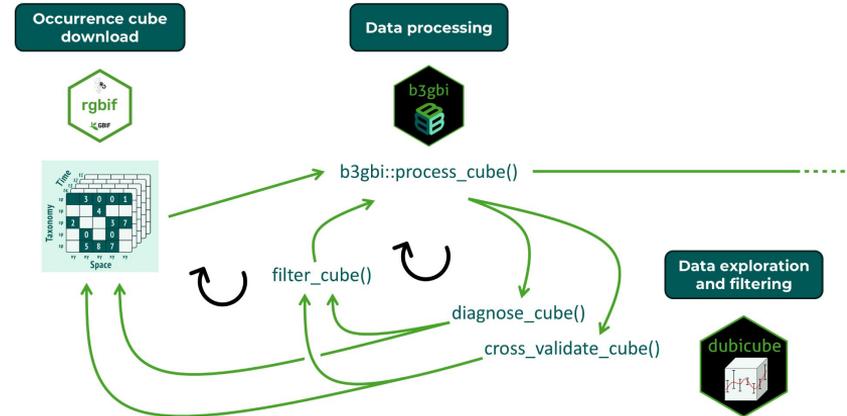
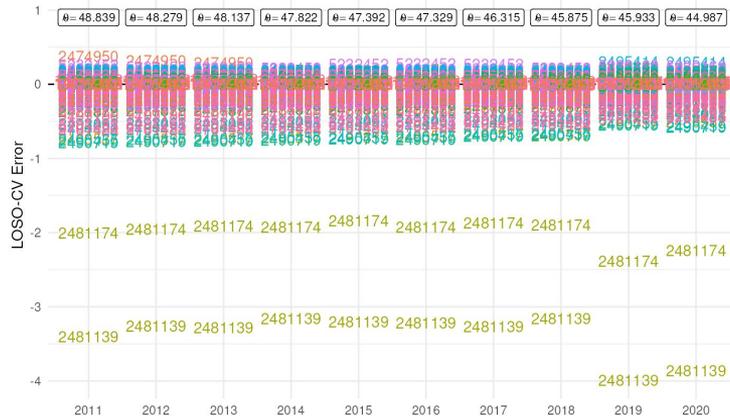


# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

### Indicator workflow

- **dubicube**
  - Data exploration for occurrence cubes and uncertainty calculation for indicators
- Group-level sensitivity analysis

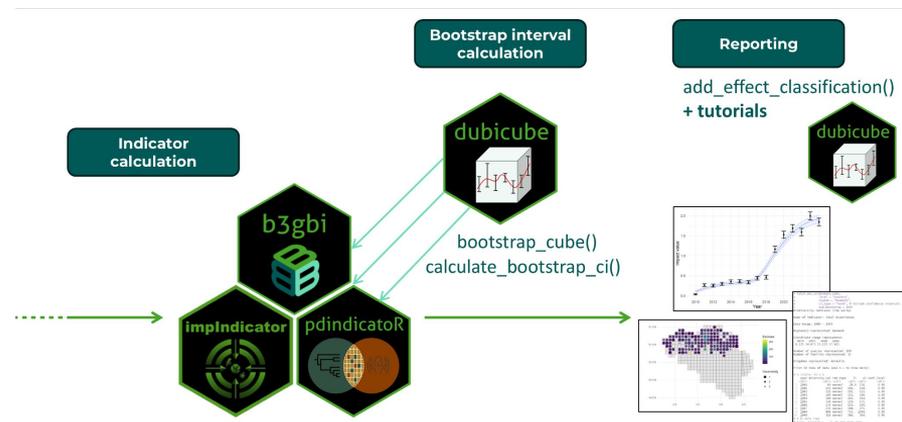
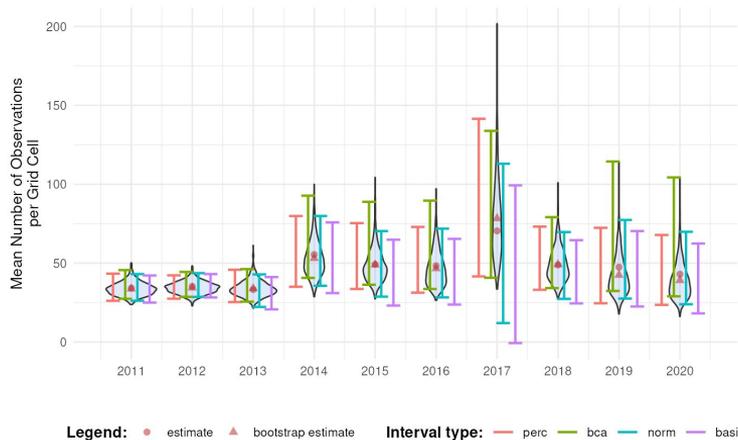


# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

### Indicator workflow

- **dubicube**
  - Data exploration for occurrence cubes and uncertainty calculation for indicators
- Indicator uncertainty calculation

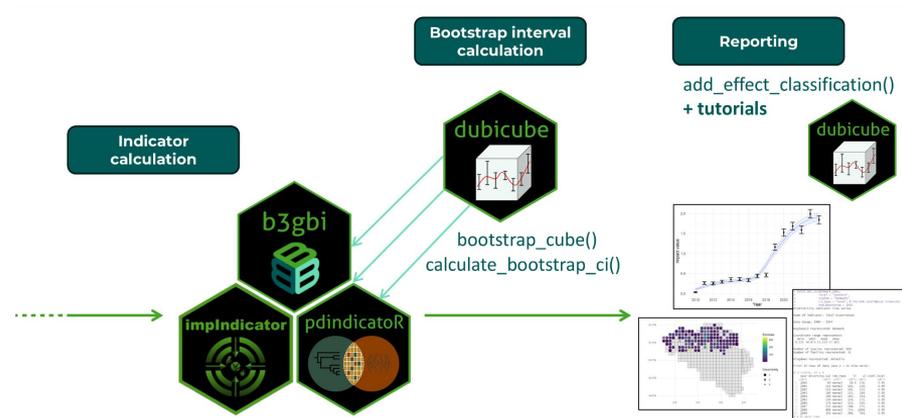
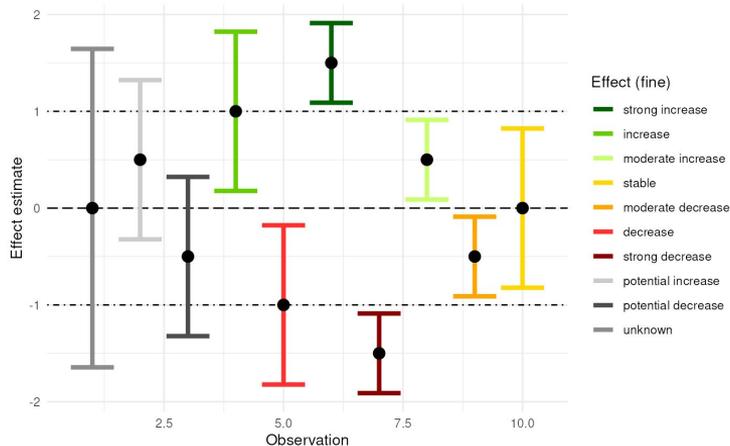


# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

### Indicator workflow

- **dubicube**
  - Data exploration for occurrence cubes and uncertainty calculation for indicators
- Indicator interpretation and visualisation (see also the [effectclass](#) package)



# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

Modelling cubes

- **dissmapr**
  - Analyse and map multi-site compositional dissimilarity ( $\zeta$ -diversity)



# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

### Modelling cubes

- **dissmapr**
  - Analyse and map multi-site compositional dissimilarity ( $\zeta$ -diversity):

How do biological communities change in response to environmental and geographic gradients?

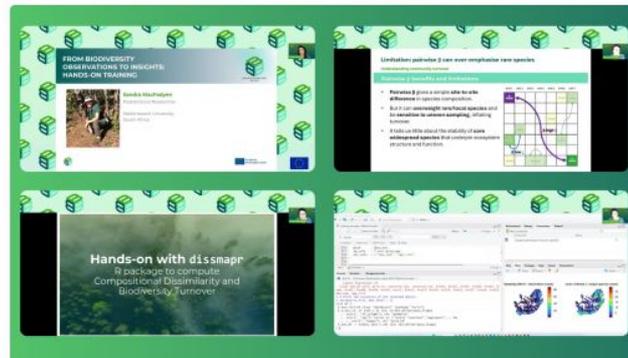
### Fourth session of B-Cubed training series: Access the recording and materials

19 March 2026

B-Cubed's [training series](#) continued with a session on Automating compositional dissimilarity and biodiversity turnover mapping with `dissmapr`. If you want to join the upcoming sessions, you can still register [here](#).

In this fourth session, held on 13 March, Sandra MacFadyen focused on `dissmapr`, an open-source R framework that automates compositional dissimilarity and turnover analysis.

- [Slides](#)
- [Recording](#)
- [Q&A and R script](#)



Training session on session on Automating compositional dissimilarity and biodiversity turnover mapping with `dissmapr`

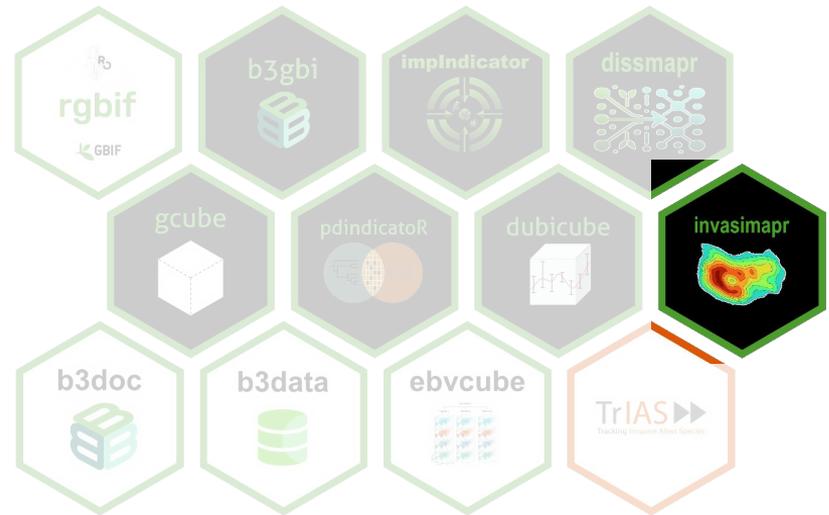


# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

Modelling cubes

- **invasimapr**
  - Estimate and map invasion fitness



# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

Modelling cubes

- **invasimapr**

- Estimate and map invasion fitness:

Can a species successfully establish at a site, given local environmental conditions and resident community structure?

### B-Cubed training series continues: Access the second session recording and materials

5 March 2026

B-Cubed's [training series](#) continued with a session on Occurrence cubes and biological invasions. Even if you missed previous sessions, you can still register [here](#) to join the upcoming ones.

The second session, held on 27 February, focused on occurrence cubes and their application to biological invasions.

- [Slides](#)
- [Recording](#)
- [Q&A](#)

During the session, Maarten Trekels (Meise Botanic Garden) presented the possibilities of the [b3alien Python package](#), which provides a technical solution to support tracking Target 6 of the Kunming-Montreal Global Biodiversity Framework (KM-GBF).

Sandra MacFadyen (Stellenbosch University) delved into the details of the [Invasibility Cube](#), which integrates trait, environmental (and site), and community (species) data to quantify invasion fitness and generate spatial indicators of site invasibility and species and/or trait invasiveness.



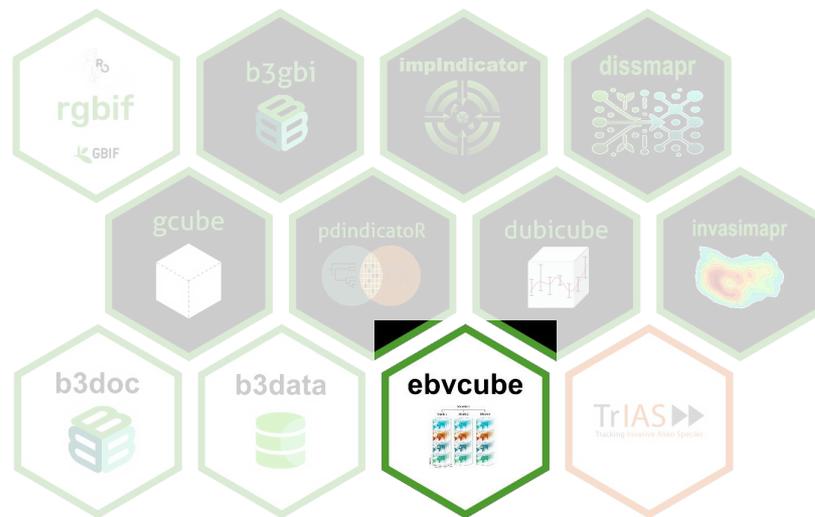
Session on 27 February - Occurrence cubes and biological invasions

# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

Other projects

- **ebvcube**
  - Access and visualise data cubes of Essential Biodiversity Variables (EBVs)

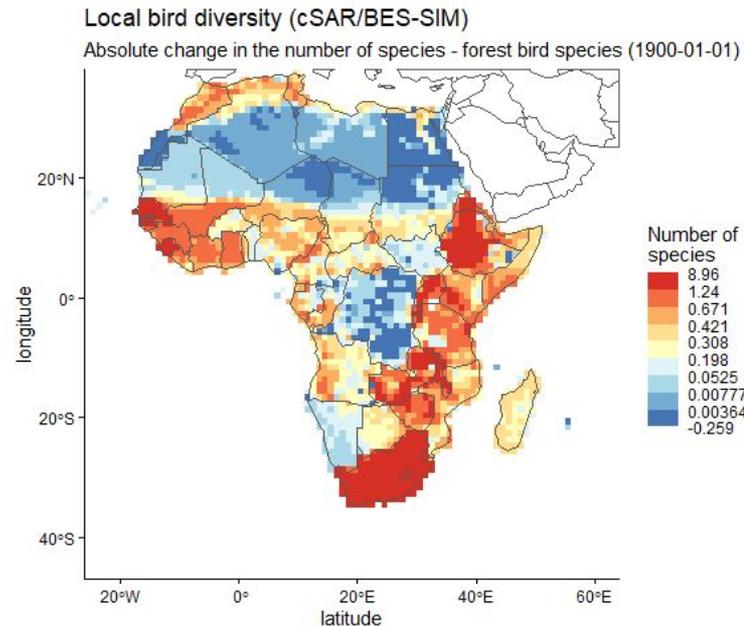


# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

### Other projects

- **ebvcube**
  - Access and visualise data cubes of Essential Biodiversity Variables (EBVs)
- Work with data of the EBV netCDFs
  - downloaded from the [EBV Data Portal](#)
- Visualise data

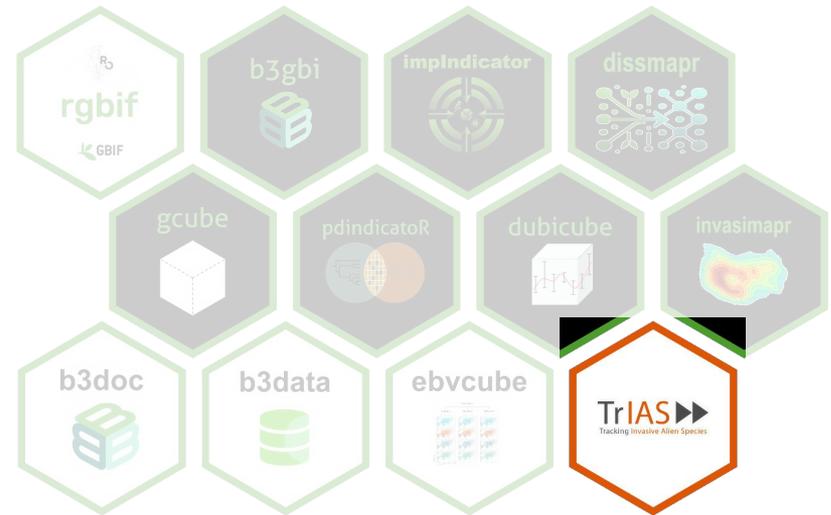


# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

Other projects

- **trias**
  - Functionality for the TrIAS and LIFE RIPARIAS projects



# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

### Other projects

- **trias**
- Trends of invasive species in Belgium
  - [alien species portal](#)

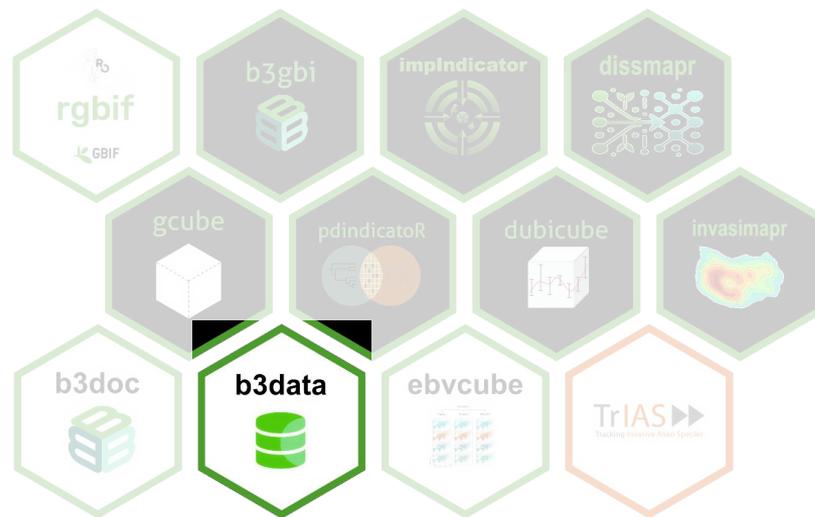


# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

Data

- **b3data**
  - Frictionless data package for the b3verse



# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

### Data

- **b3data**
  - Frictionless data package for the b3verse
- Frictionless?
  - **Problem:** Data are often messy, missing context (metadata), and difficult to move between different software tools
  - **Solution:** Frictionless Data = open-source toolkit and set of standards designed to make data "interoperable" → it works everywhere



# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

### Data

- **b3data**
  - Frictionless data package for the b3verse
- Frictionless?
- Data package?
  - Bundles raw data files (like CSVs) with their "instruction manual"
    - `datapackage.json`: A machine-readable file that describes the data's schema, origin, and license



# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

### Data

- **b3data**
  - Frictionless data package for the b3verse
- Dedicated data package for **b3verse** packages
  - Example occurrence cubes
  - Spatial reference grids
- All datasets are version-controlled on Zenodo
- Can be loaded directly into R



# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

Data

- **b3data**
  - Frictionless data package for the b3verse
    - See also [this guide](#)

Step 1 — Load the frictionless R package

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



# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

### Data

- **b3data**
  - Frictionless data package for the b3verse
    - See also [this guide](#)

#### Step 2 — Read the package descriptor from Zenodo

The content of the data package can be consulted using `read_package()`.

```
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.
```



# b3verse, an ecosystem of R packages

## A closer look at the b3verse packages

### Data

- **b3data**
  - Frictionless data package for the b3verse
    - See also [this guide](#)

#### Step 3 — Import a resource (dataset)

Tabular datasets 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>
```



# Downloading cubes with rgbif

Ward Langeroot



# Downloading cubes with rgbif

## Download cubes from script

- We can get occurrence cubes directly with **rgbif**
- What do we need?
  - a. GBIF credentials
  - b. SQL query
  - c. R script



<https://dyte.io/blog/automation-at-dyte/>

# Downloading cubes with rgbif

## Download cubes from script

### a. GBIF credentials

- See [this rgbif tutorial](#)
- Problems with access rights? → contact [helpdesk@gbif.org](mailto:helpdesk@gbif.org)

The **best way** to allow rgbif access to your GBIF credentials is to save them in your **.Renviron** file.

The easiest way to edit this file is by running:

```
install.packages("usethis")  
usethis::edit_r_environ()
```

Edit your **.Renviron** to look like this:

```
USER = jwaller  
PSWD = safe_fake_password_123  
MAIL = jwaller@gbif.org
```



# Downloading cubes with rgbif

## Download cubes from script

### b. SQL query

- Training session 24 February 2026
- Tutorials: [rgbif website](#), [B-Cubed documentation](#), [GBIF website](#)

#### B-Cubed training series begins: Access the first session recording and materials

24 February 2026

B-Cubed's [training series](#) has officially started, showcasing emerging approaches that help make biodiversity data more actionable in practice. If you haven't signed up yet, register [here](#) to join the upcoming sessions.

The first session, held on 20 February, introduced participants to a [service](#) from the Global Biodiversity Information Facility (GBIF) that enables users to easily create and download species occurrence cubes from GBIF-mediated data using SQL queries.

- [Slides](#)
- [Recording](#)
- [Q&A](#)

The session provided an overview of the service and live demonstrations with practical examples. It was led by Andrew Rodrigues (GBIF) and Lina Estupinan Suarez (Martin Luther University Halle-Wittenberg), who guided participants through the service and answered questions in the Q&A.



Session on 20 February - Creating species occurrence cubes



# Downloading cubes with rgbif

## Download cubes from script

- b. SQL query **Select dimensions  
(temporal, spatial, taxonomical)**

```
GBIF_MGRSCode(  
  1000,  
  decimalLatitude,  
  decimalLongitude,  
  COALESCE(coordinateUncertaintyInMeters, 1000)  
) AS mgrsCode,
```

```
SELECT  
  -- Dimensions:  
  \"year\",  
  GBIF_MGRSCode(  
    1000,  
    decimalLatitude,  
    decimalLongitude,  
    COALESCE(coordinateUncertaintyInMeters, 1000)  
  ) AS mgrsCode,  
  speciesKey,  
  species,  
  \"order\",  
  family,  
  genus,  
  -- Measurements  
  COUNT(*) AS n,  
  MIN(COALESCE(coordinateUncertaintyInMeters, 1000)) AS minCoordinateUncertaintyInMeters,  
  -- Higher taxon measurement  
  IF(ISNULL(\"order\"), NULL, SUM(COUNT(*)) OVER (PARTITION BY \"order\", \"year\")) AS orderCount  
FROM  
  occurrence  
WHERE occurrenceStatus = 'PRESENT'  
  AND countryCode = 'BE'  
  AND \"year\" >= 2007  
  AND \"year\" <= 2023  
  AND (coordinateUncertaintyInMeters <= 1000 OR coordinateUncertaintyInMeters IS NULL)  
  AND speciesKey IS NOT NULL  
  AND NOT ARRAY_CONTAINS(issue, 'ZERO_COORDINATE')  
  AND NOT ARRAY_CONTAINS(issue, 'COORDINATE_OUT_OF_RANGE')  
  AND NOT ARRAY_CONTAINS(issue, 'COORDINATE_INVALID')  
  AND NOT ARRAY_CONTAINS(issue, 'COUNTRY_COORDINATE_MISMATCH')  
  AND class = 'Aves'  
GROUP BY  
  \"year\",  
  mgrsCode,  
  speciesKey,  
  \"order\",  
  family,  
  genus,  
  species  
ORDER BY  
  \"year\" ASC,  
  mgrsCode ASC,  
  speciesKey ASC
```









# Downloading cubes with rgbif

## Download cubes from script

### c. R script

```
# SQL query
my_sql_query <- "... "

# Start a download on GBIF servers
cube_download <- rgbif::occ_download_sql(
  user = Sys.getenv("USER"),
  pwd = Sys.getenv("PSWD"),
  email = Sys.getenv("MAIL"),
  q = my_sql_query
)
```

# Downloading cubes with rgbif

## Download cubes from script

### c. R script

```
# SQL query
my_sql_query <- "...

# Start a download on GBIF servers
cube_download <- rgbif::occ_download_sql(
  user = Sys.getenv("USER"),
  pwd = Sys.getenv("PSWD"),
  email = Sys.getenv("MAIL"),
  q = my_sql_query
)

# Check status of download and wait to finish
rgbif::occ_download_wait(cube_download)
#> status: preparing
#> status: running
#> status: succeeded
#> download is done, status: succeeded<<gbif download metadata>>
#> ...
```



# Downloading cubes with rgbif

## Download cubes from script

### c. R script

```
# SQL query
my_sql_query <- "...

# Start a download on GBIF servers
cube_download <- rgbif::occ_download_sql(
  user = Sys.getenv("USER"),
  pwd = Sys.getenv("PSWD"),
  email = Sys.getenv("MAIL"),
  q = my_sql_query
)

# Check status of download and wait to finish
rgbif::occ_download_wait(cube_download)
#> status: preparing
#> status: running
#> status: succeeded
#> download is done, status: succeeded<<gbif download metadata>>
#> ...

# Retrieve the download from GBIF
occ_cube <- rgbif::occ_download_get(cube_download) |>
  rgbif::occ_download_import()
#> Download file size: 1.55 MB
#> On disk at ...
```



# Downloading cubes with rgbif

## Download cubes from script

### c. R script

```
# View cube
head(occ_cube)
#> # A tibble: 6 × 9
#>   year mgrscode specieskey species          order          family      genus      n mincoordinateuncertaintyi...1
#>   <int> <chr>      <int> <chr>      <chr>          <chr>          <chr>      <int>      <dbl>
#> 1  2022 31UDS48    2480964 Morus bassanus Suliformes      Sulidae      Morus        1    10000
#> 2  2022 31UDS48    2481174 Larus fuscus   Charadriiformes Laridae      Larus        1    10000
#> 3  2022 31UDS48    2481433 Fulmarus glacialis Procariiformes Procariidae Fulmarus     1    10000
#> 4  2022 31UDS49    2481174 Larus fuscus   Charadriiformes Laridae      Larus        2    10000
#> 5  2022 31UDS49    2481342 Uria aalge     Charadriiformes Alcidae      Uria         1    10000
#> 6  2022 31UDS49    2481433 Fulmarus glacialis Procariiformes Procariidae Fulmarus     2    10000
#> # i abbreviated name: 1mincoordinateuncertaintyinmeters
```

Disclaimer: I used a smaller query for this example than the query explained above (e.g. limited years, no order count).



# Highlighting the b3gbi R package

Shawn Dove



# Analyse and plot your biodiversity data cube in 3 simple steps

1

## INGEST

`process_cube()`

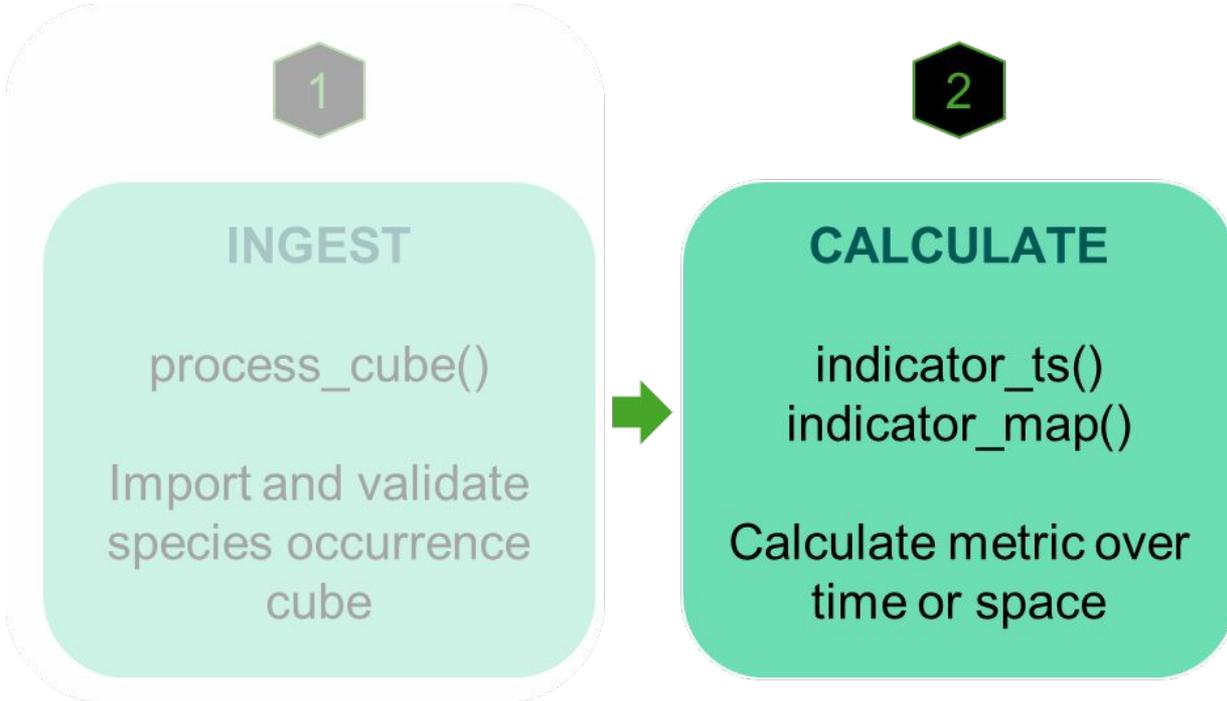
Import and validate  
species occurrence  
cube



Custom occurrence cubes can be downloaded for free from the [gbif.org](http://gbif.org) website or using the `rgbif` R package.

Or, create a simulated cube using the `gcube` R package.

**b3gbi will handle the rest!**



18 metrics available:

- richness
- evenness
- Hill diversity
- rarity
- taxonomic distinctness
- occupancy turnover
- etc...

Integrated uncertainty calculation for time series

Crop grid using custom shape files

1

## INGEST

`process_cube()`

Import and validate  
species occurrence  
cube

2

## CALCULATE

`indicator_ts()`  
`indicator_map()`

Calculate metric over  
time or space

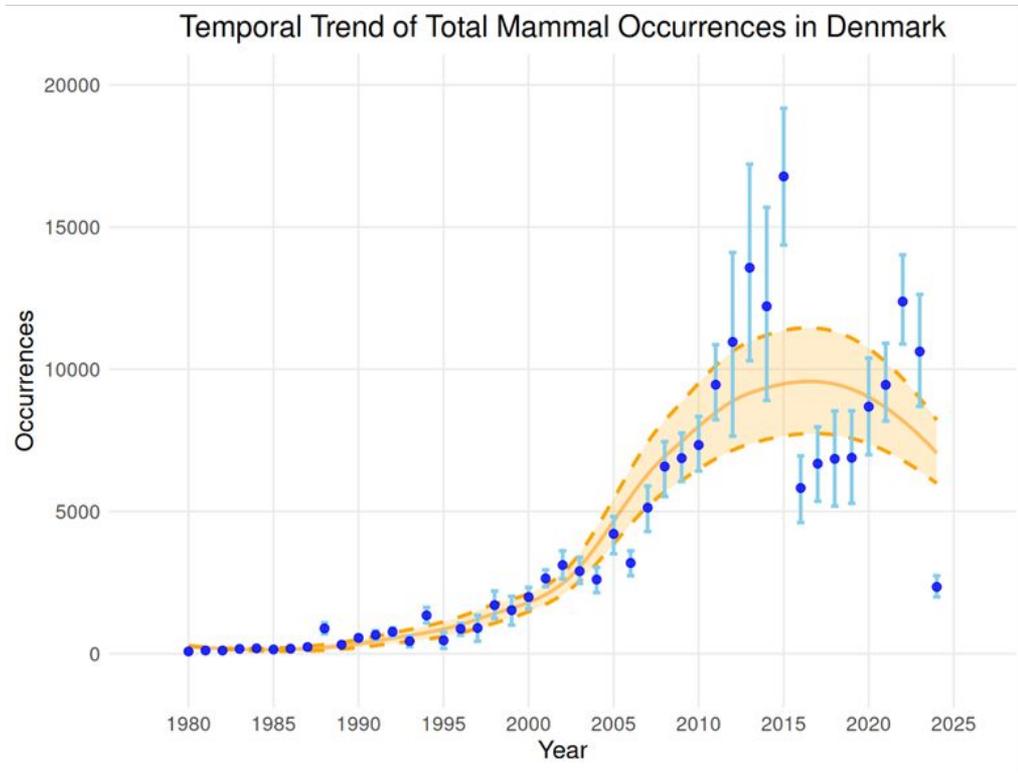
3

## VISUALIZE

`plot()`  
`plot_mv()`

Generate  
publication-quality  
map or time series





## ggplot2 integration

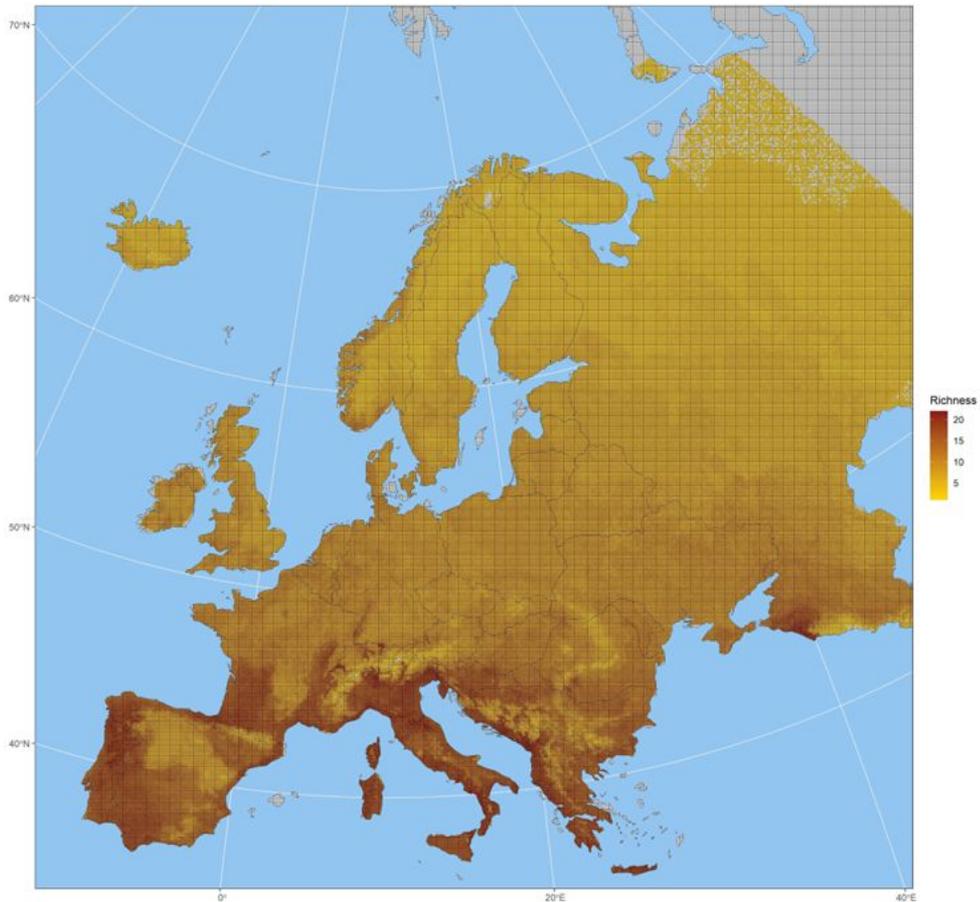
3

**VISUALIZE**

**plot()**

Generate  
publication-quality  
map or time series





## rnaturalearth integration

3

**VISUALIZE**

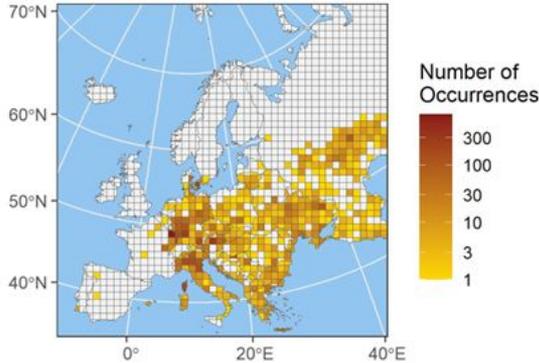
plot()

Generate  
publication-quality  
map or time series

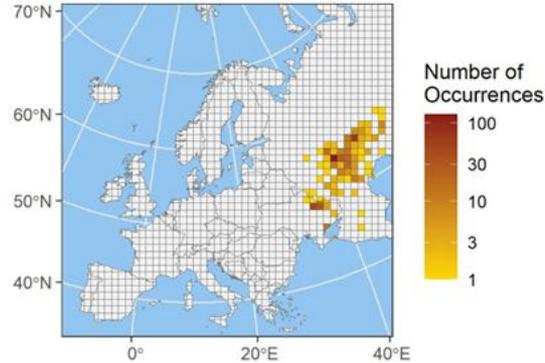


## Species Occurrences

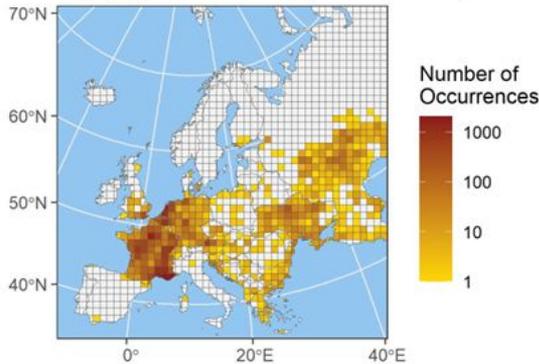
*Bufo viridis* (Laurenti, 1768)



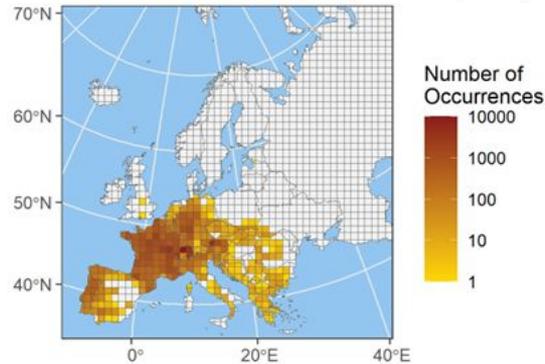
*Pelobates vespertinus* (Pallas, 1771)



*Pelophylax ridibundus* (Pallas, 1771)



*Salamandra salamandra* (Linnaeus, 1758)



## rnaturalearth integration

3

**VISUALIZE**

plot()

Generate  
publication-quality  
map or time series

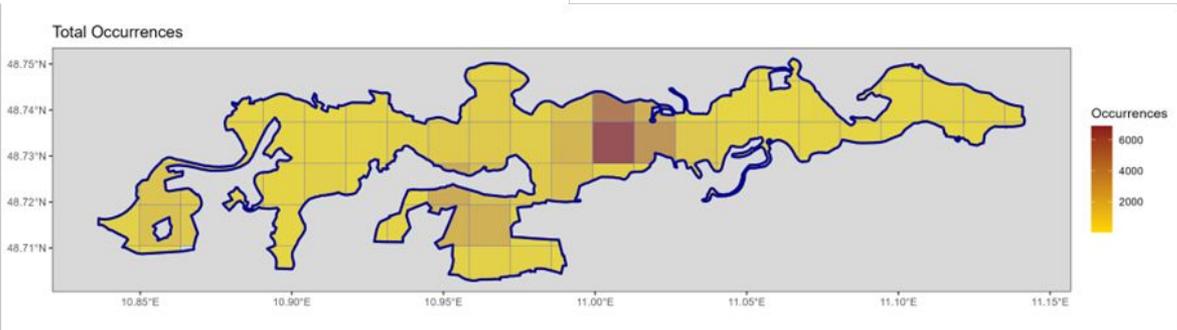
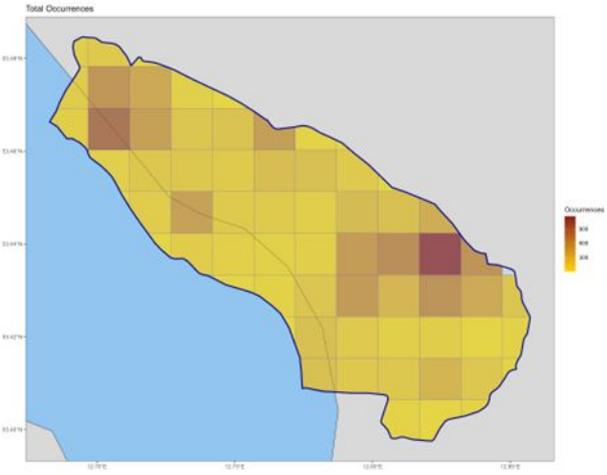
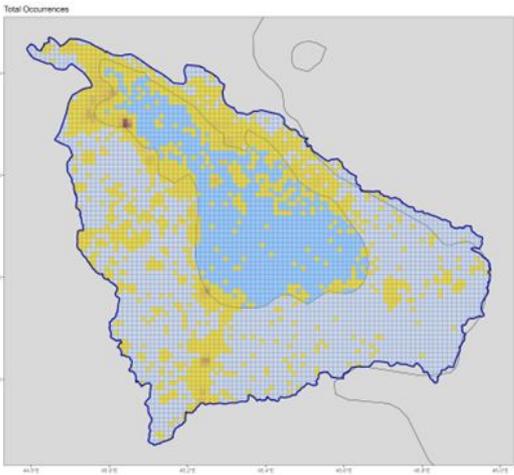
# shapefile integration

3

**VISUALIZE**

plot()

Generate  
publication-quality  
map or time series



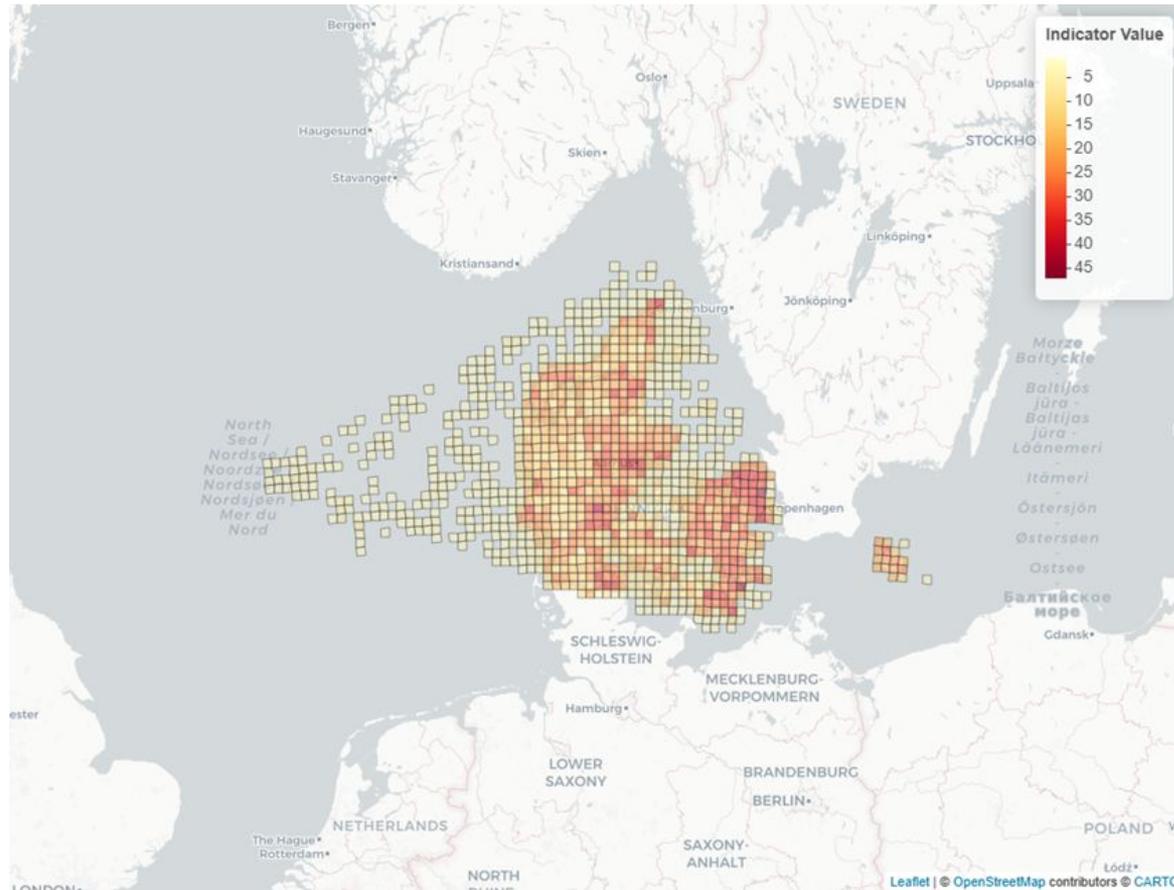
# mapview integration

3

**VISUALIZE**

`plot_mv()`

Generate  
publication-quality  
map or time series



# b3gbi: a powerful and flexible indicators package



Supports multiple grid reference systems with automated detection:

Military Grid Reference System (MGRS)

Extended Quarter Degree Grid Cells (EQDGC)

European Environment Agency (EEA) reference grid

Icosahedral Snyder Equal Area aperture 3 hexagonal (ISEA3H) reference grid

Plot your results using any compatible Coordinate Reference System (CRS)

Add custom ggplot2 code

Plot interactive maps with different base layers



## B-Cubed: General Biodiversity Indicators

Welcome to the B-Cubed: Biodiversity Indicators Shiny app!

The B-Cubed: Biodiversity Indicators Shiny app uses the R package [b3gbi](#) to calculate and visualise widely used biodiversity indicators from a data cube; either one created using [GBIF](#) or one created from your own data.

Start by uploading your data cube using the file browser in the left-hand panel. You can also use this panel to choose the biodiversity indicator(s), taxa, geographical area, and temporal window of interest for your data. Use the tabs to visualize the outputs.

**Data** **Analysis & Filters** Summary Map Time-series Table Export Background References About

Visualization Options

**Biodiversity Indicator**

Abundance-Based Rarity

Customize Region

**Map resolution**

Medium (50m)

**Spatial resolution in kilometers or degrees (depending on grid type)**

0.25

**Date range:**

1862 2000 2024

1862 1878 1895 1911 1927 1943 1960 1976 1992 2009 2024

Subset by family

**What am I looking at?**

Abundance-Based Rarity for all input cube taxa in all input cube regions from 2000 to 2024

**Background information on this indicator:**

**Rarity**

Rarity is the scarcity or infrequency of a particular species in an area. A rare species might have a small population size, a limited distribution, or a unique ecological niche (Maciel, 2021; Rabinowitz, 1981). Rarity can also be a biodiversity indicator when summed over multiple species in an area, and may provide important insight for determining conservation priorities. When measured over time, rarity may indicate potential threats or changes in the environment.

**Abundance-Based Rarity**

Abundance-based rarity is the inverse of the proportion of total occurrences represented by a particular species. The total summed rarity for each grid cell or year is calculated (sum the rarity values of each species present there). It is calculated as:

$$\sum_{i=1}^S 1/p_i$$

where S is the number of species and pi is the proportion of occurrences represented by species i.

**\*Note: Outdated!**

Graphical  
user  
interface  
available

Download:  
[github.com/b-cubed-eu/b3gbi-gui](https://github.com/b-cubed-eu/b3gbi-gui)

Online:  
<https://bcc9vd-shawn-dove.shinyapps.io/b3gbi-gui/>

# BREAK TIME

visit <https://github.com/shawndove/b3gbi-demo>  
if you want to follow along



# A practical case study using the b3verse

Jasmijn



# Calculating regional indicators in Europe using the B-Cubed workflow

In this case study, the **B-Cubed workflows will be tested** for Flanders, a region of Europe where species occurrence data are abundant.

## The expected results include

- Making the **selected indicators available** through a public dashboard that can serve as inspiration for other dashboards
- **Ensuring interoperability** by maintaining close contact with other dashboard maintainers, for instance, by providing all code in an R package.



The screenshot displays the Vlaams Biodiversiteitsportaal website. At the top, there are logos for TRIAS, the Instituut Natuur- en Bosonderzoek, and the Vlaanderen logo. The main navigation bar includes 'Start', 'Checklist indicators', 'Species information', 'Early alert', and 'Other dashboards'. Below this, three panels are visible: 'Checklist indicators' with a line graph showing trends from 2008 to 2020; 'Species information' with a grid of colored dots representing species occurrences; and 'Early alert' with a silhouette of a person taking a photo. The main content area features a large image of a bird with a search bar overlaid. Below the bird image, there are statistics for 'Waarnemingen' (37,21,628), 'Soorten' (12,820), 'Datasets' (138), and 'Organisaties' (7). The footer includes the Biodiversity.be logo and the text 'BELGIAN BIODIVERSITY PLATFORM FOR SCIENCE, POLICY, AND PRACTICE'.

# Calculating regional indicators in Europe using the B-Cubed workflow

The implemented indicators can be subdivided into:

- **General biodiversity indicators** (based on **b3gbi**, for instance, cumulative species richness, relative species richness, etc.);
- **Phylogenetic indicators** (based on **pdindicatorR**);
- **Invasive Alien Species indicators** (based on **TrIAS** and **b3alien** but extended with additional indicators necessary for reporting (e.g. rate of establishment, proportion of non-native species, comparison of species occupancy between periods, TrIAS indicators);
- Extra indicators that are used for IAS reporting might be added to the list, based on stakeholder needs.

Extra attention will be given to a comparison between Natura 2000 versus non-Natura 2000 habitats when applying these indicators, calculation and interpretation of indicator uncertainty, and taking into account **survey effort**.





## Flanders use case

Demonstrating B-Cubed workflows

 unsplash

 b3gbi

 impIndicator

 pdindicatorR

This dashboard showcases developed workflows within [the B-Cubed project](#) for the region of Flanders, a region of Europe where species occurrence data are abundant.

The implemented indicators in this dashboard can be subdivided into:

- General biodiversity indicators (based on [b3gbi](#), for instance, cumulative species richness, relative species richness, etc.);
- Phylogenetic indicators (based on [pdindicatorR](#));
- Invasive Alien Species indicators (based on [impIndicator](#), [TriAS](#) and [b3alien](#))

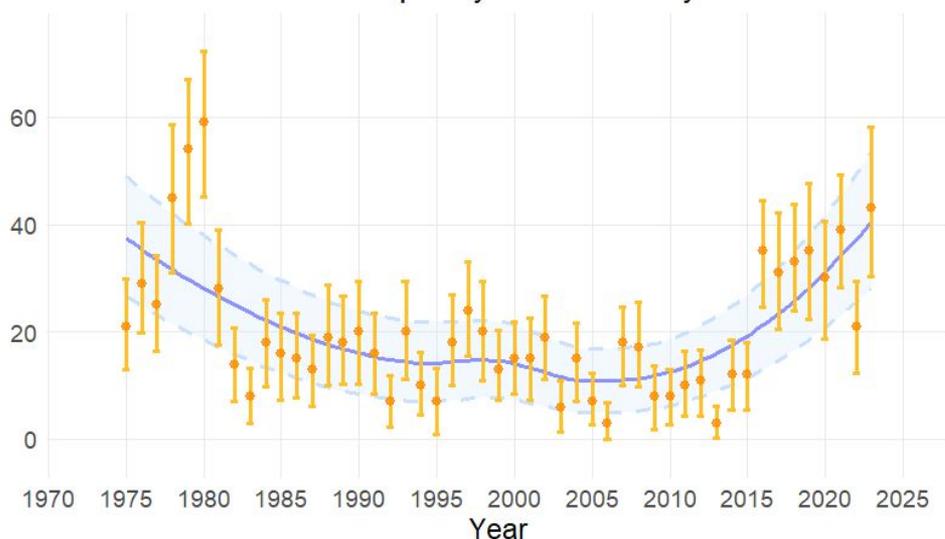
# General indicators

*Centaurea cyanus*

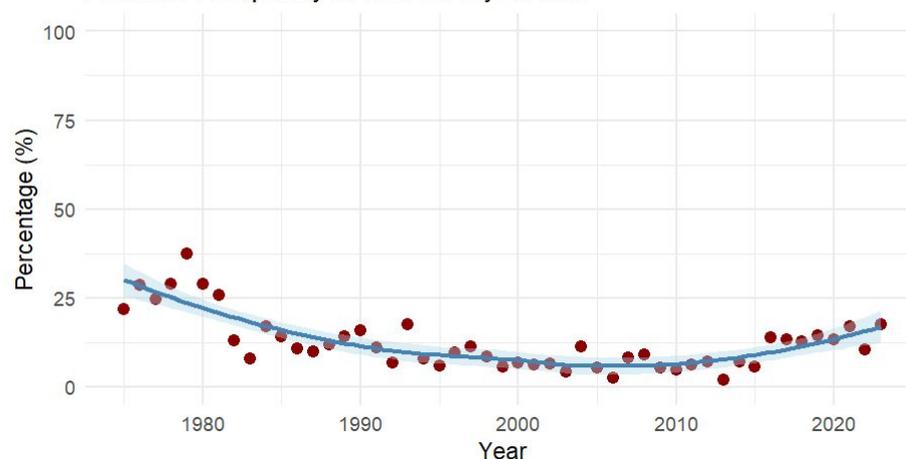


(c) Kai-Philipp Schablewski CC-BY-NC

### Absolute occupancy of well surveyed cells



### Relative occupancy of well surveyed cells

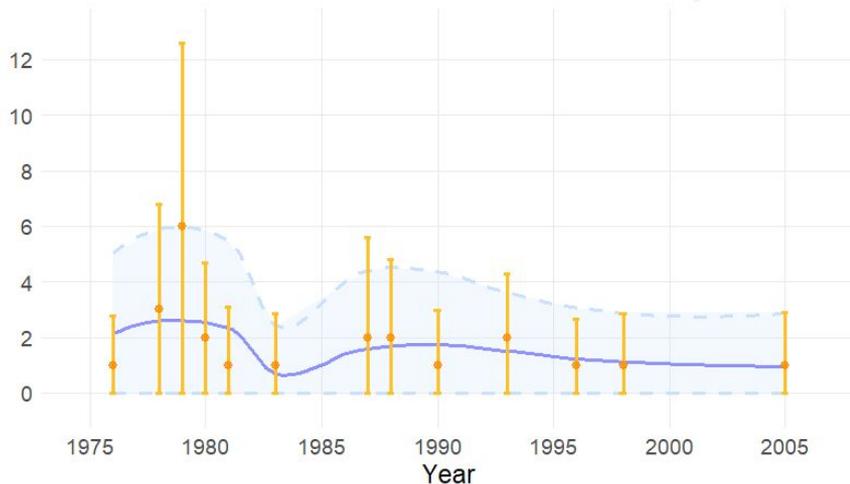


# General indicators

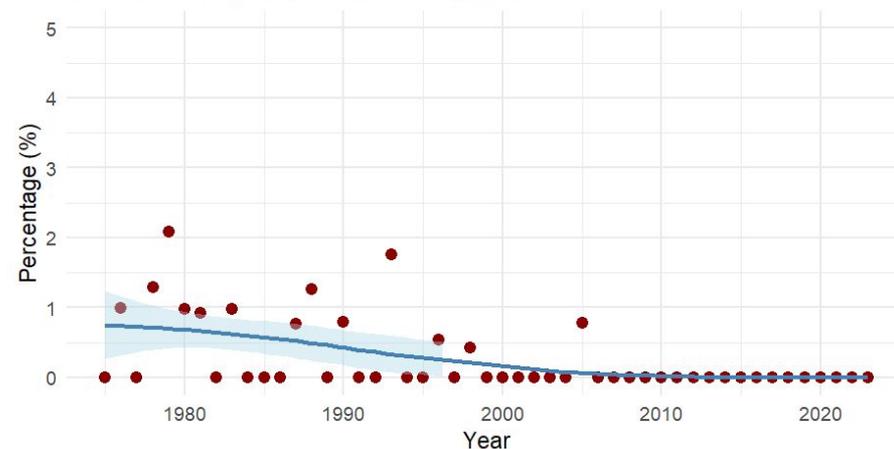
*Arnosseris minima*



Absolute number of occurrences in well surveyed cells



Relative occupancy of well surveyed cells

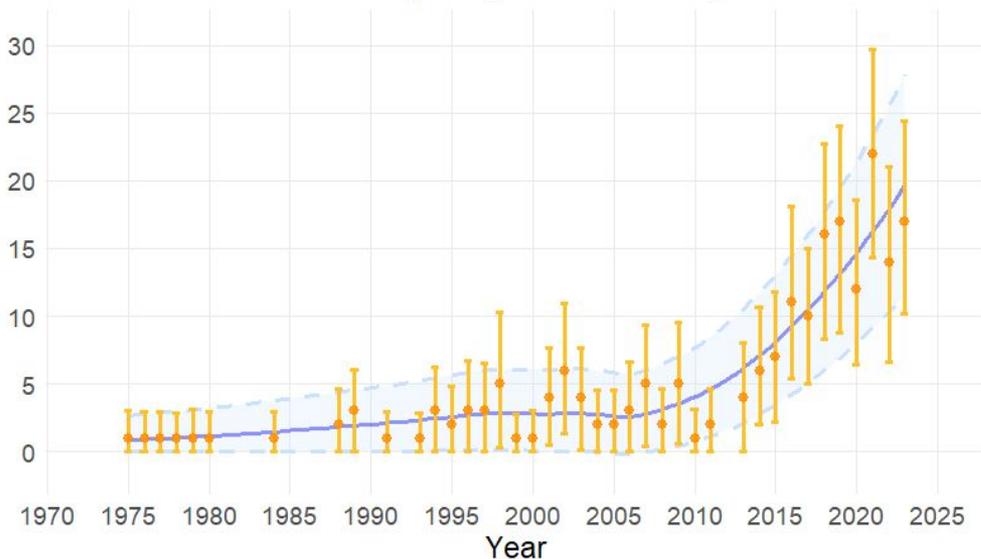


# General indicators

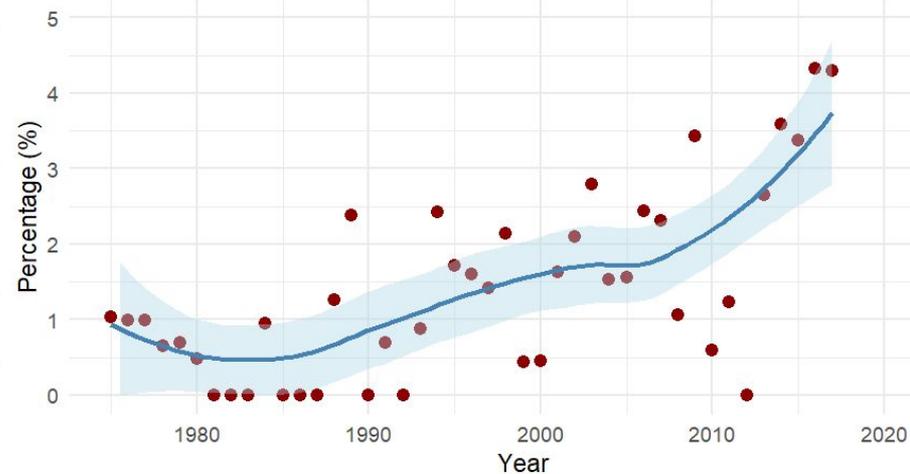
*Ophrys apifera*



Absolute occupancy of well surveyed cells

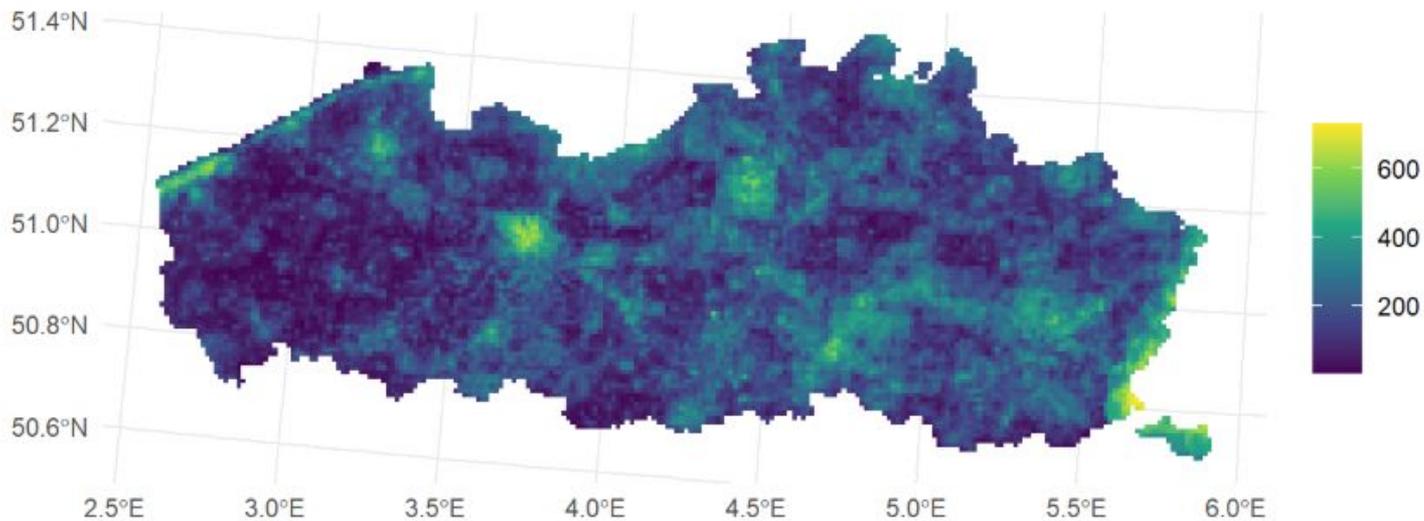


Relative occupancy of well surveyed cells



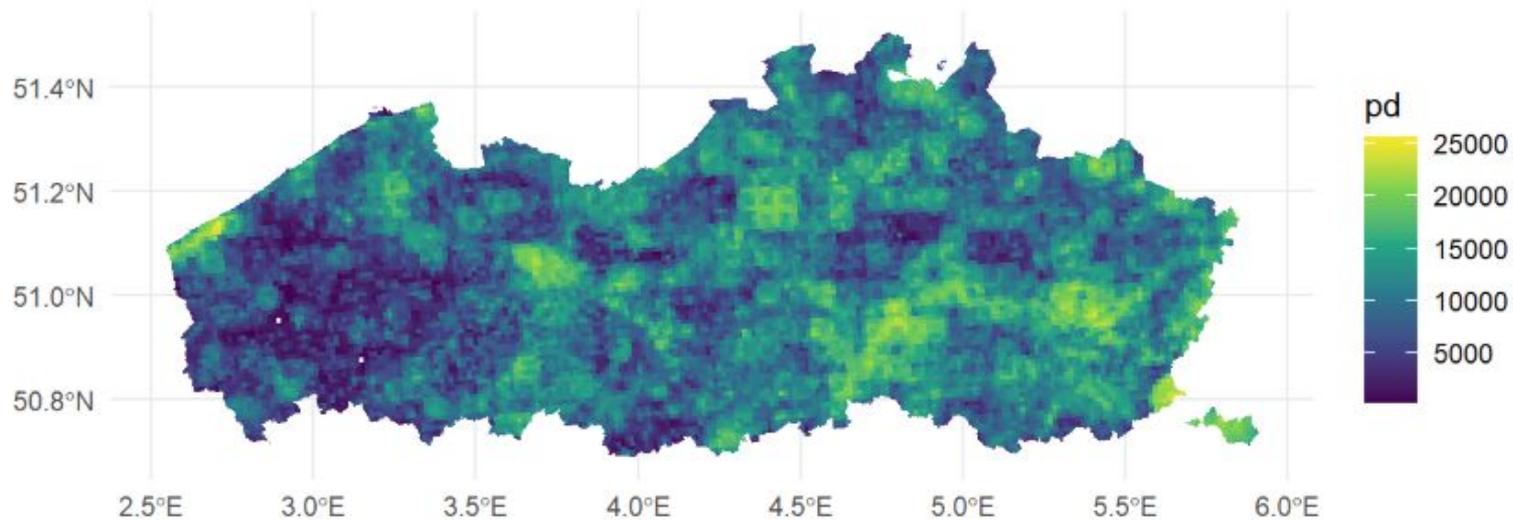
# General indicators

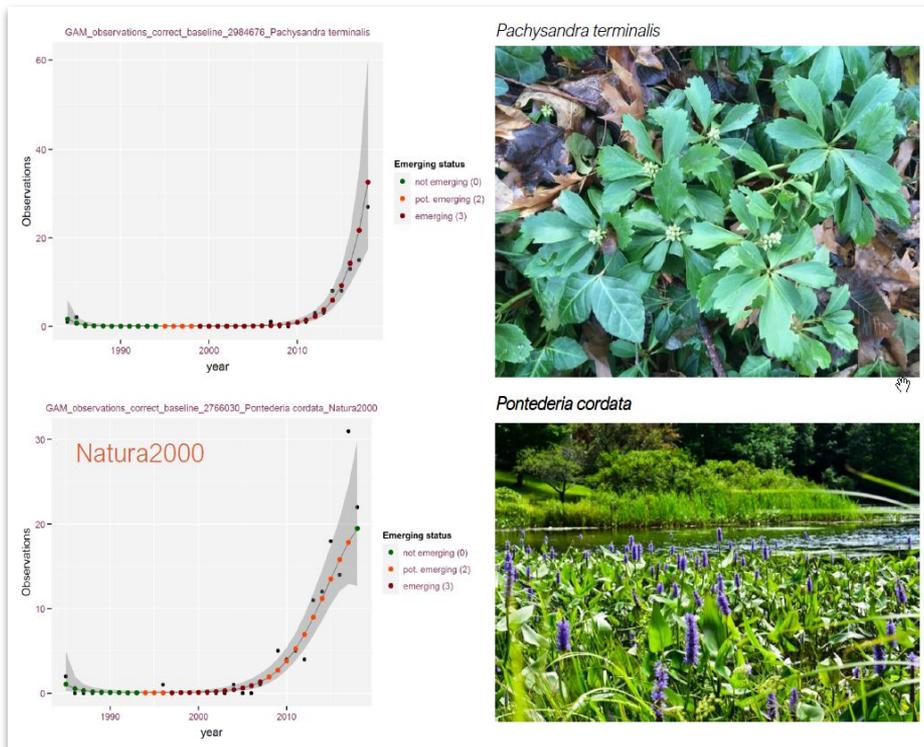
Observed species richness



# General indicators

## Phylogenetic diversity





## Alien Species Portal

<https://alienspecies.inbo.be>

# IAS indicators

## Overview of TRIAS indicators



### Checklist-based indicators

- Number of new introductions of alien species per year

- Cumulative number of introductions of alien species

- Pathways associated with introductions of alien species

### Occurrence-based indicators

- Detect appearing and reappearing species per year

- Assessing emerging status of alien species

- Ranking species per emerging status

- Define taxonomic distribution of emerging species

- Species observations and occupancy in Belgian protected areas

- Status of alien species in Belgian protected areas

## Alien Species Portal

<https://alienspecies.inbo.be>

## Target 6 (b3alien)



Kunming-Montreal  
**GLOBAL BIODIVERSITY FRAMEWORK**

GBF HOME // TARGET 6

### Target 6

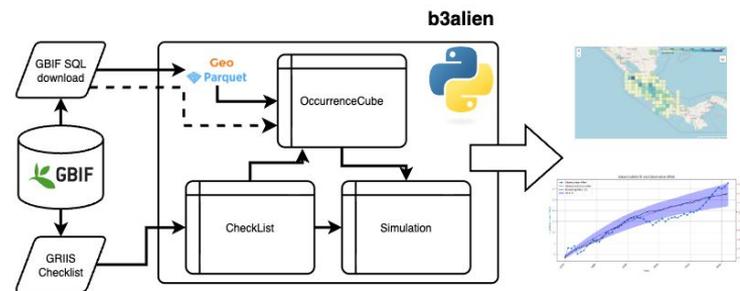
#### Reduce the Introduction of Invasive Alien Species by 50% and Minimize Their Impact

*Eliminate, minimize, reduce and or mitigate the impacts of invasive alien species on biodiversity and ecosystem services by identifying and managing pathways of the introduction of alien species, preventing the introduction and establishment of priority invasive alien species, reducing the rates of introduction and establishment of other known or potential invasive alien species by at least 50 per cent, by 2030, eradicating or controlling invasive alien species especially in priority sites, such as islands.*

Following are the guidance notes prepared by the Secretariat for Target 6



b3alien: a Python package to calculate the Global Biodiversity Framework Target 6 Headline Indicator



B-Cubed training series continues: Access the second session recording and materials

5 March 2026

B-Cubed's training series continued with a session on Occurrence cubes and biological invasions. Even if you missed previous sessions, you can still register here to join the upcoming ones.

The second session, held on 27 February, focused on occurrence cubes and their application to biological invasions.

- Slides
- Recording
- USA

During the session, Maarten Trekels (Meise Botanic Garden) presented the possibilities of the b3alien Python package, which provides a technical solution to support tracking Target 6 of the Kunming-Montreal Global Biodiversity Framework (KM-GBF).

Sandra MacFadyen (Stellenbosch University) delved into the details of the Invasibility Cube, which integrates trait, environmental (and site), and community (species) data to quantify invasion fitness and generate spatial indicators of site invasibility and species and/or trait invasiveness.



Session on 27 February - Occurrence cubes and biological invasions

## Global Register of Introduced and Invasive Species - Belgium

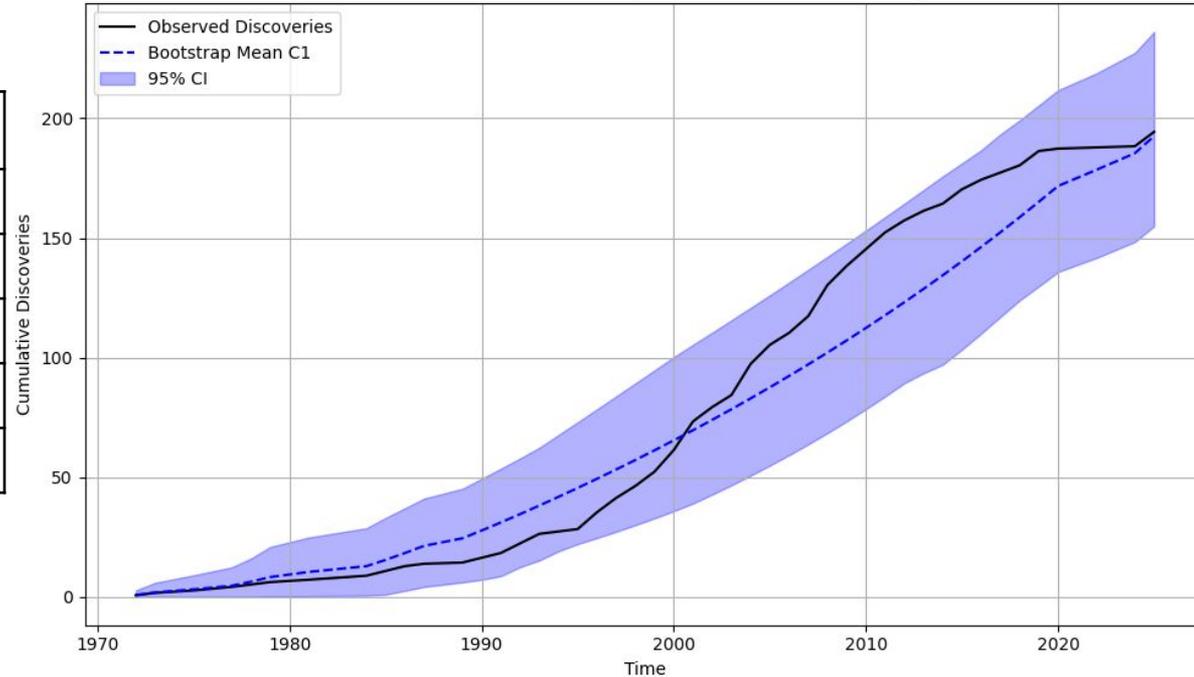
Published by [Invasive Species Specialist Group ISSG](#)

Desmet P • Reyserhove L • Oldoni D • Groom Q • Adriaens T • Vanderhoeven S • Pagad S

## Target 6 (b3alien)

Year	Annual_Rate	Annual_Rate_Error
2019	6.498157	1.035277
2020	6.660950	1.121160
2022	6.822542	1.216755
2024	6.992717	1.318645
2025	7.177649	1.417874

Best case scenario

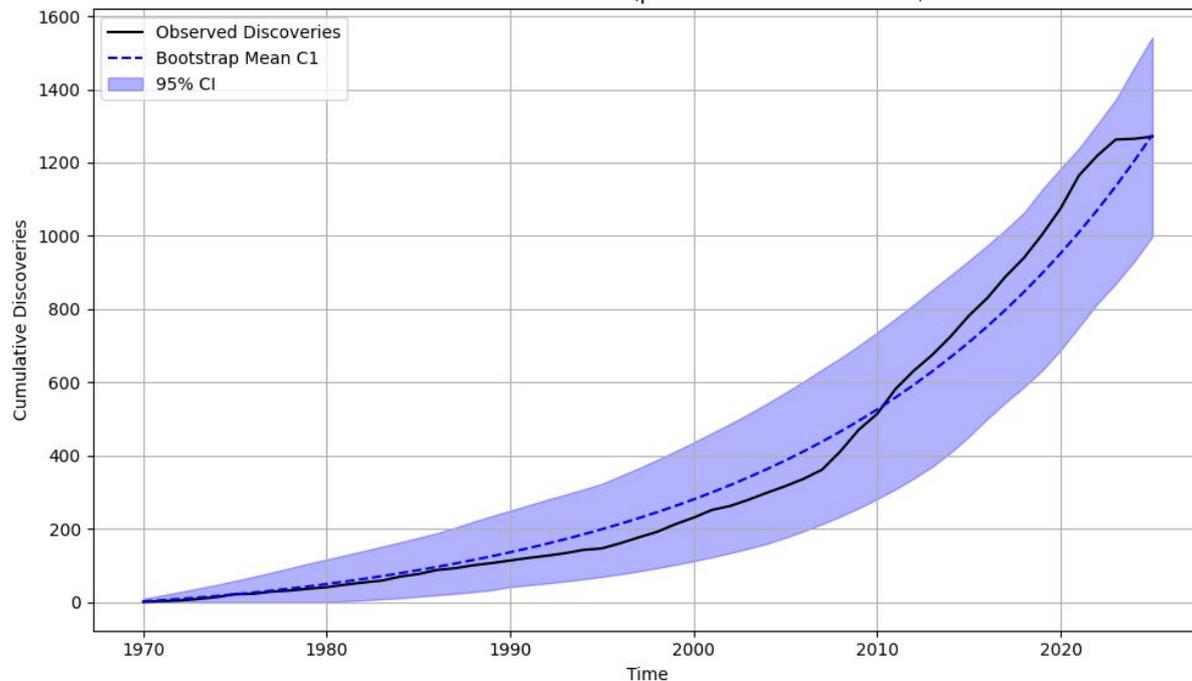
Solow-Costello Fit with CI ( $\beta_1$  95% CI: 0.0004 – 0.0590)

## Global Register of Introduced and Invasive Species - Belgium

Published by [Invasive Species Specialist Group ISSG](#)

Desmet P • Reyserhove L • Oldoni D • Groom Q • Adriaens T • Vanderhoeven S • Pagad S

## Target 6 (b3alien)

Solow-Costello Fit with CI ( $\beta$ : 95% CI: 0.0221 - 0.0998)

Worst case scenario

Year	Annual_Rate	Annual_Rate_Error
2021	57.713091	7.638794
2022	61.226267	8.923800
2023	64.972153	10.442058
2024	68.965698	12.222458
2025	73.223060	14.304139

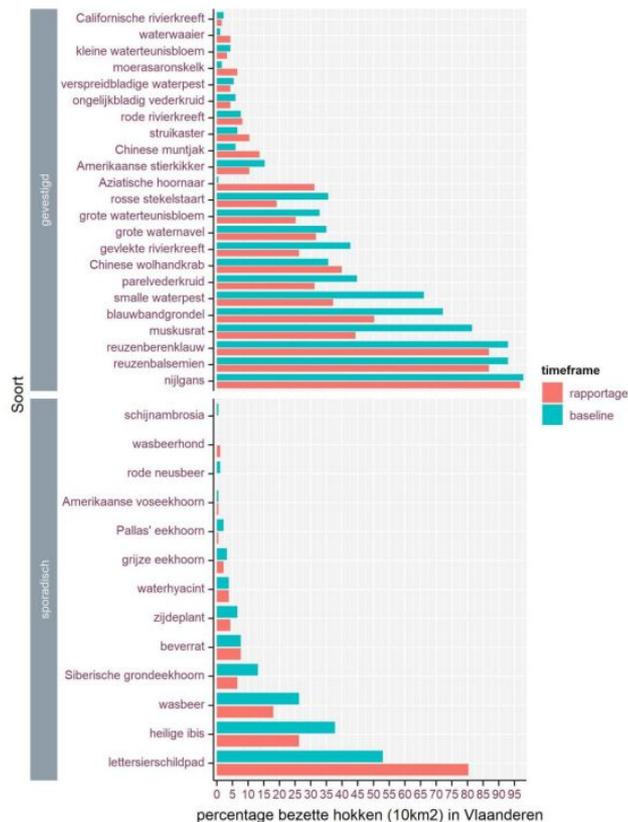
# IAS indicators

## EU concern occupancy species (update of existing indicator)

Adriaens et al. 2020  
(doi.org/10.21436/inbor.19288287)



Biodiversity Building Blocks for policy



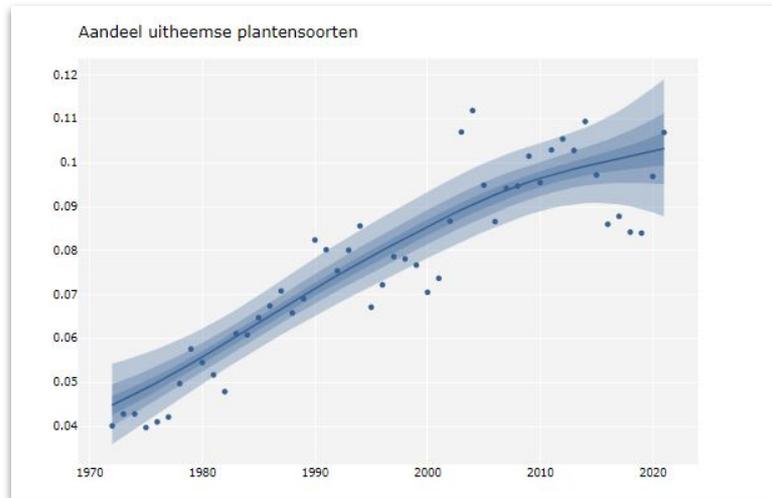
**Alien Species Portal**

<https://alienspecies.inbo.be>

# IAS indicators

Extra: Percentage of exotic plants per km2 (update of existing indicator)

<https://www.vlaanderen.be/inbo/indicatoren/aandeel-uitheemse-planten>



# Thank you!

Ward Langerart, Shawn dove &  
Jasmijn Hillaert



B-Cubed Newsletter



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