BIODIVERSITY
BUILDING
BLOCKS FOR
POLICY

LEGACY BOOKLET

Funded by
the European Union

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Project Overview

B-Cubed aimed to standardise access to biodiversity data, helping transform fragmented biodiversity records into timely, policy-relevant indicators. This was achieved by developing a service to create "species occurrence cubes", which then served as the basis for models and indicator of past, current and future biodiversity. To ensure its results can be reused, the project created exemplary workflows for modelling and indicator calculation, as well as a suite of guides, tutorials and hands-on training sessions. The application and usefulness of B-Cubed's algorithms and software are demonstrated through the project's four case studies, which consider a variety of environments, regions and challenges to maximise their relevance to stakeholders and policy-makers and to test the extremes of the tools. They cover testing B-Cubed workflows in the region of Flanders, using indicators to assess the status of biological invasions and their management in South Africa, optimising assessments and reporting of the Habitats Directive in Europe, and assessing the capacity of species occurrence cubes to monitor Ramsar sites.

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Consortium

- Meise Botanic Garden
- Global Biodiversity Information Facility
- Research Institute for Nature and Forest
- University of Bologna
- Justus-Liebig-University Giessen
- Ovidius University of Constanța
- South African National Biodiversity Institute
- Stellenbosch University
- Pensoft Publishers
- German Centre for Integrative Biodiversity Research (iDiv) Halle-Jena-Leipzig
- French Institute for Research in Computer Science and Automation
- University of Aveiro
- University of L'Aquila

Kick-off meeting, 2023, Brussels, Belgium

Annual Meeting, 2024, Montpellier, France

Annual Meeting, 2025, Leipzig, Germany

Table of Contents

1. Building species occurrence cubes 7

2. Modelled cubes 11
Overview of modelled cubes 12
Suitability Cube 14
Dissimilarity Cube 15
Network Invasibility Cube 18
DeepMaxent 21
Criteria for producing reliable indicators and trends from occurrence cubes 23

3. Indicators of biodiversity change and quality measures 24
Biodiversity indicators (b3gbi R package) 25
Phylogenetic diversity indicators (pdindicatoR) 26
Impacts of alien taxa indicators (impIndicator) 27
Indicators of robustness (dubicube) 29
Workflows for the calculation of the indicators (b3verse) 31

4. Guidelines, tutorials and software requirements for data and indicator implementation 33
Software development guide and quality assessments 34
B-Cubed documentation website 35
Advancing FAIR biodiversity science and policy 35

5. Stakeholder engagement and dissemination 38
Alignment with other European and international biodiversity initiatives 39
Hackathon 39
Training sessions 40
Policy briefs 41
Open access project collections 42

1

BUILDING SPECIES OCCURRENCE CUBES

Standardising biodiversity data

B-Cubed designed, developed and deployed a service to create "species occurrence cubes". It is provided by the Global Biodiversity Information Facility (GBIF) and allows users to aggregate the vast amount of species occurrence data (i.e. when and where species have been observed) into custom downloads. This facilitates the creation of Essential Biodiversity Variables (EBVs) and indicators, aiding biodiversity management and policy decisions.

Specification for a new data format and service

A new format was designed to aggregate species occurrence data along geographic, temporal and taxonomic dimensions allowing users to obtain, for example, the number of occurrences for a plant family, for each year and for each decimal degree grid cell. The specification describes what spatial reference grids should be offered, how to handle occurrences with a larger spatial uncertainty than those grids, and what measures to provide (e.g. count, minimum coordinate uncertainty, sampling bias, etc.). The specification also describes the service to produce such cubes.

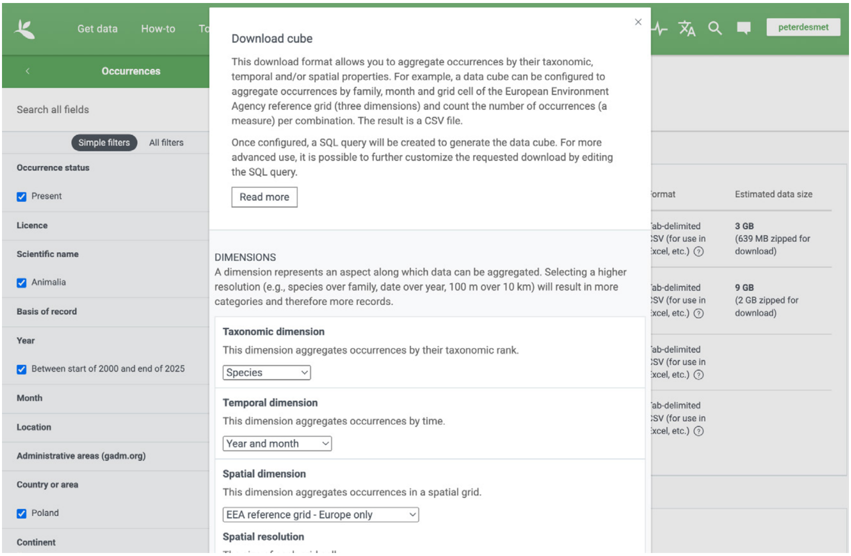
Read the specification at **https://docs.b-cubed.eu/guides/occurrence-cube/.**

The GBIF SQL Download API

The specification was implemented by GBIF as a new service that allows users to query and aggregate species occurrence data with the Structured Query Language (SQL). This well-known language can handle diverse and complex data operations and can be used for more than the generation of data cubes. The service also provides a number of functions that shield users from having to create complex aggregation queries themselves (such as grid assignment).

Any registered user of GBIF can use the service. The easiest way to do so is through the GBIF website (**https://www.gbif.org/**), where one can create a cube through a series of dropdown menus and checkboxes. No SQL knowledge is required for this, but advanced users can switch to a SQL editor to customise their query further.

Users can also interact with the service programmatically using the command line interface or the updated libraries in R (rgbif) and Python (pygbif). As with other GBIF occurrence download formats, all successful queries are assigned unique and permanent DOIs. This enables FAIR citation, attributes data publishers and aids reproducibility of downstream analyses.



Occurrence status

☑ Present

Licence

Scientific name

☑ Animalia

Basis of record

Year

☑ Between start of 2000 and end of 2025

Month

Location

Administrative areas (gadm.org)

Country or area

☑ Poland

Continent

Download cube

This download format allows you to aggregate occurrences by their taxonomic, temporal and/or spatial properties. For example, a data cube can be configured to aggregate occurrences by family, month and grid cell of the European Environment Agency reference grid (three dimensions) and count the number of occurrences (a measure) per combination. The result is a CSV file.

Once configured, a SQL query will be created to generate the data cube. For more advanced use, it is possible to further customize the requested download by editing the SQL query.

DIMENSIONS
A dimension represents an aspect along which data can be aggregated. Selecting a higher resolution (e.g., species over family, date over year, 100 m over 10 km) will result in more categories and therefore more records.

Taxonomic dimension
This dimension aggregates occurrences by their taxonomic rank.
Species

Temporal dimension
This dimension aggregates occurrences by time.
Year and month

Spatial dimension
This dimension aggregates occurrences in a spatial grid.
EEA reference grid - Europe only

Spatial resolution

ormat	Estimated data size
ab-delimited SV (for use in xcel, etc.)	3 GB (639 MB zipped for download)
ab-delimited SV (for use in xcel, etc.)	9 GB (2 GB zipped for download)
ab-delimited SV (for use in xcel, etc.)	
ab-delimited SV (for use in xcel, etc.)	

Figure: Screenshot of the GBIF.org download page, where users are presented with the option to format data as a cube.

Learn how to create a cube at
https://docs.b-cubed.eu/tutorials/download-a-cube-from-gbif/

Facilitating the use of biodiversity data

By providing species occurrence measures across user-defined dimensions and resolutions, cubes significantly expand the usability of GBIF-mediated data. The ability for users to define biodiversity dimensions across time, space and taxa and obtain species occurrence counts at those resolutions will improve integration with other data sources. For example, species occurrences have an important role in calibrating and validating biodiversity models derived from satellite imagery, but to date, differences in temporal and spatial resolutions have required considerable data processing. By better matching the scale and resolution, data cubes can aid users in building more robust models of species distribution and biodiversity change more efficiently, improve biodiversity baselines and monitor changes over time.

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2

MODELLED CUBES

Building on species occurrence cubes, B-Cubed developed a set of modelled cube approaches that extend biodiversity data from aggregation and reporting to prediction, interpretation, and decision support. These approaches translate occurrence records and associated environmental information into policy-relevant products that help users assess species distributions, community turnover, invasion risk, and the reliability of model outputs through space and time. Together, they show how occurrence cubes can underpin a new generation of transparent, scalable, and reproducible biodiversity modelling workflows.

Overview of modelled cubes

The modelled cubes developed in B-Cubed address complementary ecological questions at different levels of organisation. The Suitability Cube focuses on species-level model applicability, helping users understand where species distribution model predictions are robust and where they are uncertain. The Dissimilarity Cube shifts attention to communities, quantifying how species assemblages differ across space and time and how these patterns may change under future scenarios. The Network Invasibility Cube integrates invader traits, abiotic suitability, and resident community context to assess where biological invasions are most likely and which species pose the greatest risk. DeepMaxent provides a scalable deep-learning framework for species distribution modelling that can incorporate biodiversity cubes alongside environmental, remote-sensing, and other heterogeneous predictors.

Taken together, these approaches demonstrate how B-Cubed moves from biodiversity data cubes as a standardised data product to biodiversity modelling cubes as a framework for analysis, forecasting, and policy support. They provide complementary tools for understanding where species may occur, how communities reorganise, where invasions are most likely, and how confidently these patterns can be interpreted.

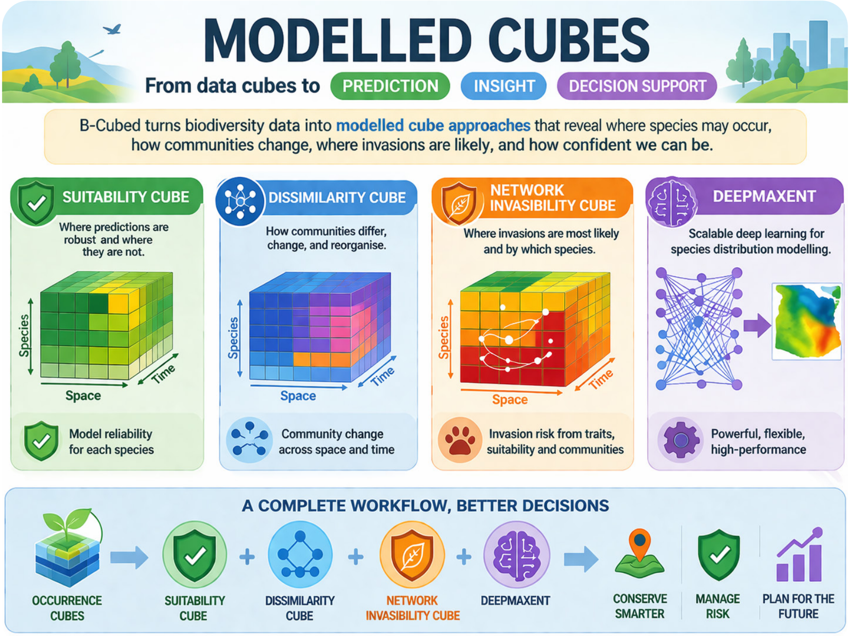

Figure: Overview of modelled cubes transforming biodiversity data into prediction, insight, and decision support.

Suitability Cube

The Suitability Cube is a conceptual and operational framework designed to evaluate biodiversity data fitness-for-use across multiple analytical contexts. The output is a three-dimensional data cube (cell × species × time) that integrates indicators (Dissimilarity Index, Area of Applicability and Hypervolume of the species' niche) derived from the same environmental variables used as inputs to the SDMs. This cube provides a reproducible and transparent framework for exploring how species occupy environmental space, identifying areas of high uncertainty or extrapolation, and evaluating the robustness of model predictions through space and time.

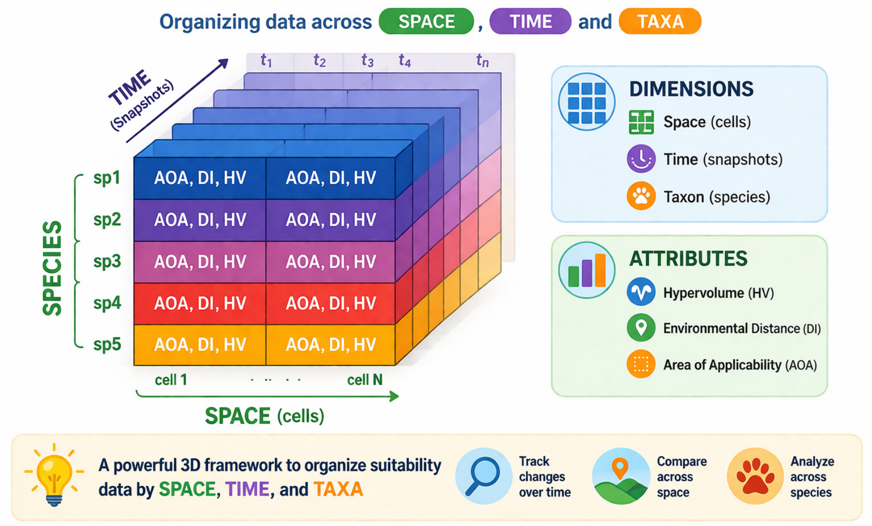

Figure: Conceptual structure of the Suitability Cube, organised along spatial, taxonomic, and temporal dimensions

References

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Dissimilarity Cube

The Dissimilarity Cube is a reproducible, multidimensional product that maps how communities (not just single species) differ across space and time. It combines species-occurrence records with environmental covariates to quantify compositional turnover using order-wise metrics, like zeta (ζ) diversity, and then models and maps turnover and bioregions, including under future scenarios.

The Dissimilarity Cube turns biodiversity records into clear, mappable signals of community change, thereby helping identify stable regions, shifting assemblages, and areas at risk of ecological reorganisation.

Conservation and monitoring often need to understand how whole assemblages change across landscapes, not just where a species might occur. Community-level turnover and bioregional patterns provide this complementary perspective. The Dissimilarity Cube formalises multi-site dissimilarities in a consistent data-cube structure, making change comparable across regions, taxa, and time.

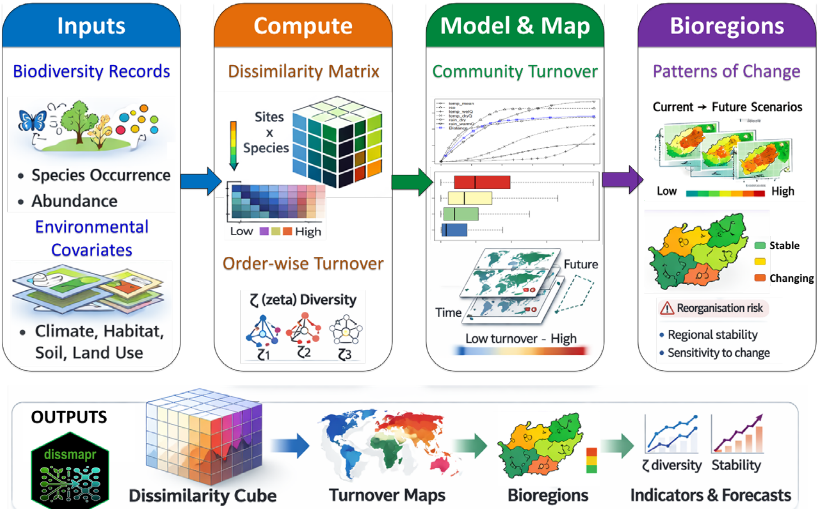

Figure: Workflow of the dissmapr package for biodiversity dissimilarity and turnover analysis.

The framework integrates species occurrence data, environmental predictors, and order-wise dissimilarity metrics (zeta-diversity) to compute, predict, and map compositional turnover. Core functions handle data acquisition, spatial aggregation, variable preparation, dissimilarity computation, predictive modelling, and spatial visualisation. This modular workflow enables independent and reproducible analyses of biodiversity structure and bioregional change across scales.

The objective of the Dissimilarity Cubes is to deliver a standard, scalable workflow that:

- computes multisite compositional turnover (ζ-diversity) from site-by-species data,
- links turnover to environmental and geographic drivers using Multi-Site GDM (i-splines), and
- produces spatial surfaces, bioregions, and scenario-based change maps for decision support.

By making turnover and bioregional boundaries explicit and forecastable, the cube supports: monitoring of ecological stability vs. change, detecting emerging “novel” community configurations, and targeting conservation planning to places where assemblages are most likely to reorganise under pressure.

Some of the key outputs are order-wise dissimilarity metrics (e.g. ζ_2), continuous turnover surfaces, bioregional partitions (k-means/PAM/hierarchical/GMM), scenario change maps, and i-spline partial dependence plots. In the documented demonstration (South African butterflies; >55k GBIF records aggregated to 0.5° and linked to WorldClim plus effort/richness layers), geographic distance dominated turnover, sampling effort was the next strongest driver, and rainfall contributed modestly. Including sampling effort increased deviance explained to ~30–37%, while omitting effort reduced it below 10%, highlighting how uneven sampling can obscure ecological signals. Sensitivity mapping further separated uncertainty from clustering choices versus climate-driven shifts in bioregions.

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McGeoch, M. A., Latombe, G., Andrew, N. R., Nakagawa, S., Nipperess, D. A., Roigé, M., et al. (2019). Measuring continuous compositional change using decline in zeta diversity. *Ecology and Evolution*, 9(21), 12864–12874. **https://doi.org/10.1002/ecy.2832**

Network Invasibility Cube

The Network Invasibility Cube is a unified, transparent framework for assessing invasion risk by combining invader traits, abiotic suitability, and biotic resistance from resident communities into invasion-fitness and establishment-probability surfaces across sites and species. It converts complex invasion ecology into decision-ready indicators by identifying which invaders are most likely to establish, where invasions are most likely, and why (which traits and conditions drive risk).

Biological invasions are a major driver of biodiversity loss, and establishment depends jointly on environmental conditions, resident community context, and invader traits. Traditional approaches often treat these drivers separately; the cube integrates them into a single interoperable structure to avoid fragmented and inconsistent assessments.

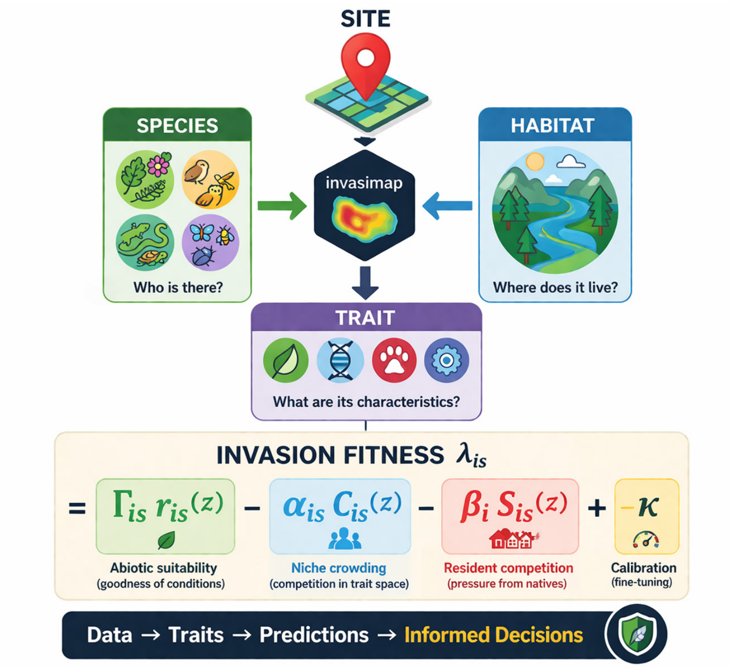

Figure: invasimapr workflow links data access, preparation, trait-space modelling, resident predictors, and slope estimation to the invasion fitness equation.

The invasion fitness formula decomposes into four components: abiotic suitability $\Gamma_{is} r_{is}^{(z)}$ (green), niche crowding penalty $\alpha_{is} C_{is}^{(z)}$ (blue), resident saturation penalty $\beta_i S_{is}^{(z)}$ (red), and a calibration offset k (grey). Each component is derived from specific workflow modules, converging on predicted invader establishment and summarised results, which provide actionable outputs to policy.

The objective is to provide a modular, reproducible workflow (implemented in invasimapr) that:

- constructs a shared trait space and quantifies trait-based crowding/biotic pressure,
- models resident baselines (suitability and saturation),
- computes invasion fitness λ and transforms it into establishment probability *P*, and
- summarises outputs into clear indicators for policy and management.

The cube supports risk assessment and prioritisation by flagging invasion "hotspots" and high-risk species-trait combinations, enabling more targeted surveillance, pathway control, and site-level mitigation, while remaining comparable across taxa, regions, and scenarios.

Key outputs include site × invader invasion-fitness matrices λ, establishment probabilities *P*, trait-space diagnostics, species invasiveness rankings, site invasibility maps, and trait-effect summaries. Mechanistically, invasion fitness weights abiotic suitability, trait-based niche crowding (biotic resistance), and resident competition/saturation; $\lambda > 0$ indicates higher establishment likelihood, which can be mapped to λ via logistic/probit transformations. Visual outputs explicitly contrast abiotic opportunity versus biotic pressure (trait-similar crowding), highlighting where invasion is most plausible (high suitability, low crowding). Final summaries distil model outputs into decision-ready rankings and hotspot maps suitable for reporting and iterative policy updates.

References

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DeepMaxent

DeepMaxent is a deep learning framework for species distribution modelling that integrates the maximum entropy principle with neural networks. Beyond classical environmental variables, it provides a flexible foundation to incorporate complex and heterogeneous predictors such as remote sensing imagery, climate projections, ecological context, and multimodal biodiversity data. The method relies on a normalised Poisson point-process loss, enabling scalable training with stochastic gradient descent and efficient multi-species modelling while accounting for spatial sampling biases. DeepMaxent improves predictive accuracy compared to classical Maxent and opens new opportunities for large-scale, multimodal biodiversity monitoring using deep learning.

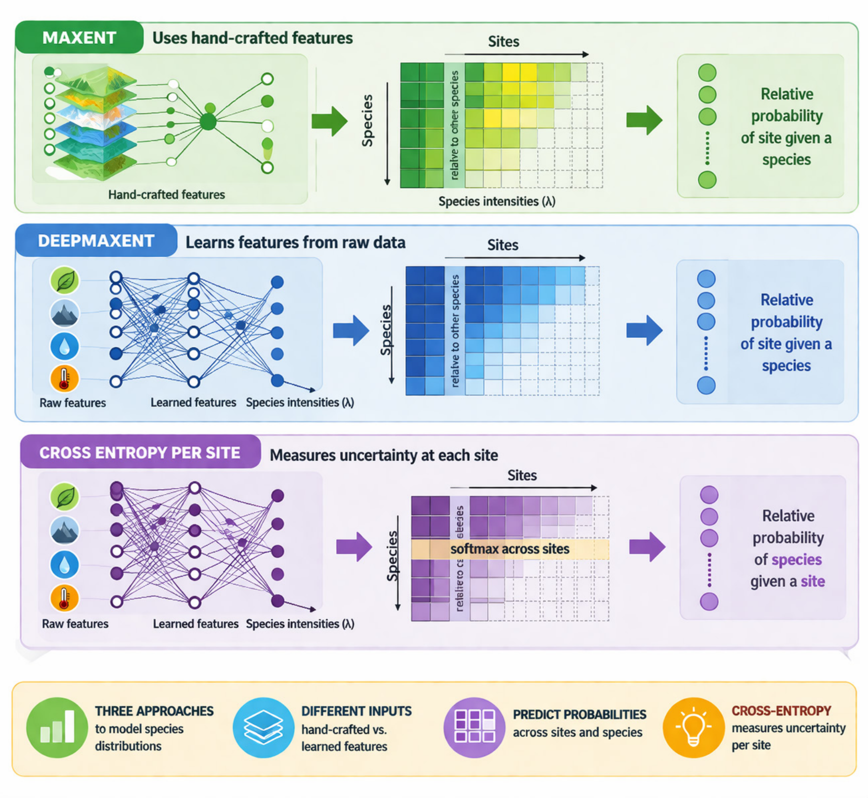

Figure: Illustration of three species distribution modelling approaches (Maxent, DeepMaxent, and a common cross-entropy).

Maxent relies on handcrafted environmental features and trains an independent model for each species. DeepMaxent uses a single deep learning model to predict multiple species simultaneously, incorporating batch normalisation across samples to standardise feature representations. In contrast, the commonly used cross-entropy approach applies normalisation along the species dimension, focusing on predicting the presence of species at each site rather than modelling species jointly.

References

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DeepMaxent: A neural network using the maximum entropy principle for Species Distribution Modelling developed in the B-Cubed project **https://github.com/RYCKEWAERT/deepmaxent**

Criteria for producing reliable indicators and trends from occurrence cubes

By comparing status and trend estimates from aggregated data cubes with those obtained from structured monitoring data, B-Cubed developed guidelines for producing reliable indicators and trends from occurrence cubes. These guidelines emphasise the importance of clearly defining the scope of the analysis so that data are aggregated at an appropriate level, conducting an exploratory assessment of the aggregated data to identify common gaps or errors, and applying targeted filtering. All filtering, harmonisation, and data-quality decisions should be documented in a transparent and traceable manner.

References

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3

INDICATORS OF BIODIVERSITY CHANGE AND QUALITY MEASURES

Biodiversity indicators (b3gbi R package)

The b3gbi R package is a computational tool designed to efficiently analyse large-scale species occurrence data, such as those from GBIF, to produce consistent insights into global biodiversity trends. It works by processing species occurrence cubes to automatically calculate standardised indicators (e.g., species richness and change over time), quantify uncertainty, and present results through customisable maps and time series. It aims to improve the accessibility, reproducibility, and reliability of biodiversity analyses to better support conservation and environmental decision-making.

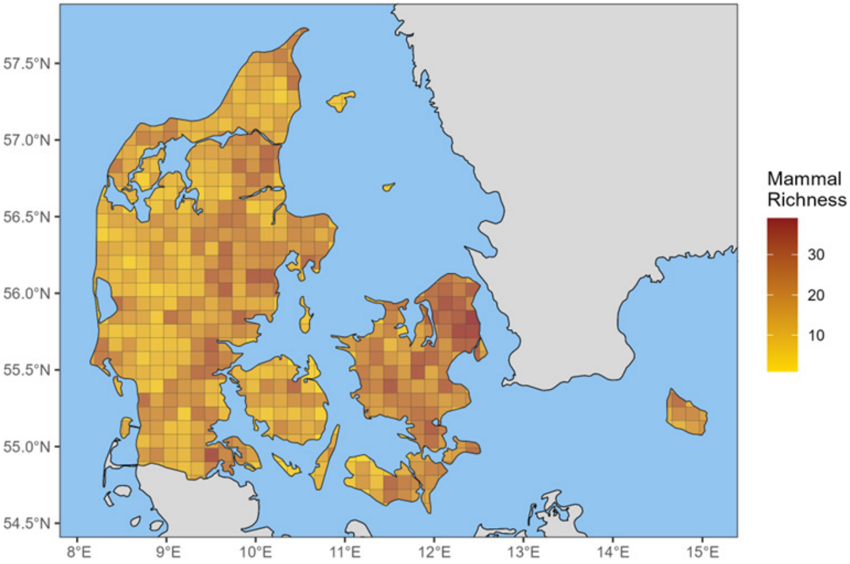

Figure: Observed Land Mammal Richness in Denmark: 1980–2020

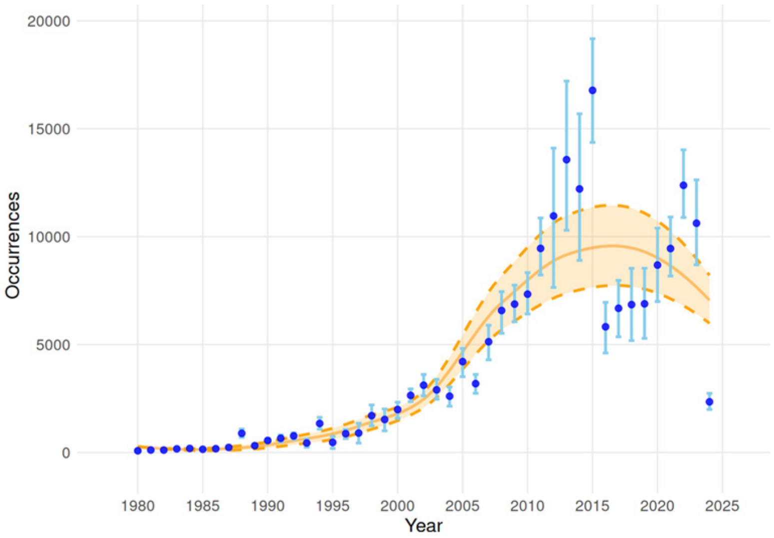

Figure: Temporal Trends of Total Mammal Occurrences in Denmark, largely reflecting the increase in survey effort in the 21st century and changes in the mobilisation of data.

References

Dove, S. (2026). b3gbi: General Biodiversity Indicators for Biodiversity Data Cubes. R package version 0.8.15, **https://github.com/b-cubed-eu/b3gbi**

Phylogenetic diversity indicators (pdindicatoR)

The pdindicatoR package was developed to facilitate producing phylogenetic diversity (PD) maps from user-provided phylogenetic trees and GBIF species occurrence cubes. The workflow output highlights phylogenetic diversity hotspots and quantifies the proportion of PD currently safeguarded within existing protected areas. The package can be used as a tool to locate hotspots of phylogenetic diversity, guide conservation planning by identifying priority regions for protection and assisting with long-term monitoring and reporting on PD conservation status.

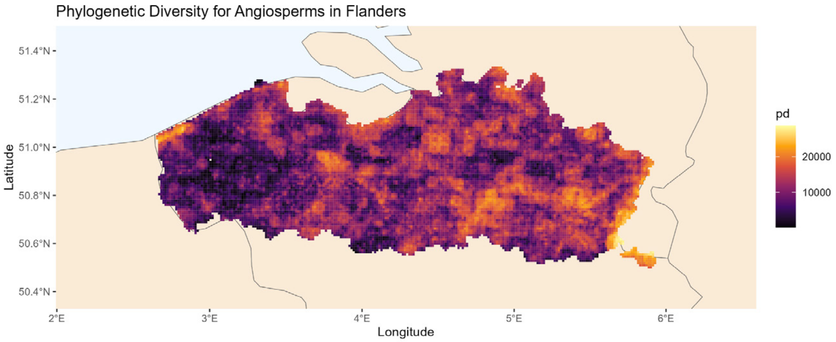

Figure: Phylogenetic Diversity for Angiosperms in Flanders

References

Breugelmans, L., Trekels, M., Hendrickx, L. (2024) pdindicatoR: Calculate and visualize a phylogenetic diversity indicators based on species occurrence data cubes (Version 0.1.0). **https://doi.org/10.5281/zenodo.14237551**

Impacts of alien taxa indicators (impIndicator)

The Impacts of alien taxa indicators present a straightforward method for estimating the harm caused by alien (non-native) species, using freely available data and a clear, step-by-step process. As non-native species spread and multiply, they can seriously affect local plants, animals, and entire ecosystems, not to mention impacts on agriculture and health. By combining information about where these alien species occur (from online databases) with the evaluations of their ecological effects (from an international standardised process that gathers information on impacts and collates them into a standard score), we developed a practical tool that gives an “impact value.” This value reflects both how widespread a species is and how serious its negative effects can be. Researchers, conservationists, and policymakers can use these values to identify which non-native species are likely to be problematic, allowing managers to address the urgent future problems. This method thus helps guide actions to protect biodiversity and maintain healthy ecosystems into the future.

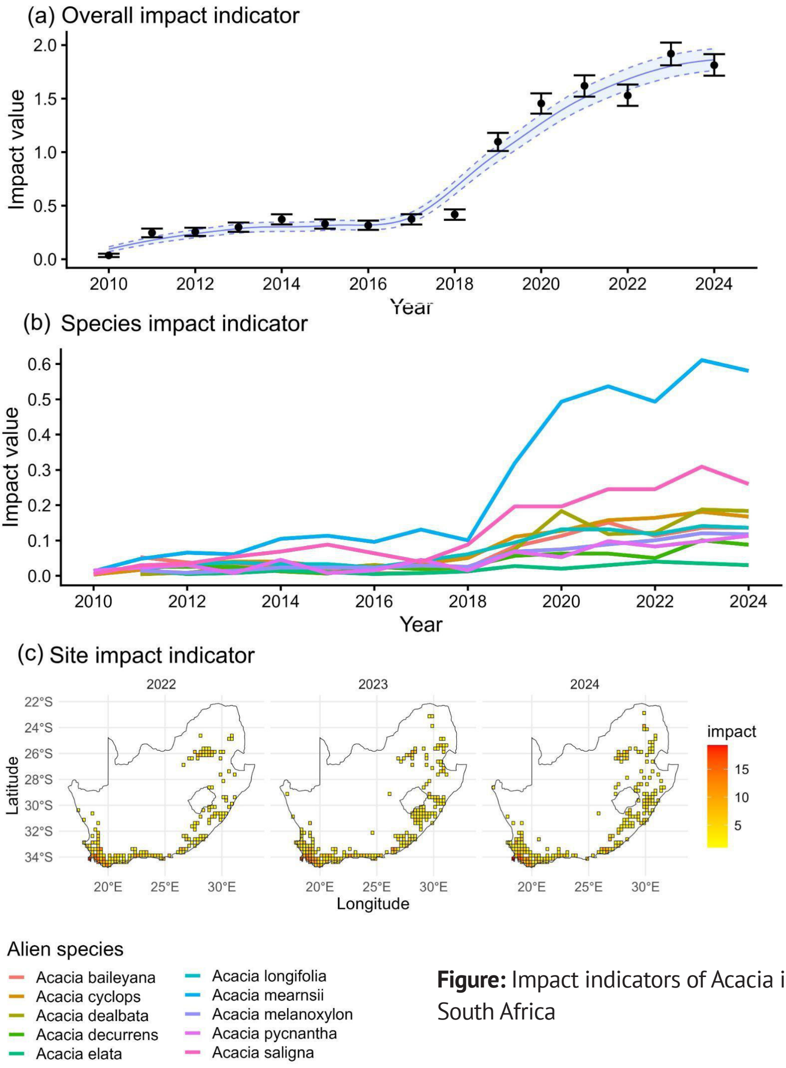

Figure: Impact indicators of Acacia in South Africa

References

Yahaya, M. M., Kumschick, S., MacFadyen, S., Landi, P., & Hui, C.(2026). impIndicator: Impact Indicators of Alien Taxa (Version 0.6.0) [Computer software]. **https://doi.org/10.5281/zenodo.15052675**

Indicators of robustness (dubicube)

The R package dubicube supports exploratory analysis, uncertainty quantification, and evidence-based interpretation of biodiversity indicators. It tackles the need to assess the reliability and interpretability of biodiversity indicators derived from species occurrence data by implementing methods to evaluate data robustness, identify limitations in spatial, temporal, and taxonomic coverage, and quantify how sensitive indicators are to individual species. Uncertainty is explicitly estimated using resampling techniques, allowing confidence intervals and effect classifications to support cautious interpretation of trends. Together, these approaches reduce the risk of overconfidence in indicator results and improve transparency in analysis. All proposed methods are implemented in the R package dubicube, which supports exploratory analysis, uncertainty quantification, and evidence-based interpretation of biodiversity indicators.

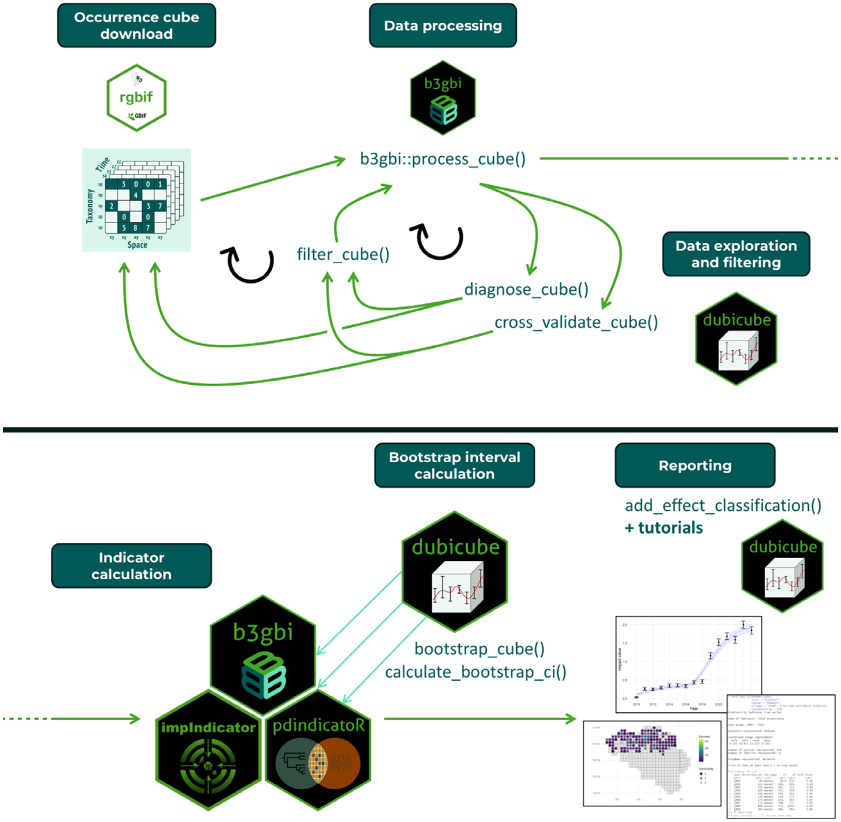

Figure: dubicube functionality within the indicator calculation workflow. Data exploration can be done by evaluating diagnostics or group-specific sensitivity analysis using cross-validation. Based on these results, it can be decided to filter the data or to generate a new data cube. The package can also be used to calculate confidence intervals for indicators based on bootstrap resampling and plays an important role in reporting.

References

Langeraert, W., & Van Daele, T. (2026) dubicube: Calculation and Interpretation of Data Cube Indicator Uncertainty (Version 0.11.1) [Computer software]. **https://doi.org/10.5281/zenodo.14850237**

Workflows for the calculation of the indicators (b3verse)

The b3verse is an integrated ecosystem comprising eleven R packages and the b3data data package. The b3verse consolidates biodiversity indicator workflows into a coherent, reproducible, and open-source framework, covering general biodiversity indicators (e.g. b3gbi), phylogenetic diversity (pdindicatoR), alien species impacts (impIndicator), uncertainty and robustness assessment (dubicube), and modelling tools such as dissmapr and invasimapr. The ecosystem follows strict development guidelines, includes automated testing and continuous integration via R-universe, and is permanently archived on Zenodo. Comprehensive documentation and tutorials ensure accessibility, and the modular design provides the technical foundation for cloud-based dashboards and policy-oriented applications.

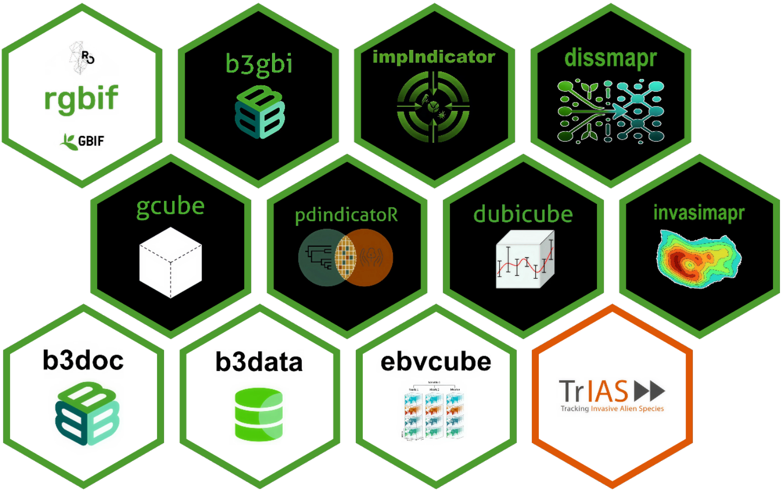

Figure: b3verse R packages

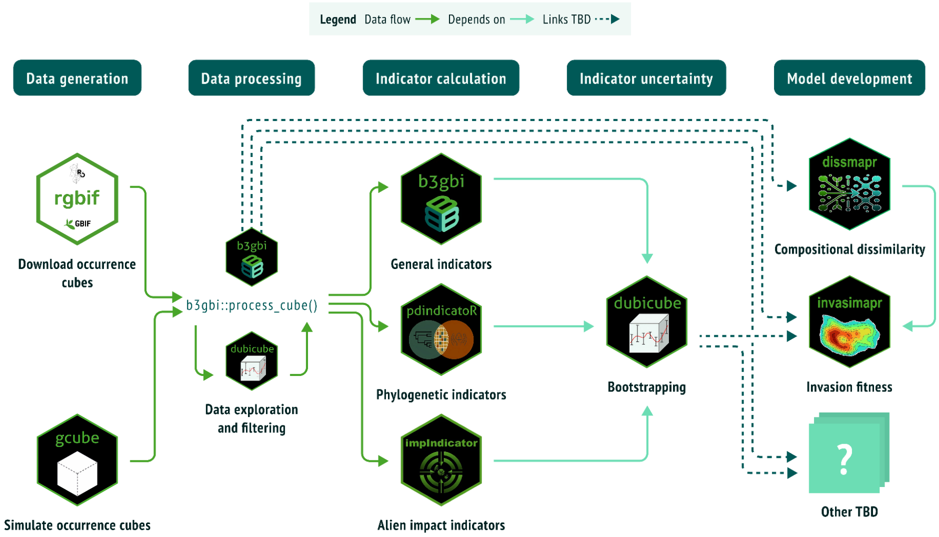

Figure: How data and indicators developed by B-Cubed connect

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Langeraert, 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/

4

GUIDELINES, TUTORIALS AND SOFTWARE REQUIREMENTS FOR DATA AND INDICATOR IMPLEMENTATION

The reproducible use of B-Cubed's data products and indicators is ensured by establishing specifications and guidelines. This included defining quality requirements, implementing and testing procedures, and documenting best practices to guarantee openness, portability and technical readiness. Comprehensive and user-friendly documentation has been developed to support the use of species occurrence cubes across different cloud providers. In addition, the technical knowledge generated throughout the project is centralised, ensuring that all B-Cubed data products are not only openly available, but also fully Findable, Accessible, Interoperable and Reproducible (FAIR), strengthening their long-term scientific and policy impact.

Software development guide and quality assessments

The B-Cubed software development guide (**https://docs.b-cubed.eu/guides/software-development/**) establishes the high-level quality requirements for all software tools, computational workflows, and digital resources developed within the consortium. It establishes a consistent open-source development lifecycle that promotes transparency, collaboration, and reuse both within and beyond the project.

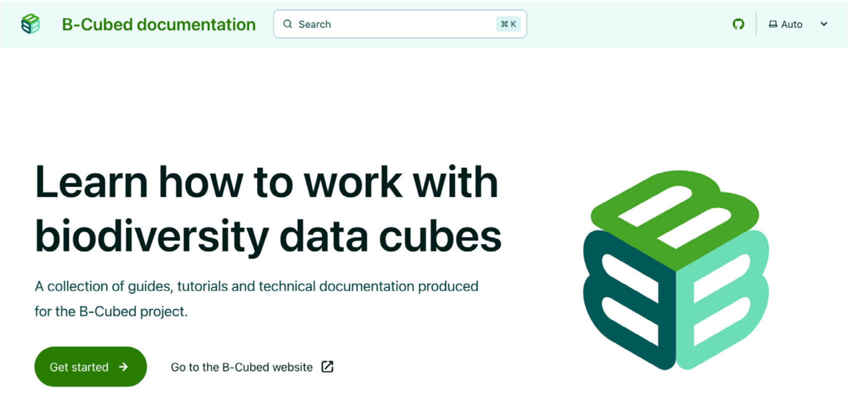
The guide provides clear instructions and examples on repository management, inclusion of useful metadata, licensing under the permissive MIT licence, and the adoption of collaborative workflows such as the GitHub flow. Specific best practices are detailed for development in R and Python, ensuring consistency and technical robustness.

Quality assessments confirm that B-Cubed software tools comply strongly with the defined openness and quality standards (81% overall compliance), with continuous improvement observed throughout the project. The interoperable “b3verse” of R packages and associated documentation ensures robust, reusable and sustainable digital outputs.

B-Cubed documentation website

The B-Cubed documentation website (**https://docs.b-cubed.eu/**) serves as the public, searchable and peer-reviewed access point for all technical knowledge produced within the project. The platform hosts guides, tutorials, and technical documentation, ensuring accessibility for both developers and end users.

The website is built using the Astro/Starlight static site generator and hosted on GitHub Pages, providing a low-maintenance and sustainable infrastructure. All content undergoes peer review through GitHub Pull Requests to ensure high editorial and technical standards. A semi-automated workflow integrates externally maintained tutorials (such as R vignettes) directly into the main documentation platform, maintaining coherence while enabling distributed contributions.



Learn how to work with biodiversity data cubes

A collection of guides, tutorials and technical documentation produced for the B-Cubed project.

Figure: B-Cubed documentation website

Advancing FAIR biodiversity science and policy

B-Cubed's work also contributes to advancing FAIR principles for the project's geospatial data products and strengthening their interoperability within the broader biodiversity data ecosystem. This work includes collaboration with the GEO BON Essential Biodiversity Variables (EBV) **Data Portal** and the **EBVCube format**.

New taxonomic fields were implemented within the EBVCube metadata structure and made programmatically accessible via an API. These enhancements strengthen the findability, accessibility, interoperability and reproducibility of B-Cubed data products within the broader biodiversity data ecosystem. Together, these efforts establish a traceable data mobilisation workflow and enable open access to well-documented and machine-readable, gridded spatial data. By aligning data sharing practices with international standards, the project supported evidence-based biodiversity monitoring and contributed to the strategic objectives of the European Green Deal Data Space.

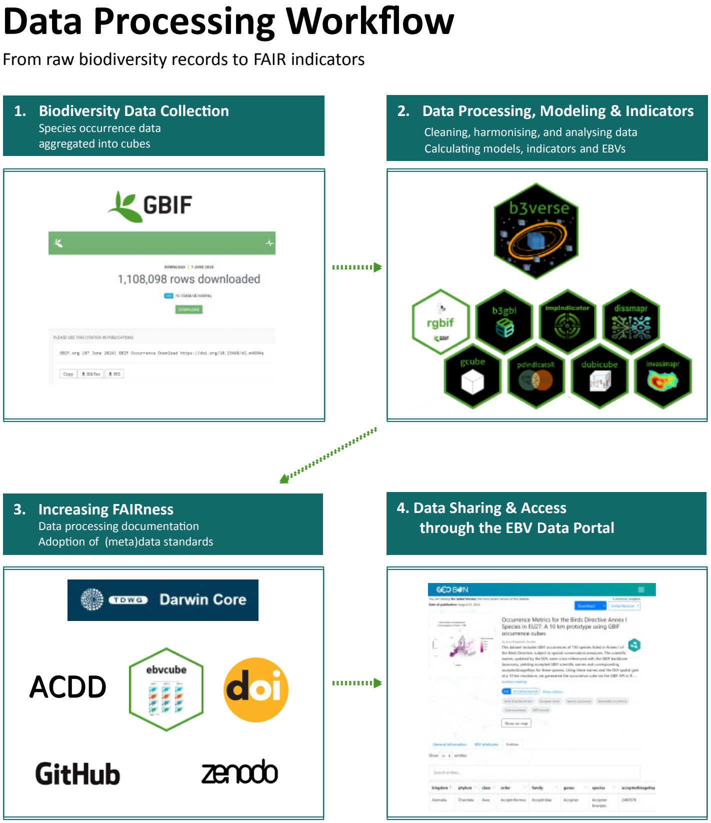


Figure: Schematic of data mobilisation for species occurrence records using the data cubes approach. Examples: [1]10.15468/dl.gxk3vh; [2]10.5281/zenodo.13798783; [3]10.25829/w0vf54.

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5

STAKEHOLDER ENGAGEMENT AND DISSEMINATION

To maximise the impact of its results, B-Cubed worked closely with stakeholders to align project objectives, provide training opportunities and disseminate results. We have also utilised various outreach platforms to disseminate B-Cubed's results, including newsletters, press releases, and social media channels, to reach a wide and diverse audience.

Alignment with other European and international biodiversity initiatives

B-Cubed analysed other European and international initiatives and created actionable insights to enhance the use of biodiversity indicators in policy decision-making. In this way, some critical gaps such as the need for open workflows, harmonised datasets, and alignment with existing data platforms, were identified. This policy work (**https://b-cubed.eu/policy**) helped B-Cubed bridge the gap between policy and indicators and led to greater use of biodiversity indicators in policy decisions. The project has developed specific tools for harmonising datasets, adapting workflows for known indicators, and piloted new workflows for indicators that were lacking methodology.

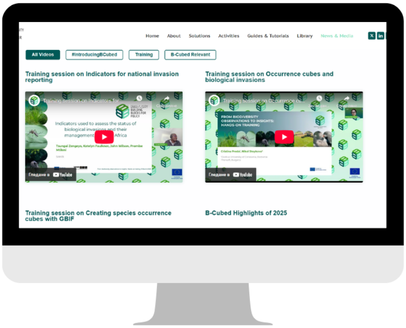
Furthermore, B-Cubed has been actively collaborating with its sister projects (FAIR Information Cubes – FAIRiCube, All Data 4 Green Deal – AD4GD, Urban Data Space for Green Deal – USAGE) and other projects such as Bio-Agora, COOP4CBD, EarthMonitorOrg, EuropaBON, BioDT, BMD, OneSTOP, MAMBO and GUARDEN, fostering valuable partnerships.

Hackathon

B-Cubed organised a 4-day hackathon with the common goal to standardise biodiversity data in order to enhance efficiency and accessibility. The event brought together biodiversity informaticians, researchers, and practitioners who are passionate about leveraging biodiversity data for impactful solutions. During the Hackathon, participants had the chance to experiment with data cubes and channel creativity into innovative solutions for a variety of biodiversity challenges. The contributions made during the Hackathon played a pivotal role in advancing data cube technology, aiding in the enhancement of data preservation and monitoring on a global scale.

Figure: Participants in B-Cubed's Hackathon

Training sessions



Training session on Indicators for national invasion reporting

Training session on Occurrence cubes and biological invasions

Training session on Creating species occurrence cubes with GBIF

B-Cubed Highlights of 2025

The main technological achievements of B-Cubed were highlighted with a series of training sessions on working with biodiversity data cubes and indicators. They focus on the SQL service to download biodiversity data cubes from GBIF-mediated data, R packages developed throughout the project, using biodiversity indicators and other tools. The training sessions and their recordings present the project's results in an accessible and engaging way, making them easier to understand and use. They are available on B-Cubed's YouTube channel and project website (**https://b-cubed.eu/videos?categoryId=2**) where viewers can explore the project's outcomes in more detail.

Policy briefs

B-Cubed created several policy briefs that address key areas of scientific and technological advancements relevant to policy and practice. They focus on effective biodiversity monitoring using FAIR data and indicators, the Green Deal Data Space, the benefits of countries using GBIF, as well as on the data pipelines used by the project and the outcomes of B-Cubed's case studies.

All of the project's policy briefs are available on **https://b-cubed.eu/project-materials**.

POLICY BRIEF

BIODIVERSITY
BUILDING
BLOCKS FOR
POLICY

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Effective biodiversity monitoring requires FAIR data and FAIR models for FAIR indicators

Findable,
Accessible,
Interoperable, and
Reusable!

Key messages

- Headline indicators are a valuable starting point for **consistently monitoring the goals and targets** in the Kunming-Montreal Global Biodiversity Framework (GBF). However, Parties to the Convention on Biological Diversity (CBD) will need to couple these with additional indicators and would **benefit from shared data and methodologies**.

POLICY BRIEF

AD4GD

BIODIVERSITY BUILDING BLOCKS FOR POLICY

FAIRiCUBE

USAGE

UNLOCKING THE FULL POTENTIAL OF THE GREEN DEAL DATA SPACE

Making environmental data work for Europe's green transition

Environmental data are essential enablers of the European Green Deal. They support informed decision-making, underpin effective regulation, drive innovation, and empower society to act. Yet today, much of these data remains fragmented, inaccessible, or underutilised, creating significant barriers that limit Europe's progress towards its climate goals.

The Green Deal Data Space (GDDS) is envisioned as a solution to overcome these challenges and foster trusted exchange of public and private data across all areas of the green transition. To be effective, the GDDS must uphold the principles of Findability, Accessibility, Interoperability and Reusability (FAIR). Four projects—AD4GD, B-Cubed, FAIRiCUBE and USAGE—funded under the HORIZON-CL6-2021-GOVERNANCE-01-17 call have explored and documented the requirements for successfully achieving

- **Ensure resilient semantic interoperability on top of strong technical foundations.** Promote and enrich comprehensive controlled vocabularies with stable, well-defined concepts under established ontology frameworks, supported by technical infrastructure and governance for adaptability and long-term sustainability.
- **Recognise and resource the effort behind metadata.** Foster interoperability among varied metadata formats to ease the work of producers and users, and expand existing metadata standards to cover critical overlooked elements. Assure resources for metadata creation.
- **Enable data exchange between diverse stakeholders of the GDDS.** Develop effective strategies that

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TrIAS
Tracking Invasive Alien Species

BIODIVERSITY BUILDING BLOCKS FOR POLICY

OneSTOP

Why countries need the Global Biodiversity Information Facility: Lessons from Belgium

DOI 10.5281/zenodo.16890980

Quentin Groom[1], Tim Adriaens[2], Peter Desmet[2], Sonia Vanderhoeven[3], Nikol Yovcheva[4]

[1]Meise Botanic Garden, Meise, Belgium, [2]Research Institute for Nature and Forest, Brussels, Belgium, [3]Belgian Biodiversity Platform, Université Libre de Bruxelles, Belgium, [4]Pensoft Publishers, Sofia, Bulgaria

As global challenges such as biodiversity loss, invasive species, and climate change intensify, open biodiversity data infrastructures like the **Global Biodiversity Information Facility** (GBIF) offer vital tools for evidence-based decision-making, placing the best available research evidence at the heart of policy development and implementation[1]. Belgium's experience demonstrates how participation in GBIF enhances national capacity, supports scientific excellence, and delivers significant economic, ecological, and strategic returns for biodiversity science, policy and practice. This policy brief encourages governments to follow Belgium's lead in leveraging GBIF to support sustainable development, conservation, and innovation.

Belgium as a biodiversity data powerhouse

Belgium contributes over 55 million species observation records to GBIF, including 5.8 million in 2024 alone. 42 million records about Belgian biodiversity come from over 1,400 datasets, many of which originate from institutions abroad. This reflects Belgium's global integration in biodiversity research and the strategic importance of open data.

Institutions such as **Meise Botanic Garden, The Royal Belgian Institute of Natural Sciences, Flanders Marine Institute, The Research Institute for Nature and Forest, Natuurpunt**, **Belgian Biodiversity Platform, and the Universities of Liège and Ghent** play leading roles, actively publishing data, shaping national and international collaborations and promoting evidence-based decision-making processes. These efforts enhance European biodiversity monitoring and support transnational research on species distribution, ecosystem change, and conservation priorities.

1 Young, E., & Quinn, L. (2012). ***Making research evidence matter: A guide to policy advocacy in transition countries***. Open Society Foundations. http://advocacyguide.icpolicyadvocacy.org

Funded by
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POLICY BRIEF

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Data pipelines for policy-relevant indicators

Quentin Groom[1], Nikol Stoykova[2], Andrew Rodrigues[3], Jasmijn Hillaert[4], Lina M. Estupinan Suarez[5], Sandra MacFadyen[6] Ward Langeraert[7]

[1] Meise Botanic Garden, Meise, Belgium
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[3] Global Biodiversity Information Facility, Copenhagen, Denmark
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[6] Mathematical Sciences, Stellenbosch University, South Africa
[7] Research Institute for Nature and Forest, Brussels, Belgium

Key messages

- Automated data pipelines make it possible to turn scattered biodiversity records into up-to-date indicators that support evidence-based policymaking.
- Tools such as GBIF's data cube service, combined with a collection of open-source R packages provide standardised, interoperable, and FAIR-compliant workflows for analysing and sharing biodiversity data.
- While these tools are mainly used by scientific and technical teams, the outputs they support, such as dashboards, reports, and indicators, deliver clear, accessible evidence to policymakers, improving the timeliness of biodiversity information.

Funded by
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Open access project collections

To ensure effective communication and dissemination, B-Cubed has established a project collection in the Research Ideas and Outcomes (RIO) journal (**https://doi.org/10.3897/rio.coll.233**) and communities in Zenodo (**https://zenodo.org/communities/b3**) and GitHub (**https://github.com/b-cubed-eu**). In this way, the project's full research cycle was made transparent and easily accessible, ensuring compliance with the FAIR principles.

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RIO collection: **https://riojournal.com/topical_collection/233/**

Zenodo community: **https://zenodo.org/communities/b3/records?q=&l=list&p=1&s=10**

GitHub community: **https://github.com/b-cubed-eu**

Website: **https://b-cubed.eu/**

YouTube channel: **https://www.youtube.com/@B-CubedProject**

Policy briefs: **https://b-cubed.eu/project-materials**

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