

B-Cubed

Biodiversity Building Blocks for Policy

Documentation on Modelled Cubes

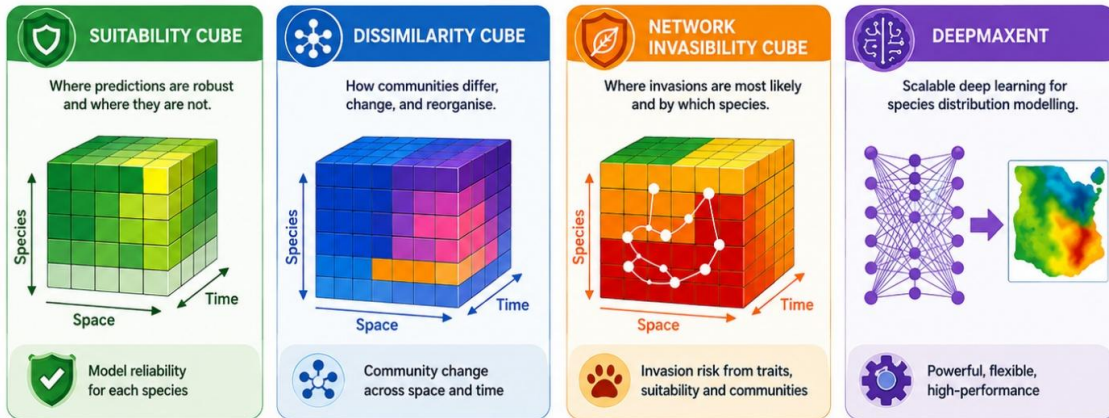
A Summary of Deliverable D4.1

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B-Cubed turns biodiversity data into **modelled cube approaches** that reveal where species may occur, how communities change, where invasions are likely, and how confident we can be.



1. 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.

2. Overview of Modelled Cubes

Modelling Current and Future Scenarios

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.

Three modelled data cubes were developed, each addressing a different ecological dimension but sharing common data inputs. Interoperability is achieved through consistent structuring of biodiversity inputs into site-by-species, site-by-environment, and species-by-trait matrices. This

common backbone enables the cubes to be linked: Suitability predictions can feed into the Invasibility Cube as measures of environmental match; Dissimilarity outputs can contextualise invasion risk by identifying which communities are undergoing compositional change; and all three cubes can be layered to produce integrated risk assessments.

3. Suitability Cube

The Suitability Cube is a conceptual and operational framework for evaluating the fitness-for-use of species distribution model outputs across analytical contexts. Its structure is a three-dimensional cube organised by space, species, and time, with each cell containing indicators that describe the reliability and interpretability of model predictions.

These indicators include the Dissimilarity Index, the Area of Applicability, and the Hypervolume of the species' niche, all derived from the same environmental variables used to fit the species distribution models. By integrating these measures into a common cube structure, the Suitability Cube enables users to evaluate not just what a model predicts but how far those predictions can be trusted in any given location and time period.

This makes the Suitability Cube especially valuable for identifying where model outputs are sufficiently robust for downstream indicator development and where predictions should be interpreted with caution.

The Suitability Cube workflow proceeds through four main phases: (1) data acquisition, gathering species occurrence records and environmental layers; (2) pre-processing, including cleaning, spatial alignment, and variable selection; (3) indicator computation, calculating the Dissimilarity Index, Area of Applicability, and Hypervolume for each species-site-time combination; and (4) cube building, assembling the results into a structured, multidimensional output. All scripts are openly available on GitHub under an MIT licence, supporting full reproducibility.

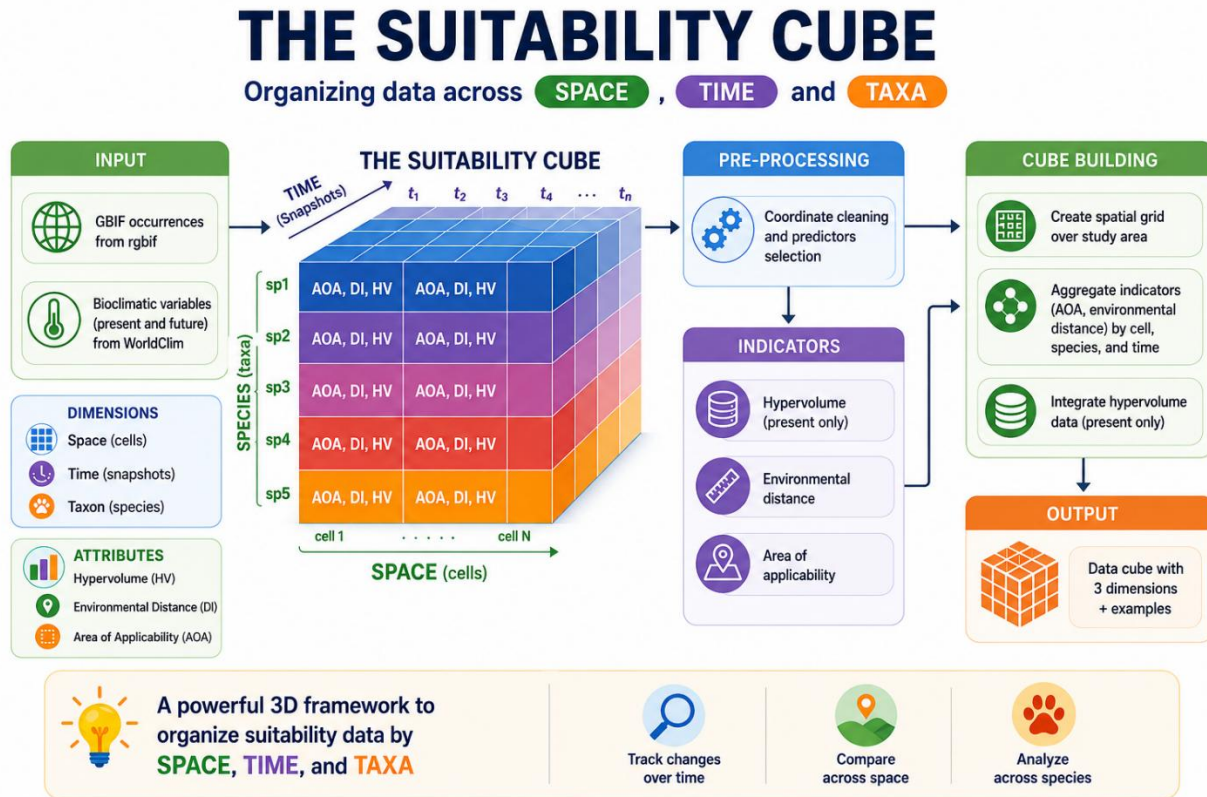


Figure 1: Three-dimensional structure of the Suitability Cube, organised across space, time, and taxa, with three diagnostic indicators (Dissimilarity Index, Area of Applicability, Hypervolume).

4. Dissimilarity Cube

The Dissimilarity Cube works at the community level, mapping how groups of species differ from one place to another and how communities may reorganise under future conditions. Using zeta diversity, it extends traditional pairwise comparisons to capture shared species across multiple sites simultaneously, providing a richer picture of compositional turnover.

Implemented through the **dissmapr** R package, the cube identifies ecological regions, tracks shifts in species assemblages, and highlights areas at risk of losing ecological resilience or undergoing reorganisation. Key outputs include order-wise dissimilarity metrics, continuous turnover maps, bioregional partitions, and scenario-based change maps.

By capturing multi-site compositional patterns rather than simple pairwise differences, the Dissimilarity Cube reveals how biodiversity is structured across landscapes. This information is essential for bioregional classification, conservation planning, and tracking ecological responses

to environmental change. Dissimilarity outputs can also feed directly into the Invasibility Cube, providing community context for invasion risk assessments.

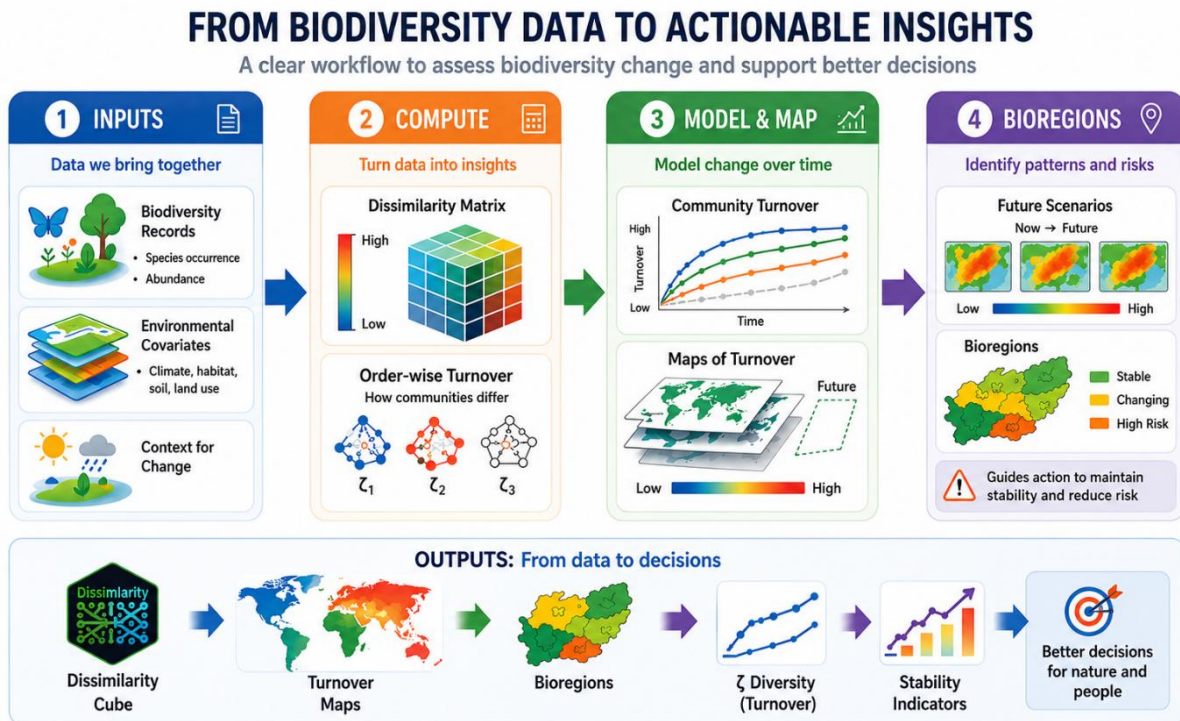


Figure 2: Conceptual overview of the *dissmapr* workflow for compositional dissimilarity and biodiversity turnover analysis.

5. Network Invasibility Cube

The Network Invasibility Cube focuses on invasive alien species, one of the most serious threats to biodiversity worldwide. By combining species traits, occurrences, and interaction models, it evaluates how invasions disrupt native communities, estimates which systems are most vulnerable, and provides species-level risk rankings.

Implemented through the **invasimapr** R package, it quantifies invasion fitness, the net potential for a newcomer to establish given local environmental conditions and resident community resistance. Outputs include site-level invasibility maps, species invasiveness rankings, and trait-environment diagnostics.

The cube integrates three components: abiotic suitability (whether the physical environment supports the invader), biotic resistance (whether the resident community can repel the

newcomer), and invader traits (characteristics that determine competitive ability and establishment success). By combining these dimensions, the Network Invasibility Cube provides a comprehensive picture of invasion risk that goes beyond simple environmental matching.

Outputs can be used to prioritise surveillance efforts, target early-detection programmes, and guide management strategies for invasive alien species across regions and taxonomic groups.

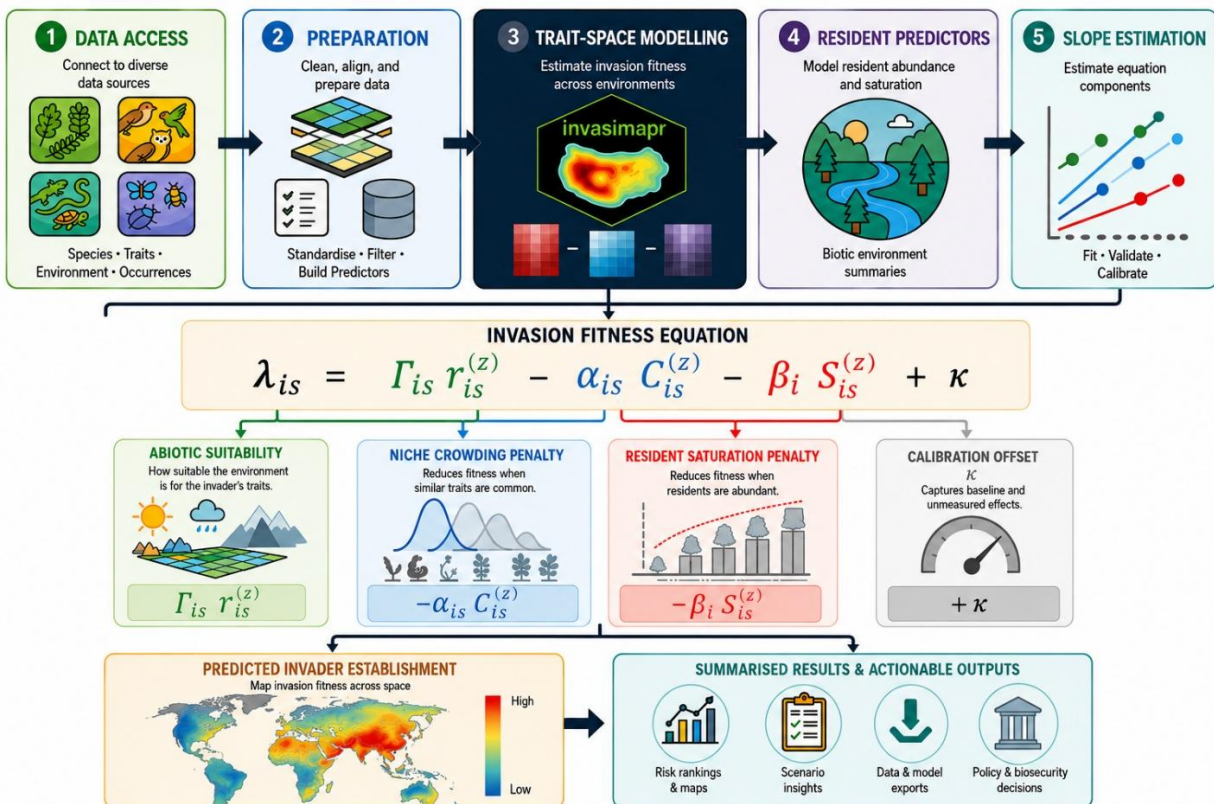


Figure 3: The invasion fitness concept showing how abiotic suitability, niche crowding, and resident competition combine to determine whether an invasive species can establish at a given site.

6. Criteria for Producing Reliable Indicators

The development of modelled cubes within B-Cubed is guided by a set of criteria intended to ensure that the resulting indicators are scientifically sound, operationally useful, and policy-relevant. These criteria include transparency (all methods and code are openly documented), reproducibility (workflows can be re-run with updated data or alternative parameters), and interpretability (outputs are accompanied by uncertainty measures and guidance on appropriate use).

Each modelled cube produces indicators that describe not only a predicted pattern (such as species suitability, community dissimilarity, or invasion risk) but also the confidence with which that pattern can be interpreted. This dual focus on prediction and reliability distinguishes the B-Cubed approach from conventional modelling workflows, where uncertainty is often reported separately or not at all.

By embedding reliability assessment directly within the cube structure, B-Cubed ensures that downstream users, whether researchers, policymakers, or conservation practitioners, can make informed decisions about where and how to apply the model outputs.

7. Implications for Monitoring and Policy

The cube framework provides scalable, reproducible, and decision-relevant outputs that align with emerging biodiversity monitoring frameworks such as the post-2020 Global Biodiversity Framework. Suitability cubes help identify priority areas for conservation and restoration. Dissimilarity cubes support bioregional classification and tracking of community-level change. Invasibility cubes enable early warning and targeted management of invasion risks.

All workflows are modular and adaptable to new taxa, regions, and policy questions. Each cube complies with FAIR data principles, ensuring that outputs can be shared, reproduced, and built upon by the broader scientific and policy community.

8. Resources and Further Reading

Documentation and Guides

- **Suitability Cube Guide:** docs.b-cubed.eu/guides/suitability-cube
- **Dissimilarity Cube Guide:** docs.b-cubed.eu/guides/dissimilarity-cube
- **Invasibility Cube Guide:** docs.b-cubed.eu/guides/invasibility-cube

R Packages

- **dissmapr:** b-cubed-eu.github.io/dissmapr
- **invasimapr:** b-cubed-eu.github.io/invasimapr

Full Citation

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