

BON in a Box: An Open and Collaborative Platform for Biodiversity Monitoring, Indicator Calculation, and Reporting



Jory Griffith^{1,2}, Jean-Michel Lord^{1,3}, Michael D. Catchen^{2,3,5}, María Isabel Arce-Plata⁵, Guillaume Blanchet¹¹, Manuel Fernandez Galvez Bohorquez⁴, Matusan Chandramohan², María Camilla Diaz-Corzo^{4,11}, Dominique Gravel¹¹, César Gutiérrez⁴, Isabelle Helfenstein¹⁵, Sean Hoban¹³, Jamie M. Kass^{1,7}, Linda Laikre¹⁶, Guillaume Larocque^{2,3}, Deborah M. Leigh^{18,19,20,21}, Brian Leung², Alicia Mastretta-Yanes¹⁴, Katie L. Millette^{1,2,3}, Diego Moreno, María Alejandra Molina-Berbeo⁴, Kari E. Norman^{5,8}, María Helena Olaya Rodríguez⁴, Simon Pahls¹⁵, Kaitlyn Perreira², Pedro Peres-Neto¹⁰, Timothée Poisot^{1,3,5}, Laura J. Pollock^{2,3}, Juan Carlos Rey-Velasco⁴, Víctor J. Rincón-Parra¹¹, Claudia Rössli¹⁵, François Rousseu¹¹, Lina María Sánchez-Clavijo⁴, Meredith C. Schuman¹⁵, Oliver Selmoni¹⁵, Jessica M. da Silva¹⁷, Erika Suarez-Valencia⁴, Thilina Surasinghe^{1,9}, Eren Turak^{1,6}, Luis Fernando Urbina Gonzalez⁴, Sarah Valentin¹², Noah Wightman², Juan Zuloaga¹, Maria-Cecilia Londoño^{1,4}, Andrew Gonzalez^{1,2,3}

Corresponding Author: jory.griffith@mcgill.ca

¹ Group on Earth Observations Biodiversity Observation Network (GEO BON), ² McGill University, Québec, Canada, ³ Quebec Center for Biodiversity Science, Québec, Canada, ⁴ Instituto de Investigación de Recursos Biológicos Alexander von Humboldt, Bogotá, Colombia, ⁵ Université de Montréal, Québec, Canada, ⁶ Department of Planning and Environment, New South Wales, Australia, ⁷ Tohoku University, Miyagi, Japan, ⁸ USDA Forest Service, Rocky Mountain Research Station, NM, USA, ⁹ Bridgewater State University, ¹⁰ Concordia University, Québec, Canada, ¹¹ Université de Sherbrooke, Québec, Canada, ¹² Centre de coopération internationale en recherche agronomique pour le développement, France, ¹³ Morton Arboretum, IL, USA, ¹⁴ Comisión Nacional para el Conocimiento y Uso de la Biodiversidad, ¹⁵ Universität Zürich, Switzerland, ¹⁶ Stockholms universitet, Sweden, ¹⁷ South African National Biodiversity Institute, ¹⁸ WSL Zurich, Switzerland, ¹⁹ LOEWE Centre for Translational Biodiversity Genomics (TBG), ²⁰ Senckenberg Research Institute, Weimar, Germany, ²¹ Institute of Ecology, Evolution, and Diversity, Faculty of Biosciences, Goethe University, Frankfurt, Germany

Abstract

The Convention on Biological Diversity's Kunming-Montreal Global Biodiversity Framework (GBF) sets ambitious goals to protect and restore biodiversity. It includes a Monitoring Framework that mandates countries to track progress toward these goals using indicators that summarize biodiversity trends. Calculating indicators is challenging for countries due to technical barriers, lack of available data and tools, and capacity bottlenecks. BON in a Box, an open tool for biodiversity modeling and indicator calculation developed by the Group on Earth Observations Biodiversity Observation Network, is designed to address these challenges. It connects individual analyses into pipelines that convert data into essential biodiversity variables and indicators and can be run locally or on the cloud. These pipelines are community-built, customizable, and can analyze public or user datasets. BON in a Box provides a comprehensive and accessible tool for scientists and policymakers around the world to track progress toward the GBF and make biodiversity management decisions.

1. The GBF and the need created by the Monitoring Framework

Biodiversity loss represents a profound threat to ecosystems and human well-being, demanding urgent global actions to implement effective conservation strategies and comprehensive biodiversity monitoring (Gonzalez et al. 2023a). The Kunming-Montreal Global Biodiversity Framework (GBF) of the United Nations Convention on Biological Diversity (CBD) articulates the commitment of Parties to protect and restore biodiversity while maintaining nature's essential contributions to people (CBD 2022). The ambitions of the agreement are captured by 23 action targets to be achieved by 2030 and four outcome-focused goals for 2050 (CBD 2022). To meet these objectives, countries are aligning their governmental plans and programs with the GBF through their national biodiversity strategies and action plans (NBSAPs) to ensure that necessary measures are integrated into national policy and practice (Perino et al. 2021, Sandström et al. 2023).

The GBF is accompanied by a Monitoring Framework that provides a set of indicators to evaluate progress towards its goals and targets (CBD 2022). Indicators are quantitative metrics that summarize the status and trends of different aspects of biodiversity, from genetic diversity to ecosystem health (Noss 1990). Indicators in the Monitoring Framework are associated with different targets, and Parties are required to calculate and report them to the CBD. For example, the Red List Index (RLI) measures changes in species extinction risk over time and is aligned with Goal A and Target 4 of the GBF, which focus on halting human-induced extinctions (CBD 2022, Raimondo et al. 2023). Similarly, the Protected Connected Index (ProtConn) evaluates progress toward Target 3, which aims to establish well-connected protected area networks that cover 30% of terrestrial and marine areas by 2030 (Saura et al. 2017, 2018; CBD 2022). Indicators such as the RLI and ProtConn also inform policy by identifying areas where

Glossary

Term	Definition
Biodiversity Monitoring	Biodiversity monitoring is the collection of primary biodiversity, ecosystem, and environmental data over space and time, synthesis of these data into essential variables, attribution to drivers of change, and calculation indicators of biodiversity status and reporting of these indicator trends to inform conservation and restoration objectives.
Biodiversity Observation Network (BON)	A network of observation sites or stations and/or a network of experts and groups who collect and analyze biodiversity data for different needs. A BON coordinates monitoring efforts to support conservation policy and/or management action from national biodiversity strategies and action plans. A BON can be regional (e.g., Europe, Asia-Pacific), national (e.g., Japan), or thematic (e.g., Marine, Freshwater).
Global Biodiversity Framework (GBF)	The latest agreement of the United Nations Convention on Biological Diversity (CBD) adopted by 196 Parties at its 15th Conference of the Parties in December 2022. The GBF sets an ambitious pathway to reach a global vision of living in harmony with nature and halting biodiversity loss by 2050 and supports the achievement of the Sustainable Development Goals (CBD 2022).
GBF Goals	The GBF specifies 4 long-term goals to achieve before 2050. These aim to A) protect and restore nature by ensuring the integrity of ecosystems and halting species extinctions, B) prosper with nature by managing nature's contributions to people and supporting sustainable development, C) share benefits equally by increasing the monetary and non-monetary benefit sharing of genetic resources and upholding indigenous rights, and D) invest and collaborate by ensuring adequate means of implementation of the GBF, including financial resources, capacity building, and technical and scientific cooperation (CBD 2022).
GBF Target	The GBF specifies 23 urgent action-oriented targets for Parties to the CBD to meet before 2030 to help achieve the four long-term goals of the framework. These targets aim to reduce threats to biodiversity, meet people's needs through the sustainable use of biodiversity and benefit-sharing, and develop tools and solutions for implementing the framework (CBD 2022).
GBF Monitoring Framework	The Monitoring framework is designed to track progress toward the goals and targets of the GBF through a set of indicators. It emphasizes the need for consistent data collection, reporting, and evaluation at national and global levels to ensure accountability and transparency. It calls upon the development of national and regional monitoring systems, including the technologies, tools, networks and communities needed to sustain monitoring.

Glossary

Term	Definition
Parties	Member states including 196 countries and the EU that have ratified the CBD treaty. Parties negotiate to adopt and/or revise CBD strategies and frameworks during the biennial Conference of the Parties.
Essential Biodiversity Variables (EBV)	“A biological variable that critically contributes to the characterization of Earth’s biodiversity; they are a minimum set of common, and complementary set of observable variables across the dimensions of biodiversity that can be used to create indicators of system-level biodiversity trends” (after Brummitt et al. (2017)). EBVs provide scalable, comparable metrics that can be aggregated into time-series or spatial maps, enabling the detection of patterns and drivers of biodiversity change.
Indicator	A derived metric informed by biodiversity datasets (e.g., EBVs) that summarizes biodiversity information into a single value that can help track changes in biodiversity status or the pressures affecting it, thereby providing measurable data that informs policy decisions and conservation actions. In the context of the GBF, an indicator is used to assess progress toward the framework’s goals and targets.
Script	A sequence of code written in a programming language that accomplishes a single task, such as data cleaning, analysis, visualization, or modeling.
Pipeline	A sequence of steps connected to automate an entire analysis workflow, from the input parameters to the analysis result.
Modular Software	A software design philosophy where every script does <i>one</i> thing well, and one thing only (part of the UNIX philosophy). It results in smaller scripts that are easier to combine, maintain, and re-use.

conservation efforts, such as the establishment of protected areas, can maximize contributions to specific biodiversity goals (e.g., protecting threatened species or maximizing connectivity; [Nicholson et al. \(2012\)](#)). Together, these indicators are intended to provide a streamlined yet comprehensive framework for understanding the current state of biodiversity, tracking changes over time, and guiding conservation actions to meet the targets of the GBF. However, the practical implementation of the Monitoring Framework poses significant challenges. With the first national reports due in less than two years ([CBD 2022](#)), many Parties require significant scientific and technical support to meet these reporting and planning requirements. The Group on Earth Observations Biodiversity

Observation Network (GEO BON) has been invited by the Conference of the Parties to the CBD to support the implementation of the GBF’s Monitoring Framework. GEO BON is an international network of over 3400 researchers in 149 countries dedicated to improving the collection, coordination, and dissemination of biodiversity information at the global, regional, and national scales. The GEO BON network includes a number of Biodiversity Observation Networks (BONs), or networks of researchers monitoring biodiversity across systems and scales. BONs can be national (e.g., France BON, Japan BON), regional (e.g., Europa BON, Asia-Pacific BON), or thematic (e.g., Marine BON, Freshwater BON). The initiative to support the Monitoring Framework builds on more than a decade of effort by GEO BON to support monitoring biodiversity for action, improving access to biodiversity information globally, and bridging the gap between biodiversity science, monitoring, and policy to provide more effective responses to the biodiversity crisis ([Navarro et al. 2017](#)). One notable GEO BON initiative is the development of the Essential Biodiversity Variables (EBV) framework, which standardizes measurements to capture the various dimensions of biodiversity ([Pereira et al. 2013](#), [Brummitt et al. 2017](#)). The EBV framework identifies a standardized set of variables essential for assessing the status and trends of populations, communities, and ecosystems ([Pereira et al. 2013](#)). There are six classes of EBVs designed to capture different aspects of biodiversity from genes to ecosystems, each with the flexibility to be calculated with multiple measurement approaches across multiple scales (e.g., regional, national), realms (e.g., Essential Ocean Variables; EOVs), and taxa ([Turak et al. 2017a](#), [Schmeller et al. 2017](#), [Kissling et al. 2018](#), [Muller-Karger et al. 2018](#), [Jetz et al. 2019](#), [Hoban et al. 2022](#)). Ideally, EBVs would be directly measured with comprehensive sampling, but in practice they are usually modelled or estimated from available data; therefore, EBVs serve as a conceptual intermediate between direct observations and biodiversity indicators ([Pereira et al. 2013](#)). Importantly, unlike indicators, EBVs are robust to changes in policy and legislation

because they represent the state of biodiversity without reference to any targets (Turak et al. 2017b). Because they are systematically collected over time and space, EBVs provide the standardized information needed to derive indicators of biodiversity change (Fig. 1). The calculation of EBVs and indicators presents significant challenges for Parties reporting to the GBF (Affinito et al. 2024). Even with access to appropriate data and methods, assembling workflows to compute indicators and EBVs is complex. The methodologies for indicator calculation are often embedded within scientific publications, and associated computer code is not always openly available, requiring significant effort and expertise to interpret and implement (Orr et al. 2022, Affinito et al. 2024). For many Parties, limited resources and technical capacity hinder their ability to apply these methods and meet the commitments outlined in the Monitoring Framework and the GBF (Affinito et al. 2024). This is especially true for BONs and other organizations that represent broad geographic regions with many linguistic and sociopolitical differences (e.g., Asia-Pacific BON; Takeuchi et al. (2021)). Parties with the capacity to calculate indicators often invest substantial time, effort, and resources into independently developing workflows instead of sharing them across borders. Additionally, tools for indicator calculation are often difficult to find or access and rely on opaque, black-box methodologies that lack customization options and fail to incorporate user-specific data. This closed method of calculation complicates auditing processes and makes cross-Party comparisons challenging, which may undermine trust in the reported conclusions. Ensuring greater transparency, accessibility, and standardization in these workflows is therefore essential to enhance efficiency and foster confidence in biodiversity monitoring efforts. There is a pressing need for an open analysis toolkit to streamline and simplify the calculation of EBVs and indicators for a wide range of users, including Parties to the CBD, the scientific community, and natural resource managers who collaborate with stakeholders such as local communities, industries, NGOs, policymakers,

and intergovernmental organizations (Navarro et al. 2017, Orr et al. 2022). To effectively meet the needs of this diverse group of users, such a platform must be scientifically rigorous, user-friendly, interoperable, fully transparent, and customizable. It should enable seamless integration of data from publicly available datasets while also allowing for the incorporation of user-provided data, recognizing that many countries have national-level data not included in global repositories. Additionally, the toolkit must support calculations across multiple spatial and temporal scales, as the success of the Monitoring Framework for the GBF relies on coordinated efforts by subnational and national actors, each measuring biodiversity change at their operational scales. Here, we introduce the BON in a Box modeling tool, an initiative of GEO BON designed to facilitate the calculation of EBVs and indicators. We emphasize the importance of providing countries, organizations, and biodiversity monitoring practitioners with a comprehensive set of tools to overcome multiple technical barriers. Addressing these challenges would enable more accurate assessments of biodiversity, help prioritize areas for sampling and conservation, and support tracking progress toward the targets outlined in the GBF. We demonstrate how BON in a Box addresses these needs by hosting community-contributed analysis pipelines developed by experts to organize and streamline the process of generating policy-relevant biodiversity information, making it more accessible and actionable. We outline the current capabilities of BON in a Box, share our vision for its continuing development, and invite collaborators to contribute their expertise to enhance and expand this initiative. Ultimately, we hope BON in a Box will support biodiversity policy at all levels, from guiding monitoring efforts and tracking progress to informing meaningful conservation and management actions worldwide.

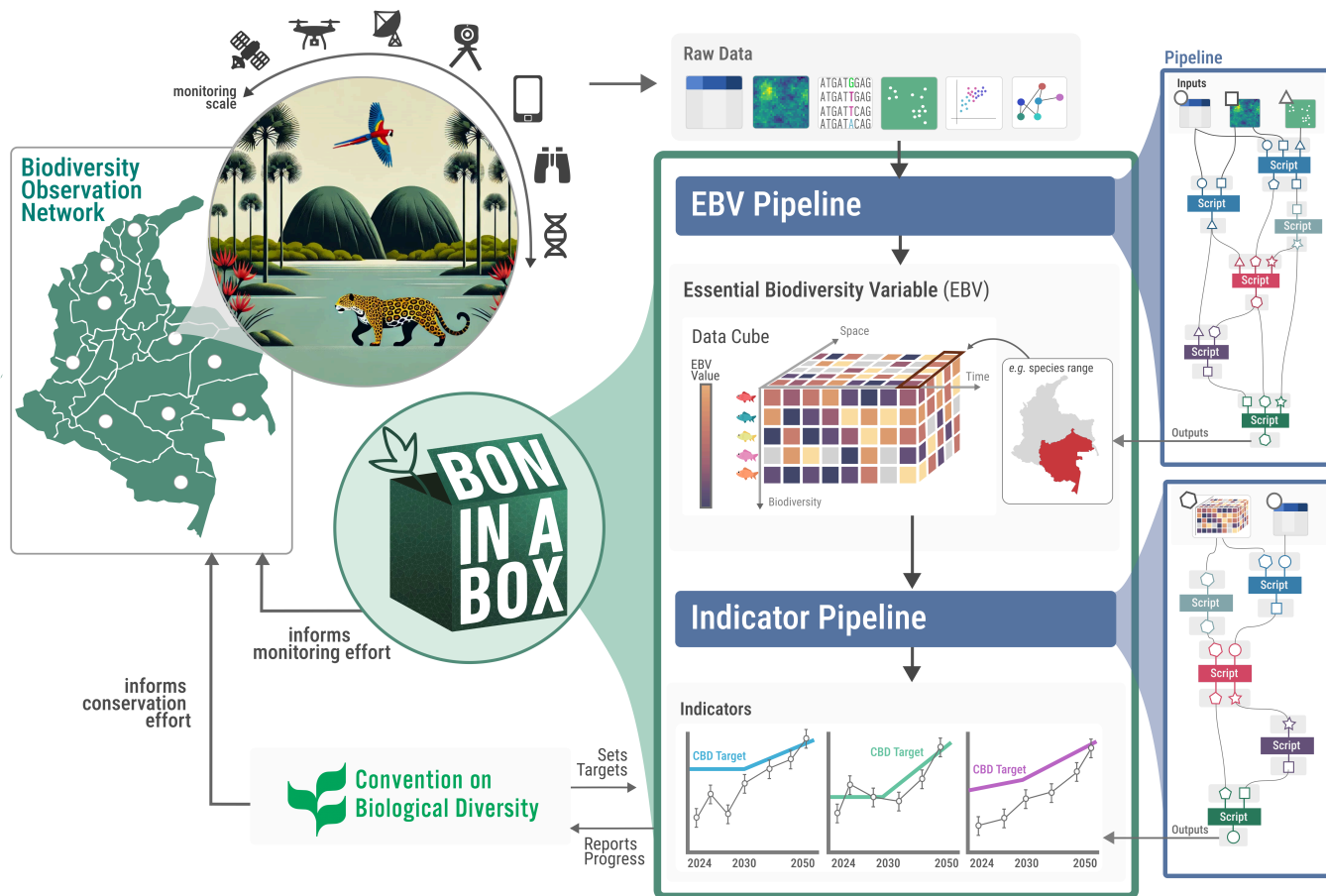


Figure 1: BON in a Box can help with both informing monitoring efforts through sampling prioritization and assessing biodiversity change by calculating both EBVs and indicators. This information is used to report to multilateral agreements such as the Convention on Biological Diversity and also used to inform conservation efforts and assess the progress from these efforts. BON in a Box becomes a tool for many levels of conservation policy by increasing the quality and accessibility of biodiversity information.

2. The BON in a Box Platform

2.1. Overview

The BON in a Box modeling tool is part of a larger platform to share knowledge, tools, and computational resources and support the establishment and operation of Biodiversity Observation Networks (BONs). BON in a Box began as a platform where users could access tools relevant for BON implementation and management (Langer and Londono Murcia 2021). Later, it expanded to include a catalog of biodiversity monitoring projects, enabling users to search for projects, connect with project leaders, and expand their network (<https://boninabox.geobon.org/projects>). The tool described here is the most recent addition to BON in a Box and was developed collaboratively by the GEO

BON Secretariat and the Quebec Centre for Biodiversity Science in Montreal, Canada, and the Alexander von Humboldt Institute in Bogotá, Colombia. This new feature enhances the platform’s capacity to support biodiversity monitoring and reporting efforts globally. The modelling tool (hereafter referred to as BON in a Box) hosts a variety of community-contributed analysis pipelines for calculating EBVs and indicators. BON in a Box is unique in its combination of technical values that reinforce GEO BON values of excellence, collaboration, and shared purpose, as well as transparency, openness, and inclusivity, throughout its network (Table 1). By allowing users to share these analyses, BON in a Box fosters coordination and standardization among Biodiversity Observation Networks (BONs), countries, and organizations, promoting collaborative

and efficient biodiversity monitoring efforts (Figure 1). The pipelines in BON in a Box are workflows that have been adapted by the contributor to function as pipelines within the tool. A workflow is a sequence of steps required to run an analysis from start to finish. These steps may be consolidated into a single script or separated into multiple scripts, but typically need to be executed sequentially, often requiring manual intervention. In BON in a Box, workflows are adapted to become automated analysis pipelines that run an entire analysis with the push of a button, producing results that can be downloaded and viewed in an interactive dashboard. Each step of the workflow is divided into modular, stand-alone scripts, each designed to perform a specific task and generate an output (Figure 2). The scripts are connected through inputs and outputs within the BON in a Box pipeline editor. The input of a script can either be an output of a previous script in a compatible format (e.g., GeoTiff, CSV, GeoJSON) or can be provided directly by the user through a form automatically generated for each pipeline. Because each step is modular, scripts written in different programming languages (e.g., R, Python, Julia) can be connected in a single pipeline and commonly used scripts can be reused in other pipelines. Users can view and download the intermediate results and code for each script, ensuring full transparency throughout the process. Additionally, every script and pipeline are thoroughly documented with accompanying annotations, providing clear explanations of the scientific context, purpose, inputs, outputs, and relevant citations. This enables others to easily understand, adopt, and adapt the pipelines to suit their specific needs and contexts.

BON in a Box pipelines are designed to be generalizable to different taxa, countries, and regions. Each pipeline generates a form with parameters that can be input by the user. Instead of having to manually edit code to adapt it to another context (e.g., species, region, spatial scale, coordinate reference system), users can edit the input form and run the pipeline again with new parameters. The results of all previous

Pipeline

an interconnected set of scripts
for entire EBV and Indicator workflows

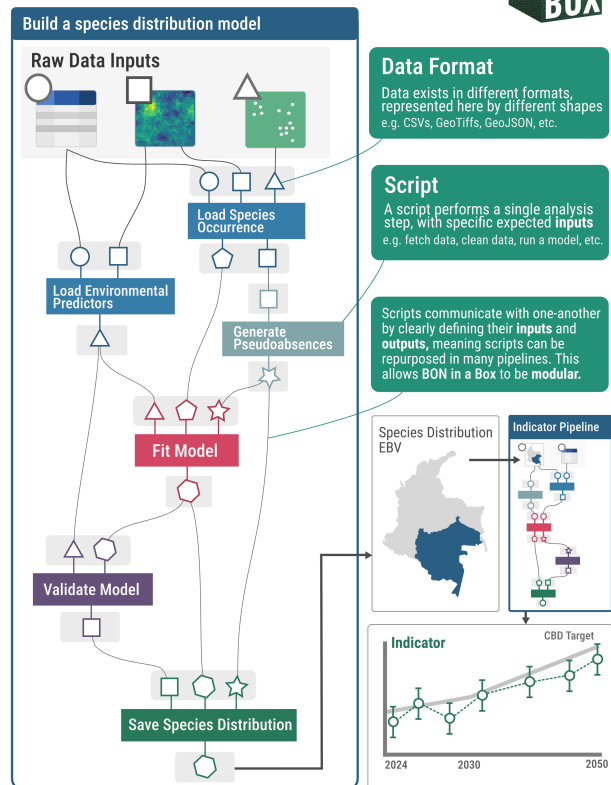


Figure 2: A BON in a Box pipeline is an interconnected set of **scripts** that automate the process of turning raw data into **EBVs** and **indicators**. **Scripts** are completely and connected via inputs and outputs, which can also be downloaded and viewed as intermediate results. These **pipelines** are fully customizable and can be tailored to user needs.

pipeline runs are saved and can be accessed at any time. Additionally, BON in a Box pipelines can be run with publicly available data, user-provided data, or a combination of both. Countries or organizations often have their own datasets rooted in local knowledge and relevant to specific local contexts, which can lead to distrust when they are presented with pre-calculated indicators based on global data. To address this, BON in a Box allows users to run pipelines using their own data without needing to share it publicly. To deal with sensitive data such as the locations of threatened species, the tool can be deployed locally on any server or computer and data does not need to leave the organization. When such data are not available,

pipelines can pull directly from a variety of publicly available datasets such as GBIF (GBIF 2024), GEO BON's EBV portal (Langer et al. 2022), and IUCN (IUCN 2023). In comparison to other tools, BON in a Box is unique in its ability to run a wide array of community-contributed and customizable biodiversity analyses that can be viewed in a user-friendly dashboard (see Table 2 for comparison to other platforms). In sum, BON in a Box is a tool for organizing and sharing analyses for generating useful biodiversity information in an open and organized way, reducing duplication of effort between scientists, increasing capacity in areas with less resources, and helping to connect to existing global observing systems (e.g., Global Ocean Observing System).

2.2. The vision

Our vision is for BON in a Box to become a comprehensive platform that optimizes biodiversity monitoring efforts, provides standardized and curated tools for calculating biodiversity variables and indicators, and lowers barriers to sharing biodiversity knowledge. To achieve this vision, we aim to 1) expand the range of EBVs and indicators available within BON in a Box by increasing the number and geographic representation of users and collaborators; 2) improve accessibility by making the tool more user-friendly and usable on a large scale; 3) develop pipelines to guide sampling prioritization and monitoring efforts effectively; and 4) establish pipeline standards, a crediting system, and a peer-review model to attract contributors and ensure the scientific rigor and quality of all contributed pipelines.

2.2.1. Open pipelines for the community

We aim to expand the range of pipelines available in BON in a Box to include all GEO BON EBVs and indicators in the Monitoring Framework that require modeling. We will achieve this by leveraging the expertise of the GEO BON community and beyond to develop and contribute these pipelines to BON in a Box. Additionally, we aim to further expand BON in a Box as a tool for collaboration beyond the context of the GBF. We hope to

host a number of additional pipelines that are relevant to the needs of different Biodiversity Observation Networks (BONs), governments, NGOs, and other organizations. BON in a Box has huge potential as a tool for any collaborative project or network to access, share, and standardize analysis workflows to calculate EBVs and indicators that are relevant to a variety of contexts. For example, a national, regional, or thematic BON could host their own instance of BON in a Box to develop and test pipelines that are useful to them. Then, when a pipeline has been validated for use in a broader context outside of the network, they can share it publicly in the main BON in a Box tool. By facilitating collaboration within and between BONs, BON in a Box should become a necessary tool to help form the Global Biodiversity Observation System (GBIOS; Gonzalez et al. (2023a)).

2.2.2. Accessibility

Another goal of BON in a Box is to increase accessibility and usability of the platform. BON in a Box is currently a downloadable software, but we plan to make it a globally accessible web platform. Additionally, we will make platform improvements to enable wider use and greater computing capabilities by integrating the platform with remote, scalable high-performance computing resources. This approach ensures that even users without sufficient cyberinfrastructure can run analysis pipelines and easily compute and download results for their country or region of interest. To further improve accessibility, we plan to make BON in a Box available in multiple languages, broadening its usability across the globe. A key goal of BON in a Box is to improve biodiversity monitoring from the ground up by developing a suite of pipelines to guide sampling prioritization and address gaps in biodiversity data. The many shortfalls in existing biodiversity data (Hortal et al. 2015) present fundamental challenges to generating reliable biodiversity indicators (Orr et al. 2022). Additionally, countries and organizations often have limited resources to establish and sustain biodiversity monitoring programs. Therefore, a critical component

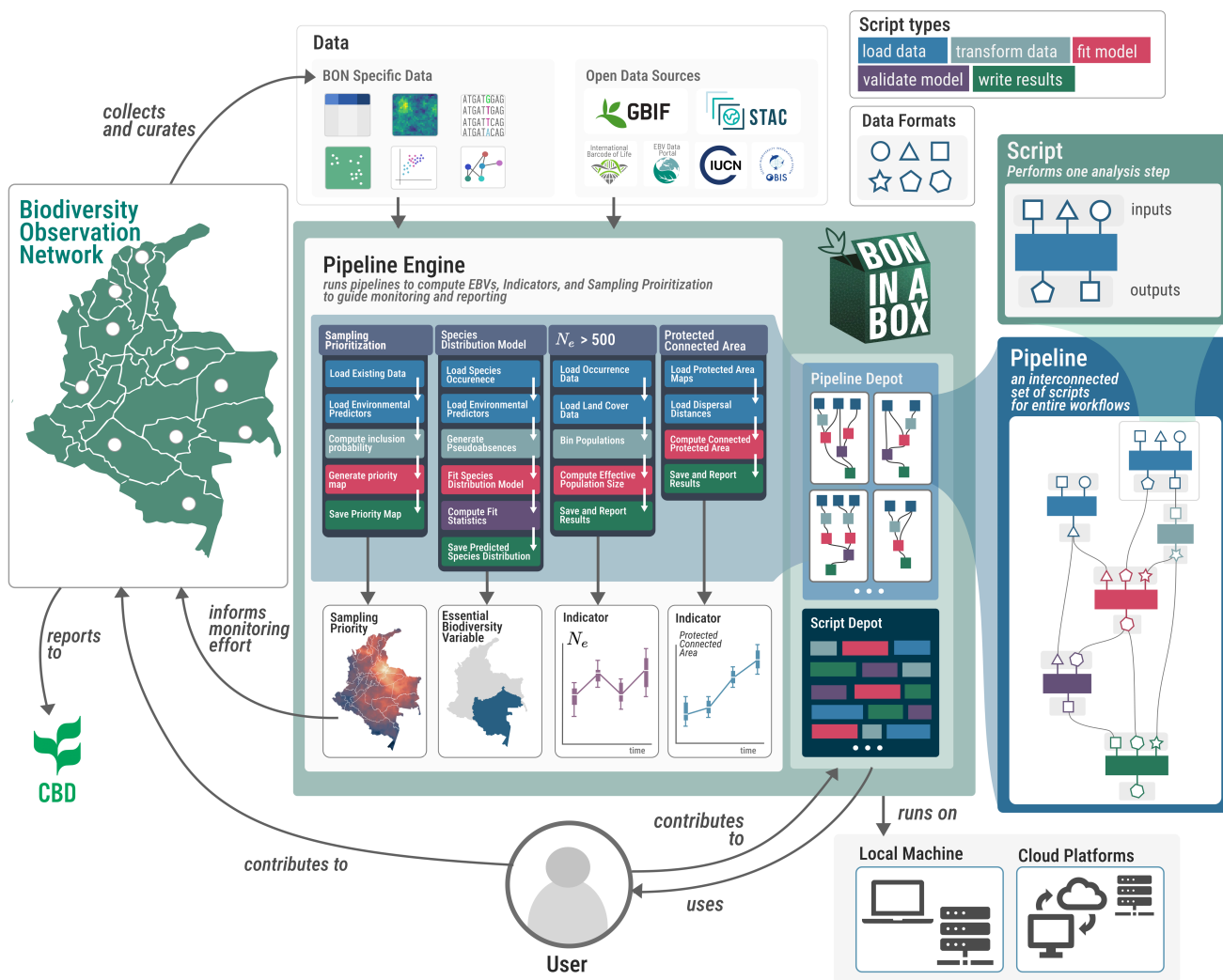


Figure 3: BON in a Box is a tool that aims to increase the quality of and access to biodiversity information by informing monitoring efforts (sampling prioritization) and calculating EBVs (e.g. SDMs) and indicators (e.g. $N_e > 500$) in an open, standardized, and user-friendly way. BON in a Box contains pipelines, or a set of individual steps (scripts) that perform an analysis from start to finish in an automated way by connecting the input of one script to the output of the next. pipelines can be run with publically available data, user-provided (BON specific) data, or both. All pipelines are contributed by members of the scientific community. Each script in a pipeline is added to the script depot and can be reused in future pipelines, and therefore each contribution to the pipeline engine strengthens the whole tool. BON in a Box can be run on a local computer or on a remote server (cloud platform).

of successfully implementing the Monitoring Framework is the development of optimally designed biodiversity monitoring programs that efficiently and robustly detect biodiversity change and attribute them to causal drivers (Gonzalez et al. 2023b). An essential aspect of the BON in a Box vision is a comprehensive toolkit to identify data gaps, guide spatial sampling prioritization, and support the design of local monitoring projects to inform decision-making and conservation efforts. By optimizing the

effectiveness and coverage of BONs, the toolkit will contribute to generating more robust data, providing decision-makers with stronger evidence to guide conservation actions.

2.2.3. Peer Review

To ensure consistency and quality and incentivize contributors, we will develop a peer review and publishing process for contributed pipelines. Attracting contributors may remain a challenge as long as pipeline development is unrecognized by traditional academic crediting

systems, a persistent issue in the field of software development for ecology (Merow et al. 2023). To address this, pipelines will be published in Diamond Open Access (publish for free) journals, where contributions form micro-publications with DOIs. This removes the higher burden of submitting a traditional software note, maintains the unity of the BON in a Box ecosystem by centralizing the addition of tools, incentivizes researchers to contribute pipelines, and encourages users to cite the specific pipelines and steps used in their reporting. Additionally, a peer-review process will ensure the quality of BON in a Box pipelines. Adoption and collaboration with BON in a Box by policymakers relies on the guarantee that the pipeline delivers best-in-class outputs tailored to their needs, both because they rely on sound research, and because the standards of software engineering are high. In line with this model, we propose a peer-review process where experts from the GEO BON network provide feedback on contributed analysis scripts and pipelines. Reviewers will be provided with a standard checklist to evaluate criteria such as the functionality of the pipeline, the scientific rigor of the methods, clarity of the documentation, generalizability, and whether there are clear guidelines for interpretation. Reviewers will have the opportunity to learn about analyses and tools that are being developed in their field and create new networks with other researchers. Because the pipelines are built around the idea of re-usable steps, any peer review on a single pipeline is likely to improve the quality and trustworthiness of the entire ecosystem. In sum, our vision is to create a living tool that is frequently developed and strengthened by the users and the diverse network of GEO BON scientists and collaborators (Figure 3). The tool will support biodiversity policy at every level, improving biodiversity information by guiding monitoring efforts, assessing biodiversity change, and informing action.

3. Examples of BON in a Box pipelines

3.1. Species Distribution Models

Knowing where species are is essential for understanding the distribution of biodiversity and informing conservation efforts. However, less than 10% of the world is well-sampled, and even the longest running and consistently monitored biodiversity observation networks have substantial data gaps in space, taxonomy, and time (Hughes et al. 2021). Therefore, it is necessary to use species distribution models (SDMs) to provide more comprehensive estimates of species distributions. SDMs use a range of methods from regression to machine-learning to make spatially explicit predictions on where species are likely to occur based on associations between environmental variables and known species occurrences (Guisan et al. 2017). The outputs of these models inform the 'Species Distributions' EBV that can be used as a key base layer for many applications. These include making maps and predictions for impacts of environmental stressors, habitat suitability for at-risk species, biodiversity hotspots, high-priority locations for protected areas, sampling gaps and prioritization for future sampling, and indicators such as the Biodiversity Habitat Index (BHI), Species Habitat Index (SHI), and Species Protection Index (SPI). A wide diversity of open programming tools exist for SDMs, and while using them together improves analytical standards (Kass et al. 2024), they require some technical expertise. BON in a Box contains automated pipelines that build state-of-the-art SDMs with these open tools, validate and report their performance, and provide visualizations to facilitate interpretation of their outputs, which can then be directly plugged into pipelines as base layers to calculate indicators. This allows users to calculate indicators based on existing SDM outputs or SDM pipelines without completely redoing analyses and without having to download SDMs or large raster files on their computer.

3.2. Proportion of populations with an effective size $N_e > 500$

BON in a Box has partnered with the “Genes from Space” team hosted by the International Space Science Institute (<https://teams.issibern.ch/genesfromspace/>) to integrate a pipeline to calculate the headline genetic indicator (A.4) of the GBF: the proportion of populations within species with an effective population size $N_e > 500$ (CBD 2022), otherwise known as the $N_e > 500$ indicator (Mastretta-Yanes et al. 2024). N_e , which is listed as the ‘Effective Population Size’ EBV, is a standard metric in population genetics that relates to genetic changes from generation to generation, including the loss of genetic diversity (Hoban et al. 2022). N_e is related to census size (N_c), but typically much lower because of fluctuating population size, unequal sex ratio, unequal contribution of offspring by parents, and nonrandom mating (Frankham 1995). Populations with N_e greater than 500 are considered to have sufficient genetic variation to maintain genetic diversity and population viability (Franklin 1980). For a given species, the $N_e > 500$ indicator is calculated as the proportion of populations in a given region with N_e exceeding 500. N_e can be directly measured through genetic sequencing or indirectly estimated from N_c assuming a conservative $N_e : N_c$ ratio of 0.1 (Hoban et al. 2022). Census data has been found to be readily available for many species, enabling the calculation of this indicator when genetic data is lacking (see Mastretta-Yanes et al. (2024)). To scale capacity to report on this headline indicator for species for which genetic data is not available, the “Genes from Space” team created a pilot method to estimate N_e using publicly available Earth observation data. The pipeline uses satellite-derived land cover data to estimate the size of suitable habitat for locations where the species of interest was observed (e.g., based on GBIF occurrences). Given a population density estimate, the habitat size for different populations is then converted into N_c and then N_e using an assumed or previously observed ratio between N_e and N_c . The pipeline also

reports a separate genetic diversity indicator, “Populations maintained” (PM). In the future, the pipeline will be updated to allow users to include genetic, trait, and other more specific information into the definition of populations and assessment of habitat or population condition to increase the accuracy of N_e and PM estimates. Because DNA sequence information and long-term census monitoring data is rare, this pipeline allows users to estimate a proxy for $N_e > 500$ even when DNA and N_c data are not available. Connecting these estimates to frequently updated Earth observation data allows assessment of short-term changes in the estimates (several times per year), allowing managers to detect changes in the indicator at an early stage.

3.3. Protected Connected Index

Designing well-connected protected areas is critical to slow biodiversity loss and reach Target 3 of the CBD, which aims to protect 30% of well-connected land by 2030 (Saura et al. 2018, CBD 2022). Connectivity reflects the capacity of the landscape to facilitate the movement of species, which drives processes such as dispersal and gene flow, maintaining the stability and integrity of different ecosystems over time. ProtConn, a component indicator in the Monitoring Framework, measures the percentage of a given country or region that is both protected and connected (Saura et al. 2017). ProtConn is calculated by estimating the probability that species can move between protected areas based on their distance from one another. BON in a Box includes a pipeline to calculate ProtConn using the World Database of Protected areas or user input protected area polygons (IUCN 2023). The user inputs a dispersal distance based on dispersal estimates for a species or taxonomic group of interest (Saura et al. 2019). This indicator is useful to not only evaluate the connectedness of current protected areas, but also to assure that future protected areas are strategically placed to maximize connectivity for a wide variety of species.

3.4. Sampling Prioritization

The vast majority of Earth’s surface and oceans currently lack robust data about the biodiversity they possess. There are many gaps in biodiversity data, and these gaps are multifaceted—aside from spatial biases, there are large discrepancies in coverage across different taxonomic groups, functional traits, and interactions between species (Hortal et al. 2015). Biodiversity monitoring that reliably informs decision making is only possible if we have sufficient data to detect and attribute changes in biodiversity and ecosystem function (Gonzalez et al. 2023b). This poses a challenge for monitoring many aspects of biodiversity, because there are some components for which we simply cannot collect data everywhere, all the time. There are many practical limitations on the scope of biodiversity monitoring programs, but a major one is funding. For decision makers to develop scientifically supported policies to reach the GBF targets, it is necessary to choose where to collect new data to get as much useful information as possible from a monitoring program. Furthermore, there are many GBF targets, and allocating monitoring effort toward different targets may force trade-offs. In this context, determining where monitoring effort is likely to result in actionable information is essential (Canessa et al. 2015, Raymond et al. 2020). A central component of BON in a Box is providing users with methods for prioritizing where to collect data to fill in gaps in our monitoring effort. This includes methods for balancing data collection across a set of environmental variables, taxa, or monitoring targets, or for extending existing BON sites to improve coverage. These methods can also adaptively improve where we choose to sample based on the data a BON collects. For example, pipelines for computing SDMs also produce maps of model uncertainty, which can be combined with other data (like sampling accessibility, climatic and ecosystem rarity, or other factors) to produce sampling prioritization maps to improve the monitoring of species distributions. Furthermore, BON in a Box offers a set of diagnostic tools to evaluate the efficacy of planned samples and enables “what-

if” scenarios for stakeholders to consider the alternative BON designs. Using existing data to guide future monitoring efforts ensures we fill biodiversity data gaps to most effectively and efficiently inform conservation policy.

4. Service Model

Critical to the success and reach of BON in a Box is a service model that will make it accessible to users and adapt the access type to their technical capacities and expected development needs. GEO BON maintains BON in a Box as a service to its member organizations. GEO BON is an open network with 3500 members from 1900 organizations distributed across 149 countries spanning many of the Parties to the UN CBD. This represents a large and heterogeneous network reflecting a diversity of needs and levels of expertise, which the service model must cater to. To reflect this diversity, we propose a model that allows a range of users access to BON in a Box services through collaboration with the GEO BON team. One of the major goals of BON in a Box is to build capacity for Parties that have fewer resources to calculate indicators for reporting. Our service model reflects this mission by including training to transfer knowledge to local stakeholders about how to use the platform in their biodiversity monitoring programs. The three distinct options can be co-developed with the user to suit their current technical demands but maintain an eye on likely future needs (Figure 4):

- Option 1: A member downloads BON in a Box from the GEO BON GitHub repository and runs analyses on their local computer or server. Initial set-up or continued support is offered by the GEO BON team. This option requires that a user is comfortable with the technical demands of hosting and running the platform themselves.
- Option 2: A member runs an analysis remotely on an instance hosted on the GEO BON server. Various levels of support by GEO BON experts regarding data and pipeline selection would be offered to accompany the organization.

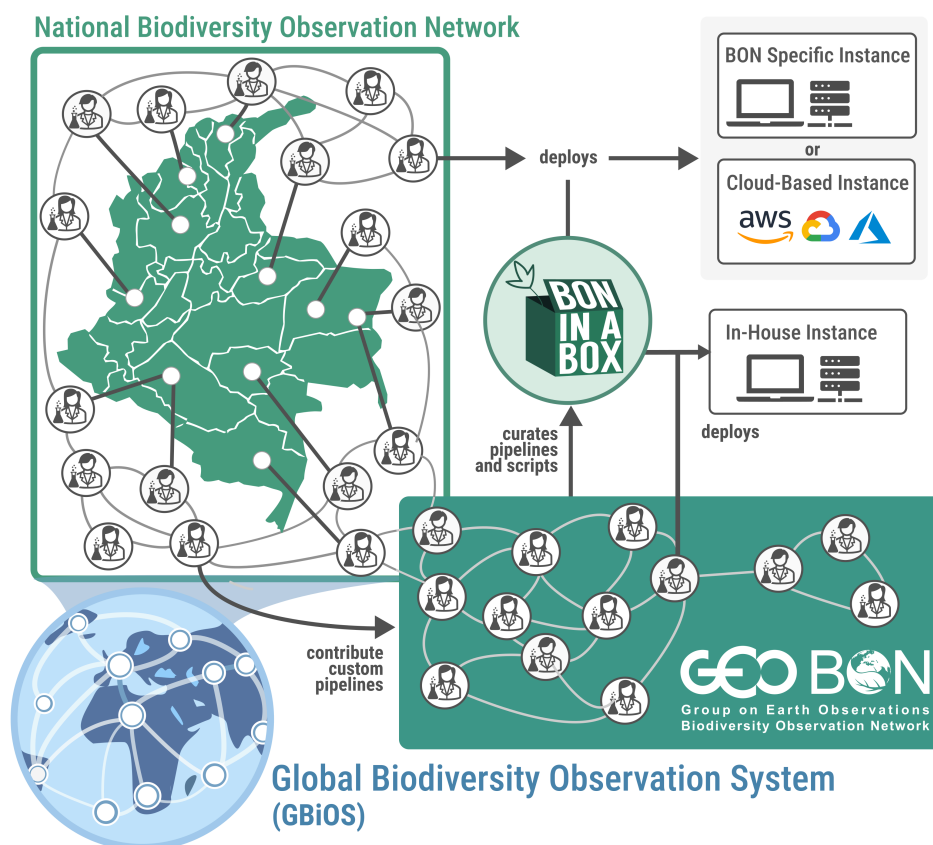


Figure 4: Service model and community support from the GEO BON network to countries and other organizations wishing to implement BON in a Box. Users from national or regional BONs can choose from three potential options – running a local instance, running an instance on a cloud-computing platform, or consulting with GEO BON to run an in-house analysis – depending on the technical demands of the project and the amount of support required. This aims to cater to a range of user needs and capacities.

- Option 3: The GEO BON team runs the analysis (end to end) for a member organization on the GEO BON server. The analysis is run by the BON in a Box team after a period of analysis co-design, data exploration, and indicator selection with the user. Once pipelines are developed and customized to the needs of the member organization, the GEO BON team provides training to integrate the tool into their monitoring program.

We expect many countries to implement BON in a Box in support of their national monitoring frameworks under the GBF. Funding would be sought to fund the appropriate service model to cover the time and computational needs of the team composed of country and GEO BON experts. The funding would also support the development of bespoke data-to-indicator pipelines within the country's instance of BON in a Box so that the progress stated

in their NBSAP can be reported reliably, repeatedly, and transparently. Other potential clients include businesses and corporations seeking to implement an instance of BON in a Box under one of these three options. Small businesses may need one or two indicators and may choose option 3, while large corporations may have sufficient in-house expertise to adopt option 1 or 2. Corporate members may wish to fund an open-ended development of their instance of BON in a Box to encompass indicator calculations across their value chain and comply with new biodiversity Environmental, Social, and Governance (ESG) norms (e.g., Corporate Sustainability Reporting Directive in Europe). This adaptable service model aims to respond to an ever-growing range of needs among members and users. The ultimate goal is to raise the funding to allow continued development of the

BON in a Box service and garner support for its continued development.

5. Conclusion

Through BON in a Box, we can host a collection of state-of-the-art pipelines that transform data into EBVs and indicators to assist with many aspects of biodiversity monitoring, planning, and reporting. By making analysis pipelines readily available to organizations, countries, and other parties of the CBD, BON in a Box could become an integral part of national, regional, and thematic BONs. BON in a Box generates biodiversity information relevant for prioritizing monitoring areas, biodiversity-inclusive spatial planning, assessing and reporting progress towards restoration and protection targets of the GBF, and many other applications at many scales. BON in a Box can help government agencies, BONs, and other major contributors to biodiversity monitoring maximize the benefits of resources allocated to biodiversity research by increasing the use and impact of their work and allowing them to benefit from the work of others. BON in a Box is being developed to match user needs, and early input from governments and contributors supporting them will help to better match the sequence of pipeline development in BON in a Box to priorities of users. BON in a Box is intended to assist with the establishment of a global biodiversity observing system (GBIOS) where biodiversity information is shared across organizations, borders, and scales to enable collective action (Gonzalez et al. 2023a), but this requires large-scale effort and collaboration. To achieve this vision, we encourage organizations or individuals producing EBV or indicator workflows, or have a major role in funding, guiding or supporting those who produce such code, to contribute to BON in a Box.

Acknowledgements

We are grateful for the support of Amy Luers, a donation from the Microsoft Corporation, the Liber Ero Chair in Biodiversity Conservation, and the Digital Research Alliance of Canada for providing computing resources since the early phases of BON in a Box. We would also like to

thank the founding organizations, including the Québec Centre for Biodiversity Science, McGill University, Instituto de Investigación de Recursos Biológicos Alexander von Humboldt, Université de Sherbrooke, Université de Montréal, and Concordia University.

Funding Information

The development of the new version of BON in a Box pipeline engine and monitoring projects portal was made possible thanks to an initial donation from Microsoft. TP and KN were funded through the Discretionary Award 223764/Z/21/Z in Data for Science and Health from the Wellcome Trust. TP and MIAP were funded by the Fondation Courtois. The ISSI international team “Genes from Space” is funded by the International Space Science Institute ISSI and the pipeline development was funded through the canton of Zurich and the NOMIS foundation.

References

- Affinito F, Williams J M, Campbell J E, et al (2024) Progress in developing and operationalizing the Monitoring Framework of the Global Biodiversity Framework. *Nature Ecology & Evolution* 1–9. <https://doi.org/10.1038/s41559-024-02566-7>
- Brummitt N, Regan E C, Weatherdon L V, et al (2017) Taking stock of nature: Essential biodiversity variables explained. *Biological Conservation* 213:252–255. <https://doi.org/10.1016/j.biocon.2016.09.006>
- Canessa S, Guillera-Arroita G, Lahoz-Monfort J J, et al (2015) When do we need more data? A primer on calculating the value of information for applied ecologists. *Methods in Ecology and Evolution* 6:1219–1228. <https://doi.org/10.1111/2041-210X.12423>
- CBD (2022) Kunming-Montreal Global Biodiversity Framework
- Frankham R (1995) Effective population size/adult population size ratios in wildlife: a review. *Genetical Research* 66:95–107. <https://doi.org/10.1017/s0016672300034455>
- Franklin (1980) *Conservation Biology: An Evolutionary-Ecological Perspective*. Chapter 8: Evolutionary Change in Small Populations. 135–149
- GBIF (2024) Global Biodiversity Information Facility. <https://www.gbif.org/>
- Gonzalez A, Chase J M, O'Connor M I (2023b) A framework for the detection and attribution of biodiversity change.

- Philosophical Transactions of the Royal Society B: Biological Sciences 378:20220182. <https://doi.org/10.1098/rstb.2022.0182>
- Gonzalez A, Vihervaara P, Balvanera P, et al (2023a) A global biodiversity observing system to unite monitoring and guide action. *Nature Ecology & Evolution* 7:1947–1952. <https://doi.org/10.1038/s41559-023-02171-0>
- Guisan A, Zimmermann N E, Thuiller W (eds) (2017) *Habitat Suitability and Distribution Models With Applications in R. Habitat Suitability and Distribution Models: With Applications in R i-i*
- Hoban S, Archer F I, Bertola L D, et al (2022) Global genetic diversity status and trends: towards a suite of Essential Biodiversity Variables (EBVs) for genetic composition. *Biological Reviews* 97:1511–1538. <https://doi.org/10.1111/brv.12852>
- Hortal J, Bello F d, Diniz-Filho J A F, et al (2015) Seven Shortfalls that Beset Large-Scale Knowledge of Biodiversity. *Annual Review of Ecology, Evolution, and Systematics* 46:523–549. <https://doi.org/10.1146/annurev-ecolsys-112414-054400>
- Hughes A C, Orr M C, Ma K, et al (2021) Sampling biases shape our view of the natural world. *Ecography* 44:1259–1269. <https://doi.org/10.1111/ecog.05926>
- IUCN (2023) International Union for Conservation of Nature. <https://www.iucn.org/>
- Jetz W, McGeoch M A, Guralnick R, et al (2019) Essential biodiversity variables for mapping and monitoring species populations. *Nature Ecology & Evolution* 3:539–551. <https://doi.org/10.1038/s41559-019-0826-1>
- Kass J M, Smith A B, Warren D L, et al (2024) Achieving higher standards in species distribution modeling by leveraging the diversity of available software. *Ecography*. <https://doi.org/10.1111/ecog.07346>
- Kissling W D, Ahumada J A, Bowser A, et al (2018) Building essential biodiversity variables (EBVs) of species distribution and abundance at a global scale. *Biological Reviews* 93:600–625. <https://doi.org/10.1111/brv.12359>
- Langer C, Fernández N, Quöß L, et al (2022) Cataloging Essential Biodiversity Variables with the EBV Data Portal. *Biodiversity Information Science and Standards* 6:e93593. <https://doi.org/10.3897/biss.6.93593>
- Langer C, Londono Murcia M C (2021) BON in a Box - a platform for biodiversity monitoring tools. <https://zenodo.org/doi/10.5281/zenodo.13913382>
- Mastretta-Yanes A, Silva J M da, Grueber C E, et al (2024) Multinational evaluation of genetic diversity indicators for the Kunming-Montreal Global Biodiversity Framework. *Ecology Letters* 27:e14461. <https://doi.org/10.1111/ele.14461>
- Merow C, Boyle B, Enquist B J, et al (2023) Better incentives are needed to reward academic software development. *Nature Ecology & Evolution* 7:626–627. <https://doi.org/10.1038/s41559-023-02008-w>
- Muller-Karger F E, Miloslavich P, Bax N J, et al (2018) Advancing Marine Biological Observations and Data Requirements of the Complementary Essential Ocean Variables (EOVs) and Essential Biodiversity Variables (EBVs) Frameworks. *Frontiers in Marine Science* 5. <https://doi.org/10.3389/fmars.2018.00211>
- Navarro L M, Fernández N, Guerra C, et al (2017) Monitoring biodiversity change through effective global coordination. *Current Opinion in Environmental Sustainability* 29:158–169. <https://doi.org/10.1016/j.cosust.2018.02.005>
- Nicholson E, Collen B, Barausse A, et al (2012) Making Robust Policy Decisions Using Global Biodiversity Indicators. *PLOS ONE* 7:e41128. <https://doi.org/10.1371/journal.pone.0041128>
- Noss R F (1990) Indicators for Monitoring Biodiversity: A Hierarchical Approach. *Conservation Biology* 4:355–364. <https://doi.org/10.1111/j.1523-1739.1990.tb00309.x>
- Orr M C, Hughes A C, Costello M J, Qiao H (2022) Biodiversity data synthesis is critical for realizing a functional post-2020 framework. *Biological Conservation* 274:109735. <https://doi.org/10.1016/j.biocon.2022.109735>
- Pereira H M, Ferrier S, Walters M, et al (2013) Essential Biodiversity Variables. *Science* 339:277–278. <https://doi.org/10.1126/science.1229931>
- Perino A, Pereira H M, Felipe-Lucia M, et al (2021) Biodiversity post-2020: Closing the gap between global targets and national-level implementation. *Conservation Letters* 15. <https://doi.org/10.1111/conl.12848>
- Raimondo D, Young B E, Brooks T M, et al (2023) Using Red List Indices to monitor extinction risk at national scales. *Conservation Science and Practice* 5:e12854. <https://doi.org/10.1111/csp2.12854>
- Raymond C V, McCune J L, Rosner-Katz H, et al (2020) Combining species distribution models and value of information analysis for spatial allocation of conservation resources. *Journal of Applied Ecology* 57:819–830. <https://doi.org/10.1111/1365-2664.13580>
- Sandström C, Ring I, Olschewski R, et al (2023) Mainstreaming biodiversity and nature’s contributions to people in Europe and Central Asia: insights from IPBES to inform the CBD post-2020 agenda. *Ecosystems and People* 19. <https://doi.org/10.1080/26395916.2022.2138553>
- Saura S, Bastin L, Battistella L, et al (2017) Protected areas in the world’s ecoregions: How well connected are they?. *Ecological Indicators* 76:144–158. <https://doi.org/10.1016/j.ecolind.2016.12.047>
- Saura S, Bertzky B, Bastin L, et al (2018) Protected area connectivity: Shortfalls in global targets and country-level priorities. *Biological Conservation* 219:53–67. <https://doi.org/10.1016/j.biocon.2017.12.020>
- Saura S, Bertzky B, Bastin L, et al (2019) Global trends in protected area connectivity from 2010 to 2018. *Biological Conservation* 238:108183. <https://doi.org/10.1016/j.biocon.2019.07.028>

- Schmeller D S, Mihoub J-B, Bowser A, et al (2017) An operational definition of essential biodiversity variables. *Biodiversity and Conservation* 26:2967–2972. <https://doi.org/10.1007/s10531-017-1386-9>
- Takeuchi Y, Muraoka H, Yamakita T, et al (2021) The Asia-Pacific Biodiversity Observation Network: 10-year achievements and new strategies to 2030. *Ecological Research* 36:232–257. <https://doi.org/10.1111/1440-1703.12212>
- Turak E, Brazill-Boast J, Cooney T, et al (2017b) Using the essential biodiversity variables framework to measure biodiversity change at national scale. *Biological Conservation* 213:264–271. <https://doi.org/10.1016/j.biocon.2016.08.019>
- Turak E, Harrison I, Dudgeon D, et al (2017a) Essential Biodiversity Variables for measuring change in global freshwater biodiversity. *Biological Conservation* 213:272–279. <https://doi.org/10.1016/j.biocon.2016.09.005>

Appendix

Resumen

El Marco Mundial de Biodiversidad de Kunming-Montreal (MMB) del Convenio sobre la Diversidad Biológica establece objetivos ambiciosos para proteger y restaurar la biodiversidad. Incluye un marco de seguimiento que obliga a los países a evaluar el progreso hacia dichos objetivos mediante indicadores que resuman las tendencias de la biodiversidad. El cálculo de los indicadores supone un reto para los países debido a las barreras técnicas, falta de datos y herramientas disponibles y limitaciones en capacidades. Para hacer frente a estos retos, la Red de Observación de la Biodiversidad del Grupo de Observaciones de la Tierra desarrolló BON in a Box, una herramienta abierta para el modelamiento y cálculo de indicadores de biodiversidad. Esta herramienta agrupa flujos de trabajo que conectan análisis individuales para transformar datos en variables esenciales de biodiversidad e indicadores, y que pueden ejecutarse localmente o en la nube. Estos flujos de trabajo son creados por la comunidad, son personalizables y sirven para analizar conjuntos de datos públicos o de los usuarios. BON in a Box ofrece una herramienta integral y accesible a científicos y tomadores de decisiones de todo el mundo tanto para seguir el progreso hacia el MMB como para tomar decisiones de gestión de biodiversidad.

Résumé

Le Cadre mondial pour la biodiversité (CMB) de Kunming-Montréal fixe des objectifs ambitieux pour la protection et la restauration de la biodiversité. Il comprend un cadre de suivi qui requiert le suivi des progrès accomplis par les pays dans la réalisation de ces objectifs, à l'aide d'un ensemble d'indicateurs qui résument les tendances de la biodiversité et d'autres processus complexes. Le calcul de ces indicateurs est un défi pour les pays en raison des difficultés techniques, du manque de données, de l'indisponibilité des outils, et de la faible disponibilité des experts. L'outil de calcul et de modélisation d'indicateurs de BON in a Box, développé par le Réseau d'observation de la biodiversité du Group on Earth Observations (GEO BON), est un logiciel libre conçu pour relever ce défi : il transforme les données en variables de biodiversité essentielles et en indicateurs, par des chaînes de traitement - ou pipeline - pouvant être exécutées soit localement ou dans le nuage. Produits par la communauté, ces pipelines sont personnalisables et peuvent analyser des ensembles de données publiques ou fournies par l'utilisateur. BON in a Box offre un outil polyvalent et accessible aux scientifiques et aux décideurs politiques du monde entier pour suivre les progrès accomplis dans la réalisation des objectifs du GBF et prendre des décisions en matière de gestion de la biodiversité.

Values	
Open and Transparent	BON in a Box is open-source, and the script’s code is fully available with links to supporting publications. Instead of presenting pre-calculated indicators with black-box methodology, the modeling tool shows all the analysis steps from raw data to indicators with intermediate results. This transparency and openness in data and methodology creates trust among data curators, scientists, and decision-makers. BON in a Box respects the FAIR and CARE data principles, and seeks to apply the FAIR principles to data processing pipelines.
Generalizable	All pipelines are generalizable to different locations, scales, and contexts. This increases the use of these methodologies by different countries and organizations and standardizes the way that biodiversity change is measured, strengthening BONs and facilitating knowledge exchange.
Modular	Dividing pipelines into clear steps not only allows the user to better understand the methods, but also allows scripts to be re-used across varied contexts. Each script has a single responsibility, and commonly used analysis scripts can be re-used in different pipelines. For instance, data cleaning scripts can be applied to multiple pipelines that utilize similar types of data, enhancing efficiency and consistency in data processing workflows (Kissling et al. 2017). Additionally, each script is interoperable through its input/output descriptions, meaning that pipelines can contain scripts and toolkits from different languages and computing environments. This modularity reduces code duplication and allows for script and pipeline customization.
Reproducible	Users can easily reproduce previous results by running an analysis pipeline with the same parameters. Additionally, pipelines can be re-run with new data, allowing results to be easily updated with new information. All pipelines are well documented with references and explanations.

Table S1: BON in a Box values. BON in a Box was designed with a set of technical values that reinforce the GEO BON values

Platform	Description	Similarities	Differences	Compatibility with BON in a Box
UN Biodiversity Lab (UNDP and UNEP 2025)	Platform with over 400 spatial data layers on nature, climate change, and sustainable development with the ability to calculate zonal statistics over these spatial layers. Includes workspaces for countries to upload their own data.	User-friendly UI with ability to calculate EBVs and indicators by doing zonal statistics on curated data layers.	No options to contribute or edit analyses. No options to run full workflows from raw data to EBVs and indicators.	BON in a Box could be used for custom analysis in user workspaces. This would require additional software development.
Restor (Crowther et al. 2022)	A community-contributed platform where users can upload their restoration projects. Using a Google Earth Engine backend, it calculates ecological statistics over polygons of restoration areas. Free but offers a paid platform for enterprise and government.	Community-contributed projects. Can calculate some metrics over the restoration areas of interest. Free to use.	No options for users to choose or run analyses themselves or change parameters. Focus on restoration projects and metrics.	BON in a Box could be used to add biodiversity-related metrics in Restor. Platform integration would require additional software development.
SyncroSim (Daniel et al. 2025)	Software platform to run simulations on geospatial data and produce forecasts that can be used in policy contexts. Offers a suite of tools for interactively comparing models across scenarios using charts and maps, with the ability to export the results to other programs.	Focus on policy-relevant information. Users can build and run reproducible workflows. User friendly interface. Processing of geospatial data. Works with R and Python coding languages.	Focus on running geospatial simulation code and forecasting. Not open source. Has a free tier.	Platform integration with BON in a Box would require additional software development.
Galaxy Ecology (The Galaxy Community 2024)	Open source platform to retrieve, process, analyze, and visualize ecological data, build on the Galaxy supercomputer network. Can analyze ecological data using scripts in a variety of languages including R, Python and Perl. This platform is the most similar platform to BON in a Box, and initial differences decreased over the years.	Community-contributed. Open source. Analyzes ecological data that can be from publicly available sources or uploaded by the user. Can run R or Python scripts with Conda dependencies. Graphical user interface to run code through forms. Graphical user interface to assemble workflows (pipelines) combining individual scripts. Can be used on the cloud or deployed locally.	Public instance linked to Galaxy supercomputer infrastructure (vs Digital Research Alliance of Canada). Scripts are described in XML (vs YAML). Galaxy Ecology is a layer on top of the wider Galaxy initiative.	API calls are possible between platforms. Script-level compatibility would require development, but would allow the use of scripts from one platform directly in a pipeline of the other platform, on a single infrastructure.
Wallace EcoMod (Kass et al. 2023)	R package with accompanying Shiny app for reproducible modeling of species niches and distributions. Gives users access to public online biodiversity databases to build and evaluate species distribution models, and also to visualize their predictions on an interactive map. Users can contribute modules to expand functionality, instructional text is included, and code can be downloaded to rerun analyses.	Can be expanded with community contributions. Instructs users on every step of the workflow. Interactive. Modular. Open-source. Reproducible.	Focused on species distribution modelling, does not currently calculate other EBVs or indicators. Shiny app (currently can be run only in R).	Potential to build species distribution models in Wallace EcoMod as a pipeline in BON in a Box using the R package. Such models could then be used for downstream analyses that require the 'Species Distributions' EBV.
map.me biodiversity (Görgen and Bhandari 2024)	R package for analyzing a number of biodiversity related indicators and biodiversity threats based on publicly available geospatial datasets. Supports computationally efficient routines and parallel computing in cloud infrastructures.	Supports computationally intensive analyses. Open source with publicly available code. Uses publicly available geospatial layers.	R package with no dedicated user interface. No option for direct community contribution. Users cannot provide their own data layers.	Potential to run map.me analyses as a pipeline in BON in a Box using the R package.
OpenForis (FAO 2025)	Set of free and open source software platforms that help countries measure, monitor, and report on forestry progress and make science-based decisions.	Open source. Geospatial data processing and analysis.	Includes other tools for data collection and management. No option for direct community contribution. Focus on forest ecosystems and policy.	Platform integration with BON in a Box would require additional software development.
EBV workflow templates (Lumbierres et al. 2024)	Templates to describe three workflow components (data collection and sampling, data integration, and modelling) for generating EBVs. Developed by EuropaBON, it outlines a number of	Focus on FAIR principles and interoperability. Community-contributed: developed through a workshop involving stakeholders. Aims to standardize methods, share knowledge, and improve access to biodiversity information.	Not a software: outlines process but does not calculate EBVs. Focus on EBVs relevant to Europe.	Can use workflow templates to guide development of analysis pipelines within BON in a Box.

Platform	Description	Similarities	Differences	Compatibility with BON in a Box
	EBVs that are relevant to a European context.			
Map of Life (Jetz et al. 2012)	A platform offering curated species distribution models which are used to calculate a number of indicators (e.g., species habitat index). Results are presented in an interactive dashboard which can be customized by countries.	Calculates EBVs and indicators. Interactive user-friendly dashboard.	No option for direct community contribution. Not open source. No option to see or run code (the results are pre-calculated, and in some cases expert-validated).	BON in a Box uses the MoL public API to get range maps. Further platform integration with BON in a Box would require additional software development.
openEO Platform (openEO consortium 2025)	Builds on the openEO API, which allows users to connect with earth observation cloud backends in a simple and unified way. Provides intuitive programming libraries to process a wide variety of earth observation datasets as well as processing infrastructure.	Open source. User friendly front end to run code. Supports R and Python.	Provides processing infrastructure. Focused on workflows to process satellite data. Very detailed visual programming tool (i.e. a box is a single mathematical operation vs a whole script).	Could send jobs from BON in a Box to OpenEO Platform to run on computing infrastructure, especially when the processing of large amounts of ESA satellite data is required.
b3gbi (B-Cubed 2025)	R package for calculating and plotting biodiversity indicators from GBIF occurrence cubes.	Open source. Focus on policy-relevant indicators. Analysis of GBIF data.	R package, not a platform. No option for direct community contribution.	Potential to run R functions as analysis pipelines within BON in a Box.

Table S2: BON in a Box values. BON in a Box was designed with a set of technical values that reinforce the GEO BON values

Appendix References

B-cubed-EU. B3GBI: B-Cubed EU Global Biodiversity Indicators [GitHub repository]. GitHub. Accessed January 24, 2025. <https://github.com/b-cubed-eu/b3gbi>

Crowther TW, Thomas SM, Hoogen J van den, Robmann N, Chavarría A, Cottam A, Cole R, Elliott T, Clark E, Max S, Danylo O, Rowe C. 2022. Restor: Transparency and connectivity for the global environmental movement. *One Earth* 5: 476–481.

Daniel, C., Hughes, J., Lucet, V., Embrey, A., Birchard, K., Frid, L., Kennedy, T., & Senthivasan, S. (2025). rsyncosim: The R Interface to ‘SyncroSim’ (Version 2.0.2) [Software]. Available at <https://syncosim.github.io/rsyncosim/>

FAO, OpenForis: Free Tools for Environmental Monitoring, Food and Agriculture Organization of the United Nations. Accessed January 24, 2025. <https://openforis.org>. Görden, D, Bhandari, O. 2024. mapme.biodiversity: Efficient monitoring of Global Biodiversity Portfolios. R package version 0.9.3. <https://CRAN.R-project.org/package=mapme.biodiversity>.

Jetz W, McPherson JM, Guralnick RP. 2012. Integrating biodiversity distribution knowledge: toward a global map of life. *Trends in Ecology & Evolution* 27: 151–159.

Kass JM, Pinilla-Buitrago GE, Paz A, Johnson BA, Grisales-Betancur V, Meenan SI, Attali D, Broennimann O, Galante PJ, Maitner BS, Owens HL, Varela S, Aiello-Lammens ME, Merow C, Blair ME, Anderson RP. 2023. wallace 2: a shiny app for modeling species niches and distributions redesigned to facilitate expansion via module contributions. *Ecography* 2023: e06547.

Lumbierres M, Abecasis D, Alcaraz-Segura D, Alison J, Álvarez-Presas M, Anderle M, Avci F, Bajocco S, Baldo M, Beja P, Bergamini A, Bergami C, Blanco-Aguiar JA, Boada J, Bonn A, Borges P, Borgwardt F, Borja A, Breeze T, Brotons L, Brucet S, Bruelheide H, Buttigieg PL, Buzan E, Calderón-Sanou I, Camacho A, Camacho-Santamans A, Campanaro A, Cani A, Cariñanos P, Carvalho L,

Castellan G, Castro A, Ceia-Hasse A, Chianucci F, Chowdhury S, C. Lima A, Costa V, Crespo D, Crepaz H, Dahlkamp A, De Knijf G, De Koning K, Demars BOL, De Stefano M, Desmet P, Diem A, Díaz-Delgado R, Díaz Martín B, Drakare S, Eljasik P, Falaschi M, Fernandes I, Fernández Bejarano SJ, Fernandez N, Fernández-López J, Ferrara C, Ferré Codina A, Fiegenbaum H, Floccia F, Galbusera P, Galdies J, Gañán M, Garcia-Gonzalez F, Garzoli L, Gundersen H, Haysom KA, Hedenås H, Heremans S, Hilpold A, Hinojo B, Holmgren K, Hunger S, Huybrechts P, Hvilsum C, Ilarri M, Illa-Bachs E, Isaac N, Jandt U, Jankauskaite G, Junker J, Kahlert M, Kamilaris A, Kasmi Y, Kiran H, Koma Z, Kranstauber B, Kopatz A, Lanzén A, Lecegui Carnero V, Lever JJ, Liqueste C, Luque S, Madon B, Majaneva M, Manea E, March D, Marco M, Martínez-López J, Martínez-Vicente V, McCallum I, Méndez M, Milanovic M, Moe SJ, Morant D, Muir MAK, Müllerová J, Múrria C, Musche M, Nascimbene J, Nestola E, Oggioni A, Oikonomou A, Oldoni D, Ott D, Pace G, Padubidri C, Palomino Gaviria AP, Paniccia C, Pereira HM, Pérez-Girón JC, Pérez-Haase A, Petriccione B, Philipson P, Pit IR, Pladevall-Izard E, Pop DA, Puerta-Piñero C, Quaranta M, Radoux J, Rasmussen JJ, Renan I, Reubens J, Roeoesli C, Rolph S, Rūsiņa S, Samoila C, Santana J, Schakel JK, Schepers L, Schletterer M, Schmidt-Kloiber A, Seeber J, Shi Y, Shinneman S, Smets B, Soares J, Soccodato A, Solé-Medina A, Sorvari J, Sousa R, Souza AT, Souza Dias A, Spinosa A, Strasser T, Thulin SM, Trottet A, Turicchia E, Uriarte A, Vagenas G, Valdez J, Vallefucio F, Van de Putte AP, Van Grunsven RHA, Vicente J, Villegas-Rios D, Villero D, Viti MM, Vriend SJG, Walentowitz A, Ward RJ, Wijesingha J, Zhang J, Ziemba A, Zimmermann J, Kissling WD. 2024. EuropaBON EBV workflow templates. openEO Consortium. n.d. openEO Platform. Accessed January 24, 2025. <https://openeo.org>.

The Galaxy Community. 2024. The Galaxy platform for accessible, reproducible, and collaborative data analyses: 2024 update. *Nucleic Acids Research* 52: W83–W94.

United Nations Development Programme (UNDP), United Nations Environment Programme (UNEP), and UN Biodiversity Lab, UN Biodiversity Lab. Accessed January 24, 2025. <https://unbiodiversitylab.org>.