

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



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Abstract

Biodiversity loss is a critical global challenge. The Kunming-Montréal Global Biodiversity Framework (GBF) sets ambitious goals to protect ecosystems, halt species loss, and enhance biodiversity. The GBF's Monitoring Framework requires countries to track progress toward biodiversity targets using a standardized set of indicators that summarize complex trends in biodiversity. However, the calculation of these indicators can be challenging due to technical barriers, lack of available data and tools, and capacity bottlenecks, hindering countries' ability to implement the monitoring framework. BON in a Box, developed by the Group on Earth Observations Biodiversity Observation Network (GEO BON), is an open-source platform designed to address this challenge. It provides accessible tools for calculating Essential Biodiversity Variables (EBVs) and indicators — helping scientists, policymakers, and conservation practitioners prioritize monitoring areas, understand biodiversity trends, and track progress toward the targets of the GBF. BON in a Box automates the process of turning raw data into EBVs and indicators by connecting individual analysis steps into pipelines that can be run with minimal technical expertise. The pipelines are fully modular, customizable, open, and transparent, with options for users to use publicly available data or input their own proprietary data. Pipelines are all contributed by GEO BON collaborators, promoting knowledge sharing and scientific collaboration. BON in a Box is a collaborative platform for turning data into useful information to guide monitoring efforts, understand biodiversity change, make informed conservation decisions, and track progress toward meeting the targets of the GBF.

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

Biodiversity loss poses a significant threat to ecosystems and human well-being, necessitating urgent global actions targeting effective conservation strategies and comprehensive biodiversity monitoring (Gonzalez et al. 2023a). The Kunming-Montréal **Global Biodiversity Framework** (GBF) of the United Nations Convention on Biological Diversity (CBD) defines the commitment by Parties to the CBD to protect and restore biodiversity, and maintain nature's contributions to people (Milner-Gulland et al. 2021, McGowan et al. 2024). The ambitions of the agreement are captured by twenty-three action targets to be reached by 2030, and four outcome-focused goals for 2050. Through their national biodiversity strategies and action plans (NBSAPs), countries are aligning their governmental plans and programs to reflect the necessary measures set out by the Convention and the **GBF**.

To track progress towards the targets of the **GBF**, the Monitoring Framework provides a set of **indicators** for GBF Parties to report. Biodiversity **indicators** summarize trends in monitoring data into a simple metric of biodiversity change over time. These **indicators** are important for understanding past change, predicting future change, and informing conservation policy (Stevenson et al. 2021). Each of the **indicators** evaluates progress relating to the goals and targets of the **GBF**. For example, the Red List Index (RLI) measures the trend in extinction risk of species over time, and relates to Goal A and Target 4 of the **GBF**, which focuses on halting human-induced species extinctions (Nicholson et al. 2024). These **indicators** can also inform policy, such as where to place new protected areas to maximize biodiversity conservation (Nicholson et al. 2012). The Protected Connected Index (ProtConn) can assess progress toward Target 3 (30% of all lands are protected and connected by 2030) while also informing the establishment of new protected

Glossary

Term	Definition
Biodiversity Observation Network (BON)	A network of observation sites or stations and/or a network of experts and groups who produce and use biodiversity data for different needs. A BON coordinates observations and monitoring to support policy prompting conservation 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)	An agreement that sets an ambitious pathway to reach a global vision of living in harmony with nature and halting biodiversity loss by 2050. As of now, 196 parties have signed the Global Biodiversity Framework, which was adopted at the 15th Conference of the Parties to the Convention on Biological Diversity (CBD) in December 2022.
GBF Target	The GBF specifies 23 action targets for parties to the CBD to meet before 2030. For example, target 1 aims to have 30% of land and seas protected and connected by 2030.
GBF Monitoring Framework	A framework 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.
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))
Indicator	A biodiversity indicator summarizes one or more EBVs into a single value that can help track changes in biodiversity status, such as species populations, ecosystem health, and habitat extent, thereby providing measurable data that informs policy decisions and conservation actions. In the context of the GBF, an indicator is a specific metric used to assess progress toward the framework's goals and targets.
Script	A piece of code written in a programming language that accomplishes a single task, such as data cleaning, analysis, visualization, and modeling.
Pipeline	A set of scripts connected to complete an entire analysis workflow that is automated from start to finish, operating under user-specified or default parameters.
Modular Software	A software design philosophy where every script does one 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.

areas to maximize connectivity (Saura et al. 2017, 2018). Together, these **indicators** provide a simplified but comprehensive view of the state of biodiversity and how it is changing over time to inform conservation action and assess progress toward the targets of the **GBF**. However, the implementation of the monitoring framework is complex, and many parties require scientific and technical support.

The Group on Earth Observations Biodiversity Observation Network (GEO BON) and other relevant organizations, have been invited by the Conference of the Parties to the CBD to support Parties in putting the **GBF**'s Monitoring Framework (Decision 15/5) into practice. GEO BON is an international network of over 3300 researchers dedicated to improving the acquisition, coordination, and delivery of biodiversity information at the global, regional, and national levels. This work builds on a decade of effort by GEO BON to improve accessibility to biodiversity information globally, to bridge the gap between science and policy to better respond to the biodiversity crisis (Navarro et al. 2017).

One such effort is the development of the **Essential Biodiversity Variable** (EBV) framework developed by GEO BON to standardize measurements and capture different aspects of biodiversity (Pereira et al. 2013). The **EBV** framework identifies an optimum set of variables needed to understand the current state of populations and ecosystems (Pereira et al. 2013) and the ecosystem services they provide (Balvanera et al. 2022, Schwantes et al. 2024). **EBVs** can be thought of as a conceptual intermediate between observations (raw data) and **indicators** (Kissling et al. 2018). The definitions of **EBVs** are designed to be agnostic to specific taxa and general enough to allow for multiple measurement approaches. Importantly, unlike **indicators**, **EBVs** are robust to changes in policy and legislation (Schmeller et al. 2017). **EBVs** can be calculated at regional, national, and subnational scales (Vihervaara et al. 2017, Turak et al. 2017a, Bellingham et al. 2020) and measured in terrestrial, marine, and freshwater realms (Turak et al. 2017b, Schmeller et al. 2017, Muller-Karger et al. 2018). These **EBVs**, collected

over time and space, provide the standardized information necessary to calculate **indicators** of biodiversity change (Figure 1).

GEO BON has defined six classes of **EBVs**, to capture different aspects of biodiversity: genetic composition, species populations, species traits, community composition, ecosystem functioning, and ecosystem structure (Kissling et al. 2018, Jetz et al. 2019, Hoban et al. 2022). For example, one **EBV** in the genetic composition class is effective population size, which can be measured through genetic sequencing or estimated from population monitoring data (Hoban et al. 2022). This **EBV** directly supports one of the headline **indicators** of the **GBF**, the proportion of populations within species with an effective population size > 500 (Mastretta-Yanes et al. 2024). To support the production of **EBVs**, GEO BON created the **EBV** data portal (Langer et al. 2022) which hosts processed raster layers that can be used for **EBV** estimation and ultimately the calculation of **indicators**.

However, the calculation of **EBVs** and **indicators** can be complex, and technical barriers in their calculation is one of the major challenges for parties in reporting to the **GBF** (Orr et al. 2022). Even when the appropriate data and methods are available, assembling an analysis workflow to calculate **indicators** and **EBVs** from raw data can be difficult. **Indicators** calculation methods are often hidden in scientific publications and the code is not always open, requiring effort and expertise to decipher and implement them (Affinito et al. 2024). Parties may lack the capacity to apply these methods, hindering their ability to fulfill the commitments of the Monitoring Framework and the **GBF** (Affinito et al. 2024). This may be particularly true of parties operating in areas without strong computing capacity, which can make the calculation of **EBVs** and **indicators** prohibitively expensive. Even if parties do have the capacity to calculate **indicators**, they may invest effort, time, and resources into independently developing analysis workflows that already exist but are not easily discoverable or customizable. Additionally, tools to calculate indicators typically use black-box methods with no capacity for customization,

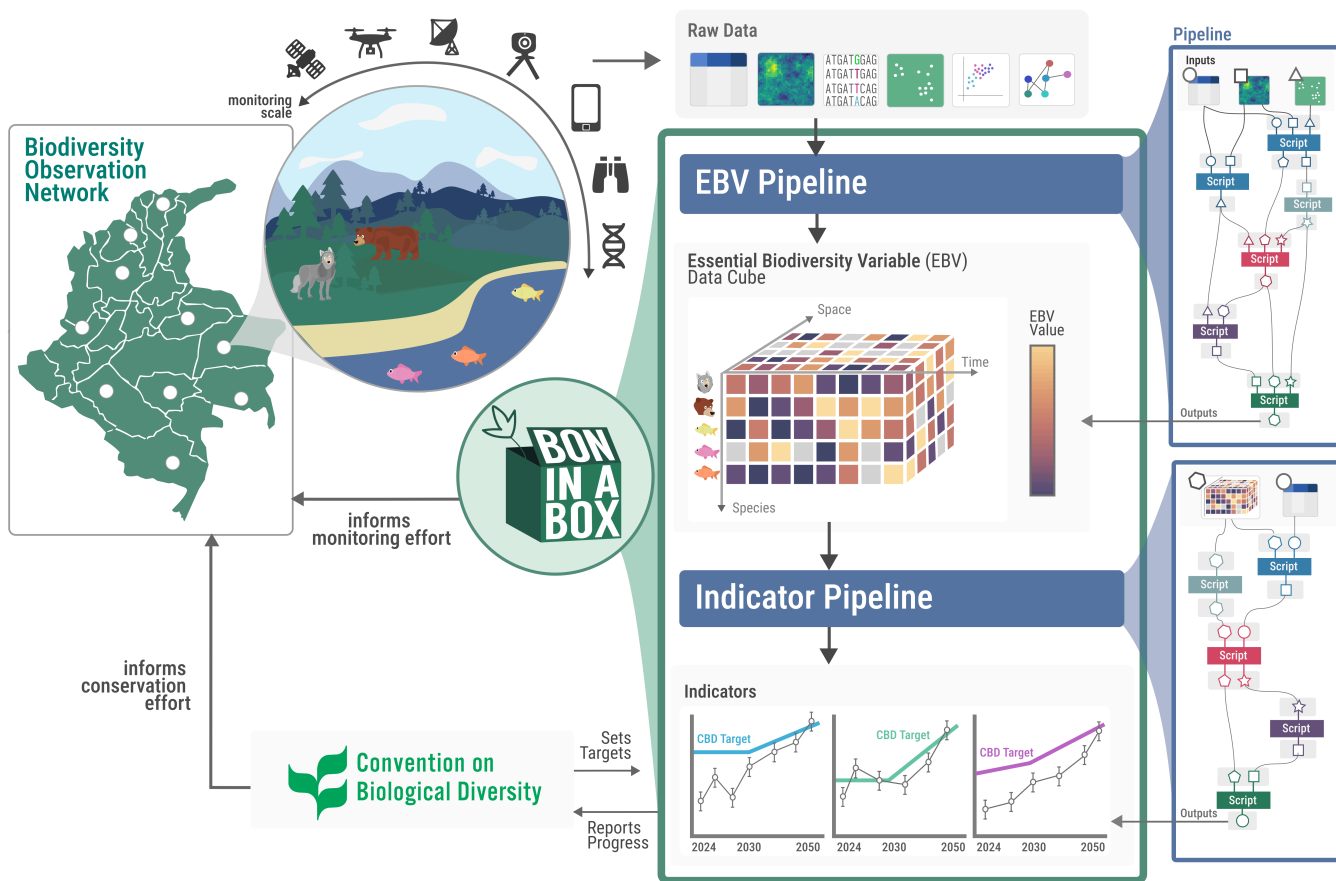


Figure 1: BON in a Box can help with both informing monitoring efforts through sampling prioritization and assessing biodiversity change by calculating both **EBVs** and **indicators**. This information is used to report to multilateral agreements such as the Convention on Biological Diversity and also 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.

incorporation of user data, or the ability to generate estimates across scales, and they are not always easily discoverable or readily available. The closed nature of these **pipelines** also makes them difficult to audit, which can erode trust in their conclusions.

Therefore, there is a pressing need for an open analysis toolkit that can integrate and simplify the process of calculating **EBVs** and **indicators** for a variety of users, including the scientific community, natural resource managers, local communities, industries, NGOs, policymakers, and intergovernmental bodies (Navarro et al. 2017, Orr et al. 2022). To serve the needs of this diverse group of users, this analysis platform must be accurate, user-friendly, interoperable, fully transparent, and customizable. It needs the ability to both pull data

from publicly available datasets and allow inputs of user data when available. Additionally, the tool must be able to calculate **EBVs** and **indicators** across scales, as the success of the monitoring framework for the **GBF** relies on cooperation between subnational and national actors who need to measure biodiversity change at their respective scales of operation.

Here, we describe the BON in a Box modeling platform (hereafter, BON in a Box), an initiative of GEO BON to facilitate the calculation of **EBVs** and **indicators** by scientists and policymakers to assist with conservation planning and reporting to the CBD. We highlight the need for countries and partner organizations to have a comprehensive set of tools that removes the technical barriers of calculating **EBVs** and **indicators** to better assess the current state of

biodiversity, prioritize areas for sampling and conservation, and track progress toward the targets of the GBF. We describe how BON in a Box can fill this need by creating analysis **pipelines** to automate the process of calculating **EBVs** and **indicators** and prioritizing sampling areas. We describe the current capabilities of BON in a Box and our vision for its future, and we call for collaborators to contribute to this project and help us achieve this vision. Ultimately, we hope that BON in a Box can assist in all levels of biodiversity policy around the world, from guiding monitoring efforts to assessing progress to informing action.

2. The BON in a Box Platform

2.1. Overview

BON in a Box is a platform for sharing knowledge, tools, and computational resources to facilitate the establishment and operation of **Biodiversity Observation Networks (BONs)** and intended to assist countries, regions, and organizations in setting up or improving biodiversity observing systems. It provides guidance for harmonizing biodiversity observations, amplifying the capacity for data analyses, thereby supporting the integration of **EBVs** to track biodiversity change. The original version of BON in a Box allowed users to search for tools relevant for **BON** implementation and management. The next version included a catalog of biodiversity monitoring projects, allowing users to search projects, connect with leaders, and expand their network. The most recent addition to BON in a Box described here includes a modeling tool to assist in calculating **EBVs** and **indicators** for reporting. This modeling tool was developed through a collaborative effort between the GEO BON secretariat, the Québec Centre for Biodiversity Science, in Montréal, Canada and Humboldt Institute in Bogotá, Colombia with the goal of lowering the barrier for decision-makers to turn data into **indicators** to assess the state of biodiversity. The backbone of the modeling tool is the **pipeline** engine, which automates the process of turning raw data into **indicators** that can be used in assessing biodiversity change, informing conservation efforts, and reporting to

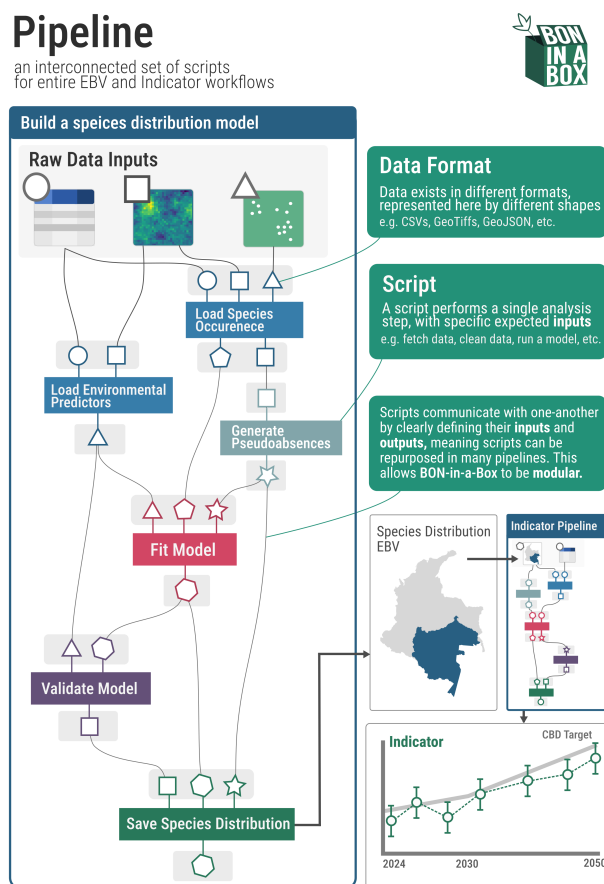


Figure 2: A BON in a Box pipeline is an interconnected set of **scripts** that automate the process of turning raw data into **EBVs** and **indicators**. **Scripts** are completely and connected via inputs and outputs, which can also be downloaded and viewed as intermediate results. These **pipelines**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

the GBF and other environmental agreements. The browser-based user interface allows users to input the parameters that they are interested in (e.g. data, country or region of interest, species, parameters of the model, etc.), press a button to run the code, and visualize and download the results. The BON in a Box platform is intended to transform GEO BON's current capacity to support parties in the implementation of the GBF's monitoring framework, including the establishment of a global biodiversity observing system (GBIOS, [Gonzalez et al. \(2023a\)](#)).

In the context of biodiversity monitoring, a workflow dictates the path from raw biodiversity data to **EBVs** and **indicators** using different analytical tools. This is usually accomplished with a series of steps that are run sequentially,

with manual intervention, using the results from the previous step as inputs for the next. The BON in a Box **pipeline** engine automates these workflows by connecting these individual steps into **pipelines** that run an entire analysis with the push of a button (Figure 2). Each step of the workflow is separated into **modular** stand-alone **scripts** that perform a task and produce an output. The output of a **scripts** can be in a variety of formats (GeoTiff, CSV, GeoJSON, etc.) and becomes an input for the next step. Because each step is **modular**, **scripts** written in different programming languages (R, Python, Julia, etc.) can be connected in a single **pipeline**. Facilitating the centralization of code, which allows the management of workflows from different **scripts** through a single interface and enables the reuse of common **scripts** in other **pipelines** and contexts. For example, a common step such as pulling and cleaning GBIF data can be used in a variety of **pipelines**, reducing the need to re-write code. Users can view the **scripts**' intermediate results and code, creating a fully transparent process. BON in a Box is a community-driven initiative, and all **pipelines** are contributed and reviewed by collaborators, supporting GEO BON's mission of coordination and knowledge sharing between biodiversity observation networks.

BON in a Box **pipelines** are designed to be generalizable to different taxa, countries, and regions. Because of the openness and **modularity** of BON in a Box **pipelines**, they can be customized for a variety of user needs. The user can run the **pipelines** with publicly available data, user-provided data, or a combination of both (Fig. 1). For example, **pipelines** can pull from publicly available datasets such as GBIF, GEO BON's **EBVs** portal (Langer et al. 2022) and IUCN database. Additionally, individual **pipeline** steps can be added or modified to tailor the analyses to a specific use and context. This leads to four potential levels of customization: 1) a standard **pipeline** with user-provided data, 2) a standard **pipeline** with user-provided and public data, 3) a customized **pipeline** with public data, and 4) a customized **pipeline** with user-provided and public data. To deal with sensitive data, such as

the locations of threatened species, the engine was built in containers so it can be deployed locally on any server or computer. Therefore, the sensitive data does not have to leave the organization in order to be used in a BON in a Box **pipeline**. Currently, BON in a Box can be installed on a local computer using container technology and used to run analysis **pipelines** to calculate a number of **indicators** with the press of a button, turning publicly available or user-input data into **EBVs** and **indicators**. The results (both final products, and intermediate steps) of running these **pipelines** can be saved, and viewed in an interactive dashboard. In sum, BON in a Box is a platform to calculate **EBVs** and **indicators** with little to no coding experience through community-contributed, open, and customizable analysis **pipelines**, significantly lowering the barrier to access of biodiversity information for scientists and decision-makers.

2.2. The vision

Our vision is for BON in a Box to become a comprehensive platform for **BONs** that optimizes monitoring efforts, offers standardized and curated tools for calculating biodiversity variables and **indicators**, and in general lowers barriers for sharing biodiversity knowledge. To achieve this, we plan to 1) expand the breadth of **EBVs** and **indicators** that are available in BON in a Box and make the tool more accessible, 2) create pipelines to guide sampling prioritization and monitoring efforts, 3) increase the number and global representation of contributors to BON in a Box and 4) implement a peer-review model for contributed **pipelines**.

We intend to increase the number of analysis **pipelines** that are available in BON in a Box to include all of the GEO BON **EBVs** and **indicators** in the Monitoring Framework. We will also engage **BONs**, governments, NGOs, and other organizations in contributing to other **indicators** that are useful to them. We aim to host BON in a Box as a web platform that will be globally available, allowing **EBV** and **indicator pipelines** to be run using remote and scalable computing resources. This will allow users without coding expertise or cyberinfrastructure

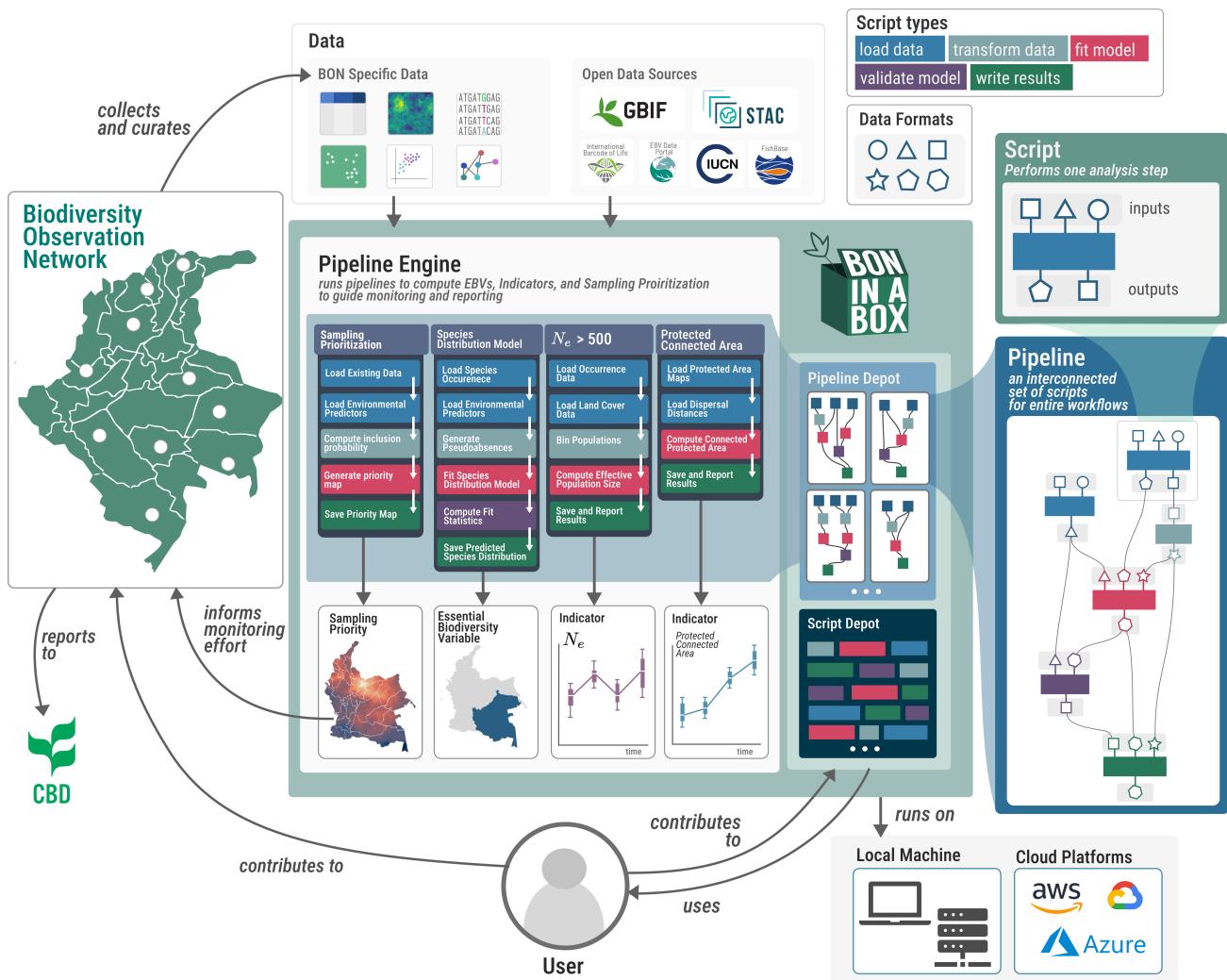


Figure 3: BON in a Box is a tool that aims to increase the quality of and access to biodiversity information by informing monitoring efforts (sampling prioritization) and calculating EBVs (e.g. SDMs) and indicators (e.g. $N_e > 500$) in an open, standardized, and user-friendly way. BON in a Box contains 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).

to run analysis pipelines and easily compute and download results for their country or region of interest in the form of a report with results, maps, figures, and interpretations.

Another primary 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 fill the gaps in biodiversity data. A fundamental challenge to reporting on the targets of the GBF is the many shortfalls in existing biodiversity data (Hortal et al. 2015). Countries

have limited resources to create biodiversity monitoring programs. Therefore, a key aspect of a successful implementation of the GBF monitoring framework will be the development of optimally designed biodiversity monitoring programs that can both efficiently and robustly detect and attribute biodiversity change to causal drivers (Gonzalez et al. 2023b). An essential aspect of the BON in a Box vision – in the name itself – is a toolkit to identify data gaps and guide spatial sampling prioritization and the design of local BONs to best inform decision making and conservation effort. This would include tools for

expanding existing **BONs** and prioritization of different regions based on current knowledge, powered by the **EBVs/indicators** computed using the **pipeline** engine. This will enable biodiversity monitoring best suited to inform decision makers to guide action toward meeting the **GBF Targets**.

In order to achieve our vision for this comprehensive tool to help improve our understanding of the current status and trends of biodiversity and the capacity of countries to report to multilateral agreements, we need the diverse expertise of GEO BON members. Contributing analysis **pipelines** to BON in a Box widens the impact and scope of research by increasing the use of analyses and tools for biodiversity monitoring and policymaking. When researchers develop new **indicators** and methods, they can stay hidden in the literature and require expertise to implement in a policy context. By including **pipelines** in BON in a Box, researchers will be able to reach a wider audience and increase the application of their analyses. Attracting contributors may remain an issue for as long as the work of **pipeline** development is unrecognized, especially using traditional academic crediting mechanisms. For this purpose, **pipelines** will be published in a Diamond OA (publish for free) journal, 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, incentivises researchers to contribute **pipelines**, and encourages users to cite the specific **pipelines** and steps used in their reporting.

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 test code and outputs of the **pipelines**, check for errors, and evaluate the scientific rigor of the results, as well as

evaluating whether the **pipeline** is user-friendly, generalizable, and easy to interpret for a non-expert. The reviewer will be provided with a standard checklist to evaluate these criteria, and, similar to the manuscript review process, will determine whether the **pipelines** need major or minor revisions before being published on the BON in a Box platform. 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 constantly developed and strengthened by the users and the diverse network of GEO BON scientists and collaborators. The tool will support biodiversity policy at every level, aiding in improving biodiversity information by guiding monitoring efforts, assessing biodiversity change, and informing action.

2.3. Comparison to other platforms

BON in a Box offers a unique **modular** platform for open access, analysis, and visualization of biodiversity data made and managed by scientists, but it is important to note that it exists within an ecosystem of complementary tools. Some are primarily interactive maps that offer suites of visualization tools for **indicators**. For example, the [UN Biodiversity Lab](#) offers a diverse array of basemaps and statistics by country, and [Restor](#) functions as a data-sharing platform with information about ecological restoration projects around the world ([Crowther et al. 2022](#)). Of the interactive platforms that are primarily analysis tools, some are managed by companies or corporate groups and can help calculate **indicators**. [Syncrosim](#) is a company-produced software for streamlined geospatial analysis and forecasting that packages results for decision makers, and it has both free and paid versions for increased data storage and support. Other interactive platforms for analysis are developed and managed primarily by the scientific community. Wallace EcoMod

is an open, GUI-based R application for interactive species distribution modeling and related analyses that has a **modular** structure and includes educational materials for teaching (Kass et al. 2023). Finally, Galaxy Ecology is also a **modular** and GUI-based platform that serves a host of tools for ecological analysis (including Wallace EcoMod) and cloud computing options (Royaux et al. 2024). Yet other platforms are code-based and require programming experience to navigate. The MAPME project's R package map.me biodiversity is an extensive and open analysis toolbox for calculating **indicators** extracted from **EBVs** and other layers through spatial aggregation operations while leveraging cloud computing (Görgeten et al. 2024). Snakemake is a workflow management system similar to the **pipeline** engine of BON in a Box in many ways, but with a focus on bioinformatic workflows and general accessibility for non-technical users (Köster and Rahmann 2012). EuropaBON has developed **EBVs** workflow templates designed to capture comprehensive descriptions about the three workflow components: data collection and sampling; data integration; and modeling (Lumbierres et al. 2024).

BON in a Box's strength draws from its policy and community-driven development, which focuses contributions on the gap between existing data and reporting for biodiversity targets. Where other efforts with similar open-source, **modular** philosophies (e.g. Galaxy Ecology) provide a platform for any contribution under the broad umbrella of ecological analysis, BON in a Box's clarity of purpose guides community and **pipeline** growth. This ensures that future development uniquely furthers the project's goals, which are framed by the requirements of the KM-GBF, its monitoring framework, and potential future agreements made by parties to the CBD. This approach also improves adaptability and synergy between **pipeline** contributions, as the scope of **scripts** use and **pipeline** overlap are well-defined. BON in a Box is unique in its combination of technical values that reinforce the GEO BON values of excellence, collaboration and shared purpose,

transparency and openness, and inclusivity throughout its network (Table 1).

Values

Open and Transparent

The modeling tool 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.

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 **pipelines** 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.

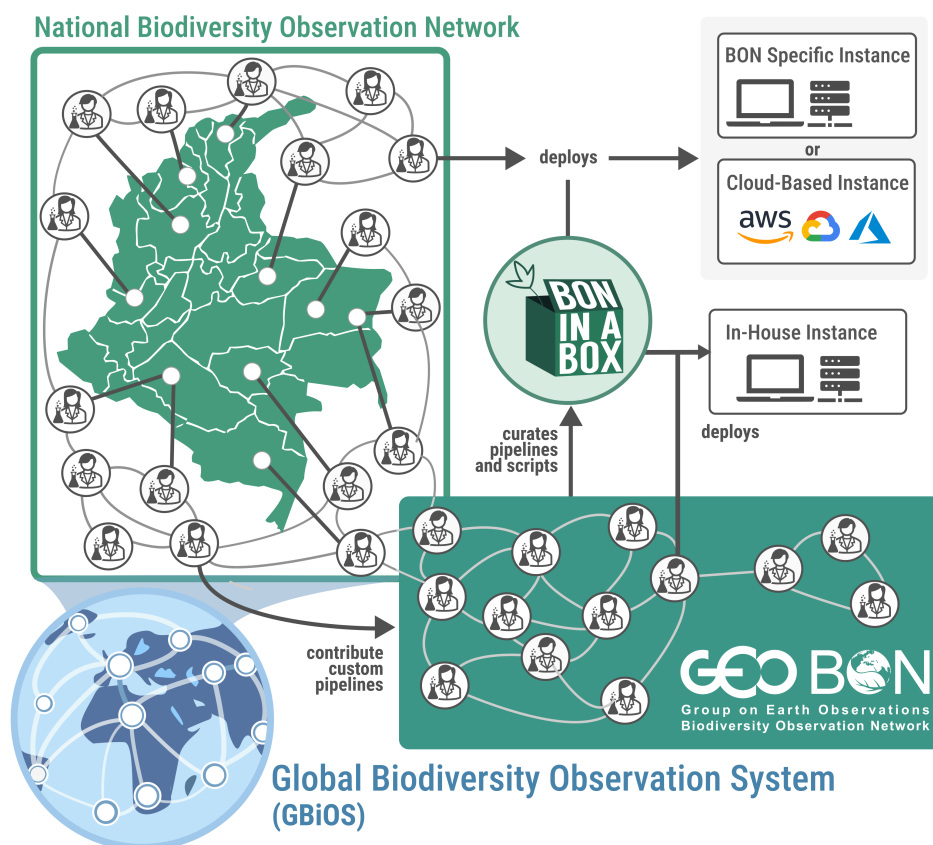


Figure 4: Service model and community support from the GEO BON network to countries and other organizations wishing to implement BON in a Box. Users from national or regional BONs can choose from three potential options – running a local instance, running an instance on a cloud-computing platform, or 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.

2.4. Service Model

Critical to the success and reach of BON in a Box is a service model that makes it accessible to users and adapts 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 3300 members, and 1800 member 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. The service model must cater to a broad range of needs.

To reflect this diversity, we propose a model that allows a range of users access to BON in a Box services and through collaboration with the GEO BON team. The three distinct options can be co-developed with the user to suite their current

technical demands but maintain an eye on likely future needs:

- **Option 1:** A member runs an analysis on a local instance of BON in a Box obtained from the GEO-BON GitHub repository. Initial set-up support is offered by the GEO-BON team. This option requires that a user is comfortable with the
- **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.
- **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 **indicators** selection with the user.

We expect many countries may wish to implement BON in a Box to support the implementation 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 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; Figure 4). This adaptable service model aims to respond to an ever growing range of needs among a constellation of members and users. The ultimate goal is to raise the funding that allows continued development of the BON in a Box service and garner support for its continued development.

3. Pipeline Examples

3.1. Species Distribution Models

Knowing where species are is essential for understanding the distribution of biodiversity and informing conservation efforts, and this information is needed to estimate the ‘species distributions’ **EBVs** in the ‘species populations’ class. 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 (Hughes et al. 2021). Information on species occurrences is often sparse with considerable spatial and

taxonomic biases (Hughes et al. 2021). We therefore need to fill these data gaps using predictive models that can provide more comprehensive estimates of where species are. Species distribution models (SDMs) represent a range of methods from regression to machine-learning, and they predict where species are likely to occur based on associations between environmental variables and known occurrences (Elith and Leathwick 2009), (Guisan et al. 2017). Range estimates from these models can be used as key base layers for a wide variety of applications including making maps and predictions for: impacts of environmental stressors on species, habitat suitability for at-risk species, biodiversity hotspots across a region, locations of conservation priorities and protected area expansion, sampling gaps and prioritization for future sampling, and a range of biodiversity **indicators** including the Biodiversity Habitat Index (BHI), Species Habitat Index (SHI), and Species Protection Index (SPI). There is currently a wide variety of open programming tools for SDMs, including those that gather and process data on species and the environment; fit and validate models; tune model complexity; correct for methodological biases; assess model predictions and extrapolation; and assemble metadata for reproducibility; as well as a growing number of interactive applications (Kass et al. 2023, Sillero et al. 2023). BON in a Box mobilizes these tools into automated **pipelines** that build state-of-the-art SDMs, validate and report their performance, and provide visualizations to facilitate interpretation of their outputs. SDM **pipelines** offered in BON in a Box simplify the process of modeling this important **EBVs** and provide important base layers for a number of **indicator** calculations.

3.2. $N_e > 500$

BON in a Box has partnered with the “Genes from Space” team at the International Space Science Institute to integrate a **pipeline** to calculate $N_e > 500$, headline **indicator** A.4 of the GBF (The proportion of populations within species with an effective population size > 500). $N_e > 500$ measures the overall maintenance of genetic diversity and adaptive capacity within

species. The effective population (N_e) is the number of individuals that contribute offspring to the next generation. An effective population size (N_e) of more than 500 individuals per population is considered sufficient to maintain genetic diversity and population viability. The $N_e > 500$ **indicator** measures the proportion of populations within each species with an effective population size above 500, averaged across all species. Therefore, $N_e > 500$ measures the genetic status of species and populations. $N_e > 500$ can be directly measured through genetic sequencing or indirectly estimated from census population size (N_c ; [Hoban et al. \(2020\)](#)). However, both genetic sequencing data and long-term population monitoring data is often not available for most species in most areas. The “Genes from Space” team has created a method to estimate $N_e > 500$ for a number of species using publicly available satellite data. The **pipeline** creates polygons of populations using occurrence data, land cover data, and dispersal distances, estimates census population sizes from population polygons and known densities, and estimates effective population size (N_e) from census population size. The **indicator** is calculated as the proportion of species’ populations that have an $N_e > 500$, averaged over all species. This **pipeline** is available on BON in a Box, where users can calculate $N_e > 500$ for a species and region of interest without having to sample populations or sequence genes, greatly improving capacity to report on this headline **indicator**.

3.3. Protected Connected Index

ProtConn, or the Protected Connected Index, is a component **indicator** for goal A of the GBF (CBD 2022b). ProtConn measures the percent of a given country or region that is protected and connected, meaning that species can easily move between them to facilitate gene flow and reduce extinction risk ([Saura et al. 2017](#)). ProtConn is calculated by determining 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 for protected areas in a given country or region using the World Database of Protected areas or

user input protected area polygons. The user inputs a dispersal distance based on dispersal estimates for a species or group of species of interest. Users can assess the current state of protected areas, or calculate ProtConn with sets of proposed protected areas. ProtConn 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. 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](#)).

3.4. Sampling prioritization

The vast majority of Earth’s surface and oceans currently lack robust data about the biodiversity that exists there. 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 can’t collect data everywhere, all the time. There are many practical limitations on the scope of biodiversity monitoring programs — primarily funding. For decision makers to develop scientifically supported policy 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. Further, 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 not just with a toolbox to compute EBVs and **indicators**, but also methods for prioritizing where to collect data to fill in gaps in our

monitoring effort. For example, **pipelines** for computing Species Distribution Models (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. Using existing data to guide future monitoring efforts ensures we fill biodiversity data gaps to most effectively and efficiently inform conservation policy and ensure nations can meet the GBF targets.

4. How countries and other parties of the CBD can use BON-in-a-Box

The standardized tools and workflows in BON in a Box for calculating **EBVs** and **indicators** can help **BONs** to provide globally consistent information to governments and other reporting entities. They can also help **BONs** to generate information specifically tailored to support on-the-ground actions by government agencies and other decision-makers. Examples include identifying optimal locations for habitat protection and restoration for threatened species, designing new protected areas, or implementing other effective area-based conservation measures (OECM).

The ways in which **BONs** may use and contribute to BON in a Box will depend on their resources, governance, and respective roles in generating biodiversity information, and these factors vary greatly among existing **BONs**. One example is Freshwater BON (**FW-BON**), a thematic **BON** with a global agenda. FWBON is a voluntary community of practice established in 2017 with no dedicated, central funding, nor specified end date. Another example is Asia-Pacific BON (**APBON**), a regional **BON** founded in 2009 representing an expansive area and a wide variety of countries (Takeuchi et al. 2021). Like FWBON, APBON operates as a voluntary organization without central funding. Sharply contrasting with these is **EuropaBON**, a project-based, regional **BON** with substantial resources at the center. Like the earlier iteration **EUBON**, EuropaBON has generated **substantial outputs** in

its short life-time, December 2020 to May 2024. Unlike EuropaBON or APBON, FWBON does not directly engage in monitoring or the calculation of **indicators**, but instead provides guidance and supports its members to contribute to tracking global change in freshwater biodiversity (Turak et al. 2017a, Cantonati et al. 2020). Unlike FWBON, regional **BONs** like APBON and EuropaBON accumulate information for multiple ecosystems (terrestrial, marine, freshwater). They also represent countries within their region and thus strive for their active participation, though regions with extreme diversity in language, culture, and sociopolitics like APBON face great challenges regarding data-sharing and collaborative activities. FWBON and APBON have a large proportion of members representing developing countries that often lack the coordination and resources to contribute biodiversity information efficiently to make comprehensive regional estimates. Hence, direct engagement of groups like FWBON and APBON in the development of BON in a Box and the inclusion of specific guidance and tools could greatly enhance the availability of biodiversity information to help governments meet action targets and reporting requirements for the **GBF**.

Latin American countries, led by Colombia, are organizing to strengthen regional coordination and formalize participation in a **BON** called K2A Hub Latam. Colombia's experience in designing and implementing **pipeline** workflows to calculate biodiversity **indicators** in BON in a Box (including **EBVs** and other **indicators** of national interest) is driving the adoption of this tool across the region. This network helps better identify regional needs and expectations regarding BON in a Box, fostering collaboration in developing new workflows, sharing local experiences, and providing relevant information to adapt and improve BON in a Box according to the specific needs of each country. **BONs** which aim to have a direct role in calculating **EBVs** and **indicators** vary greatly in their technical skills and capacity. Also, **BONs** that have comparably low or high capacity might be lacking in very different capabilities. For example, some **BONs** or governments might

have well-developed systems for assembling and processing raw species occurrence data for input to SDMs, yet little capacity to calculate Red List Index metrics (Raimondo et al. 2023) from primary data or generate biodiversity maps and cost surfaces for input to run spatial prioritization analyses that can inform reserve design and planning (e.g., Watts et al. (2017)). The different modules in BON in a Box enable **BONs** to use standardized and accessible tools to address the specific gaps in their capabilities. Even when **BONs** succeed and can generate and process primary data and calculate **indicators**, the outputs may not be comparable with those produced by other **BONs** and governments because of their lack of generality. For example, EuropaBON has generated a suite of **EBV values** for Europe with foci on specific taxa and ecosystems. Given differences in geography, biodiversity, and culture, APBON may have different priorities regarding which taxa and ecosystems to focus on, which would make it difficult to directly compare **EBVs** estimates between these regions (Takeuchi et al. in prep). BON in a Box could help by harmonizing these estimates and others for the purposes of evenly comparing regional **EBVs** estimates and of calculating standardized, global **EBVs** and **indicators** for reporting to the CBD. Harvesting outputs from various efforts (e.g., those with national, regional, or global scopes) to generate **EBVs** estimates and combining them will likely require new functions and/or modules, and cooperation among **BONs** could help produce such tools for use in BON in a Box **pipelines**.

5. Conclusion

We believe that through open collaboration across the globe, we can host a collection of state of the art data-to-indicator **pipelines** that will assist with all aspects of biodiversity monitoring, planning, and reporting, from prioritizing sampling areas to tracking change to implementing the global biodiversity monitoring framework in countries across the world. By making these **pipelines** readily available to organizations, countries, and other parties of the CBD, BON in a Box can contribute to

turning raw data into biodiversity information that can be used for multiple tasks. These include prioritizing monitoring areas, biodiversity-inclusive spatial planning, assessing and reporting progress towards restoration and protection targets to the CBD and other multilateral agreements. BON in a Box can help government agencies, biodiversity observation networks, 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 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 the parties. This is especially important as national reporting deadlines for the KM GBF are quickly **approaching**. 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. 2023b), but this requires large-scale effort and collaboration. To achieve this vision, we encourage organizations or individuals producing **EBVs** or **indicator** code or have a major role in funding, guiding or supporting those who produce such code to contribute to BON in a Box.

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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>
- Balvanera P, Brauman K A, Cord A F, et al (2022) Essential ecosystem service variables for monitoring progress towards sustainability. *Current Opinion in Environmental Sustainability* 54:101152. <https://doi.org/10.1016/j.cosust.2022.101152>
- Bellingham P J, Richardson S J, Gormley A M, et al (2020) Implementing integrated measurements of Essential Biodiversity Variables at a national scale. *Ecological Solutions and Evidence* 1:e12025. <https://doi.org/10.1002/2688-8319.12025>
- 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-Aroita 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>
- Cantonati M, Poikane S, Pringle C M, et al (2020) Characteristics, Main Impacts, and Stewardship of Natural and Artificial Freshwater Environments: Consequences for Biodiversity Conservation. *Water* 12:260. <https://doi.org/10.3390/w12010260>
- Crowther T W, Thomas S M, Hoogen J v d, et al (2022) Restor: Transparency and connectivity for the global environmental movement. *One Earth* 5:476–481. <https://doi.org/10.1016/j.oneear.2022.04.003>
- Elith J, Leathwick J R (2009) Species Distribution Models: Ecological Explanation and Prediction Across Space and Time. *Annual Review of Ecology, Evolution, and Systematics* 40:677–697. <https://doi.org/10.1146/annurev.ecolsys.110308.120159>
- 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>
- Hoban S, Bruford M, D'Urban Jackson J, et al (2020) Genetic diversity targets and indicators in the CBD post-2020 Global Biodiversity Framework must be improved. *Biological Conservation* 248:108654. <https://doi.org/10.1016/j.biocon.2020.108654>
- 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>
- 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, Pinilla-Buitrago G E, Paz A, et al (2023) wallace 2: a shiny app for modeling species niches and distributions redesigned to facilitate expansion via module contributions. *Ecography* 2023:e6547. <https://doi.org/10.1111/ecog.06547>
- 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>
- Köster J, Rahmann S (2012) Snakemake—a scalable bioinformatics workflow engine. *Bioinformatics* 28:2520–2522. <https://doi.org/10.1093/bioinformatics/bts480>
- 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>
- Lumbierres M, Abecasis D, Alcaraz-Segura D, et al (2024) EuropaBON EBV workflow templates. <https://doi.org/10.5281/zenodo.10971094>
- 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>
- McGowan P J K, Hutchinson A, Brooks T M, et al (2024) Understanding and achieving species elements in the Kunming–Montreal Global Biodiversity Framework. *BioScience* biae65. <https://doi.org/10.1093/biosci/biae065>
- Milner-Gulland E J, Addison P, Arlidge W N S, et al (2021) Four steps for the Earth: mainstreaming the post-2020 global biodiversity framework. *One Earth* 4:75–87. <https://doi.org/10.1016/j.oneear.2020.12.011>
- 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, Andrade A, Brooks T M, et al (2024) Roles of the Red List of Ecosystems in the Kunming-Montreal Global Biodiversity Framework. *Nature Ecology & Evolution* 8:614–621. https://doi.org/10.1038/s41559-023-02320-5
- 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
- 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
- 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
- Royaux C, Mihoub J-B, Jossé M, et al (2024) Guidance framework to apply best practices in ecological data analysis: Lessons learned from building Galaxy-Ecology
- 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
- 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
- Schwantes A M, Firkowski C R, Affinito F, et al (2024) Monitoring ecosystem services with essential ecosystem service variables. *Frontiers in Ecology and the Environment* 22:e2792. https://doi.org/10.1002/fee.2792
- Sillero N, Campos J C, Arenas-Castro S, Barbosa A M (2023) A curated list of R packages for ecological niche modelling. *Ecological Modelling* 476:110242. https://doi.org/10.1016/j.ecolmodel.2022.110242
- Stevenson S L, Watermeyer K, Caggiano G, et al (2021) Matching biodiversity indicators to policy needs. *Conservation Biology* 35:522–532. https://doi.org/10.1111/cobi.13575
- 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 (2017a) 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 (2017b) 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
- Vihervaara P, Auvinen A-P, Mononen L, et al (2017) How Essential Biodiversity Variables and remote sensing can help national biodiversity monitoring. *Global Ecology and Conservation* 10:43–59. https://doi.org/10.1016/j.gecco.2017.01.007
- Watts M E, Stewart R R, Martin T G, et al (2017) Systematic Conservation Planning with Marxan. *Learning Landscape Ecology: A Practical Guide to Concepts and Techniques* 211–227