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Biologist's Toolbox

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

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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 because of fragmented biodiversity monitoring efforts, technical barriers, a lack of available data and tools, and capacity bottlenecks. The BON in a Box platform for biodiversity monitoring and indicator calculation, developed by the Group on Earth Observations Biodiversity Observation Network, was created to address these challenges by providing open, transparent, and reproducible analysis pipelines that convert data into essential biodiversity variables and indicators. These pipelines are built by experts and contributed by the community, follow FAIR principles, and help scientists apply their research to coordinate biodiversity monitoring efforts, build capacity to track progress toward the GBF, and affect policy change.

Keywords: biodiversity goals and targets, biodiversity observation network, capacity building, Convention on Biological Diversity, essential biodiversity variables

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. 2023b). 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 2022a). The ambitions of the agreement are captured by 23 action targets to be achieved by 2030 and four outcome-focused goals for 2050 (CBD 2022a, Hughes and Grumbine 2023). To meet these objectives, countries are aligning their governmental plans and programs with the GBF through their national biodiversity strategies and action plans to ensure that necessary measures are integrated into national policy and practice (Perino et al. 2022, Sandström et al. 2023).

The GBF is accompanied by a monitoring framework that provides a set of indicators to evaluate progress toward the GBF's

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goals and targets (CBD 2022b). 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. There are 36 headline and 14 binary indicators which parties are required to report to the CBD, and 52 component and 257 complimentary indicators that are voluntary for reporting and provide additional insight into the status and trends of biodiversity. For example, the Red List Index headline indicator measures changes in species extinction risk over time and is aligned with goal A and target 4 of the GBF, which are focused on halting human-induced extinctions (CBD 2022a, 2022b, Raimondo et al. 2023). Similarly, the Protected Connected Index (ProtConn) component indicator evaluates progress toward target 3, which aims to establish well-connected protected area networks that cover 30% of terrestrial and marine areas by 2030 (CBD 2022a, 2022b, Saura et al. 2017, 2018). The indicators in the monitoring framework are intended to provide a streamlined but comprehensive structure 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 and reporting burden of the monitoring framework pose significant challenges. With the seventh national reports due by 28 February 2026 (CBD 2022c) and the eighth reports due by June 2029, many parties require significant scientific and technical support to compile data, calculate indicators, and validate their national values to meet these reporting requirements.

The Group on Earth Observations Biodiversity Observation Network (GEO BON), among other organizations, has been invited by the Conference of the Parties to the CBD to support the implementation of the GBF and its monitoring framework. GEO BON is an international network of over 3900 researchers in 158 countries dedicated to improving the collection, coordination, and dissemination of biodiversity information at the global, regional, and national scales. GEO BON supports the monitoring framework by building on more than a decade of effort by GEO BON experts to monitor biodiversity, improve access to biodiversity information, and bridge the gaps among biodiversity science, monitoring, and policy to provide more effective responses to the goals of the GBF (Navarro et al. 2017). For example, GEO BON has assembled biodiversity observation networks (BONs), which are organized networks of researchers monitoring biodiversity across national (e.g., China BON, Colombia BON, France BON, Japan BON) and regional scales (e.g., Europa BON, Asia-Pacific BON, Arctic BON) or thematic realms (e.g., Marine BON, Freshwater BON, Omic BON, Soil BON, Move BON).

Another notable GEO BON initiative is the development of the essential biodiversity variables (EBV) framework, which identifies a standardized set of variables to assess the status and trends of biodiversity (Pereira et al. 2013, Brummitt et al. 2017). 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), and taxa (Schmeller et al. 2017b, Turak et al. 2017b, 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. 2017a). Given they are systematically collected over time and space, EBVs provide the standardized information needed to derive indicators of biodiversity change (figure 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 them is complex. The methodologies for indicator calculation are often embedded within scientific publications, and the associated computer code is not always openly available, requiring significant effort and expertise to interpret, recalculate, or implement (Orr et al. 2022, 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, and methodological differences in calculation can make cross-party comparisons challenging (Bhatt et al. 2020, Kühl et al. 2020, Kumagai and Niamir 2022). Additionally, many parties have concerns about maintaining sovereignty over data, analysis, and interpretation and do not want to rely on tools that use opaque, black-box methodologies or fail to incorporate country-specific data (Gonzalez and Londoño 2022). Ensuring greater transparency, accessibility, and standardization in these workflows is therefore essential to enhance efficiency and foster confidence in biodiversity monitoring and reporting efforts (Kumagai and Niamir 2022).

There is a pressing need for an open analysis platform 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, nongovernmental organizations, 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 user-friendly, interoperable, fully transparent, customizable, and underpinned by scientific best practices. It should enable seamless integration of data from publicly available data sets while also allowing for the incorporation of user-provided data, recognizing that many users have local data not included in national or global repositories (Güntsch et al. 2025). Additionally, the platform 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 (Navarro et al. 2017, Muthee et al. 2022, Hébert et al. 2025).

Here, we introduce the newest version of BON in a Box as a platform to organize, share, and run analyses to calculate EBVs and indicators. We emphasize the importance of mobilizing the scientific expertise of the GEO BON community and providing countries, organizations, and BONs with an extensive and carefully curated 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 and peer-reviewed 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

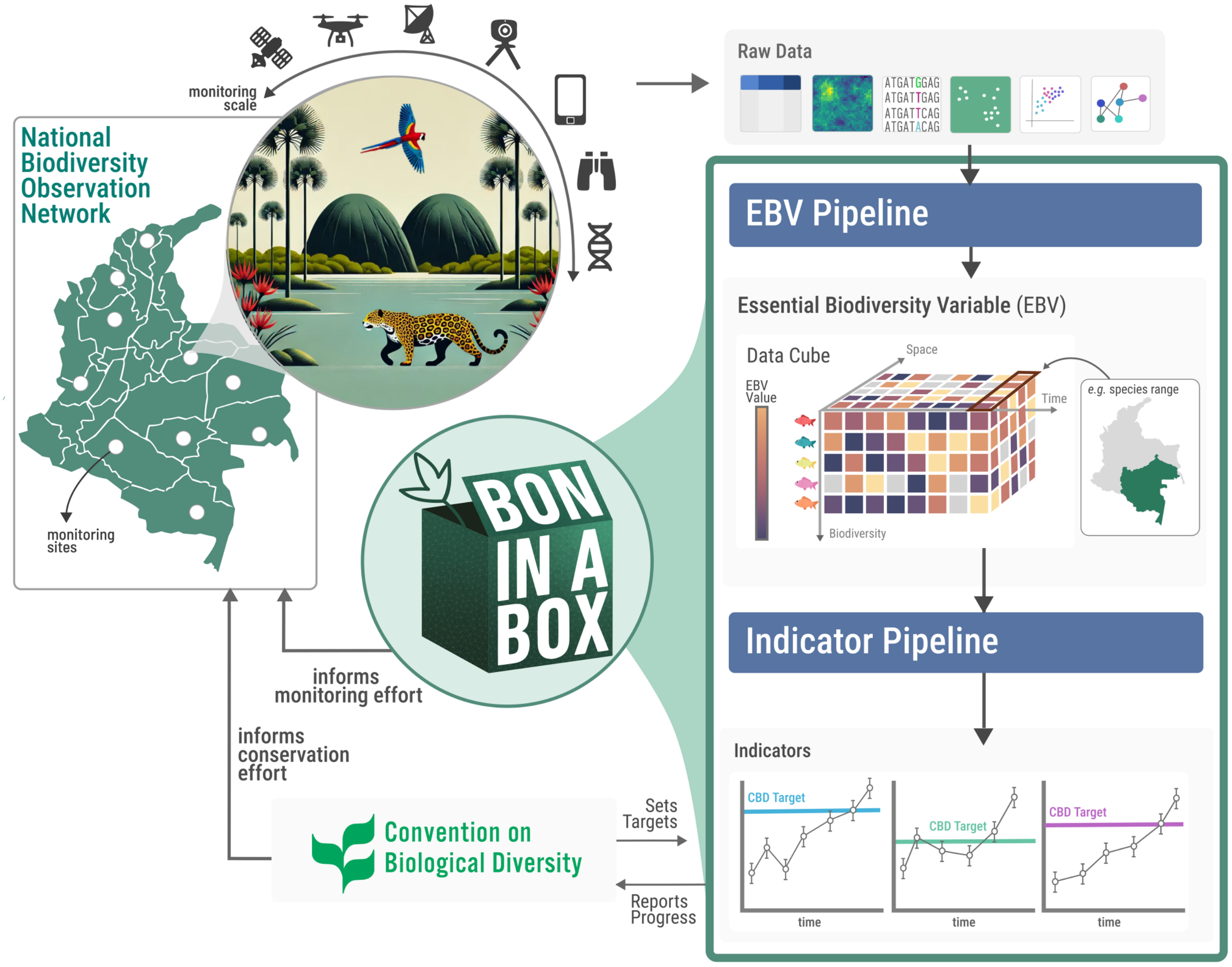


Figure 1. BON in a Box can help inform monitoring efforts by prioritizing sampling areas and assessing biodiversity change by executing complex workflows that generate EBVs and indicators from raw data. An example national BON for Colombia is shown on the left, with each dot representing a given monitoring site. On the right, an example EBV for a hypothetical community of cichlid fishes in Colombia is produced from raw data, resulting in a data cube of this EBV across different locations and times. This EBV then contributes to computation of a hypothetical indicator, which would support national, subnational, and thematic BONs in reporting to the United Nations Convention on Biological Diversity, while also guiding conservation planning and assessing progress toward biodiversity goals.

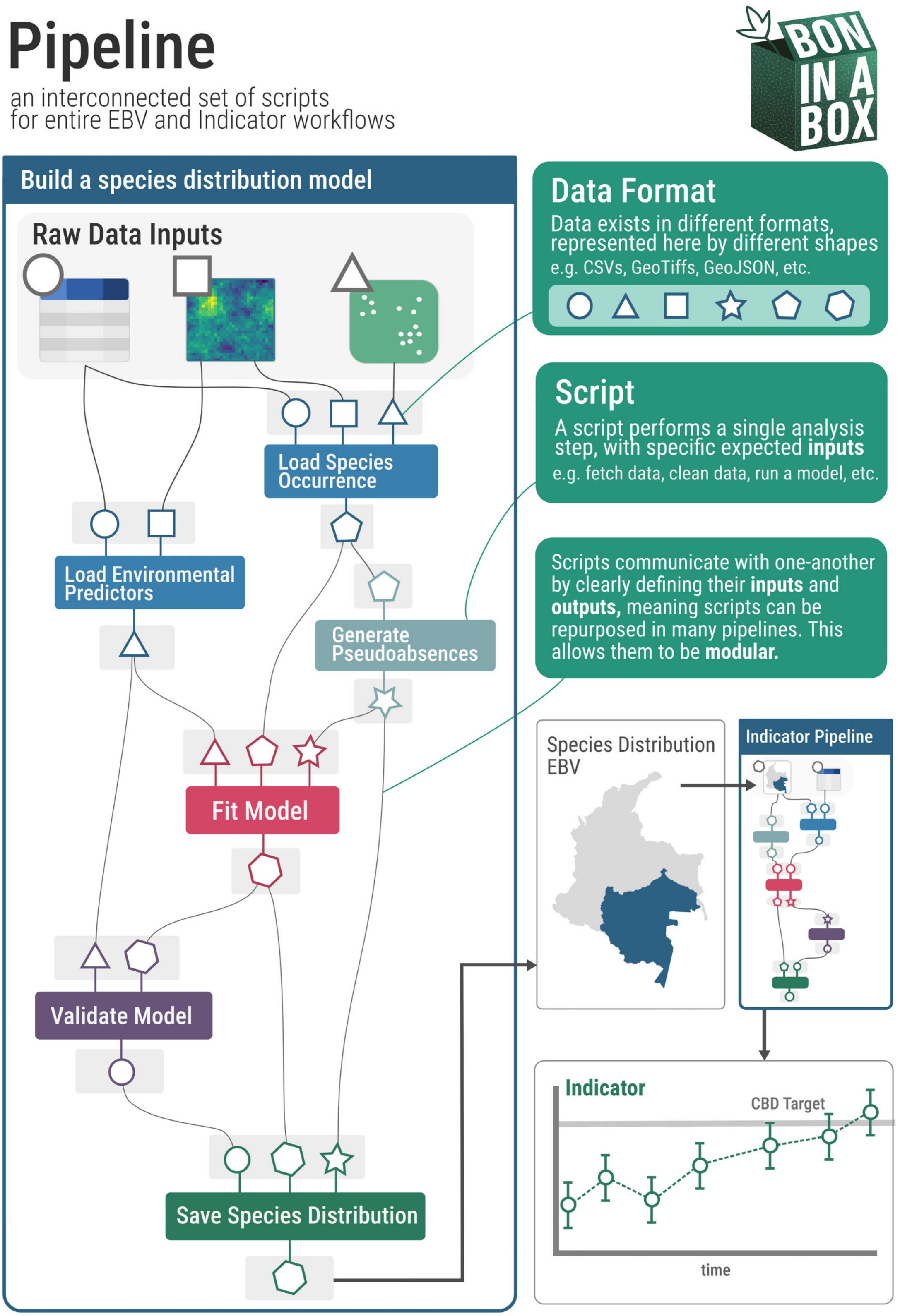
BON in a Box will support biodiversity policy at all levels, from guiding monitoring efforts and tracking progress to informing meaningful conservation and management actions worldwide.

BON in a Box overview

BON in a Box began as a portal where users can find and share projects and tools (Navarro et al. 2017, Langer and Londoño-Murcia 2021) to support the establishment and operation of BONs. In the present article, we introduce the next version of the BON in a Box platform (https://boninabox.geobon.org), 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. The new version of BON in a Box enhances the platform's capacity to support biodiversity monitoring and reporting efforts globally by providing a toolkit to share and run analyses to calculate EBVs and indicators in an open, transparent, and standardized way. BON in a Box follows an open source and bottom-up approach that reinforces the GEO BON values of excellence, collaboration, and shared purpose, as well as transparency, openness, and inclusivity throughout its network (supplemental table S1). By allowing users to share their analysis methods, BON in a Box fosters coordination and standardization among BONs, countries, and organizations, promoting collaborative and efficient biodiversity monitoring efforts (figure 1).

The software underlying BON in a Box, hereafter referred to as *the pipeline engine*, provides a user interface to build, parameterize, and run analysis pipelines and to view their outputs in an interactive dashboard. Users can launch the pipeline engine by cloning a GitHub repository onto their computer and can modify code and run pipelines directly from that folder. The pipeline engine is built on containerization technology, using Docker and Docker Compose to create reproducible and isolated execution environments. This ensures that pipelines run consistently, regardless of the host machine's configuration. The pipeline engine maintains data sovereignty by running on the user's own computer or server infrastructure through the use of the containerized web microservices. This architecture allows the BON in a Box pipeline engine to be highly portable, customizable, and decentralized.

Pipelines are connected sequences of steps to run analyses from start to finish in an automated way without manual inter-



Pipeline

an interconnected set of scripts for entire EBV and Indicator workflows

Data Format

Data exists in different formats, represented here by different shapes e.g. CSVs, GeoTiffs, GeoJSON, etc.

Script

A script performs a single analysis step, with specific expected **inputs** e.g. fetch data, clean data, run a model, etc.

Scripts communicate with one-another by clearly defining their **inputs** and **outputs,** meaning scripts can be repurposed in many pipelines. This allows them to be **modular.**

Figure 2. A BON in a Box pipeline is a series of interconnected, modular scripts to automate the transformation of data into EBVs and indicators. Each script is linked through inputs and outputs of particular file types (represented by different shapes), which can also be accessed and downloaded as intermediate results. These pipelines are fully customizable, allowing users to adapt them to meet specific needs and contexts.

vention (figure 2). Contributors can build a pipeline in BON in a Box on the basis of an existing workflow that calculates an EBV or indicator. Building a pipeline involves separating the workflow into steps, which are represented by individual scripts parameterized with custom inputs and outputs specified and described through a YAML file. These scripts are then connected to form pipelines in 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, GeoPackage) or can be provided directly by the user through a form automatically generated for each pipeline. Because inputs and outputs are in standard file formats, scripts written in different programming languages (e.g., R, Python, Julia) can be connected in a single pipeline. Additionally, scripts are designed to be modular, meaning they perform a specific task and can be easily combined in different ways and reused in other pipelines. Users can view and download the intermediate results and code for each script, ensuring full transparency throughout the process. Additionally, each script and pipeline is thoroughly documented with accompanying annotations, providing clear explanations of the scientific context, purpose, inputs, outputs, and relevant citations. BON in a Box pipelines and scripts adhere to the FAIR principles by ensuring they are findable through metadata and persistent identifiers, accessible via open and well-documented interfaces, interoperable through the use of common file formats and standard coding languages, and reusable through their detailed documentation and modular design. 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. Rather than manually editing code to adapt for different contexts, (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 runs are saved and can be accessed by the user 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 local data sets rooted in knowledge and context and may distrust precalculated data layers or indicators generated with global data. Additionally, they may be concerned about maintaining sovereignty over their data and how it is used (Gonzalez and Londoño 2022). To address these concerns, BON in a Box allows users to run each pipeline using custom data, and because it can be deployed locally on any server or computer, these data do not need to leave the organization. When such data are not available, pipelines can pull directly from a variety of publicly available data sets such as GBIF (2025), GEO BON's EBV portal (Langer et al. 2022), and the International Union for Conservation of Nature (IUCN 2025). 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 interface (see supplemental table S2 for a comparison to other platforms).

The strength of BON in a Box as a community-contributed platform is its foundation of scientific expertise by GEO BON members. BON in a Box provides a platform to mobilize and operationalize the varied knowledge of the growing community of GEO BON members as both pipeline contributors and reviewers. Experts who have developed a workflow to calculate EBVs or indicators can share these analyses in a user-friendly, transparent, and reproducible way. This bottom-up approach helps disseminate the research of scientists and bridge the gap between scientists and policymakers by increasing the usability and interpretability of analysis methods. Additionally, all BON in a Box pipelines will be peer-reviewed and curated by GEO BON experts, ensuring that they deliver scientifically sound outputs for users. Reviewers are provided with a standard checklist to evaluate criteria such as the functionality of the pipeline, scientific rigor of the methods, clarity of the documentation and guidelines for interpretation, generalizability, and novelty. Pipeline code is published in an open-access repository and given a DOI, incentivizing researchers by making their pipelines accessible and enabling users to cite them in their reporting. BON in a Box helps GEO BON achieve the vision of a globally coordinated network of biodiversity researchers by allowing the community to share, review, and build on analyses to generate useful biodiversity information.

BON in a Box is a simple but powerful platform designed to support a wide range of users, from researchers to policymakers. We see the platform as having two main user groups: users who both contribute and run pipelines and users who only run them. The first group is expected to consist primarily of academic researchers, government agencies, or nongovernmental organizations working on biodiversity analyses intended for broader use. BON in a Box simplifies the process of organizing, sharing, and testing biodiversity analyses for these users, allowing for more collaborative and transparent development. These users may also run and build on pipelines developed by others for their own research or to inform policy decisions. The second group represents those who need to calculate biodiversity metrics for reporting to the CBD or other entities (e.g., the financial sector). These users still need to have domain knowledge of biodiversity to parameterize the pipelines and validate the outputs (e.g., a scientist in a national environmental ministry) but are not involved in indicator development. For these users, access to BON in a Box pipelines saves time, money, and resources; helps build capacity; and ensures that the methods are scientifically robust. In summary, BON in a Box is a platform that helps increase collaboration between scientists and bridge the gap between science and implementation of the GBF's monitoring framework by creating a more harmonized and open biodiversity knowledge system.

Pipeline examples

The following section describes examples of pipelines available in BON in a Box. It demonstrates the ability of the platform to support a wide range of use cases (figure 3).

Species distribution models

Determining the change in extent of species' geographic ranges is essential for understanding trends in biodiversity patterns related to goal A of the GBF. However, less than 7% of the world is well sampled (at 5 kilometer resolution), 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 employ these data to build species distribution models (SDMs) to estimate species distributions. SDMs use a range of modeling methods, from simple linear or envelope models to machine-learning approaches, to make spatially explicit predictions of where species are likely to occur on the basis of 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 appli-

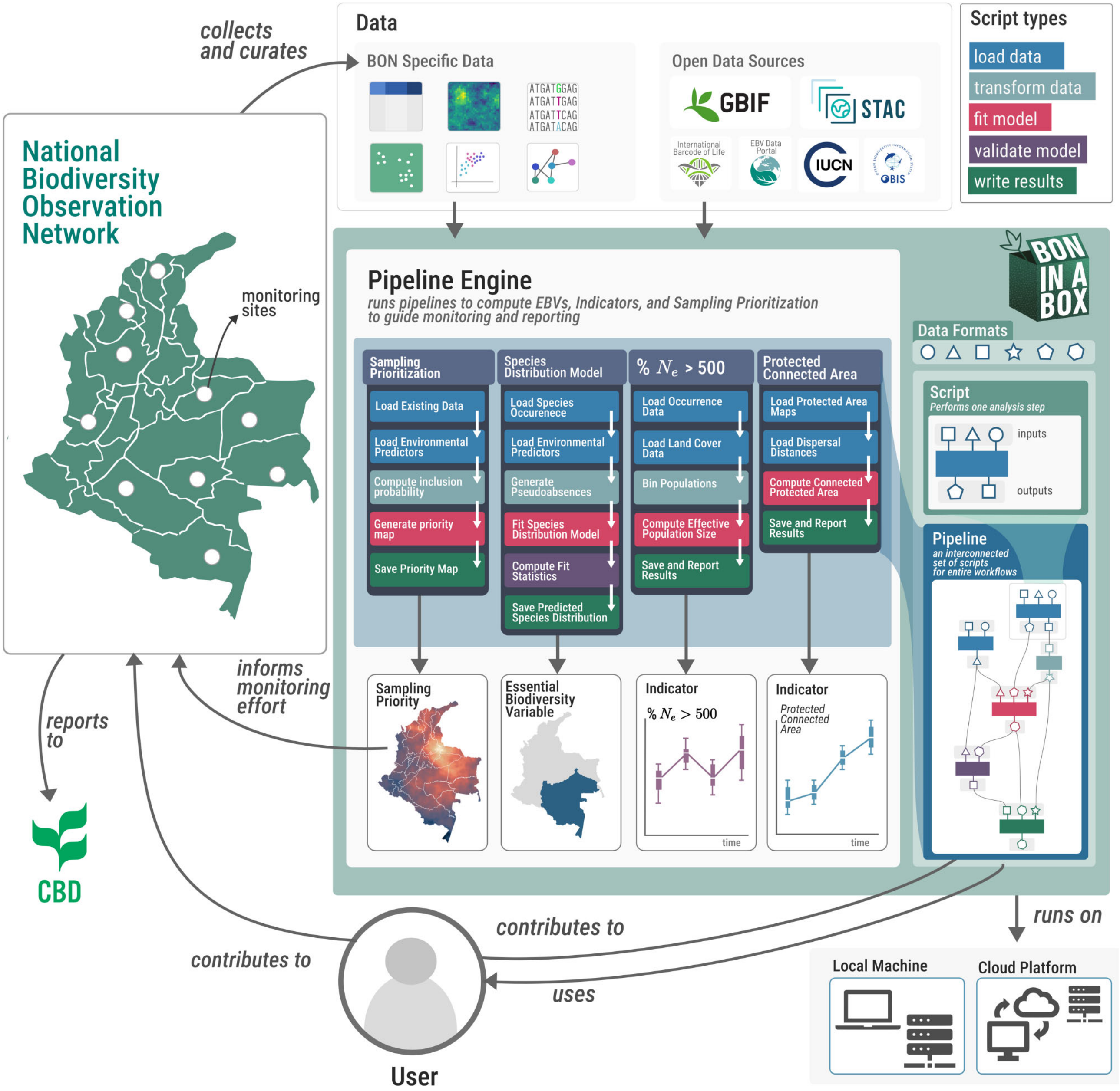


Figure 3. The service model for how BON in a Box can be used to facilitate a global biodiversity observation system (Gonzalez et al. 2023b). Community support from the GEO BON network both maintains BON in a Box, and aids countries and other organizations in implementing BON in a Box. Users from national or regional BONs (e.g., users from a particular monitoring site for the Colombia BON on the left) can choose to either run their own instance or consult 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.

cations. 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 (Ferrier et al. 2004), Species Habitat Index (Powers and Jetz 2019), and Species Protection Index (Jetz et al. 2022). A wide diversity of open programming tools exist for SDMs, and although using them together improves analytical standards (Kass et al. 2025), they require some technical expertise. BON in a Box contains automated pipelines that build expert-supported SDMs using various methods such as boosted regression trees (Elith et al. 2008), maximum entropy (Phillips et al. 2017), and effort-weighted log-Gaussian Cox processes (Simpson et al. 2016). Users can run, adjust parameters, validate and measure performance, and visualize their outputs, which can then be directly plugged into pipelines as base layers to calculate indicators. This allows users to calculate indicators on the basis of existing SDM outputs or SDM pipelines without repeating analyses or downloading large files to local computers.

Proportion of populations with an effective size larger than 500

BON in a Box can also be used to beta-test and pioneer new methodologies. The BON in a Box team 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 over 500 (CBD 2022b), otherwise known as the $N_e > 500$ indicator (Hoban et al. 2020, Mastretta-Yanes and da Silva et al. 2024). Effective population size (N_e), which is listed as an 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 the number of mature individuals (census size, N_c) but is 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 Ne 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). The global assessment required by the GBF is not feasible through genetic sequencing alone because access to remote or hazardous regions and resources for sequencing at scale are limited (i.e., due to required costs and person-hours). Census data are readily available for many species, which enable the calculation of this indicator using the N_e:N_c ratio when genetic data is lacking (Mastretta-Yanes and da Silva et al. 2024). To scale capacity to report on this headline indicator for more species and regions, the Genes from Space team created a pilot method to estimate N_c 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., on the basis of GBIF occurrences). Given a population density estimate, the habitat size for different populations is used to estimate N_c and then N_e using the ratio between N_e and N_c known from expert knowledge, following the approach demonstrated in Mastretta-Yanes and da Silva and colleagues (2024) for the national indicator assessment in Belgium. The pipeline also reports the genetic diversity indicator populations maintained (PM), a complementary indicator in the GBF (Hoban et al. 2020). 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 (Hoban et al. 2020). Given that DNA sequence information and long-term census monitoring data are rare for most monitored species, this pipeline allows users to estimate the $N_e > 500$ indicator when no other data are available, and to prioritize species or regions for *in situ* monitoring.

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 2022b). 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 on the basis of their distance from one another. The BON in a Box ProtConn pipeline uses the R package Makurhini (Godínez-Gómez et al. 2025) to calculate the percentage of land area that is protected and connected and compares it with CBD targets. The pipeline calculates ProtConn using the World Database of Protected Areas (UNEP-WCMC and IUCN 2025) or user input protected area polygons. The user also specifies 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.

Vision

Our vision is for BON in a Box to become a comprehensive platform that optimizes biodiversity monitoring efforts, provides a standardized and curated platform for calculating biodiversity variables and indicators, and lowers barriers to sharing and reporting biodiversity information. To achieve this vision, we aim to improve accessibility by making the pipeline engine more user-friendly and usable on a large scale, to expand the range of EBVs and indicators available within BON in a Box and integrate with CBD reporting mechanisms, to develop pipelines to guide sampling prioritization and monitoring efforts effectively, and to implement a service model to better adapt BON in a Box to the needs of its users. We outline these priorities below and discuss how they will help increase the usability and impact of the platform.

Accessibility

We are working on improving the BON in a Box platform to increase accessibility and usability. Although it is currently offered as a downloadable software, we plan to host a globally accessible web platform. Additionally, improvements are underway to enable wider use and greater computing capabilities by integrating the platform with remote, scalable high-performance computing resources. This approach will ensure that even users without sufficient cyberinfrastructure can run analysis pipelines and easily compute and download results for their country or region of interest.

Expand pipeline offerings and integrate with CBD reporting mechanisms

By leveraging the expertise of the GEO BON community and beyond, we are in the process of expanding the range of pipelines available to include all GEO BON EBVs and indicators in the GBF monitoring framework. We are in discussions with the CBD about linking BON in a Box with their reporting mechanisms to streamline the process for parties calculating and reporting with indicators.

Additionally, we are expanding BON in a Box as a platform 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 BONs, governments, nongovernmental organizations, and other organizations. BON in a Box has huge potential as a platform 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 on their own server infrastructure to run, 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 platform. By facilitating collaboration within and between BONs, BON in a Box can become a necessary platform in forming the Global Biodiversity Observing System (Gonzalez et al. 2023b)—an international monitoring system comprising a network of BONs.

Sampling prioritization

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 detecting and attributing changes in biodiversity and ecosystem function (Gonzalez et al. 2023a) and generating reliable biodiversity indicators (Orr et al. 2022). Additionally, countries and organizations often have limited resources to establish and sustain biodiversity monitoring programs (Schmeller et al. 2017a). Therefore, a critical component of successfully implementing the Monitoring Framework is the development of well-designed biodiversity monitoring programs that efficiently and robustly detect biodiversity change and attribute them to causal drivers (Gonzalez et al. 2023a). 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, these pipelines will contribute to generating more robust data, providing decision-makers with stronger evidence to guide conservation actions.

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 adapted to their technical capacities and expected development needs. BON in a Box is free to install and use, but customization will be needed for the diverse set of potential users, including the many parties to the CBD. We propose a service model that allows a range of users access to BON in a Box services through collaboration with GEO BON experts and the BON in a Box team. Three distinct options can be codeveloped with the user to suit their current technical demands but maintain an eye on likely future needs.

The first option is that a member or member organization downloads BON in a Box from the GEO BON GitHub repository and runs analyses on their local computer or server. Initial setup 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. This is a free tier and recommended for scientists or organizations using BON in a Box to collaboratively develop and contribute pipelines, aimed at those with adequate knowledge to parameterize and validate pipeline outputs themselves.

Under option 2, an organization runs an analysis remotely on an instance hosted on the GEO BON server. Various levels of support by GEO BON experts would be offered to the organization regarding data and pipeline selection and training on how to use the platform. This tier would be recommended for institutional users who want to run pipelines for generating reports, but require guidance on which pipelines to use and how to parameterize them to achieve desired results.

With option 3, the GEO BON team runs the analysis (end to end) for an organization on the GEO BON server. The analysis is run by the BON in a Box team after a period of analysis codesign, 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 platform into their monitoring program. This option is recommended for parties or organizations that require custom pipelines tailored to their context and priorities.

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 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 national biodiversity strategies and action plans 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, whereas 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 norms (e.g., the 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.

In summary, our vision is to create a living toolkit that is frequently developed and strengthened by the users and the diverse network of GEO BON experts and collaborators (figure 4). The platform will support biodiversity policy at every level, improving biodiversity information by guiding monitoring efforts, assessing biodiversity change, and informing action.

Caveats

Although BON in a Box helps simplify the process of creating and running biodiversity monitoring workflows, it is important to note several considerations and limitations. Producing accurate results from BON in a Box pipelines requires knowledge of the system that is being analyzed. There may be multiple pipelines for the same analysis—for example, different types of species distributions models—and the user needs to be able to choose one that is suitable for the available data, species and location of interest. Additionally, the user will need some knowledge to accurately parameterize the pipelines. For example, the $N_e > 500$ pipeline requires an estimate of the population density of the species. Furthermore, all input data needs to be verified and scientifically accurate. Custom data input by users need to be correctly formatted, which likely requires preprocessing, cleaning, and verification. The outputs of BON in a Box require validation by experts in the area, and results should ideally be ground truthed. Therefore, we recommend that the results of pipelines in BON in a Box are validated by users with scientific expertise and domain knowledge on biodiversity before results are presented to policymakers.

Conclusions

Through BON in a Box, we can host a collection of open, transparent, reusable, scientifically robust pipelines that transform data into EBVs and indicators to assist with many aspects of biodiversity monitoring, planning, and reporting required by the GBF and other multilateral environmental agreements. BON in a Box generates biodiversity information relevant for prioritizing monitoring

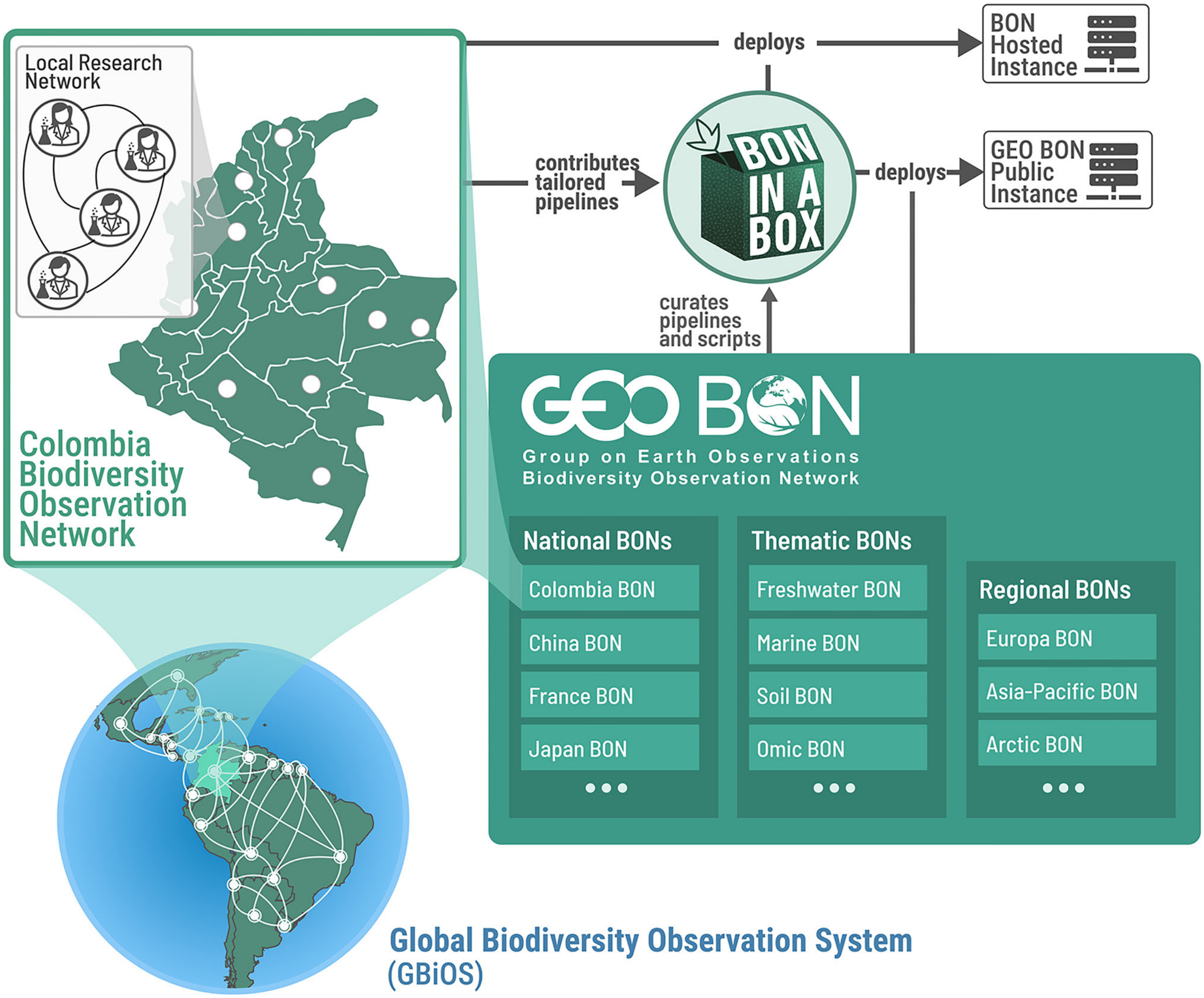


Figure 4. BON in a Box is a platform to increase the quality of and access to biodiversity information by informing monitoring efforts (sampling prioritization) and calculating EBVs (e.g., SDMs) and GBF indicators (e.g., $N_e > 500$, headline indicator A.4) in an open, standardized, and user-friendly way. BON in a Box contains pipelines, or a set of individual steps (scripts or subpipelines) 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 (see figure 2). Pipelines can be run with publicly available data, user-provided (BON derived) data, or both. All pipelines are contributed and vetted by members of the scientific community. BON in a Box can be run on a local computer or on a remote server (cloud platform).

areas, biodiversity-inclusive spatial planning, assessing and reporting progress under the monitoring framework of the GBF, and many other applications at subnational 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. By making analysis pipelines readily available to organizations, countries, and other parties of the CBD, BON in a Box facilitates knowledge transfer and overcomes many technical and capacity barriers to calculating and reporting indicators, demonstrating potential to become an integral part of the successful implementation of the monitoring framework. Additionally, it is intended to assist with the establishment of a global biodiversity observation system where biodiversity information is shared across organizations, borders, and scales, creating near-real-time updates on the status and trends of biodiversity to enable collective action (Gonzalez et al. 2023b), but this requires large-scale effort and collaboration. To achieve this vision, we welcome early input from governments and stakeholders to match the sequence of pipeline development in BON in a Box to the priorities of users. Additionally, we encourage organizations or individuals producing EBV or indicator workflows, or who have a major role in funding, guiding or supporting those who produce such code, to contribute to BON in a Box.

Authorship statement

Ms. Jory Griffith led the writing and editing of the manuscript, integrated text from co-authors, and coordinated manuscript submission. She contributed to the development and integration of many pipelines in the BON in a Box platform.

Mr. Jean-Michel Lord coordinated the manuscript planning meetings and contributed to the writing and editing of the manuscript. He has led the software development of the BON in a

Table 1. 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 of status and trend biodiversity indicators to inform conservation, restoration and sustainable use objectives.
Biodiversity Observation Network (BON)	A network of observation sites or stations 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 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).
Kunming-Montreal 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 2022a).
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 (GBF 2022a).
GBF Targets	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 (GBF 2022a).
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 on the development of national and regional monitoring systems, including the technologies, tools, networks and communities needed to sustain monitoring.
Parties	Member states including 196 countries and the EU that have ratified the CBD treaty. Parties negotiate to adopt or revise CBD strategies and frameworks during the biennial Conference of the Parties.
Essential Biodiversity Variable (EBV)	"A biological variable that critically contributes to the characterization of Earth's biodiversity; they are a minimum set of common and complementary sets 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 data sets (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. Within the GBF there are 36 headline, 13 binary, 52 component and 257 complementary indicators.
Pipeline engine	The software that allows the user to build, parameterize, and run pipelines in the BON in a Box platform.
Script	A sequence of code written in a programming language that accomplishes a single task, such as data cleaning, analysis, visualization, or modeling.
Workflow	A structured, stepwise process for analyzing data from raw data to a derived metric. This can include steps such as data cleaning, data integration, analysis, and visualization.
Pipeline	A sequence of steps connected to automate an entire analysis workflow, from the input parameters to the analysis result. In the context of BON in a Box, pipelines are scientific workflows to analyze biodiversity data that have been contributed by collaborators and adapted to be parameterized and run automatically within the pipeline engine.
Modular programming	A software design philosophy where every component does *one* thing well, and one thing only (part of the UNIX philosophy). It results in smaller pieces that are easier to combine, maintain, document and re-use.

Table 1. Continued

FAIR principles	A set of guidelines to improve management, sharing, and reuse of scientific data and digital resources. FAIR stands for *findable* (data and resources should be easy to find for both humans and machines), *accessible* (data and resources should be retrievable using open protocols), *interoperable* (data and tools should use shared, standard formats, vocabularies, and ontologies so they can work together across different systems), and *reusable* (data and resources should be well-described and licensed so others can understand, reproduce, and build on them).

Box platform and coordinated the project since the implementation of the pipeline engine.

Dr. Michael D. Catchen created the figures, and contributed to the writing and editing of the manuscript. He also contributed to pipeline development to the BON in a Box platform since the initial development of the pipeline engine.

Mrs. Maria Isabel Arce-Plata contributed to pipeline conceptualization and implementation (Species Habitat Index), editing and revision of the manuscript.

Prof. F. Guillaume Blanchet helped guide the initial design and development of the Pipeline Engine, co-led the development of two SDM pipelines, and contributed to manuscript revisions.

Mr. Mathusan Chandramohan contributed to the maintenance of the BON in a Box website, including bug fixes and feature enhancements.

Ms. M. Camila Diaz-Corzo contributed to the development of several pipelines, including the Red List Index.

Prof. Dominique Gravel helped guide the initial design and development of the pipeline engine, co-led the development of two SDM pipelines, and contributed to manuscript revisions.

Mr. César Gutiérrez contributed to the early conceptualization of BON in a Box, led the development of the project portal component for version 2.0, and participated in manuscript review.

Dr. Isabelle S. Helfenstein contributed (with many others) to the conceptual basis of BON in a Box tool for the genetic diversity indicator; contributed text on the genetic diversity indicator and tool.

Dr. Sean Hoban: contributed (with many others) to conceptual basis of BON in a Box tool for the genetic diversity indicator; wrote and edited text on the genetic diversity indicator; minor edits of text.

Prof. Jamie M. Kass contributed to writing and editing of the manuscript, as well as pipelines to calculate species-level EBVs.

Prof. Linda Laikre contributed (with many others) to the conceptual basis of BON in a Box tool for the genetic diversity indicator; contributed text on the genetic diversity indicator and tool.

Dr. Guillaume Larocque: a developer on the BON in a Box platform working on front-end design, geospatial data management, and pipeline implementation. Wrote small sections of the text and edited the paper.

Prof. Deborah M. Leigh co-contributed (with many others) to the development of the BON in a Box tool for the genetic diversity indicator; contributed to the text on the genetic diversity indicator and tool.

Prof. Brian Leung co-contributed (with others) to the development of the BON in a Box tool for SDMs, and their bias corrections.

Dr. Alicia Mastretta-Yanes contributed (with many others) to the conceptual basis of BON in a Box tool for the genetic diversity indicator; contributed text on the genetic diversity indicator and tool. Performed translations and proofread the Spanish version.

Dr. Katie L. Millette contributed (with many others) to the conceptual basis of the BON in a Box tool for the genetic diversity indicator and the writing and editing of the manuscript.

Ms. Maria Alejandra Molina Berbeo contributed by developing the pipelines, conceptualizing them, and editing the manuscript.

Mr. Dat Nguyen contributed to the development of SDM pipelines, focusing on bias correction.

Dr. Kari E. Norman contributed to conceptualization and writing of the manuscript and pipeline development.

Mrs. María Helena Olaya-Rodríguez to the conceptualization of the BON in a Box tool, the implementation of pipelines to calculate species-level EBVs, and participated in the review and editing of the overall manuscript.

Mr. Simon Pahls contributed to the development and implementation of the Genetic Diversity pipeline.

Ms. Kaitlyn Pereira contributed to the maintenance of the BON in a Box website, including bug fixes and feature enhancements.

Prof. Pedro Peres-Neto contributed to the conceptualization of BON in a Box, focusing on monitoring frameworks and user manual design, and assisted in manuscript editing.

Prof. Timothée Poisot contributed to the conceptualization of BON in a Box and its peer review mechanism, supervised pipeline development, and contributed to writing and revising the manuscript.

Prof. Laura J. Pollock contributed to the conceptualization of the new version of the BON in a Box platform. She led the development of a bias correction for SDMs, and contributed to writing and revising the manuscript.

Mr. Juan Carlos Rey-Velasco contributed to the development of several pipelines, including the Red List Index.

Mr. Victor J Rincon-Parra contributed to the development of several pipelines, including the Red List Index, and gave regular feedback on platform usability.

Dr. Claudia Roeoesli co-led the development of the genetic diversity pipeline, and contributed to manuscript writing and revision, especially the genetic diversity section.

Mr. François Rousseu contributed to the pipeline development and review (species distribution models).

Dr. Lina Maria Sánchez-Clavijo contributed to the conceptualization of the BON in a Box tool, the implementation of several pipelines to calculate species-level EBVs, and participated in the review and editing of the overall manuscript.

Prof. Meredith C. Schuman contributed (with many others) to the conceptual basis of BON in a Box tool for the genetic diversity indicator; contributed text on the genetic diversity indicator and tool.

Dr. Oliver Selmoni contributed (with many others) to the conceptual basis of BON in a Box tool for the genetic diversity indicator; contributed text on the genetic diversity indicator and tool.

Dr. Jessica M. da Silva contributed to the writing of the genetic diversity indicator and associated tool, and participated in the review and editing of the overall manuscript.

Mrs. Erika Suarez-Valencia contributed to the conceptualization of the BON in a Box tool, to the development of the project's portal, setup and testing of some pipelines and participated in the review of the overall manuscript.

Dr. Thilina D. Surasinghe contributed to designing the manuscript layout and writing/editing of the manuscript.

Dr. Eren Turak contributed to developing the conceptual basis of the manuscript, identifying the priority target audiences and writing the introduction, conclusion and other sections with a focus on EBV's and the end users of BON in a Box, especially governments, and thematic, regional and national BONs

Mr. Luis Fernando Urbina led the development of the Red List Index pipeline and several others.

Dr. Sarah Valentin contributed to the pipeline conceptualization and development (species distribution models, geospatial data extraction).

Mr. Noah Wightman co-contributed (with others) to the development of the BON in a Box tool for SDMs, specifically on correcting sampling bias and quantifying uncertainty.

Dr. Juan Zuloaga co-contributed (with others) to the pipeline conceptualization and development.

Dr. Maria-Cecilia Londoño has contributed since 2015 in the conceptualization of BON in a Box and led the team for the development of the early version that contained the tool catalog. For this new version she leads the team at the Alexander von Humboldt Institute and contributed to the proposal for funding by Microsoft.

Prof. Andrew Gonzalez conceived of the new version of the BON in a Box platform and obtained funding from Microsoft and the Liber Ero Chair.

Supplemental material

Supplemental data are available at BIOSCI online.

Data availability

All BON in a Box pipelines are available on GitHub at https://github.com/GEO-BON/bon-in-a-box-pipelines. The code for the pipeline engine software is available at https://github.com/GEO-BON/bon-in-a-box-pipeline-engine. No new data were generated or analysed for this article.

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