BIODIVERSITY BUILDING BLOCKS FOR POLICY

M20 Established list of essential biodiversity variables and indicators to be implemented

28/02/2024

Author(s): Shawn Dove, Yanina Sica, Sandra MacFadyen, Hanno Seebens

Funded by the European Union

This project receives funding from the European Union's Horizon Europe Research and Innovation Programme (ID No 101059592). Views and opinions expressed are those of the author(s) only and do not necessarily reflect those of the European Union or the European Commission. Neither the EU nor the EC can be held responsible for them.

Table of contents

Summary

This report provides a description of the general biodiversity indicators and variables that we have chosen to implement in task 5.1 of the B-Cubed project, and briefly describes the methodology, along with our reasoning and justification for choosing them.

In keeping with the goal of task 5.1, we primarily focus on general indicators and variables that are widely known or used, simple to calculate, and can be calculated from GBIF data alone. In this way we promote accessibility, ease of use, and longevity. We will implement five general indicators, namely species richness, evenness, rarity, Hill-Shannon diversity, and Hill-Simpson diversity, as well as two essential biodiversity variables, species occurrences and taxonomic distinctness. Together these should give a broad and intuitive overview of biodiversity. We will also implement three other variables, total occurrences, density of occurrences, and mean year of occurrences, which do not directly indicate biodiversity but provide helpful context for interpretation.

A secondary aspect of this task is to develop indicators to fill policy needs based on stakeholder feedback. Based on preliminary results from task 1.5 and 1.6, we identified data gaps and biases as an important theme. Specifically, we are developing an indicator of data sufficiency to measure whether any given GBIF dataset is complete enough to reliably calculate the general indicators we are implementing. We will also implement an indicator of landscape heterogeneity being developed in another task of the B-Cubed project, which can be used as a proxy indicator for biodiversity when there is not enough biodiversity data available.

Given that B-Cubed is an ongoing project and final results from stakeholder consultations are not yet available, the indicators and variables described in this milestone should not be considered final. As the task evolves, we may still implement additional indicators and/or variables to suit stakeholder needs.

List of abbreviations

BIP	Biodiversity Indicators Partnership
CBD	Convention on Biological Diversity
EBV	Essential Biodiversity Variable
EU	European Union
GBIF	Global Biodiversity Information Facility
GEO BON	Group on Earth Observations Biodiversity Observation Network
IAS	Invasive Alien Species
LPD	Living Planet Database
LPI	Living Planet Index
MEA	Multilateral Environmental Agreement
NGO	Non-Governmental Organisation
RLI	Red List Index
SRLI	Sampled Red List Index
WBI	Wild Bird Indicator

1. Introduction

Biodiversity indicators play a crucial role in monitoring biodiversity trends (Jones et al., 2011), assessing progress towards conservation goals (Buckland et al., 2012), and understanding the impacts of biodiversity policies (Nicholson et al., 2012). They also influence management decisions and resource allocation towards urgent conservation issues (Robertson & Hull, 2001). Governments use biodiversity indicators to set policies and report progress to Multilateral Environmental Agreements (MEA), non-governmental organisations (NGOs) use them to raise awareness about biodiversity issues, news media use them to report on government actions and environmental issues, researchers use them for analysis, and consultancies use them for reports (Biodiversity Indicators Partnership, 2011). They are thus a fundamental aspect of the science-policy interface.

One key aspect of indicators is that they convey information about something more than themselves and are therefore purpose-dependent (Biodiversity Indicators Partnership, 2011; Gregory et al., 2018; Wilson et al., 2016). Despite the lack of a clear definition for biodiversity, as Newman et al. (2017) point out, it broadly refers to the variation of life, structured into compositional, structural, and functional dimensions across different levels, including genetic, species, and ecosystem diversity (Fig. 1). Given its complexity, no single metric can fully capture its multifaceted nature. Consequently, a wide array of biodiversity indicators has been developed, varying from broad and simple to specific and complex.

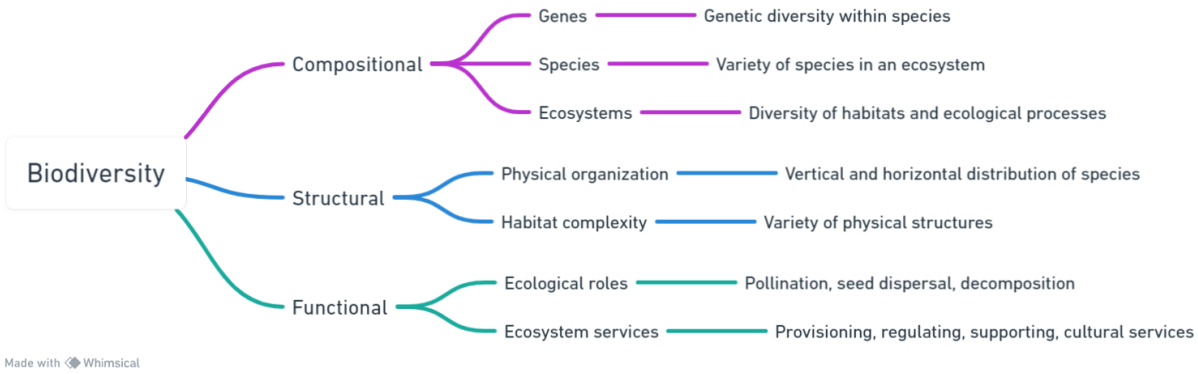

Figure 1: Simplified overview of biodiversity, illustrating its compositional, structural, and functional dimensions. This encompasses genetic variability, species richness, ecosystem types, habitat configuration, ecosystem complexity, ecological processes, and ecosystem services.

The Group on Earth Observations Biodiversity Observation Network (GEO BON) introduced the concept of Essential Biodiversity Variables (EBVs) to reduce the variety of possible biodiversity measurements to a manageable common framework of key measurements divided into six classes: genetic composition, species populations, species traits, community composition, ecosystem structure, and ecosystem function (Pereira et al., 2013). These EBVs act as intermediates between raw biodiversity data and biodiversity indicators. For example, species abundance is an EBV in the species populations class, which can be calculated from various types of survey data such as transects, aerial surveys, camera trap images, or mark-recapture,

and then feeds into biodiversity indicators such as the Living Planet Index (LPI) and the Wild Bird Index (WBI).

However, indicators and EBVs depend on access to relevant and reliable data. While advances in technology have improved tracking and counting of bird and mammal populations (Lausch et al., 2016; Nichols et al., 2011; Rose et al., 2015), our datasets are incomplete even for the most comprehensively studied taxa, and woefully lacking for others (Barnosky et al., 2011; Conde et al., 2019; Hortal et al., 2015; Jetz et al., 2019; Meyer et al., 2015; Proença et al., 2017; Turak et al., 2017). This scarcity of data hinders decisions about which species, ecosystems, or geographical areas to protect and limits our ability to assess global biodiversity comprehensively.

Volunteers have been involved in the collection of biodiversity data for more than a century, but recently the collection of biodiversity data by citizen scientists has accelerated into a global phenomenon (Chandler et al., 2017; Rapacciuolo et al., 2021) thanks in large part to the rise of internet-based platforms like eBird and iNaturalist. While sometimes opportunistic and widely varying in the degree of rigour and planning involved in their collection, citizen science datasets tend to be numerous, intensive, cover large areas, and can be used and contributed to by scientists and non-scientists alike (Rapacciuolo et al., 2021). The Global Biodiversity Information Facility (GBIF) provides a publicly accessible database of more than 2.6 billion occurrences, many of which are contributed by citizen science platforms, and is a highly valuable resource for use in indicators for policy analysis. Such a massive quantity of open data may help to solve the data crisis, but suffers from a lack of standardisation and completeness, as well as severe biases over time and space (Chandler et al., 2017; Troudet et al., 2017; Troia and McManamay, 2016). There is evidence that these issues can be partially overcome through mitigation techniques, and that after careful treatment even unstructured and opportunistic data can be safely used to calculate indicators, especially when combined with long-term monitoring data (Rapacciuolo et al., 2021). However, care and rigour should be used when performing analysis to ensure the outputs are reliable. The B-Cubed project aims to help standardise the processing and aggregation of these data. This can be facilitated by standardised, accessible, reproducible workflows.

The goal of task 5.1 of the B-Cubed project is to provide standardised publicly accessible workflows to calculate general biodiversity variables and indicators from GBIF data cubes. Preliminary work on this idea was done by the sTWIST project (Theory and Workflows for Alien and Invasive Species Tracking; e.g. McGeoch et al., 2023), which focused on developing indicators of invasive alien species (IAS) and their impacts, and the TriAS project (Tracking Invasive Alien Species; Oldoni et al., 2020), which also focused on IAS indicators and pioneered the use of GBIF data cubes. Within the sTWIST project, new indicators for alien species numbers and impacts of IAS have been developed, which are in the process of getting published. Once publicly accessible, the potential of adopting them in the B-Cubed project will be explored. The TriAS project used localised (Belgium only) high quality GBIF datasets of alien species checklists and occurrences, and provided workflows to calculate indicators related to alien species invasions. These indicators are available at https://trias-project.github.io/indicators/index.html and act as a proof of concept. In B-Cubed task 5.1 we will build on this pioneering work by providing generalised workflows to calculate a diverse set of common biodiversity variables and indicators across GBIF data cubes that cover

any taxon and/or region. These workflows can then also be applied to calculate indicators on modelled data cubes for both current distributions and future scenarios, e.g. the cubes being developed in tasks 4.1 (habitat suitability), 4.2 (multi-site generalised dissimilarity) and 4.3 (network invasibility) of the B-Cubed project.

To be relevant and useful, an indicator should address actual information needs, be responsive to change, be based in scientific theory, and have enough suitable data available to be calculated reliably. Therefore, when developing indicators, it is important to first consult with stakeholders to assess needs. This task (5.1) of the B-Cubed project is intended to both a) take advantage of existing commonly used indicators that can be calculated with occurrence data and b) develop new useful indicators based on the results of stakeholder consultations from tasks 1.5 (report on the needs for European biodiversity policy) and 1.6 (landscape analysis of biodiversity monitoring globally). At this stage tasks 1.5 and 1.6 are ongoing, with only some preliminary results available; therefore this milestone primarily focuses on the implementation of existing indicators.

We chose to focus on indicators and EBVs that are common, general, simple, widely known or used, and can be calculated from GBIF data alone, which we refer to as general biodiversity indicators. This allows for workflows with minimal dependencies and therefore increased longevity and ease of maintenance.

A secondary focus in this task is on developing new indicators of data gaps and biases. Preliminary results from stakeholder consultations in task 1.6 suggest that these are major issues for policymakers, stymieing attempts to gain a comprehensive understanding of global biodiversity and biodiversity change. Therefore, indicators that highlight and/or subvert these data gaps would be of great use to them. Furthermore, stakeholders are wary of using citizen science data in indicators for policy (preliminary results from task 1.5). Therefore, we aim to provide an indicator that evaluates whether reliable results can be obtained when applying other indicators to a given set of data.

The aim of this milestone document (M20) is to describe and justify the biodiversity indicators and variables we have chosen to implement in task 5.1.

2. Biodiversity variables and indicators

We assessed the methodology and data requirements of existing indicators and variables to determine their suitability for use with occurrence data, and selected a set of common, well-known existing indicators and variables that can be calculated exclusively from occurrence data (Table 1). In addition, we identified a gap where we can fill a policy need by developing a novel indicator, which we are calling a data sufficiency indicator. This can be calculated from GBIF occurrence data, but the development process also requires high resolution climate data, which can be freely obtained from Worldclim (Table 1). Further indicators targeted to policy needs will be determined after final results from stakeholder consultations conducted in tasks 1.5 and 1.6 are available for discussion.

Table 1: Biodiversity variables and indicators to be implemented in task 5.1

Indicator or variable	Type	Data needed	Source	Reference
Total occurrences	Variable	Occurrences	GBIF	
Density of occurrences (occ/km^2)	Variable	Occurrences	GBIF	
Mean year of occurrences (newness)	Variable	Occurrences	GBIF	
Species richness	Indicator	Occurrences	GBIF	Magurran, 1988
Evenness	Indicator	Occurrences	GBIF	Pielou, 1966; Kvålseth, 2015
Rarity	Indicator	Occurrences	GBIF	Rabinowitz, 1981
Hill-Shannon diversity	Indicator	Occurrences	GBIF	Hill, 1973
Hill-Simpson diversity	Indicator	Occurrences	GBIF	Hill, 1973
Species occurrences	EBV	Occurrences	GBIF	Pereira et al., 2013
Taxonomic distinctness	EBV	Occurrences, Taxonomy	GBIF	Clarke & Warwick, 1999
Data sufficiency	Indicator	Occurrences, Climate data	GBIF, Worldclim	Dove et al., 2023
Landscape Heterogeneity Index	Indicator	Environmental data	Google Earth Engine: Remote Sensing Data, Digital Elevation Models	MacFadyen et al., 2016

2.1. General indicators

The main focus of task 5.1 is on general biodiversity indicators, which can be calculated by anyone from publicly available datasets and give a broad overview of biodiversity. This is in contrast to specialised indicators like the Living Planet Index (LPI) that are managed and curated (e.g. the LPI is maintained and updated by the Zoological Society of London with support from the World Wide Fund for Nature), require specialised datasets (e.g. the Living Planet Database), are complicated to calculate (e.g. the LPI requires a series of complex statistical operations), and are targeted to provide specific insights (e.g. the LPI reports changes in vertebrate species population abundance over time).

2.1.1. Species richness

Species richness is the total number of species present in a sample (Magurran, 1988). It is a fundamental and commonly used measure of biodiversity, providing a simple and intuitive overview of the status of biodiversity. However, richness is not well suited to measuring

biodiversity change over time, as it only decreases when local extinctions occur and thus lags behind abundance for negative trends. While it may act as a leading indicator of alien species invasions, it will not indicate establishment because it ignores abundance. Nor will it necessarily indicate changes in local species composition, which can occur without any change in richness.

Although richness is conceptually simple, it can be measured in different ways. We will implement four different measures of richness, described below.

2.1.1.1. Observed richness

Observed richness is calculated by summing the number of unique species observed for each year or each cell. Observed richness is highly dependent on the comprehensiveness of the dataset it is being applied to. If some regions are more intensively, carefully or systematically sampled than others, this will likely reflect as higher observed richness. Observed richness also depends on the relative abundance and spatial aggregation of each species, with less abundant and less aggregated species less likely to be discovered during surveys (Hillebrand et al., 2018), as well as the detectability of each species. However, there are ways of mitigating these effects through estimation methods, as explained in section 2.1.1.3 below. Furthermore, the advent of new survey methods, such as camera traps and eDNA, has significantly altered the detectability of some species.

2.1.1.2. Cumulative richness

Cumulative richness is calculated by adding the newly observed unique species each year to a cumulative sum. This indicator provides an estimation of whether and how many new species are still being discovered in a region. While an influx of alien species could cause an increase in cumulative richness, a fast-rising trend as shown in Fig. 2 is likely an indication that the dataset is not comprehensive and therefore observed richness will provide an underestimate of species richness.

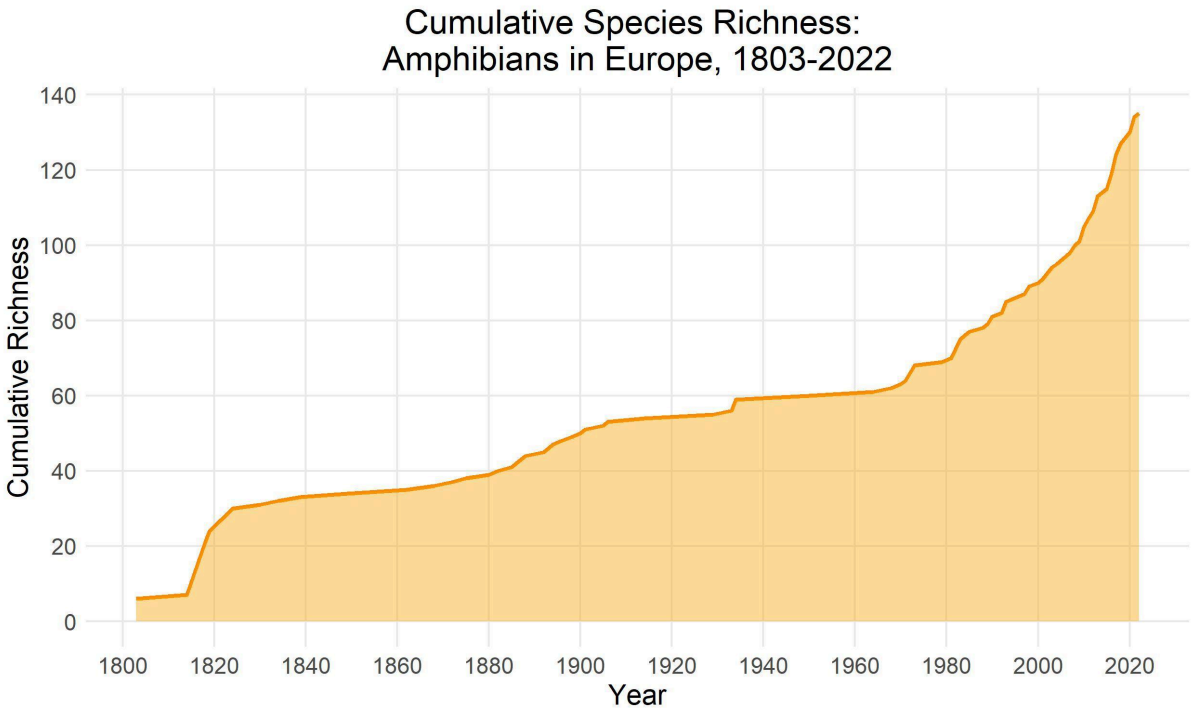

Figure 2: Cumulative species richness of amphibians in Europe, measured from 1803-2022. Source data cube contains all GBIF occurrence records of amphibians throughout Europe.

2.1.1.3. Estimated richness

Species richness can be estimated through different standardisation procedures as a way to mitigate the effects of sample size and sampling biases. One way to do this is by equalising sample size. The `specaccum` function of the VEGAN package (Dixon, 2003) for R is used to calculate a species accumulation curve (a plot of cumulative species richness as a function of sample size) for each year or grid cell. The smallest sample size from among all the grid cells or years in the dataset is then used as a reference to select richness values from each curve. This is called rarefaction. It is also possible to use a larger sample size as a reference, but this requires extrapolation of smaller samples, which is more prone to error than rarefaction.

However, results from sample-size based estimation can be problematic as they depend on both richness and evenness. A sample from a community with a more even distribution of individuals across species is likely to show higher richness than a sample of the same size from a community where many species are rare, as the rare species are less likely to appear in the sample. Similarly, a community containing a lot of species will appear less rich than it actually is if the sample size used for comparison is too small. Detectability also plays an important part; hard to detect species are less likely to appear in the sample, so communities in which rare species are more easily detectable are likely to yield richer samples.

Another way to estimate species richness is to standardise by coverage. The iNEXT package (Chao et al., 2014; Hsieh et al., 2016) for R is used to estimate species richness at an equal level of coverage (e.g. 0.95) for each cell or year in a biodiversity data cube. Coverage is the

proportion of individuals in the community belonging to species in the sample. So, at a coverage of 0.95, 95% of individuals in the community belong to species detected in the sample while 5% belong to species that are not detected in the sample. Coverage is estimated based on the frequencies of species already in the sample. It can be illustrated using a species accumulation curve, the slope of which represents the probability of detecting a new species with the next individual you sample from a community. At a sample size of zero, the slope would be one, meaning the next individual sampled has a 100% probability of being a species not already in the sample. Therefore, a coverage value of one corresponds to the asymptote of a species accumulation curve (slope of zero), meaning no new species would be uncovered through further sampling.

2.1.2. Evenness

Species evenness is a commonly used indicator that measures how uniformly individuals are distributed across species in a region or over time. It provides a complement to richness by taking relative abundance into account.

Although GBIF provides information about abundances as individual counts, the majority of entries lack this information. Hence, evenness can only be calculated using the proportions of observations rather than proportions of individuals. Strictly speaking, the evenness measures therefore indicate how uniformly species are represented in the respective data set rather than the true evenness of the ecological community.

We will provide two measures of evenness.

2.1.2.1. Pielou's evenness

First, we will implement Pielou's evenness (1966) because it is well-known and commonly used. Pielou's evenness is calculated as

$$\frac{-\sum_{i=1}^{S} p_i \times log\left(p_i\right)}{log(S)} \quad (1)$$

where S is the number of species and p_i is the proportion of occurrences represented by species *i*.

2.1.2.2. Williams' evenness

However, an analysis of evenness properties by Kvålseth (2015) showed that an evenness index introduced by Williams in 1977 in an unpublished manuscript has two important properties which Pielou's does not. The properties in question are complex mathematical properties known as the Schur-Concavity and value validity, but we attempt to describe them here more simply. If a measure of evenness is Schur-concave, it means that when the distribution of individuals becomes more evenly spread across species, the measure of evenness will stay the same or increase, but never decrease. Value validity means that an evenness index should provide

sensible and meaningful values across its range for any given distribution of species abundances. Given that these are intuitively useful properties for an evenness index, we also implement Williams' evenness index, which Kvålseth referred to as E9 but we will refer to as Williams' evenness.

Williams' evenness is calculated as

$$1 - \left[\frac{\left(S \sum_{i=1}^{S} p_i^2 - 1 \right)}{S - 1} \right]^{\frac{1}{2}} \quad (2)$$

where S is the number of species and p_i is the proportion of occurrences represented by species *i*.

2.1.3. Hill diversity

Hill (1973) introduced the concept of Hill diversity, which assumes that the number and relative abundance of species are inseparable components of diversity. Hill diversity uses a single equation to calculate multiple measures of diversity by varying a single parameter ℓ, which changes the emphasis on rare vs common species (Roswell et al., 2019). It represents the mean rarity of sampled species, and is calculated as

$$D = \left(\sum_{i=1}^{S} p_i \left(r_i \right)^l \right)^{1/l} \quad (3)$$

where *D* is diversity, *S* is the number of species, p_i is the proportion of individuals belonging to species *i*, r_i is the rarity of species *i*, and ℓ determines the rarity scale for the mean.

While ℓ can theoretically take almost any value, three common measures of diversity are special cases: species richness, and modified versions of the Shannon and Simpson diversity indices (Roswell et al., 2019). These three measures occur when ℓ takes the value of 1, 0 (or near-zero, as ℓ cannot actually take the value of 0), or -1, respectively. Richness uses an arithmetic scale (the arithmetic mean), thus giving rare species a lot of leverage. By contrast, Hill-Shannon diversity uses a logarithmic scale (the geometric mean), treating common and rare species equally, and Hill-Simpson diversity uses a reciprocal scale (the harmonic mean), giving common species higher leverage.

2.1.3.1. Species richness

Using the Hill diversity equation, richness becomes simply S, the number of species, and is thus identical to richness calculated without Hill diversity.

2.1.3.2. Hill-Shannon diversity

Hill-Shannon diversity is actually e (base of the natural log) raised to the power of the Shannon index. It is estimated for each year or cell count using the iNEXT package, standardised by coverage, as

$$e^{-\sum_{i=1}^{S} p_i ln\left(p_i\right)} \quad (4)$$

where S is the number of species and p_i is the proportion of occurrences represented by species *i*.

2.1.3.3. Hill-Simpson diversity

Hill-Simpson diversity is the inverse of the Simpson index. It is estimated using the iNEXT package for each year or cell, standardised by coverage, as

$$\frac{1}{\sum_{i=1}^{S} \left(p_i\right)^2} \quad (5)$$

where S is the number of species and p_i is the proportion of occurrences represented by species *i*.

Both Hill-Simpson and Hill-Shannon diversity describe a combination of richness and evenness that reduce the inadequacies of either measure alone.

2.1.4. Rarity

Rarity is the scarcity or infrequency of a particular species in an area. A rare species might have a small population size, a limited distribution, or a unique ecological niche (Maciel, 2021; Rabinowitz, 1981). Rarity can also be a biodiversity indicator when summed over multiple species in an area, and may provide important insight for determining conservation priorities. It can be measured in different ways, but we will provide workflows to calculate rarity by abundance (using number of occurrences as a proxy) and by area. When measured over time rarity may indicate potential threats or changes in the environment.

2.1.4.1. Abundance-based rarity

Abundance-based rarity is the inverse of the proportion of total occurrences represented by a particular species. The total summed rarity for each grid cell or year is calculated (sum the rarity values of each species present there).

$$\sum_{i=1}^{S}\left(\frac{1}{p_i}\right) \quad (6)$$

where S is the number of species and p_i is the proportion of occurrences represented by species i.

2.1.4.2. Area-based rarity

Area-based rarity is the inverse of occupancy frequency (proportion of grid cells occupied) for a particular species. The total summed rarity for each grid cell or year is calculated (sum the rarity values of each species present there).

$$\sum_{i=1}^{S}\left(\frac{1}{\frac{n_i}{N}}\right) \quad (7)$$

where S is the number of species, N is the total number of occupied grid cells, and n_i is the number of grid cells occupied by species i.

2.2. Specialised indicators

In addition to general biodiversity indicators, we will provide workflows for certain specialised indicators that provide useful biodiversity information not covered by general indicators and variables, or that advance specific policy goals or needs according to stakeholder feedback from tasks 1.5 and 1.6. Other tasks of the B-Cubed project already focus on phylogenetic indicators (task 5.2) and invasive alien species impact indicators (task 5.3), therefore task 5.1 will aim to cover another important policy need: indicators of data completeness.

2.2.1. Data sufficiency

Biodiversity sampling varies globally in intensity and methodology, with large data gaps and biases across systems, taxa, time, and space (Hughes et al., 2021). Rich countries fund more studies than poor countries. Biodiversity in the global north is far better understood than in the global south (Antonelli et al., 2023; Dove et al., 2023). Birds and mammals are better understood than reptiles and amphibians (Dove et al., 2023), which are in turn better understood than invertebrates (Cardoso et al., 2011; Hochkirch et al., 2021). Terrestrial systems are better understood than freshwater systems (Darwall et al., 2011; Dove et al., 2023). These inconsistencies exacerbate the data crisis, confounding the interpretation of biodiversity indicators and making it more difficult to determine the changing state of global biodiversity.

Citizen science datasets in open access repositories like GBIF have tremendous potential to help overcome these gaps and biases in biodiversity data. However, thus far citizen science data collection activities skew strongly toward the global north and toward charismatic taxa, especially birds, while leaving speciose invertebrate groups and diversity hotspots in the global

south poorly sampled and underrepresented (Chandler et al., 2017; Troudet et al., 2017), thus mirroring or even widening existing data collection biases. Furthermore, because citizen science data represents a variety of datasets, sometimes opportunistically collected, and without standardisation, they have broad prevalence but very poor completeness compared to systematic surveys, with the majority of grid cells being poorly surveyed (Troia and McManamay, 2016). These issues with citizen science data have resulted in underutilization and mistrust by researchers and stakeholders due to a perception that with such data it is not possible to reliably calculate trends across space and time (Rapacciuolo et al., 2021). Unfortunately, while we have some understanding of the existence and extent of biodiversity data gaps and biases, little is known about how they affect the reliability of indicator trends (Dove et al., 2023).

Pioneering work on the topic of biodiversity indicator reliability has been done for two specific indicators: the Red List Index (RLI) and the Living Planet Index (LPI). The Sampled Red List Index (SRLI) was developed to solve the problem of assessing speciose taxonomic groups without comprehensive sampling (Baillie et al., 2008). The idea was that when the RLI was calculated on a random sample of species of a specific minimum size from a particular taxa, the trend should be in the correct direction 95% of the time. The first version of the SRLI determined a set sample size of 1500 for all taxa, which was later revised to include smaller sample sizes (200 - 400) for decadal reassessments to improve efficiency (Henriques et al., 2020). Building on this work, Dove et al. (2023) produced a more flexible method for the LPI, which used a model of trend reliability to provide specific minimum sample sizes for each disaggregated regional taxonomic group in the Living Planet Database (LPD).

However, these previous studies involved biodiversity over time, while it is also often useful or important to compare biodiversity across space. The data cubes the B-Cubed project is developing are based on occurrence data and have an important spatial element. Therefore we are attempting for the first time to develop a method to measure the reliability of indicators when applied to gridded occurrence data. We will adapt and generalise the methodology developed by Dove et al. (2023) to measure whether any given set of GBIF occurrence data has a sufficient sample size (number of observations) to get reliable results when applying a given indicator.

The data sufficiency indicator will involve applying a model of reliability (e.g. a multiple regression model) to a dataset. Based on the sample size and underlying parameters and/or biases of the dataset, the result of the model will determine whether a given indicator is likely to give a sufficiently accurate result, according to a “threshold of reliability” (the term ‘reliability’ reflects that it is estimated by a model, as accuracy cannot be directly measured for indicators calculated on real world data). The threshold will be pre-determined, and the model will be built and parameterized using thousands of virtual species created using the “virtual species” R package (Leroy et al., 2016). The virtual species will be combined into virtual biodiversity cubes, which will then be sampled in multiple sizes and with different simulated biases. Indicators will be applied to the sampled cubes as well as the unsampled cubes and the results compared (e.g. using a distance measure) to determine how sample size, sample biases, and other parameters of the data affect indicator accuracy.

2.2.2. Landscape heterogeneity

In regions with a small amount of available occurrence data, proxy variables have been developed using available environmental data to estimate the potential distribution of species and hot spots of biodiversity. In large protected areas, landscape heterogeneity and complexity serve as vital indicators of biodiversity by providing a mosaic of habitats and ecological niches. Landscape diversity (or heterogeneity) represents the potential of an area to support an associated diversity of species and maintain functional diversity through ecological processes (MacFadyen et al., 2016). Heterogeneity in topography, vegetation types, and microclimates facilitates species coexistence by offering varied resources and conditions, which is essential for maintaining higher levels of biodiversity (Walz & Syrbe, 2013). Complexity, referring to the spatial arrangement and connectivity of these habitats, enhances ecosystem resilience and functionality by promoting gene flow, species dispersal, and adaptation to environmental changes (Walz & Syrbe, 2013). Moreover, biodiversity intactness and the preservation of large or contiguous wilderness areas within these landscapes are crucial for sustaining ecosystem services and natural processes (Hooper et al., 2005). Intactness indicates the degree to which human activities have impacted species abundance and ecosystem functions. High biodiversity intactness in wilderness areas signifies minimal human disturbance, which is essential for conserving species in their natural states and ensuring the long-term viability of ecological networks (Aycrigg et al., 2022). These areas act as benchmarks for assessing human impacts and can be crucial indicators of biodiversity change and quality necessary for conservation efforts aimed at preserving Earth's remaining natural habitats and their inherent biodiversity.

There are many possible ways of calculating landscape heterogeneity. While no specific method has yet been chosen, the methodology is being developed in task 4.2 (dissimilarity cube) and is intended to be implemented in task 5.1 when ready.

2.3. Essential biodiversity variables

While the focus of task 5.1 is primarily on indicators, we will also provide workflows for two EBVs that can be calculated strictly from data provided by GBIF.

2.3.1. Species occurrences

Species occurrences are mapped by calculating the total number of occurrences of a given species for each cell. This represents the occurrence frequency distribution, and also indicates the observed species distribution. The number of occurrences can act as a proxy for relative abundance of species with a similar detectability, which is an important aspect of biodiversity although not an indicator when calculated in isolation.

2.3.2. Taxonomic distinctness

Taxonomic distinctness measures the taxonomic relatedness between species, providing a measure of biodiversity that accounts for evolutionary relationships. A distance matrix based on pairwise taxonomic relationships is calculated for each cell using the taxize package (Chamberlain & Szöcs, 2013; Chamberlain et al., 2020), then taxonomic distinctness is calculated as the Taxonomic Distinctness Index (TDI; Clarke & Warwick, 1999):

$$\left(\sum_{i<j}\sum \frac{\left(\left|R_i - R_j\right|\right)}{L}\right) \Big/ \left(\frac{S(S-1)}{2}\right) \quad (8)$$

where S is the number of species, R_i and R_j are the taxonomic ranks of species i and j (from the GBIF Taxonomic Backbone), and L is the maximum number of taxonomic ranks.

2.4. Other variables

We will provide workflows for three other variables which do not provide any information about biodiversity directly, but are nonetheless useful for evaluating the quality, comprehensiveness, or age of a dataset.

2.4.1. Total occurrences

The total number of occurrences is calculated by summing the occurrences of all species observed for each cell or year. This variable provides an overview of the comprehensiveness and distribution of data in the cube being analysed, and may be helpful, or even vital, for interpreting the results of calculated indicators.

2.4.2. Density of occurrences

Density is calculated by summing the total number of occurrences per square kilometre for each cell or year. This provides similar information to total occurrences, but is adjusted for cell area.

2.4.3. Mean year of occurrence

The mean year of occurrence is calculated per cell, giving an indication of how recent the data is for each cell. A recent mean year is not necessarily an indication of quality, as some countries or regions have been conducting comprehensive biodiversity monitoring for many years and will therefore reflect an older mean year of occurrence, while others may show a recent mean year due to e.g. the sudden availability of large amounts of citizen science data.

3. Acknowledgements

B^3 (Biodiversity Building Blocks for policy) receives funding from the European Union's Horizon Europe Research and Innovation Programme (ID No 101059592). Quentin Groom, Sabrina Kumschick and Ward Langeraert provided helpful feedback on an earlier draft of the manuscript.

4. References

1. Antonelli, A., Smith, R. J., Fry, C., Simmonds, M. S., Kersey, P. J., Pritchard, H. W., ... & Qi, Y. D. (2020). *State of the World's Plants and Fungi.* Royal Botanic Gardens (Kew); Sfumato Foundation.

2. Aycrigg, J. L., Mccarley, T. R., Belote, R. T., & Martinuzzi, S. (2022). Wilderness areas in a changing landscape: changes in land use, land cover, and climate. *Ecological Applications*, 32(1), e02471.

3. Baillie, J. E., Collen, B., Amin, R., Akcakaya, H. R., Butchart, S. H., Brummitt, N., Meager, T.R., Ram, M., Hilton-Taylor, C., & Mace, G. M. (2008). Toward monitoring global biodiversity. *Conservation Letters*, *1*(1), 18-26.

4. Barnosky, A. D., Matzke, N., Tomiya, S., Wogan, G. O. U., Swartz, B., Quental, T. B., Marshall, C., McGuire, J. L., Lindsey, E. L., Maguire, K. C., Mersey, B., & Ferrer, E. A. (2011). Has the Earth's sixth mass extinction already arrived? In *Nature* (Vol. 471, Issue 7336, pp. 51–57).

5. Biodiversity Indicators Partnership. (2011). Guidance for national biodiversity indicator development and use. *UNEP World Conservation Monitoring Centre*.

6. Buckland, S. T., Baillie, S. R., Dick, J. M. P., Elston, D. A., Magurran, A. E., Scott, E. M., Smith, R. I., Somerfield, P. J., Studeny, A. C., & Watt, A. (2012). How should regional biodiversity be monitored? *Environmental and Ecological Statistics*, *19*(4), 601–626.

7. Cardoso, P., Erwin, T. L., Borges, P. A., & New, T. R. (2011). The seven impediments in invertebrate conservation and how to overcome them. *Biological conservation*, 144(11), 2647-2655.

8. Chamberlain, S. A., & Szöcs, E. (2013). taxize: taxonomic search and retrieval in R. *F1000Research*, 2.

9. Chamberlain, S., Szoecs, E., Foster, Z., Boettiger, C., Ram, K., Bartomeus, I., Baumgartner, J., O'Donnell, J., Oksanen, J., Tzovaras, B. G., Marchand, P., Tran, V., Salmon, M., Li, G., & Grenié, M. (2020). taxize: Taxonomic Information from Around the Web. R package version 0.9.98. https://github.com/ropensci/taxize.

10. Chandler, M., See, L., Copas, K., Bonde, A. M., López, B. C., Danielsen, F., Kristoffer, J., Legind, J. K., Masinde, S., Miller-Rushing, A. J., Newman, G., Rosemartin, A., & Turak, E. (2017). Contribution of citizen science towards international biodiversity monitoring. *Biological conservation*, 213, 280-294.

11. Chao, A., Gotelli, N. J., Hsieh, T. C., Sander, E. L., Ma, K. H., Colwell, R. K., & Ellison, A. M. (2014). Rarefaction and extrapolation with Hill numbers: a framework for sampling and estimation in species diversity studies. *Ecological monographs*, *84*(1), 45-67.

12. Clarke, K. R., & Warwick, R. M. (1999). The taxonomic distinctness measure of biodiversity: weighting of step lengths between hierarchical levels. Marine Ecology Progress Series, 184, 21-29.

13. Conde, D. A., Staerk, J., Colchero, F., da Silva, R., Schöley, J., Maria Baden, H., Jouvet, L., Fa, J. E., Syed, H., Jongejans, E., Meiri, S., Gaillard, J.-M., Chamberlain, S., Wilcken, J., Jones, O. R., Dahlgren, J. P., Steiner, U. K., Bland, L. M., Gomez-Mestre, I., Lebreton, J.-D., Vargas, J. G., Flesness, N., Canudas-Romo, V., Salguero-Gómez, R., Byers, O., Berg, T. J., Scheuerlein, A., Devillard, S., Schigel, D. S., Ryder, O. A., Possingham, H. P., Baudisch, A., & Vaupel, J. W. (2019). *Data gaps and opportunities for comparative and conservation biology*.

14. Darwall, W. R., Holland, R. A., Smith, K. G., Allen, D., Brooks, E. G., Katarya, V., Pollock, C. M., Shi, Y., Clausnitzer, V., Cumberlidge, N., Cuttelod, A., Dijkstra, K.-D. B., Diop, M. D., García, N., Seddon, M. B., Skelton, P. H., Snoeks, J., Tweddle, D., & Vié, J. C. (2011). Implications of bias in conservation research and investment for freshwater species. *Conservation Letters*, 4(6), 474-482.

15. Dixon, P. (2003). VEGAN, a package of R functions for community ecology. *Journal of vegetation science*, *14*(6), 927-930.

16. Dove, S., Böhm, M., Freeman, R., McRae, L., & Murrell, D. J. (2023). Quantifying reliability and data deficiency in global vertebrate population trends using the Living Planet Index. *Global Change Biology*, *29*(17), 4966-4982.

17. Gregory, R. D., Van Strien, A., Vorisek, P., Gmelig Meyling, A. W., Noble, D. G., Foppen, R. P., & Gibbons, D. W. (2005). Developing indicators for European birds. *Philosophical Transactions of the Royal Society B: Biological Sciences*, *360*(1454), 269-288.

18. Henriques, S., Böhm, M., Collen, B., Luedtke, J., Hoffmann, M., Hilton-Taylor, C., Cardoso, P., Butchart, S.H.M., & Freeman, R. (2020). Accelerating the monitoring of global biodiversity: Revisiting the sampled approach to generating Red List Indices. *Conservation Letters*, *13*(3), e12703.

19. Hill, M. O. (1973). Diversity and evenness: a unifying notation and its consequences. *Ecology*, *54*(2), 427-432.

20. Hillebrand, H., Blasius, B., Borer, E. T., Chase, J. M., Downing, J. A., Eriksson, B. K., Filstrup, C. T., Harpole, W. S., Hodapp, D., Larsen, S., Lewandowska, A. M., Seabloom, E. W., Van de Waal, D. B., & Ryabov, A. B. (2018). Biodiversity change is uncoupled from species richness trends: Consequences for conservation and monitoring. *Journal of Applied Ecology*, 55(1), 169-184.

21. Hochkirch, A., Samways, M. J., Gerlach, J., Böhm, M., Williams, P., Cardoso, P., Cumberlidge, N., Stephenson, P. J., Seddon, M. B., Clausnitzer, V., Borges, P. A. V., Mueller, G. M., Pearce-Kelly, P., Raimondo, D. C., Danielczak, A., & Dijkstra, K.-D. B. (2021). A strategy for the next decade to address data deficiency in neglected biodiversity. *Conservation Biology*, 35(2), 502-509.

22. Hooper, D. U., Chapin III, F. S., Ewel, J. J., Hector, A., Inchausti, P., Lavorel, S., ... & Wardle, D. A. (2005). Effects of biodiversity on ecosystem functioning: a consensus of current knowledge. *Ecological monographs*, 75(1), 3-35.

23. Hortal, J., de Bello, F., Diniz-Filho, J. A. F., Lewinsohn, T. M., Lobo, J. M., & Ladle, R. J. (2015). Seven Shortfalls that Beset Large-Scale Knowledge of Biodiversity. *Annual Review of Ecology, Evolution, and Systematics*, *46*, 523–549.

24. Hsieh, T. C., Ma, K. H., & Chao, A. (2016). iNEXT: an R package for rarefaction and extrapolation of species diversity (Hill numbers). *Methods in Ecology and Evolution*, *7*(12), 1451-1456.

25. Hughes, A.C., Orr, M.C., Ma, K., Costello, M.J., Waller, J., Provoost, P., Yang, Q., Zhu, C. & Qiao, H. (2021). Sampling biases shape our view of the natural world. *Ecography*, 44, 1259–1269.

26. Jetz, W., McGeoch, M. A., Guralnick, R., Ferrier, S., Beck, J., Costello, M. J., Fernandez, M., Geller, G. N., Keil, P., Merow, C., Meyer, C., Muller-Karger, F. E., Pereira, H. M., Regan, E. C., Schmeller, D. S., & Turak, E. (2019). Essential biodiversity variables for mapping and monitoring species populations. *Nature Ecology and Evolution*, *3*(4), 539–551.

27. Jones, J. P. G., Collen, B., Atkinson, G., Baxter, P. W. J., Bubb, P., Illian, J. B., Katzner, T. E., Keane, A., Loh, J., Mcdonald-Madden, E., Nicholson, E., Pereira, H. M., Possingham, H. P., Pullin, A. S., Rodrigues, A. S. L., Ruiz-Gutierrez, V., Sommerville, M., & MilnerGulland, E. J. (2011). The Why, What, and How of Global Biodiversity Indicators Beyond the 2010 Target. *Conservation Biology*, *25*(3), 450–457. https://doi.org/10.1111/j.1523- 1739.2010.01605.x

28. Kvålseth, T. O. (2015). Evenness indices once again: critical analysis of properties. *SpringerPlus*, *4*, 1-12.

29. Lausch, A., Bannehr, L., Beckmann, M., Boehm, C., Feilhauer, H., Hacker, J. M., Heurich, M., Jung, A., Klenke, R., Neumann, C., Pause, M., Rocchini, D., Schaepman, M. E., Schmidtlein, S., Schulz, K., Selsam, P., Settele, J., Skidmore, A. K., & Cord, A. F. (2016). Linking Earth Observation and taxonomic, structural and functional biodiversity: Local to ecosystem perspectives. *Ecological Indicators*, *70*, 317–339.

30. Leroy, B., Meynard, C. N., Bellard, C., & Courchamp, F. (2016). virtualspecies, an R package to generate virtual species distributions. *Ecography*, *39*(6), 599-607.

31. MacFadyen, S., Hui, C., Verburg, P. H., & Van Teeffelen, A. J. (2016). Quantifying spatiotemporal drivers of environmental heterogeneity in Kruger National Park, South Africa. *Landscape Ecology*, 31, 2013-2029.

32. Maciel, E. A. (2021). An index for assessing the rare species of a community. *Ecological Indicators*, 124, 107424.

33. Magurran, A. E. (1998). *Ecological diversity and its measurement*. Princeton University Press.

34. Meyer, C., Kreft, H., Guralnick, R., & Jetz, W. (2015). Global priorities for an effective information basis of biodiversity distributions. *Nature Communications*, *6*(8221).

35. Newman, J. A., Varner, G., & Linquist, S. (2017). *Defending biodiversity: environmental science and ethics*. Cambridge University Press

36. Nichols, J. D., O'Connell, A. F., & Karanth, K. U. (2011). Camera traps in animal ecology and conservation: What's next? In *Camera Traps in Animal Ecology: Methods and Analyses* (pp. 253–263). Springer Japan.

37. Nicholson, E., Collen, B., Barausse, A., Blanchard, J. L., Costelloe, B. T., Sullivan, K. M. E., Underwood, F. M., Burn, R. W., Fritz, S., Jones, J. P. G., McRae, L., Possingham, H. P., & Milner-Gulland, E. J. (2012). Making robust policy decisions using global biodiversity indicators. *PLoS ONE*, *7*(7).

38. Oldoni, D., Groom, Q., Adriaens, T., Davis, A. J., Reyserhove, L., Strubbe, D., ... & Desmet, P. (2020). Occurrence cubes: a new paradigm for aggregating species occurrence data. *bioRxiv*, 2020-03.

39. Pereira, H. M., Ferrier, S., Walters, M., Geller, G. N., Jongman, R. H. G., Scholes, R. J., Bruford, M. W., Brummitt, N., Butchart, S. H. M., Cardoso, A. C., Coops, N. C., Dulloo, E., Faith, D. P., Freyhof, J., Gregory, R. D., Heip, C., Höft, R., Hurtt, G., Jetz, W., … Wegmann, M. (2013). Essential biodiversity variables. *Science*, *339*(6117), 277–278.

40. Pielou, E. C. (1966). The measurement of diversity in different types of biological collections. *Journal of theoretical biology*, *13*, 131-144.

41. Proença, V., Martin, L. J., Pereira, H. M., Fernandez, M., McRae, L., Belnap, J., Böhm, M., Brummitt, N., García-Moreno, J., Gregory, R. D., Honrado, J. P., Jürgens, N., Opige, M., Schmeller, D. S., Tiago, P., & van Swaay, C. A. M. (2017). Global biodiversity monitoring: From data sources to Essential Biodiversity Variables. *Biological Conservation*, *213*, 256–263.

42. Rabinowitz, D. (1981). Seven forms of rarity. *Biological aspects of rare plant conservation*.

43. Rapacciuolo, G., Young, A., & Johnson, R. (2021). Deriving indicators of biodiversity change from unstructured community-contributed data. *Oikos*, 130(8), 1225-1239.

44. Robertson, D. P., & Hull, R. B. (2001). Essays Beyond Biology: toward a More Public Ecology for Conservation. *Conservation Biology*, *15*(4), 970–979.

45. Rose, R. A., Byler, D., Eastman, J. R., Fleishman, E., Geller, G., Goetz, S., Guild, L., Hamilton, H., Hansen, M., Headley, R., Hewson, J., Horning, N., Kaplin, B. A., Laporte, N., Leidner, A., Leimgruber, P., Morisette, J., Musinsky, J., Pintea, L., Prados, A., Radeloff, V. C., Rowen, M., Saatchi, S., Schill, S., Tabor, K., Turner, W., Vodacek, A., Vogelmann, J., Wegmann, M., Wilkie, D., & Wilson, C. (2015). Ten ways remote sensing can contribute to conservation. *Conservation Biology*, *29*(2), 350–359.

46. Roswell, M., Dushoff, J., & Winfree, R. (2021). A conceptual guide to measuring species diversity. *Oikos*, *130*(3), 321-338.

47. Troia, M. J., & McManamay, R. A. (2016). Filling in the GAPS: evaluating completeness and coverage of open-access biodiversity databases in the United States. *Ecology and evolution*, 6(14), 4654-4669.

48. Troudet, J., Grandcolas, P., Blin, A., Vignes-Lebbe, R., & Legendre, F. (2017). Taxonomic bias in biodiversity data and societal preferences. *Scientific reports*, 7(1), 9132.

49. Turak, E., Harrison, I., Dudgeon, D., Abell, R., Bush, A., Darwall, W., Finlayson, C. M., Ferrier, S., Freyhof, J., Hermoso, V., Juffe-Bignoli, D., Linke, S., Nel, J., Patricio, H. C., Pittock, J., Raghavan, R., Revenga, C., Simaika, J. P., & de Wever, A. (2017). Essential Biodiversity Variables for measuring change in global freshwater biodiversity. *Biological Conservation*, *213*, 272–279.

50. Walz, U., & Syrbe, R. U. (2013). Linking landscape structure and biodiversity. *Ecological indicators*, 31(8), 1-5.

51. Wilson, K., England, J., & Cunningham, S. (2016). Biodiversity indicators need to be fit for purpose. *The Routledge Handbook of Philosophy of Biodiversity*, 243-254.