TRADE, DEVELOPMENT &
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Evaluating aspects of biodiversity loss, and associated indicators, for application to the assessment of the impacts of agricultural commodity trade

WP2 scoping report

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The UK Research and Innovation Global Challenges Research Fund (UKRI GCRF) Trade, Development and the Environment Hub is working with over 50 partner organisations from 15 different countries. The project aims to make sustainable trade a positive force in the world by focusing on the impact of the trade of specific goods and seeking solutions to these impacts.

Section 1: Scoping and review

1.1 Introduction

Biodiversity is complex and no single indicator can capture all its different aspects. It is most commonly measured at one of three levels: by genes, species, or ecosystems. These aspects are usually measured in terms of their variety (i.e. the number of different types), quantity (how much there is of each type), and/or distribution (where biodiversity is located). The majority of biodiversity indicators (defined by Biodiversity Indicators Partnership, 2011), are based on habitat loss or taxonomically-biased measures of species richness (Hillebrand *et al.,* 2018), representing a small fraction of known biodiversity. Other fundamental aspects of biodiversity are often neglected – including aspects measured in the unit of species, such as species abundance or functional diversity, and aspects measured at other levels – particularly the genetic level. Attempts to reflect the multidimensionality and complexity of biodiversity in analyses of the impact of international trade, often come at the cost of usability and accessibility. Striking a balance between accurately representing biodiversity losses, whilst providing information in an accessible format is crucial if we are to mainstream these data in private and public sector decision and policy making.

Several global studies compare biodiversity indicators (e.g. Grenyer *et al.,* 2006; Davis & Cadotte, 2011; Marquadt *et al.,* 2019) but findings are mixed. Some have found limited convergence between indicators measuring different aspects (Marquadt *et al.,* 2019), demonstrating the relevance of including multiple dimensions of biodiversity in impact assessments. Indicators measuring the same aspect of biodiversity are more closely aligned (Marquadt *et al.,* 2019), with some studies also showing covariance between different aspects of biodiversity (Davis & Cadotte, 2011), yet this is often a reflection of scale. Hotspots of species richness across taxonomic groups frequently covary closely at biogeographic regional scales (Davis & Cadotte, 2011); however, congruence at finer scales is much lower. Importantly, cross-taxon congruence in the distribution of rare and threatened species is low and highly scale dependent (Grenyer *et al.,* 2006).

Within WP2 of the Trade Development and the Environment (Trade) Hub project, we are interested in the impacts associated with a number of important, internationally-traded, commodities. Previous research has indicated that the potential impacts on biodiversity associated with supply chain activities and trade are highly heterogeneous (e.g. Green *et al.,* 2019). These impacts are driven by the spatial distribution of species, their interface with geographically dispersed production activities, and the differences in the sub-national sourcing patterns of traders and countries. New techniques (for an example, see trase.earth) now allow connections to be made between global consumption activities and sub-nationally defined land use change (Godar *et al.,* 2015; Croft *et al.,* 2018). However, we know of no studies that have attempted to unpick how the application of different indicators might then influence the assessment of the relative impact of these supply chains on biodiversity.

In order to facilitate this type of analysis across multiple commodity and country contexts, here we evaluate the available methods for spatial assessment of biodiversity impacts that might be linked to commodity trade activities at a subnational scale. We group relevant methods according to the aspect of biodiversity they measure and highlight overlaps in input data between indicators, in order to understand alignment, similarities and complementarity between different methods. We also compare selected indicators in terms of their readiness, responsiveness, relevance and resolution to assist in decision making over use of biodiversity indicators in the context of commodity-impact assessment. We focus throughout on direct land use change impacts, however it is important to acknowledge that there are multiple pressures impacting biodiversity such as climate change and agrochemical pollution, which we don't consider.

1.2 Data filtering

We build on an extensive database of initiatives, measures, models, data providers, platforms, portals and certifications, listing over 250 sources of social and environmental measurement approaches (UNEP-WCMC, 2019). This was led by UNEP-WCMC and undertaken on behalf of the European Business & Biodiversity Platform, Aligning Biodiversity Measures for Business initiative and GCRF Trade Hub.

From this initial set, other sources were also added to incorporate the wide range of methods available for assessing biodiversity. This included indicators which had either previously been used in assessment of trade on biodiversity or were potentially compatible with our planned analyses. For example, methods for assessing species threat (Lenzen *et al.,* 2012), species persistence (Durán *et al.,* 2020; Green *et al.,* 2019) and species losses (Chaudhary *et al.,* 2015; Chaudhary & Brooks, 2018). We also intentionally incorporated aspects of biodiversity that are less widely recognised, in particular those related to functional and phylogenetic diversity (Cadotte e*t al.,* 2011; Jetz e*t al.*, 2014).

We filtered this database to include only those that explicitly considered biodiversity impacts - including proxies for biodiversity such as land cover. For example, initiative types with only a social focus - e.g. the 'Access to medicine index' - were excluded. We also excluded those initiatives that do not allow for measurement of biodiversity impacts, such as data portals, platforms and certifications. Furthermore, we only consider methods that can be applied at a sub-national level for the purposes of linking impacts to specific commodity production.

We then grouped the resulting subset of methods according to the aspect of biodiversity they measured, which are as follows:

1) Habitat quality
2) Species richness
3) Species vulnerability
4) Species abundance
5) Beta diversity
6) Phylogenetic diversity
7) Functional diversity.

Although these aspects are loosely aligned with Gabel et al. (2016), we chose to separate 'Species diversity', into 'Species richness' (the number of species) and 'Species abundance' (the number of individuals of each species), due to the number of indicators measuring specifically one or the other. Gabel et al. (2016) also classify "loss of species diversity" as a separate aspect. However, given that the methods for this rely on the same underlying data inputs, we incorporate it into 'Species richness'. Furthermore, we purposefully include aspects of biodiversity which have not previously been considered within life cycle assessment, yet reflect important dimensions of biodiversity, for example beta diversity and phylogenetic diversity.

1.3 Short descriptions of biodiversity aspects

Indicators can measure each aspect of biodiversity using different methodologies and with different data inputs. Here we outline a brief description of each identified aspect as well as a schematic demonstrating the effects of biodiversity loss within each aspect of biodiversity (Figure 1).

Habitat quality

This aspect uses land cover as a proxy for biodiversity. Land cover maps are usually generated from remotely sensed imagery (e.g. Hansen *et al.,* 2013), and can be used to analyse trends in landscape diversity, with land use change being the predominant driver. The most obvious correlates for biodiversity are habitat quality or habitat type, and as a consequence their loss or fragmentation can be used to account for biodiversity impacts. Land use is therefore commonly used in biodiversity conservation prioritisation and planning, yet this alone will say little about habitat quality. Hence some metrics not only focus on the loss of habitat but also the intactness or integrity of the habitat.

Species richness

Species richness is evaluated based on species occurrence. This is often derived from maps showing species distribution ranges or the area of suitable habitat for individual species to create a local species richness metric. The most widely used species distribution maps are developed and distributed by the IUCN Red List and Birdlife International. These are spatially explicit and at a global scale, covering the vast majority of known vertebrate species (e.g. amphibians, mammals and birds) and their conservation status.

Local species richness can also be calculated using large databases of georeferenced species occurrences such as GBIF, or databases containing local samples of biodiversity, such as PREDICTS, to model richness based on land cover and other environmental correlates. Regional or global species richness can be calculated using species-area relationships (SAR; Chaudhary *et al.,* 2015), which use habitat type and area of habitat to estimate species richness. Other modelling approaches such as BILBI also upscale databases of species records to model the spatial distribution of biodiversity on a regional or global scale.

Species vulnerability

Incorporating information on threats can be achieved in two ways. The first is by subsetting data to exclusively consider threatened species prior to calculating richness (Jenkins *et al.,* 2013). The second is by weighting species proportional to the threat that they face (de Baan *et al.,* 2015) for example, by using ordinal threat levels. The IUCN evaluates extinction risk, basing levels on a species' conservation status e.g. least concern (LC), near threatened (NT), vulnerable (VU), endangered (EN) and critically endangered (CR). These threat levels increasing in risk of extinction are based on quantitative criteria including rates of population decline, geographic range, population size, restricted habitats and the probability of extinction in the wild.

There are a number of other proxies to assess species vulnerability. Range size for example can be used to include only range-restricted (e.g. endemic) species. Alternatively, the inverse of range size (range size rarity) can be used to weight priority towards species with smaller ranges or species can be weighted according to the proportion of original habitat remaining. Other attributes too, such as habitat specialism and population density, can also be used to infer relative vulnerability. Population trends are an important consideration for species' vulnerability and population time series data (e.g. Living Planet Index) highlight species populations that are particularly vulnerable. These data can include measures of population size and density. A decline in population size therefore indicates that mortality rates are larger than fertility rates.

Species Abundance

Species abundance is the count of the number of individuals of each species. Other measures can also be used as proxies for abundance, such as biomass for plant species or number of nests recorded for bird species. The majority of methods using species abundance however do not use the total number of individuals belonging to a single species. Instead, the majority of methods measure the number of individuals of a species within a defined area. Their density can then be calculated by summing the mean densities for each species.

Abundance can also be represented as the intactness of abundance, estimating the impacts of a change in land use on species' populations relative to undisturbed ecosystems (e.g. PREDICTS). Pristine, healthy, ecosystems tend to harbour higher species abundance than disturbed and degraded ones. Degradation of an ecosystem would, therefore, result in a drop in the species abundance. This estimation relies on local species abundance data that are associated with a specific type of land use, inferring the cause of changes in land cover.

Beta Diversity

The organisation of biodiversity in space underpins ecological processes and maintains species and ecosystems through time (Socolar *et al.,* 2016). Beta diversity metrics attempt to reflect this property, and can be measured either as the ratio of regional to local species diversity, or as the dissimilarity of species composition between sites. It highlights differences in species compositional turnover across space and among habitats and helps emphasise areas of high complementarity - i.e. areas that contribute relatively more to total (gamma) diversity. Species composition across space depends on a series of bioclimatic and environmental factors. Decline in beta diversity therefore reflects the spatial homogenization of species assemblages.

Phylogenetic diversity

Phylogenetic diversity captures the shared ancestry of species and the breadth of evolutionary history, representing the evolutionary distance between coexisting species. While there are numerous ways to measure phylogenetic diversity (Véron *et al.,* 2019), here we will focus on one indicator, evolutionary distinctiveness, due to its wide use. Evolutionary distinctiveness can be calculated at different levels on the taxonomic hierarchy, including between specific species as well as between classes of populations. It is based on a phylogenetic tree; a branching diagram showing the evolutionary relationships between species.

These trees are usually created from morphological characteristics. However, more recently it has been possible to create them using genetic sequences for individuals. Depending on the production of the phylogenetic tree, branches can indicate either time since divergence of a species or the accumulation of evolutionary change over time. Phylogenetic diversity is commonly calculated as the sum of the lengths of all branches within a certain set of species, or the mean of the branch lengths can be calculated. Loss of phylogenetic diversity therefore demonstrates a decrease in species present which are less related, hence species are more clustered in a phylogenetic tree.

Functional diversity

Functional diversity refers to the extent of functional differences among the species in a community, acting as an indicator of the diversity of roles present. Such roles or functional groups are identified by physical, biochemical, behavioural or phenological traits that can influence the functioning and/or stability of an ecosystem (i.e. productivity and nutrient cycling) depending on the choice of traits. Examples of functional traits are body size, foliar phosphorus, habit (e.g. aquatic, aerial) and leaf size. Decline in functional diversity is not necessarily proportional to species richness loss as different species can share the same role in the ecosystem.

As with phylogenetic diversity, there are also numerous ways to measure functional diversity (Carmona *et al.,* 2016). Here we will focus on one main method to characterise functional diversity, the Functional Diversity Index, which captures the diversity of functional groups within a community. This is calculated in a similar way than phylogenetic diversity (i.e. based on the total branch length of a functional dendrogram). The Functional Diversity Index measures the extent of complementarity among species’ trait values by estimating the dispersion of species in trait space. For example, greater differences between species’ trait values represent greater trait complementarity and a larger Functional Diversity Index.

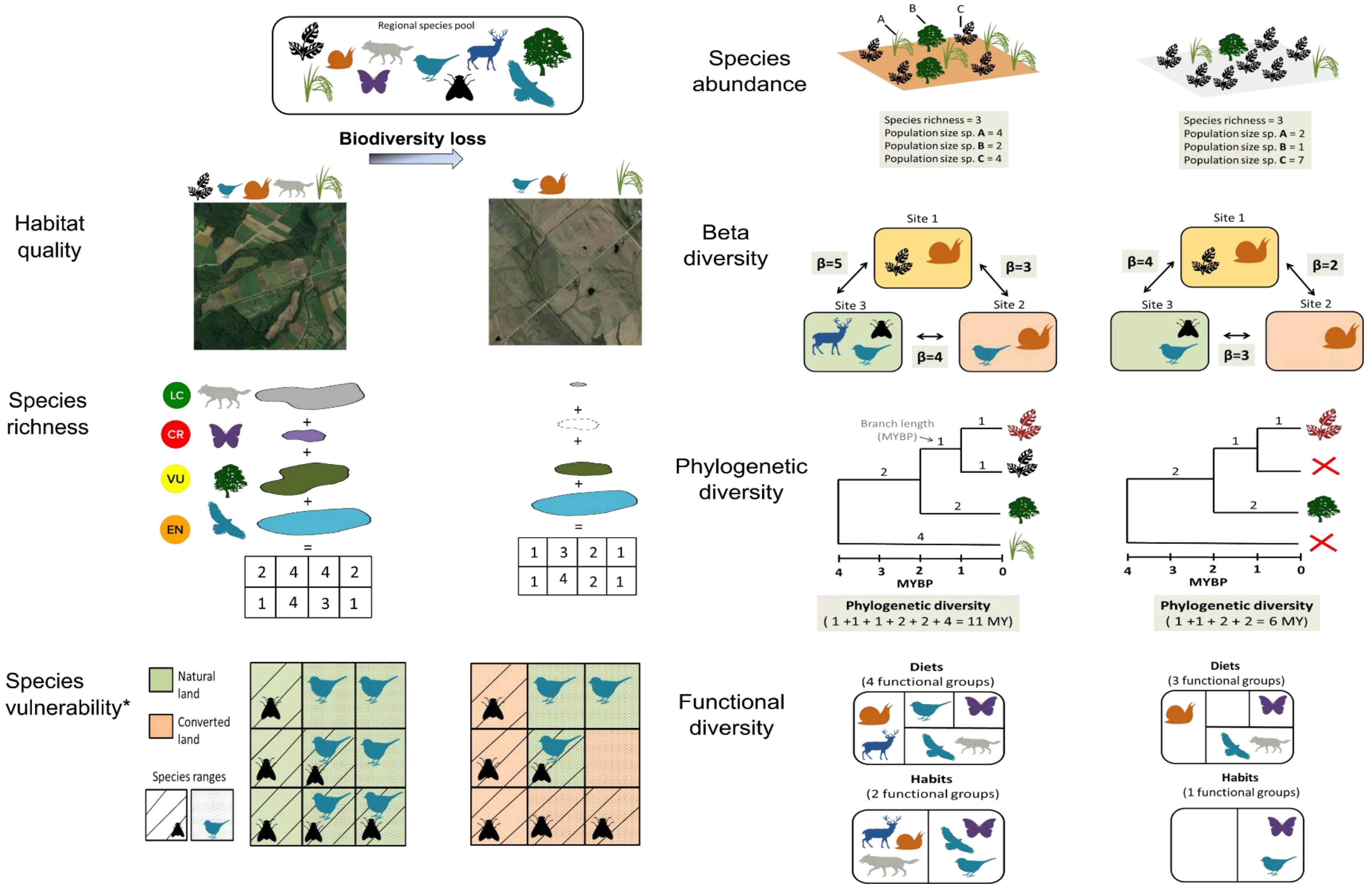

Figure 1. Schematic comparing effects of biodiversity loss on its different aspects. * Adapted from de Bann et al. (2015).

1.4 Example indicators

Within each of the aspects described above, there are a variety of indicators that have been developed to assess impacts on biodiversity and a range of specific methods available. Here we list some examples:

Table 1. Table of biodiversity aspects and a selection of indicators and example methods. Those marked with an asterisk (*) are those which we consider in more detail in Section 2.

Aspect	Indicator	Examples of methods
Habitat quality	Habitat loss	Hansen *et al.*, 2013* Potapov *et al.*, 2020 Song *et al.*, 2018
	Habitat intactness	Intact Forest Landscapes Forest Landscape Integrity Index*
	Human Appropriation of Net Primary Production	Haberl *et al.*, 2014
	Wilderness areas	Allan *et al.*, 2017
Species richness	Local species count	Jenkins *et al.*, 2013; 2015*
	Impact footprint	Verones *et al.*, 2017
	Global/regional species loss	Chaudhary *et al.*, 2015* De Baan *et al.*, 2013
Species vulnerability	Species persistence	Durán *et al.*, 2020*
	Recovery potential	Mair *et al.*, in review *
	Species threat	Lenzen *et al.*, 2009; 2012 Moran *et al.*, 2016; 2017
	Population abundance	Living Planet Index
Species abundance	Biodiversity Intactness Index	Newbold *et al.*, 2016*
	Mean Species Abundance	Alkemade *et al.*, 2009*
Beta diversity	Compositional dissimilarity	DiMarco *et al.*, 2019*
	Relative species niche width	Zelený 2009
Phylogenetic diversity	Evolutionary distinctiveness	Jetz *et al.*, 2014* Safi *et al.*, 2013
Functional diversity	FD Index	Petchey & Gaston 2002
	Ecological distinctiveness	Hidasi-Neto *et al.*, 2015*
	Ecosystem structure	Harfoot *et al.*, 2014

Section 2: Indicator comparison

2.1 Selection of indicators

To select indicators to support commodity-based comparison within the GCRF TRADE Hub, we filtered our subset of sources (Figure 2). Filtering criteria are based on a requirement for indicators to be linked effectively to models of commodity production for the examination of the impacts of agricultural expansion[1]. The first criteria is whether or not the indicator is a function of land use change; this being a primary driver of terrestrial biodiversity loss (Green *et al.,* 2005), and the underlying mechanistic link that we use to measure how agricultural commodity expansion changes the state of biodiversity.

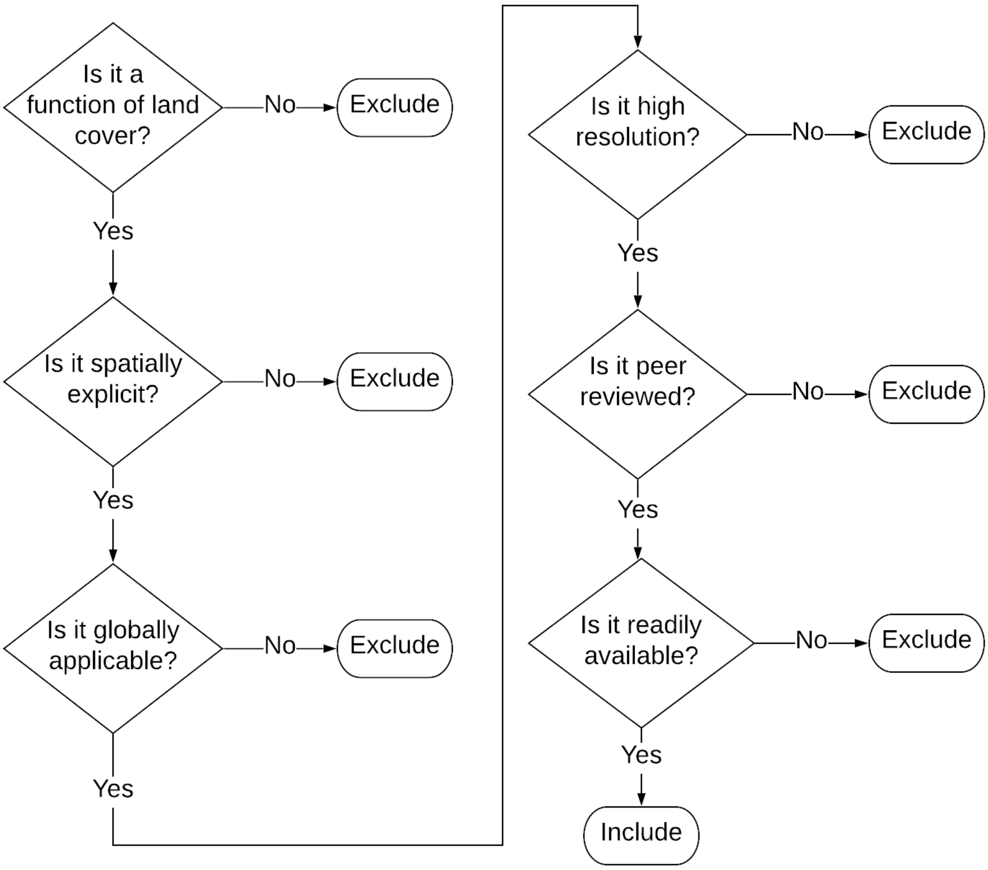

Figure 2. Decision tree used to identify appropriate indicators to include for trade assessment

High resolution (chosen here to be resolution of at least 10km*10km) is also essential for conducting sub-national analyses to enable application of methods at suitable scales for

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[1] This key requirement underpins our analyses. Hence, although certain indicators that are not a function of land use change may be important in commodity production systems, they are not relevant for this analysis.

commodity production (Joppa *et al.,* 2016)[2]. Our intention with the TRADE Hub project is to be able to compare results across country and commodity contexts, so it is also necessary that the indicator can be applied anywhere, regardless of whether this capability had been applied to date. Therefore, underlying data layers should be spatially explicit and have global applicability. Furthermore, for incorporation into our analyses, we only include methods that have been peer reviewed, and for which the data are readily available.

An initial filtered set of methods excluded methods applicable to phylogenetic and functional diversity, of which identified, pre-existing, methods were only currently available (to our knowledge) at 25km*25km or coarser. In order to ensure that methods were included that cover these important aspects of biodiversity, we therefore marginally relaxed this criterion (to a resolution of 25km*25km) in order to ensure inclusion. It is also important to note that although these methods have not been applied at finer resolutions, it is possible to do so, hence they are incorporated.

The final filtered set (see Table 1) allows comparison of methods across the biodiversity aspects, both qualitatively in this report and as applied in future analyses. Where more than one indicator was available for an aspect, we judged which was the more widely used amongst stakeholders and used that in our comparisons.

2.2 Short descriptions of selected indicators

For each of these indicators, we briefly describe the methods used to create them. We also summarise the data inputs as well as the subsequent outputs.

2.3.1 Habitat quality

2.3.1.1 Habitat loss: Tree cover loss (Hansen et al., 2013)

Methods: A series of Earth observation satellite (Landsat) data were used to map annual global forest loss, defined as tree cover, from 2000 to 2019 at a spatial resolution of 30 metres.

The study area includes all global land apart from Antarctica and a number of Arctic islands. Trees are defined as all vegetation taller than 5m in height and forest loss as a stand-replacement disturbance i.e. a disturbance that eliminates all previous trees in the stand, or the complete removal of tree cover canopy at the Landsat pixel scale. This improves on existing knowledge of global forest extent and change as it is spatially explicit and quantifies gross forest losses and gains. Outputs include pixel-level estimates of percentage tree cover,

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[2] Whilst commodity production information is often available at resolutions higher than this, when selecting appropriate biodiversity indicators for use in conjunction with production and trade assessment it is also important to consider that exclusion of biodiversity data that has a lower resolution might prevent the analysis of important biodiversity aspects. Ultimately a trade-off is likely to be needed with respect to a desire to apply data with as high a resolution as possible, and the availability of this data. Here, we choose a 10km2 threshold as this is noted by Joppa et al. 2016 to be a “minimal desirable resolution for most analyses” and is also equal to, or greater than, the resolution of most data describing sourcing patterns of commodities for international markets.

forest loss and forest gain for every year from 2000-2019, as well as trends in forest loss, using an internally consistent approach.

Data used: Tree cover loss 2000-2019 data from the University of Maryland, derived from Landsat. Supplementary data are used to identify the most biodiversity-relevant conversion - for example losses of primary tropical forest.

Outputs: Tree cover loss during the period 2000–2019, defined as a stand-replacement disturbance, or a change from a forest to non-forest state per 30 metre pixel. Encoded as either 0 (no loss) or else a value in the range 1–19, representing loss detected primarily in the year 2001–2019, respectively.

2.3.1.2 Habitat intactness: Forest Landscape Integrity Index (FLII) - Grantham et al. *(in press, Nature Communications)*

Methods: Proximity to human activity is an excellent predictor of habitat quality and, therefore, biodiversity value. This index, therefore, estimates quality by calculating direct and indirect pressure from key anthropogenic drivers as well as calculating changes to forest connectivity. Key drivers include infrastructure and agriculture which are used to calculate total recent degradation. This is combined with lost connectivity, by comparing current and potential connectivity, to create integrity scores.

Four spatially explicit datasets were combined, representing

(a) forest extent;

(b) direct pressure from high impact, localised human activities e.g. infrastructure, agriculture and recent deforestation;

(c) indirect pressure from edge effects e.g. hunting and selective logging. This presents as diffuse impacts that decline with distance to infrastructure and direct pressures;

(d) changes in forest connectivity due to forest loss.

Integrity scores are then composed of two main parts: total recent degradation and lost connectivity index. Both of these components are given equal weight for creating the integrity scores. The lost connectivity index is calculated by the change in forest configuration across an 80km radius. Connectivity is quantified by considering whether surrounding pixels are forested or not. Greater weight is then given to closer pixels with a normalized Gaussian curve (sigma = 20km) describing this relationship. This allows a very broad landscape connectivity value to be assigned to the pixel.

Once combined, an index score is calculated per pixel (300m resolution), with highest scores reflecting the highest forest health. This index was applied to forest extent for 2019, which was calculated by subtracting the annual tree cover loss 2001-2018 (Hansen *et al.,* 2013) from the global tree cover product for 2000.

In an analysis of how commodity expansion impacts on biodiversity, we can use these data in two ways:

1) We can replace the binary classification of tree cover with one that estimates the quality of the habitat for biodiversity within that patch. So forest losses in relatively

undisturbed locations are weighted more heavily than losses in highly disturbed habitats.

2) We can recalculate FLII using newly expanded cropping areas as a data input to see how these indirectly influence surrounding biodiversity.

Data used:

- Hansen et al. (2013) for forest extent
- OpenStreetMap for spatial maps of infrastructure
- Global Food Security-support Analysis Data (GFSAD) for spatial distribution of agriculture
- Beyer et al. (2020) to calculate connectivity

*Outputs: Gra*ntham et al*. (*in review) - Global map of Forest Landscape Integrity Index for 2019, highlighting three regions (USA, Equatorial Guinea and Myanmar) to demonstrate impact of pressure variables on index scores. A summary of scores for each biogeographic realm globally are also measured using the mean score, which is divided into three categories of integrity: low, medium and high.

2.3.2 Species richness

2.3.2.1 Species count: Jenkins et al. (2013)

Methods: A species count captures the number of species present within a certain area. It can be calculated using species range maps as a proxy for species occurrence. These range maps can include those based on the modelling of environmental niches, but for global analyses are more often based on species' extent of occurrence (EOO; e.g. Jenkins *et al.,* 2013). EOO is the area contained within the smallest polygon that encompasses all known or inferred occurrences, and can include large extents of habitat that are unsuitable for the species, introducing commission error (i.e. assuming that a species is present or covered when it does not). Therefore, these data should be interpreted as a 'potential' species richness. Alternatively, area of habitat (AoH) can be calculated globally by using only those habitats and environments within the EOO with which the species is associated (e.g. Rondinini *et al.,* 2011). However, it is important to note that there will still be areas within the EOO which are unoccupied because of species interactions of dispersal limitation.

For birds, data on breeding ranges are available from BirdLife International, whilst range maps for mammal and amphibian range maps are available from the International Union for the Conservation of Nature (IUCN). Information on over-wintering and migratory passage locations are also available within both datasets and the IUCN provides a number of tools for calculating species richness in ArcGIS software, counting the total number of species within each grid cell.

Data used: IUCN/Birdlife range maps, 5km resolution

Outputs: Jenkins et al. (2013; 2015): Global maps of terrestrial vertebrate diversity, showing species richness for birds, mammals and amphibians. Results include all species, threatened species and small ranged species. Overlap between the top 5% richest areas globally for the three taxa are also shown to indicate conservation priorities.

2.3.2.2 Countryside Species Area Relationship (SAR): Chaudhary et al. (2015)

Methods: Species area relationship (SAR) models predict the number of species in an area as a function of the number of species occurring in the area at a previous point in time. The classic SAR (Arrhenius, 1921) assumes all natural areas converted to human-dominated areas, such as agriculture and forestry, become completely hostile to biodiversity. This fails to capture true biodiversity change, as the assumption that non-natural habitats harbour no biodiversity is unrealistic. Hence, the classic SAR will overestimate biodiversity loss. The area required for extinction of a species is also usually larger than the sample area required to encounter the species, therefore the SAR does not accurately reflect species losses as habitat area is reduced (He & Hubbell, 2011).

Furthermore, it does not capture individual responses of species to land-use change that may vary in reality given that some species are more sensitive than others. De Baan et al. (2013) use the Matrix SAR model, which accounts for habitat heterogeneity to assess patterns of species richness in multi-habitat landscapes. Matrix effects (i.e. habitat provided by human-modified land) are incorporated into the model to account for taxon-specific responses to each component of a heterogeneous landscape. However, this model doesn't incorporate species vulnerability and assumes 100% species loss where no natural habitat remains, which is an oversimplification. Furthermore, it only considers four land use types. The Countryside SAR model, used by Chaudhary et al. (2015) in their assessment of trade impacts, builds on the classic SAR and Matrix SAR methodology, addressing these limitations. It considers a greater range of land use types, accounts for differential use of habitats by species and acknowledges that some species can tolerate human-modified habitats. It also includes assessment of vulnerability, using species specific threat levels and geographic range data. The following steps summarise the Countryside SAR approach:

Step 1: Firstly, local characterisation factors (CFs) are calculated using relative species richness to measure the response or sensitivity of taxa to land use change. This is calculated as the relative difference between plot-scale species richness in land use type and the baseline (prehistoric) natural reference area of the same biogeographic region. CFs are based on a global, quantitative analysis of peer-reviewed biodiversity surveys (De Baan *et al.*, 2013) and calculated for six land use types for five taxa (amphibians, birds, reptiles, mammals, and plants; with extension to the treatment of plants added after the method was originally developed; see below) across 804 terrestrial ecoregions.

Step 2: Local CFs are fed into the Countryside SAR model in the second step to calculate the regional species extinctions due to cumulative land use change. The model predicts losses as a function of the original number of species occurring in the natural habitat area, the remaining natural habitat and the affinity of taxon for the current land use. The relative reduction in local species richness is known as the response ratio.

Step 3: In the third step, for each ecoregion, vulnerability scores are calculated based on the fraction of each species' geographic range (endemic richness) hosted by the ecoregion and IUCN assigned threat levels for each species. Vulnerability scores are then multiplied by previously calculated SAR-predicted regional species losses, to estimate the potential global extinctions per unit of land use, with the loss of a species from all areas where it is found translated as global species loss (extinction). This creates weighted CFs (Verones *et al.,* 2013) in the unit 'global species equivalent lost per unit of land occupied or transformed'. Without the vulnerability weighting, CFs calculated in step 2 are referred to as 'unweighted CFs'.

Step 4: This step then aggregates the modelled species lost for each taxon to derive the ecosystem quality loss as measured in a unit known as 'global fraction of potentially disappeared species (PDF)'.

Chaudhary & Brooks (2018) improved upon the 2015 methodology by deriving updated CFs; adding plants to the taxa covered by the full method and including three land use intensity levels (minimal, light, and intense use) with methods also used to include the affinity of species to different intensities. The combination of datasets and methodological steps required to create the Countryside SAR is illustrated in Figure 3.

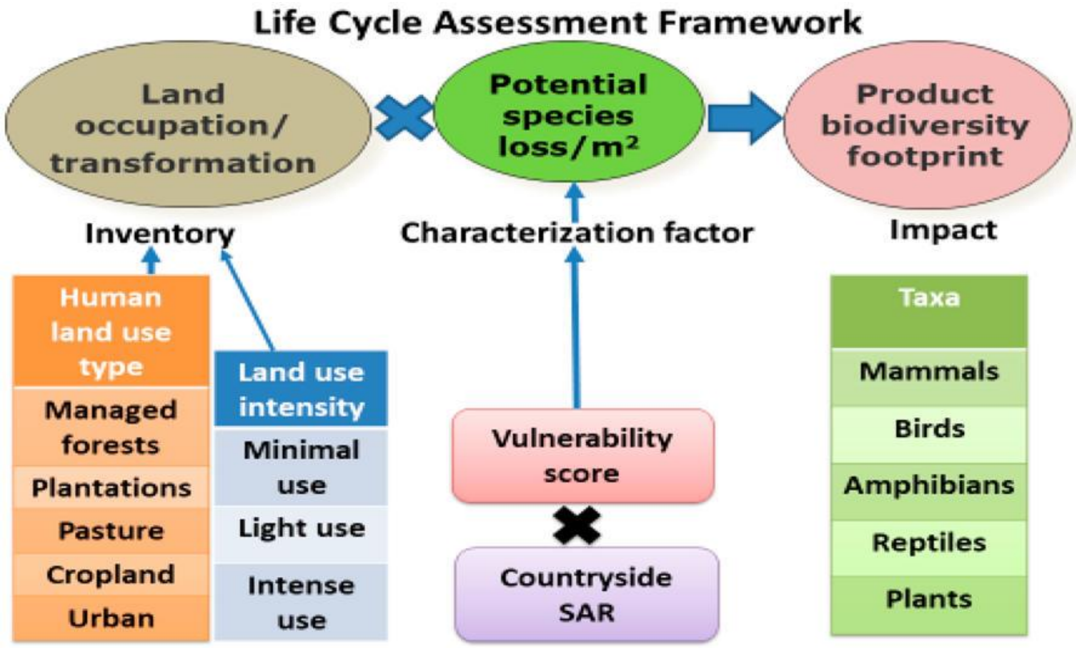

Figure 3. Overview of the Countryside SAR method (Chaudhary & Brooks, 2018).

Data used:

- land cover maps (LADA and Anthromes; 5 arc minute resolution)
- Species occurrence data (Kier *et al.,* 2005, WWF Wildlife finder)
- IUCN/Birdlife for species range maps to calculate vulnerability scores
- Ecoregion shapefiles
- FAOSTAT for area per land use type

Outputs: Chaudhary et al. *(2015);* Chaudhary & Brooks *(2018);* Chaudhary et al. *(*2016) - Global maps showing median regional occupation characterization factors per ecoregion, vulnerability scores and median global CF's per ecoregion

2.3.3 Threatened species

2.3.3.1 Recovery potential: Species Threat Abatement and Restoration (STAR)

Methods: The STAR metric quantifies the contributions that abating threats and restoring habitats in specific places offer towards reducing extinction risk. The score is calculated, globally, for amphibians, birds and mammals, and is weighted towards threatened species (CR>EN>VU>NT>LC=0). It comprises two distinct parts, the threat abatement score, and the restoration score:

1. Threat abatement: For each species, known threats (as classified by IUCN and BirdLife) are applied proportionally to their relative severity, and in proportion to the extent of their range affected. Removal of a threat in a particular location will therefore contribute to an increased threat abatement score.
2. Restoration: To calculate the potential for restoration, AoH has been mapped for 2015 and compared to a pre-industrial AoH. Habitat lost between these periods corresponds to restoration potential. AoH is mapped by constraining species ranges to elevational limits and habitat preferences using a digital elevation model (DEM) and cross-walking known habitat preferences (from IUCN) to a land cover map. This allows unsuitable areas to be removed from individual species' ranges.

The sum of STAR values across all species for a location represents the threat-abatement effort needed for all those species that would occur there to become Least Concern. For assessing biodiversity losses from habitat conversion, an inverse logic should be applied, in which the methods underpinning the restoration component of the STAR metric are used to calculate existing biodiversity value of habitat and the loss from its previous state (this could be a natural vegetation, or some other form of anthropogenic land use).

Data used:

- Species range data and threat status (IUCN, BirdLife)
- Land cover map (ESA CCI land use and cover maps)
- Digital elevation model (USGS, 2019)
- Habitat preferences (IUCN)

Outputs: Mair et al. (in review) - Global maps showing threat-abatement and restoration scores at 5km resolution for amphibians, birds and mammals per grid cell. Description available here.

2.3.3.2 Species persistence: Durán et al. (2020)

Methods: This indicator estimates changes in local population persistence, which can both be linked to specific human activities and adapted to different scales. Changes in persistence are derived from the proportional loss in species' area of habitat (AoH), which can be mapped for each point in time. Following Rondinini et al. (2011), vertebrate ranges are first clipped to a land cover map that has been harmonised (aka crosswalked) with species' habitat preferences from the IUCN habitats classification. Likewise, a digital elevation map is used to extract the parts of the range that fall within the species' altitudinal range. For plant species, for which habitat preferences are not available, range data are clipped to natural land cover classes.

AoH maps can be mapped for each point in time that will be assessed. In Durán et al. (2020) the years 2000, 2010, 2012 and 2014 were included.

For migratory species, resident, breeding and non-breeding ranges are treated separately, based on seasonal differences in habitat preferences. This accounts both for seasonal variation in habitat requirements, and for cases where the migration (and therefore survival) of a species is more threatened by changes to just one part of its migratory range.

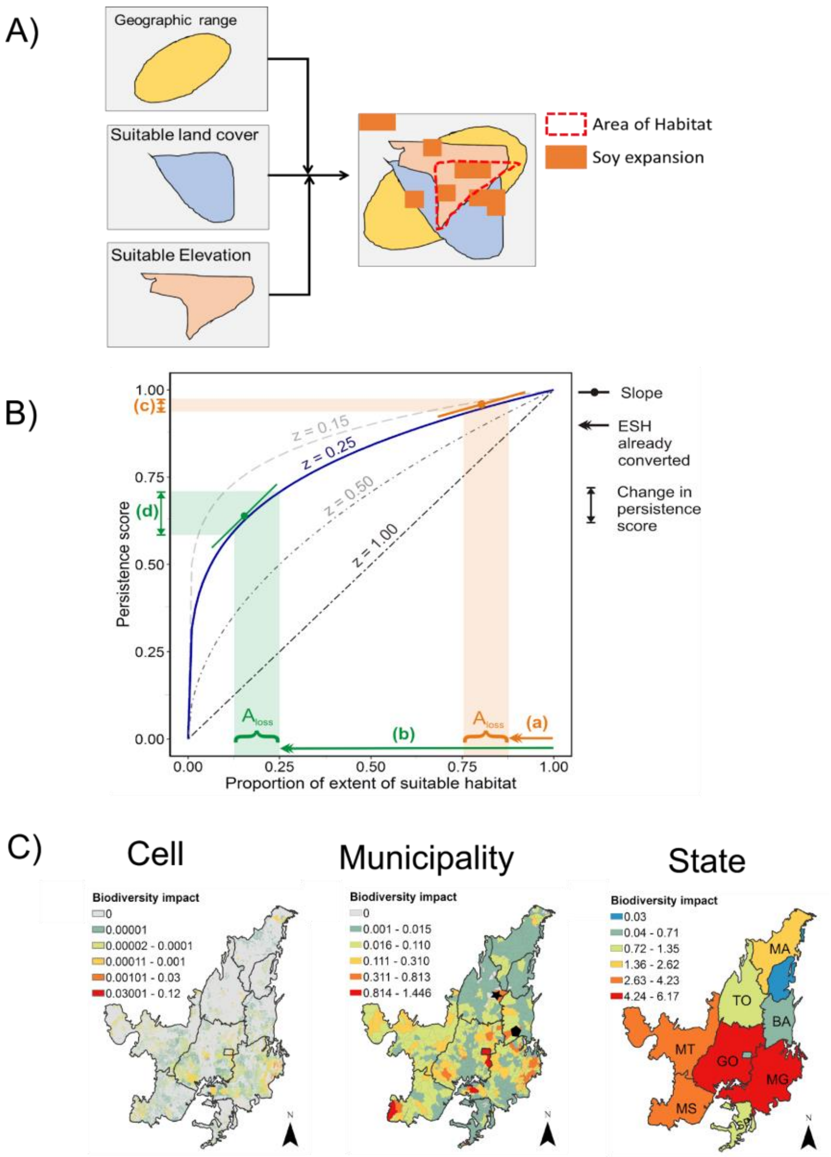

Figure 4. Schematic of method stages showing the three key main steps comprising the method: a) Mapping species' area of habitat (AoH) and calculating proportional loss of AoH due to specific land use activities (e.g. soy expansion); b) Estimating reduction in species' likelihood of persistence accounting for historical habitat loss; and c) mapping the marginal value of land use change and its biodiversity impacts across different scales.

Proportional losses of species’ AoH are calculated in relation to baseline, pre-industrial AoH maps, from which the current status can be assessed. Baseline AoH maps are produced from vegetation cover maps that represent the original or potential habitat area for the species, or from the historical extent of species ranges. The impact on population persistence of losing a given amount of AoH increases as total AoH decreases, resulting in a concave relationship between remaining AoH and local persistence. This is reflected in the power-law function used to describe the relationship between remaining habitat and persistence score. Here the exponent is set as <1 (z=0.25) so that remaining habitat for species that have lost a greater proportion of their original habitat is, relatively, more critical to the species persistence and thus receives greater weight in terms of persistence scores. This means different levels of historical habitat loss across species are accounted for. This also includes different sizes of baseline AoH, whereby species with smaller AoH present proportionally shaper declines in their remaining habitat. Although the exponent can be altered, setting it to 1 would remove the non-linear effect of cumulative historical habitat loss on species’ persistence.

When changes in AoH have been translated into persistence scores for individual species, these can be mapped as a continuous value in a gridded landscape, and then combined across species to obtain an aggregated biodiversity impact metric. The resulting pixel values reflect the species that they harbour, and their corresponding weighting factor. Hence, an area of land with many species that have lost a majority of their habitat will have a higher biodiversity impact, and an area of land with few species that have lost little of their original extent will have a lower biodiversity impact. The species used to calculate the losses can be specified (e.g. flagship species, threatened species, birds etc).

Data used:

- Species range data (IUCN, BirdLife, plant data (CNC Flora; Martinelli & Moraes, 2013))
- Land cover map (applied currently in Brazil: IBGE 2004, 2011, 2014)
- Digital elevation model (USGS, 2006)
- Habitat preferences (IUCN).

Outputs: While this is a globally applicable metric, Durán et al. (2020) used the example of soybean expansion in the Brazilian Cerrado. Two sets of outputs can be produced:

i) Changes in local population persistence linked to specific activities (e.g. commodity production). These estimates can be reported at species level, subset or group of species, or all species for which ranges and habitat preferences are available (in this case the majority of known amphibians, birds, mammals and reptiles, as well as plants);

ii) Maps of marginal loss value, which can be combined across species of interest and aggregated at different scales (e.g. municipality, state). Here gridded biodiversity impact maps were reported at 250 m resolution.

2.3.4 Species abundance

2.3.4.1 Mean Species Abundance (MSA): GLOBIO (Alkemade et al., 2009; Schipper et al., 2019)

Methods: This is an indicator of the biodiversity intactness of an area compared to its 'natural' state; with every hectare given equal weight. MSA is defined as the mean abundance of original species relative to their abundance in undisturbed ecosystems, using pristine situations as a baseline. An area with an MSA of 100% means a biodiversity that is similar to the natural situation. An MSA of 0% means a completely destroyed ecosystem, with no original species remaining.

The MSA in GLOBIO is quantified by using datasets from a meta-analysis of peer-reviewed publications which compare disturbed situations with the original. Data were extracted and MSA values calculated for each study by dividing the observed abundances of species in the disturbed situations by the abundances found in the original system described in the same publication. Values were capped at 1, so compensation by increasing species beyond their 'original' abundance over decreasing species is avoided. The mean over all species considered in the study was then calculated.

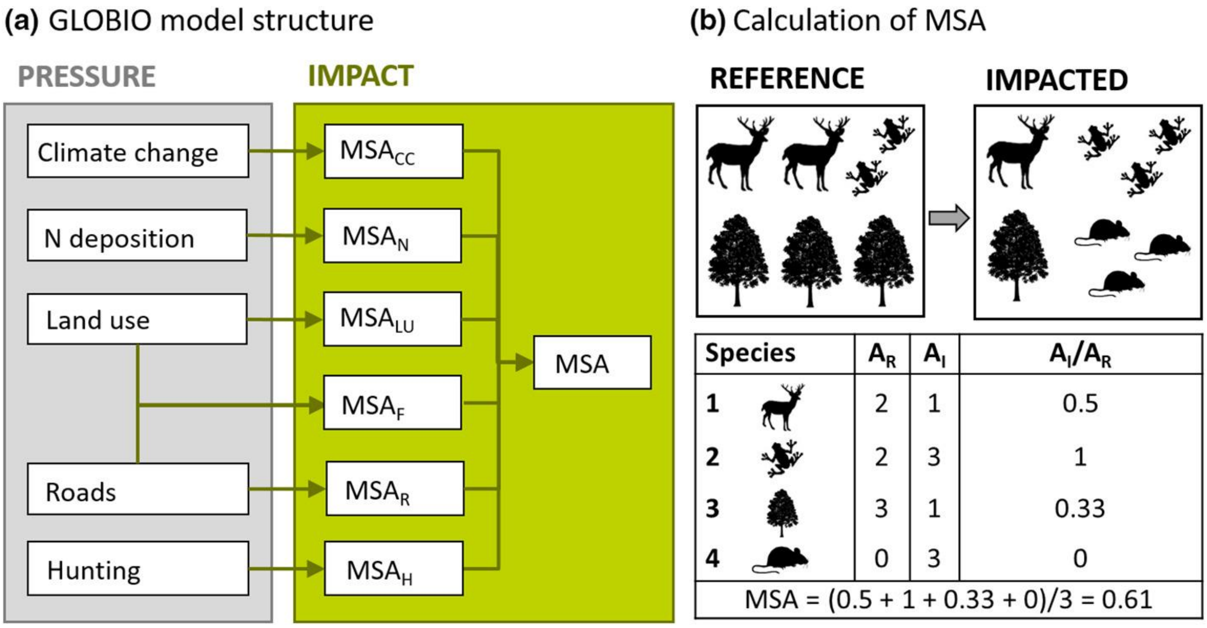

Figure 5. Summary of GLOBIO model structure and calculation of MSA (Schipper *et al.,* 2019)

Linear mixed models were used for data extracted from peer-reviewed publications for major direct and indirect human-induced drivers of impacts on natural ecosystems. Direct drivers include land use change, climate change, atmospheric N deposition, biotic exchange, atmospheric CO2 concentration, fragmentation, infrastructure and harvesting. Indirect drivers include human population density and energy use.

The MSA of each driver is calculated in GLOBIO per grid cell, using the cause-effect relationships linking environmental drivers to biodiversity impact. The MSA value for all drivers is then aggregated to produce a total MSA for each grid cell. Then, scores are aggregated across grid cells to give regional or global values. The response of individual species is not captured which is a limitation, with MSA representing the average response of the total set of species within an ecosystem.

Data used:

- ESA-CCI land cover map for 2015
- Outputs of future land use change from IAMs (0.5 degree resolution and finer)
- Databases for six human pressure-impact variables:
  - hunting, based on proximity to settlements (Benítez-López *et al.,* 2017; Benítez-López *et al.*, 2019)
  - road disturbance (Benítez-López *et al.,* 2010)
  - land use and habitat fragmentation (PREDICTS)
  - atmospheric nitrogen deposition (Midolo *et al.,* 2019)
  - climate change (Nunez *et al.,* 2019)

Outputs: The output resolution depends on the input maps. For global analyses the resolution is 0.5 by 0.5 degree (nearly 55*55 km near the equator). For national analyses often 1 by 1 km is used but can be downscaled to 300m.

2.3.4.2 Biodiversity Intactness Index (BII): Scholes & Biggs (2005); *Newbold et al. (2016)*

Methods: BII is also an indicator of biodiversity intactness. It uses data from a large and taxonomically diverse species group and is calculated for a given geographical area, relative to their reference populations, which is a baseline with minimal human impacts.

Originally conceptualised by Scholes & Biggs (2005), BII was first modelled globally by Newbold et al. (2016) as part of the PREDICTS project. This is a two-step modelling approach, followed by spatial projection of results. Firstly, site-level abundance or species richness is modelled as a function of site-level human pressure – namely land use, land use intensity, human population density and proximity to roads. This allows the model to infer the net effects of these pressures on overall abundance, therefore incoming species could compensate for loss of originally present species. Depending on the availability of pressure estimates, BII can therefore be applied at most resolutions, coarse or fine.

The second step is to then compare compositional similarity between sites in baseline land-use classes such as primary vegetation, and an adjacent site in other land use classes. The similarity measure used is the fraction of total species abundance also present in the baseline land-use class, which is calculated using an asymmetric form of the Jaccard index. The Biodiversity Intactness Index is then estimated and spatially projected according to land use. It can also be calculated for past and future dates, providing the estimates of pressures are available.

Data used:

- PREDICTS database
- Maps of four human pressure variables:
  - land use (Hurtt *et al.*, 2011)
  - land use intensity (van Asselen & Verburg, 2013)
  - human population density and proximity to roads (NASA's Socioeconomic Data and Applications Centre)

Outputs: Global maps of the biodiversity intactness of ecological assemblages in terms of the total abundance of originally occurring species. These are shown as a percentage of their total abundance in minimally disturbed primary vegetation. The total abundance and richness of species occurring in primary vegetation are also shown, at a high resolution of 1km (30 arc seconds) where pressure estimates are available.

2.3.5 Beta Diversity

2.3.5.1 Compositional dissimilarity: BILBI (Di Marco et al., 2019; Hoskins et al., 2020)

Methods: Biogeographic Infrastructure for Large-scaled Biodiversity Indicators (BILBI) is a global biodiversity modelling system developed by CSIRO (Australia's national science agency). Based on highly comprehensive data - >300 million records of >400 thousand species globally (GBIF, 2014; Map of Life - see Jetz *et al.*, 2012) - it accounts for variation across landscapes in composition of biodiversity (beta diversity[3]) so that local biodiversity losses can be calculated in terms of their contribution to gamma diversity losses (from site level to global).

Global models use generalized dissimilarity modelling (a statistical technique predicting the dissimilarity in species composition between pairs of sites as a function of environmental differences between, and spatial separation of, those sites) and species occurrence records to predict ecological similarity. The relationship between compositional turnover and environmental gradients is scaled to generate 'ecologically scaled environments' and hence continuous predictions of beta-diversity patterns across a landscape.

For each grid cell, the percentage coverage of each land-use class was multiplied by coefficients representing the estimated proportion of local species richness expected to be retained for that land use change, which were derived from global meta-analyses using the PREDICTS database. Past and future trends in habitat condition can also be generated using historical climate and land use data.

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[3] alpha diversity refers to the diversity within a site; beta diversity refers to compositional variation between locations; gamma diversity refers to total diversity across all sites.

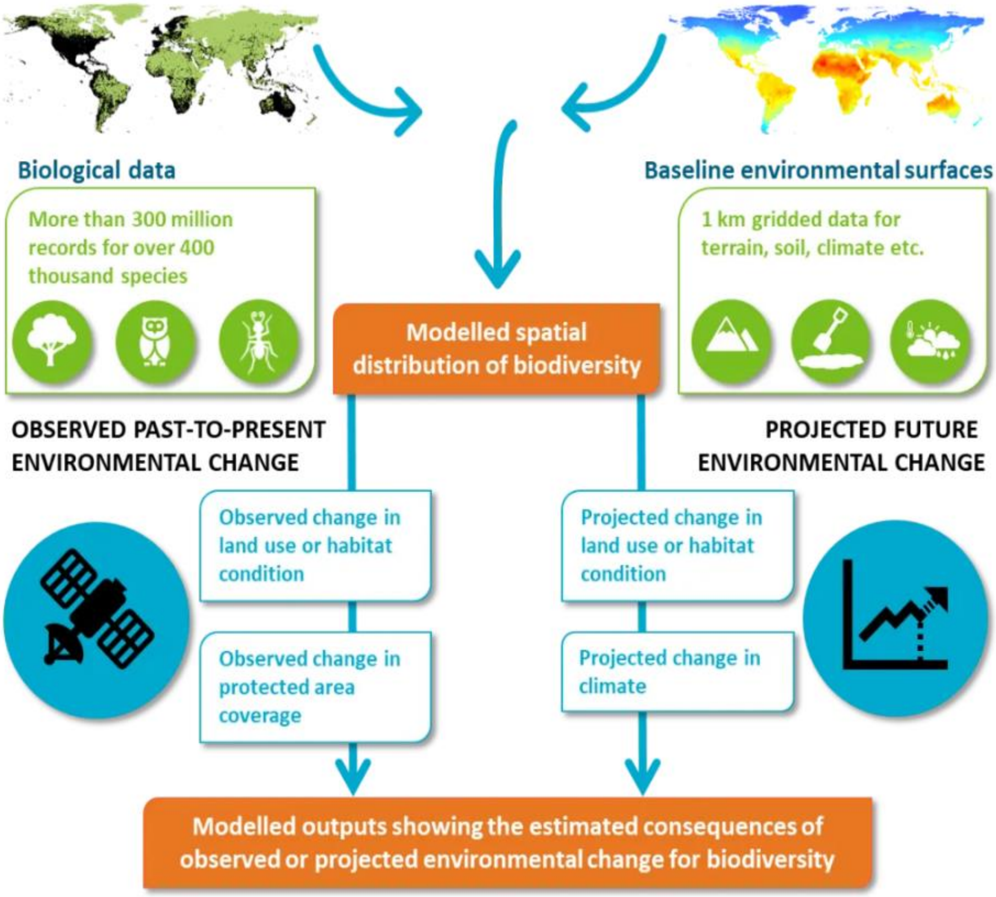

Figure 6. The components of the system that make up BILBI and report on past, present and future consequences for biodiversity. Composition of BILBI and outputs (available here)

Data used:

- GBIF plant records of vascular plant species occurrence to model compositional turnover
- PREDICTS database to generate habitat condition surfaces from estimated impacts of different types of land use change on species richness
- Species Area Relationship (SAR) used to predict the proportion of species expected to persist over the longer term
- Land-use harmonization dataset (LUH2; Hurtt *et al.,* 2017)

Outputs: DiMarco *et al.,* 2019 - This paper presents global maps of biodiversity persistence under different land use and climate change scenarios which show the estimated proportion of vascular plant species expected to persist long term. This is presented both for past land use change and under socio-economic scenarios of future land use change at 1km resolution.

2.3.6 Phylogenetic Diversity

2.3.6.1 Evolutionary distinctiveness: Jetz et al., 2014

Methods: This is a species-specific measure representing the relative contribution of a species to the total phylogenetic diversity of a clade, or how isolated a species is on its phylogenetic tree.

To calculate scores for each species, the total phylogenetic diversity of a group of organisms (a clade) is divided amongst its members. Each branch of the phylogenetic tree, represented in evolutionary time (millions of years), is divided by the number of species spanning the branch (Figure 7). The evolutionary distinctiveness of a species is defined as "the weighted sum of the branch lengths along the path from the root of an ultrametric tree to the tip, with weights determined as 1/number of tips sharing (ultimately subtending) that branch". Hence, the sum of the evolutionary distinctiveness of all species in a clade equals the total phylogenetic diversity.

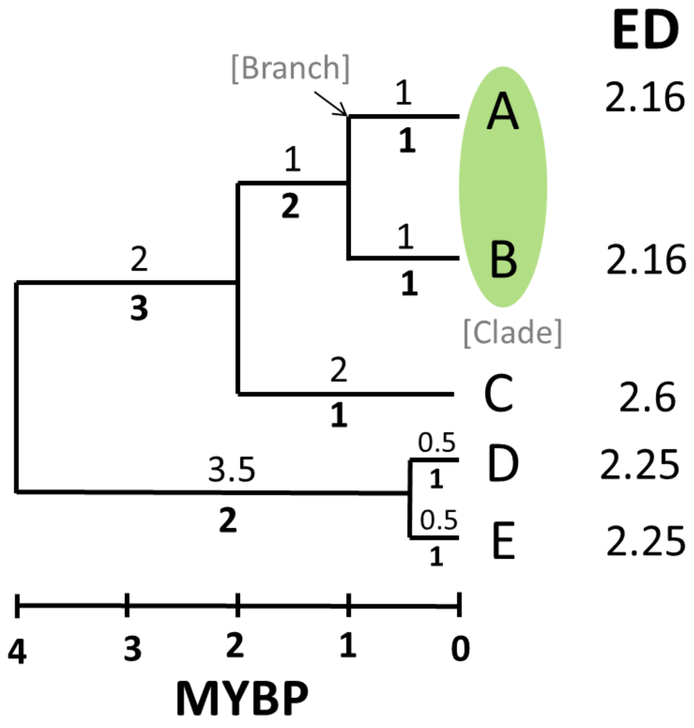

Figure 7. Hypothetical phylogeny of five species (A–E) with Evolutionary Distinctiveness (ED) scores, modified from Isaac et al. (2007). Numbers above each branch indicate the branch length in millions of years before present (MYBP); numbers below show the number of descendent species .

For example, in Figure 7, the evolutionary distinctiveness of species A is the sum of each of the three branches (1/1 + 1/2 + 2/3 = 2.16) between species A and the root. Each branch is calculated as the length of evolutionary time (in millions of years) divided by the number of species within that branch. For example, the terminal branch for species A contains just one species and is 1 million years long, therefore receives a score of 1/1. For species D and E, even though they represent a small amount of unique evolutionary history, they are the second top-ranked species; hence, evolutionary distinctiveness is not defined by length of branches alone, but also by the number of descendant species.

Scores were calculated and mapped globally by Safi et al. (2013) for mammals and amphibians, and Jetz et al. (2014) for birds. Both studies calculated evolutionary distinctiveness as above (Isaac *et al.,* 2007, Redding *et al.,* 2003). In addition, they used two approaches in order to identify priority regions of the world: a species richness based approach and a randomisation based approach. For the species richness approach the areas containing the top 5% (Safi *et al.,* 2013) and 10% (Jetz *et al.,* 2014) evolutionary distinctiveness across species were identified. In the randomisation approach, the studies identified regions with higher accumulated scores than expected by chance, but each did it in a slightly different way. Safi et al. (2013) identified where observed cumulative scores were significantly overdispersed based on a derived empirical distribution function, resulting from 1000 samples from each grid cell. Jetz et al. (2014) used a measure of phylogenetic signal of binary traits (or character dispersion on a phylogeny) called metric D (Fritz & Purvis, 2010), which allows to capture the phylogenetic clustering and randomness.

Data used:

- Phylogeny data used to calculate ED score were obtained from the following sources:
    - Mammals - Isaac et al. (2007), who used a composite ‘supertree’ from Bininda-Edmonds et al. (2007) and the taxonomy of mammals by Wilson and Reeder (2005).
    - Amphibians - Isaac et al. (2012), who based its phylogeny on Frost et al. (2006) and Roelants et al. (2007), and the taxonomy of Amphibians (Frost, 2007).
    - Birds: Jetz et al. (2014), following the taxonomy of BirdLife v3 and IOC v2.7. Phylogeny data from birdtree.org
- Species range distribution data: the IUCN RedList for mammals and amphibians, del Hoyo *et al.* (1992-2011) and also Ridgely et al. (2003) for birds.

Outputs:

- Safi et al. (2013) - this paper presents species level data of ED scores for global mammals and amphibians. Also, spatial polygons containing ED zones for both taxonomic groups. ED priority area global maps for mammals and amphibians, of 25 x 25 km to 200 x 200 km in steps of 25 km, based on the species richness and randomisation based approach as explained above.
- Jetz et al. (2014) - this paper presents species level data of ED and ESGE scores for global birds at 110 x 110 km resolution, in a Behrman equal-area projection. ED priority area global maps are for passerine and non-passerine birds.

2.3.7 Functional Diversity

2.3.7.1 Ecological distinctiveness: Hidasi-Neto et al. (2015)

Functional diversity (FD) is the variation of traits between organisms. It is estimated as the variation of traits in the functional space occupied by an ecological unit (i.e. species community, ecosystem). Different indices estimating FD attempt to capture the three primary components of FD variation: functional richness, functional evenness and functional divergence. The Functional Diversity Index developed by Petchey & Gaston (2002) captures the richness of functional groups represented by the species in a community. It is calculated in a similar way than phylogenetic diversity (PD). It is the total branch length of a functional dendrogram. FD measures the extent of complementarity among species' trait values by estimating the dispersion of species in trait space. For example, greater differences between species' trait values represent greater trait complementarity and larger FD. There are four steps to calculating FD: (1) obtaining a trait matrix, (2) converting the trait matrix into a distance matrix, (3) clustering of the distance matrix to produce a dendrogram, and (4) calculating the total branch length of the dendrogram.

It is important to note the type of traits that go into the trait matrix. One might want to select only traits that are related to the ecosystem process of interest. For example, flower colour might be excluded if the aim is to quantify diversity that is important for biomass productivity. Alternatively, some studies might be interested in traits related to species' ecological strategies, which may not directly reflect the ecosystem functions performed by the species. This is often referred to as 'ecological distinctiveness' (EcoD).

Hidasi-Neto et al. (2015) calculated and mapped the global ecological distinctiveness of 4,255 terrestrial mammals based on FD. They used information on body mass, diet, habit and activity period to produce a functional dendrogram. Since phylogenetic diversity (PD) is also calculated from dendrograms (i.e. branch distance) they combined PD values (as described in Evolutionary distinctiveness section) with FD into a single score, thus capturing both functional and phylogenetic diversity. They named it the 'Ecologically and Evolutionary Distinct and Globally Endangered (EcoEDGE)' score. By weighting this score with species' Red List category (CR, EN, VU, NT, LC), the metric assigns a higher value to those species with higher risk of extinction. From this weighting they also produced a map where only ecological distinctiveness was presented: *Ecologically distinctiveness and globally endangered species (EcoDGE).* To identify regions containing species with high EcoEDGE and EcoDGE scores, they overlaid extent of occurrence maps for species within the upper quartile of the score distributions (1,064 species) onto a grid with resolution of 1°x 1° latitude and longitude.

Data used:

- Global species distribution ranges for terrestrial mammals from the IUCN RedList.
- Functional and phylogenetic dendrograms for mammals.
- Functional traits information from Safi et al. (2011).

Outputs:

- Global map of ecologically distinctiveness (EcoED) for terrestrial mammals
- Global map of ecologically/evolutionarily distinct and globally endangered species (EcoDGE & EcoEDGE)

2.3 Interconnections between indicators

Many of the methods used in practice to assess the different aspects of biodiversity, (including the examples provided in Table 1), are underpinned by similar data layers. Figure 8 illustrates how selected examples of these biodiversity aspects and their associated methods are linked by the data inputs used to implement them. Land use change for example feeds into all aspects, whilst other data inputs may be specific to certain aspects or indicators.

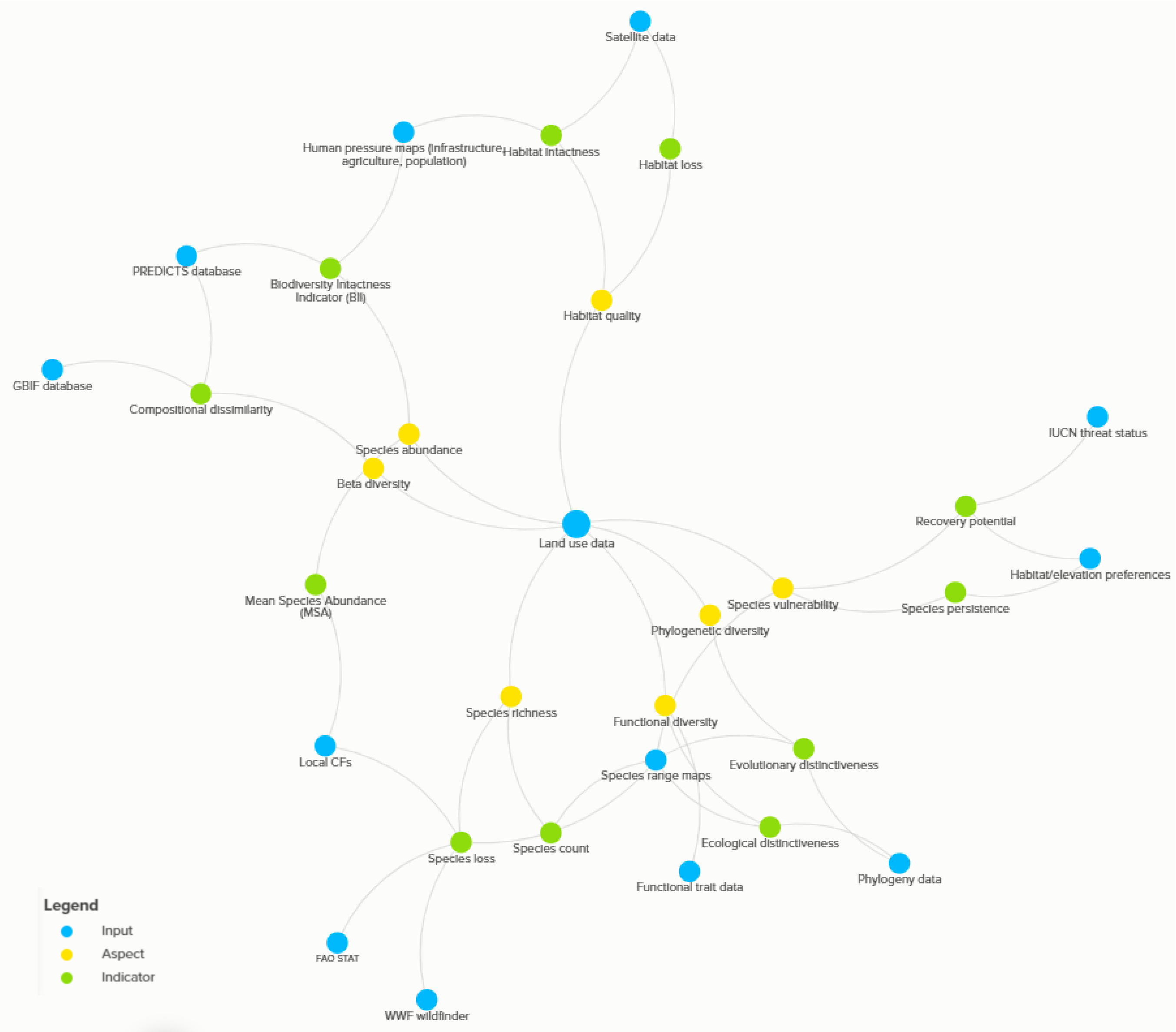

Figure 8. Diagram showing biodiversity aspects and how they are interconnected by data inputs (interactive version available here)

2.4 Indicator applicability

The applicability of an indicator ultimately depends on the context in which it is used and the answers that users seek the indicator to provide, but it is helpful to provide a summary of the key features and considerations that may factor into decisions around indicator selection. We use the following classifications as a framework for assessing indicators (Table 2):

- **Readiness:** relates to how 'ready' the indicator is for use by decision makers working in supply chains and with trade data. This includes aspects such as whether global data are available, whether data are free to use and easy to download and process, and whether users can trust that the data will be available and up-to-date in the mid- to long-term.

- **Responsiveness:** relates to how likely changes to biodiversity in locations of concern are to be reflected in observable changes in the indicator. This includes whether the indicator is sensitive to changes at the scale at which decision makers (such as procurement officers or importer country policy makers), can act (i.e. land-cover change at cell level can be translated as biodiversity impacts at municipality or state level). Also, whether the indicator measures impacts directly, or whether it measures the risk of impacts occurring (potential impacts) or simply an increase in potential pressure on biodiversity, for example.

- **Relevance:** relates to uptake by private and public actors - particularly those in supply chain decision making roles or those designing trade policy. In the case of new indicators, this is mostly assessed as whether the indicator has been designed to respond to their needs and whether such stakeholders have been involved in the development.

- **Resolution:** relates to the spatial resolution of the data, as well as the frequency of updates (e.g. are data available annually). For indicators of species diversity, it also incorporates whether data offer taxonomic specificity in their outputs. Many metrics can only be calculated for vertebrates for example, and most have some degree of taxonomic bias.

Table 2. Selected indicators and their applicability for assessment of biodiversity impacts of specific agricultural commodity production

Indicator	Readiness	Responsiveness	Relevance	Resolution
	- Coverage **- Accessibility**	**- Sensitivity** **- Pressure vs risk vs impact**	**- Use in policy or business** **- Use by academics**	**- Temporal** **- Spatial** **- Taxonomic**
Habitat loss: Hansen *et al.*, 2013	Global coverage, updated annually and freely available to download as individual 10 x 10 degree granules	Defines forest loss as stand-replacement disturbance with trees defined as taller than 5m. Measures impacts directly using habitat change as a proxy for biodiversity loss.	A globally consistent, locally relevant record of forest change, widely applicable.	30m resolution for forest cover, available from 2000-2019. Standardised definition of forest.
Habitat intactness: Forest Landscape Integrity Index	Global layer calculated, currently under review.	Captures modelled intactness of habitat, according to known anthropogenic pressures. Incorporation of integrity likely to relate more closely than simple presence/absence e.g. forest loss	Highly relevant to supply chain managers, in particular, to help identify important habitats and areas of high risk.	300m resolution, snapshot of current status. 'Forest' definition can be calibrated according to national definitions of canopy cover.
Species count: Jenkins *et al.*, 2013	Global layers freely available to download and data available on request for non commercial use.	Very sensitive to data availability and resolution used. Useful for identifying species at risk. Based on species ranges therefore able to incorporate information on land use to define species occurrence (i.e. Area of Habitat).	Data used as indicators for UN Sustainable Development Goals (SDGs). Standardised measures for easy monitoring and comparison of changes over time. Use in academia and policy.	10km resolution outputs, finer resolution can be calculated Underlying data is regularly updated, covers vast majority of known species ranges for mammals, birds and amphibians.

Indicator	Readiness	Responsiveness	Relevance	Resolution
Species loss: Countryside SAR	Globally applicable. Characterisation factors freely available to download.	Estimation of extinction risk of species, sensitive to land use, incorporates taxon sensitivity to land use change. These sensitivity parameters rely on average estimates calculated at ecoregion level. Also, estimations are not at species level and species' identities are unknown.	Commonly used in academia and life cycle impact assessment as a model for projecting extinction rates, yet highly criticized for overestimating extinctions and published characterisation factors based on relatively dated land cover datasets.	Underlying data resolution at 5 arc minute resolution (~8km). Global coverage across 804 ecoregions with varying sizes and five taxonomic groups: birds, amphibians, mammals, vascular plants and reptiles. Limited to endemic species.
Recovery potential: STAR	Global data are available and underpinning datasets are well resourced institutionally. Data will be freely available through the IBAT tool.	Risk based metric - recovery potential is based on presence of species, modelled from land use.	Developed to respond to the need for private sector and public sector actors to measure and report their contributions to species recovery within a consistent framework in the post2020 Global Biodiversity Framework.	Data are produced at 5km resolution for known threatened amphibian, bird and mammal species. Recovery potential is estimated based on changes between 2000 and 2018.
Species persistence: Durán *et al.*, 2020	Globally applicable, most of the underlying datasets are also available. Outputs available only for Cerrado biome. Maps of specific commodity crops are subject to each case study.	Ability to specify observed impacts to single species, and for specific land uses, means that results can be highly sensitive to units of land use change. Can be implemented under land use scenarios if predictions on land-use change are available.	Designed to address shortcomings of existing metrics, capturing historical habitat losses to estimate cumulative impacts and aggregating estimates across different taxa and scales. These characteristics aimed to support commodity trade assessments.	250 m resolution for the Brazilian Cerrado. Includes amphibian, bird, mammal and plant species covering the years 2000, 2010, 2012 and 2014. Can characterize biodiversity impact trends if temporal land-use change data are available.

Indicator	Readiness	Responsiveness	Relevance	Resolution
Mean Species Abundance: GLOBIO	Applicable on global and regional scales. Open source framework using open source software (Python). Scripts freely available to run the model. Underlying databases also freely available.	Captures intactness of biodiversity in response to human pressure variables under different future scenarios, as well as past and present pressure levels.	Result of international consortium. Extensive use in environmental outlook studies E.g Convention on Biological Diversity (CBD) and Intergovernmental Science-Policy Platform on Biodiversity and Ecosystem Services (IPBES)	300m resolution for outputs, impact relationships included for terrestrial plants and warm- blooded vertebrates e.g. birds and mammals. Can be used to quantify past, present and future human-induced changes
Biodiversity Intactness Index: PREDICTS	Global layer freely available for biodiversity intactness of ecological assemblages.	Quantifies species and community level responses to anthropogenic pressure.	Mainly used in academia but is relevant for answering policy related questions.	I km resolution at global scale. Reasonably representative of all major taxonomic groups and terrestrial biomes.
Compositional dissimilarity: BILBI	Global data available, excellent taxonomic and geographic coverage.	Responsive to land use change data. Losses considered in the light of neighbouring biodiversity values.	Mainly in academia. It is not straightforward to measure and is not widely understood or easy to communicate.	1km global (could do finer resolution for regional assessments). Snapshot of current status.
Evolutionary distinctiveness Jetz *et al.,* 2014	Datasets are at global scale and are available upon request to authors.	Based on species ranges therefore able to incorporate information on land use to define species occurrence (i.e. Area of Habitat).	Metric mostly used for scientific research purposes within academia. Not yet applied to land-use assessments.	Global maps for mammals and amphibians at 25km to 200km resolution, in steps of 25 km. For birds, maps are available at 110 km resolution. Represent one point in time.
Ecological distinctiveness Hidasi-Neto *et al.,* 2015	Datasets are at global scale and are available upon request to authors.	Based on species ranges therefore able to incorporate information on land use to define species occurrence (i.e. Area of Habitat).	Metric mostly used for scientific research purposes within academia. Not yet applied to land-use assessments.	Global maps for terrestrial mammals are available at 100 km resolution. Represent one point in time.

We have focused attention within this report on the different aspects of biodiversity that indicators might attempt to cover, and selected methods that implement these aspects in practice. Implementation, of course, requires (often complex) data, and - as highlighted for example in Figure 8 - there is potential for data sources to overlap considerably; particularly in cases where there are 'seminal' datasets such as IUCN data that are broadly accepted and implemented throughout the conservation science community. On the one hand, co-dependence on selected datasets can be seen as positive; ensuring that there is consistency between sources underpinning methods and helping to harmonise assessments.

Yet it is also possible that this may cause issues in the applicability of indicators; particularly where underpinning data-dependencies are obscured as part of a series of complex methodological steps. In many cases - at least partly explained by the fact that it is far from trivial to update large global datasets - land use or species information applied within the methods highlighted within this report may be years, or even decades out of date. This is a particularly pertinent consideration when indicators are applied in the context of granular commodity trade or supply-chain linked assessment; whilst 'hotspotting' of *risk* may be possible (and valuable) when using relatively dated sources, assessment of trade-linked *impact* is dependent on contemporary information that allows near- or real-time supply chain information to be linked to representative land use and species distribution data.

Likewise, interventions to improve the biodiversity conditions in regions of production (that may, for example, directly follow impact and/or risk assessment) can only be monitored for efficacy if the biodiversity indicators applied are responsive to changing conditions on the ground. It is outside the scope of this report to fully assess the methods highlighted above in terms of their data-dependency and relative utility in current and ongoing risk and/or impact assessment; the considerations highlighted in Table 2 are instead indicative of the applicability of the indicators to assessment of biodiversity risks associated with trade.

2.5 Next steps

In the next phase of the TRADE Hub project, we also intend to assess, quantitatively, how indicators vary (or not) when applied across different commodities and landscapes. We plan to focus on the following forest-risk commodities: palm oil in Indonesia, soy in Brazil, cocoa in Cote d'Ivoire and rubber in China, using recent, high resolution crop maps where available. The intention of this analysis is to assess whether indicators which cover different aspects of biodiversity correlate and, for example, whether simpler approaches could be applied as proxies for others. We also aim to compare across country-commodity contexts to examine how consistent emerging patterns between selected indicators are. This may highlight for example geographic bias or be reflective of data quality and availability.

The selected indicators in this report are the most promising in terms of the comparisons for our applied work, thus forming a probable portfolio that we will draw on for the ongoing analysis taking place in the project. Although it is likely we will use indicators selected in this report, they may not be practically applicable due to potential issues of harmonising data and applying within contexts as described in associated papers. This means recreating various indicators may be necessary for our purposes, using more recent or relevant data layers to inform the analysis. Furthermore, once the initial biodiversity comparison has been produced, we plan to use analysis results to inform which indicators to use with trade models to assess impacts of specific commodity trade on biodiversity.

Reference list

Allan, J. R., Venter, O., & Watson, J. E. (2017). Temporally inter-comparable maps of terrestrial wilderness and the Last of the Wild. *Scientific data*, *4*, 170187.

Alkemade, R., Van Oorschot, M., Miles, L., Nellemann, C., Bakkenes, M., & Ten Brink, B. (2009). GLOBIO3: a framework to investigate options for reducing global terrestrial biodiversity loss. *Ecosystems*, *12*(3), 374-390.

Arrhenius, O. (1921). Species and area. *Journal of Ecology*, 9(1), 95-99.

Benítez-López, A., Alkemade, R., & Verweij, P. A. (2010). The impacts of roads and other infrastructure on mammal and bird populations: A meta-analysis. *Biological Conservation*, 143, 1307– 1316.

Benítez-López, A., Alkemade, R., Schipper, A. M., Ingram, D. J., Verweij, P. A., Eikelboom, J. A. J., & Huijbregts, M. A. J. (2017). The impact of hunting on tropical mammal and bird populations. *Science*, 356, 180– 183.

Benítez-López, A., Santini, L., Schipper, A. M., Busana, M., & Huijbregts, M. A. J. (2019). Intact but empty forests? Patterns of hunting-induced mammal defaunation in the tropics. *PloS Biology,* 17, e3000247.

Beyer, H. L., Venter, O., Grantham, H. S., & Watson, J. E. (2020). Substantial losses in ecoregion intactness highlight urgency of globally coordinated action. *Conservation Letters*, *13*(2), e12692.

Bininda-Emonds, O. R., Cardillo, M., Jones, K. E., MacPhee, R. D., Beck, R. M., Grenyer, R., ... & Purvis, A. (2007). The delayed rise of present-day mammals. *Nature*, *446*(7135), 507-512.

Biodiversity Indicators Partnership (2011). Guidance for National Biodiversity Indicator Development and Use. *UNEP World Conservation Monitoring Centre*, Cambridge, UK. 40 pp.

Cadotte, M. W., Carscadden, K., & Mirotchnick, N. (2011). Beyond species: functional diversity and the maintenance of ecological processes and services. *Journal of applied ecology*, 48(5), 1079-1087.

Carmona, C. P., De Bello, F., Mason, N. W., & Lepš, J. (2016). Traits without borders: integrating functional diversity across scales. *Trends in ecology & evolution*, *31*(5), 382-394.

Chaudhary, A., Verones, F., De Baan, L., & Hellweg, S. (2015). Quantifying land use impacts on biodiversity: combining species–area models and vulnerability indicators. *Environmental science & technology*, *49*(16), 9987-9995.

Chaudhary, A.; Verones, F., de Baan, L., Pfister, S., Hellweg, S. Land stress (2016) Potential species loss from land use (global; PSSRg). *LCImpact, the Online Community for Life Cycle Impact Assessment.* Available at: http://www.lcimpact.eu/downloads/documents/Land_stress_chapter_LCimpact_July_17_2016.pdf.

Chaudhary, A., & Brooks, T. M. (2018). Land use intensity-specific global characterization factors to assess product biodiversity footprints. *Environmental Science & Technology*, 52(9), 5094-5104.

Croft, S. A., West, C. D., & Green, J. M. (2018). Capturing the heterogeneity of sub-national production in global trade flows. *Journal of Cleaner Production*, *203*, 1106-1118.

Davies, T. J., & Cadotte, M. W. (2011). Quantifying biodiversity: does it matter what we measure?. In Biodiversity hotspots (pp. 43-60). *Springer,* Berlin, Heidelberg.

de Baan, L., Mutel, C. L., Curran, M., Hellweg, S., & Koellner, T. (2013). Land use in life cycle assessment: global characterization factors based on regional and global potential species extinction. *Environmental science & technology*, *47*(16), 9281-9290.

de Baan, L., Curran, M., Rondinini, C., Visconti, P., Hellweg, S., & Koellner, T. (2015). High-resolution assessment of land use impacts on biodiversity in life cycle assessment using species habitat suitability models. *Environmental science & technology*, *49*(4), 2237-2244.

del Hoyo, J., Elliott, A., Sargatal, J., and Christie, D.A. eds. (1992-2011). Handbook of the Birds of the World, Volume 1-16 (Barcelona: Lynx Editions).

di Marco, M., Harwood, T. D., Hoskins, A. J., Ware, C., Hill, S. L., & Ferrier, S. (2019). Projecting impacts of global climate and land-use scenarios on plant biodiversity using compositional-turnover modelling. *Global change biology*, *25*(8), 2763-2778.

Durán, A. P., Green, J. M., West, C. D., Visconti, P., Burgess, N. D., Virah-Sawmy, M., & Balmford, A. (2020). A practical approach to measuring the biodiversity impacts of land conversion. *Methods in Ecology and Evolution*, *11*(8), 910-921.

Fritz, S. A., & Purvis, A. (2010). Selectivity in mammalian extinction risk and threat types: a new measure of phylogenetic signal strength in binary traits. *Conservation Biology*, *24*(4), 1042-1051.

Frost, D. R. (2007) Amphibian Species of the World: an online reference, version 5.

Frost, D. R., Grant, T., Faivovich, J., Bain, R. H., Haas, A., Haddad, C. F., ... & Raxworthy, C. J. (2006). The amphibian tree of life. *Bulletin of the American Museum of natural History*, *2006*(297), 1-291.

Gabel, V. M., Meier, M. S., Köpke, U., & Stolze, M. (2016). The challenges of including impacts on biodiversity in agricultural life cycle assessments. *Journal of environmental management*, *181*, 249-260.

Godar, J., Persson, U. M., Tizado, E. J., & Meyfroidt, P. (2015). Towards more accurate and policy relevant footprint analyses: tracing fine-scale socio-environmental impacts of production to consumption. *Ecological Economics*, *112*, 25-35.

Grantham, H. S., Duncan, A., Evans, T. D., Jones, K., Beyer, H., Shuster, R., ... & Clements, T. (2020). Only 40% of the world's forests are in good health. *bioRxiv*. In review doi: https://doi.org/10.1101/2020.03.05.978858

Green, R. E., Cornell, S. J., Scharlemann, J. P., & Balmford, A. (2005). Farming and the fate of wild nature. *Science*, *307*(5709), 550-555.

Green, J. M., Croft, S. A., Durán, A. P., Balmford, A. P., Burgess, N. D., Fick, S., ... & Young, L. E. (2019). Linking global drivers of agricultural trade to on-the-ground impacts on biodiversity. *Proceedings of the National Academy of Sciences*, *116*(46), 23202-23208.

Grenyer, R., Orme, C. D. L., Jackson, S. F., Thomas, G. H., Davies, R. G., Davies, T. J., ... & Ding, T. S. (2006). Global distribution and conservation of rare and threatened vertebrates. *Nature*, 444(7115), 93-96.

Haberl, H., Erb, K. H., & Krausmann, F. (2014). Human appropriation of net primary production: patterns, trends, and planetary boundaries. *Annual Review of Environment and Resources*, *39*, 363-391.

Hansen, M. C., Potapov, P. V., Moore, R., Hancher, M., Turubanova, S. A., Tyukavina, A., ... & Kommareddy, A. (2013). High-resolution global maps of 21st-century forest cover change. *Science*, *342*(6160), 850-853.

He, F., & Hubbell, S. P. (2011). Species–area relationships always overestimate extinction rates from habitat loss. *Nature*, 473(7347), 368-371.

Hidasi-Neto, J., Loyola, R., & Cianciaruso, M. V. (2015). Global and local evolutionary and ecological distinctiveness of terrestrial mammals: identifying priorities across scales. *Diversity and Distributions*, 21(5), 548-559.

Hillebrand, H., Blasius, B., Borer, E. T., Chase, J. M., Downing, J. A., Eriksson, B. K., ... & Lewandowska, A. M. (2018). Biodiversity change is uncoupled from species richness trends: Consequences for conservation and monitoring. *Journal of Applied Ecology*, 55(1), 169-184.

Hoskins, A. J., Harwood, T. D., Ware, C., Williams, K. J., Perry, J. J., Ota, N., ... & Purvis, A. (2020). BILBI: Supporting global biodiversity assessment through high-resolution macroecological modelling. *Environmental Modelling & Software*, 104806.

Hurtt, G. C., Chini, L. P., Frolking, S., Betts, R. A., Feddema, J., Fischer, G., ... & Jones, C. D. (2011). Harmonization of land-use scenarios for the period 1500–2100: 600 years of global gridded annual land-use transitions, wood harvest, and resulting secondary lands. *Climatic change*, *109*(1-2), 117.

Hurtt, G., Chini, L., Sahajpal, R., Frolking, S., Calvin,K., Fujimori, S., … Zhang, X. (2017). Land-use harmonization 2. Retrieved from https://luh.umd.edu/data.shtml

Instituto Brasileiro de Geografia e Estatística (IBGE). 2014. Cobertura e uso da terra do Brasil 2000, 2010, 2012, 2014. Available at: http://geoftp.ibge.gov.br/informacoes_ambientais/cobertura_e_uso_da_terra/mudancas/vetores/.

Isaac, N.J.B., Redding, D.W., Meredith, H.M.R., Safi, K. (2012) Phylogenetically informed conservation priorities for amphibian conservation. *PLoS one,* 7: e43912.

Isaac, N.J.B., Turvey, S.T., Collen, B., Waterman, C., Baillie JEM (2007) Mammals on the EDGE: Conservation Priorities Based on Threat and Phylogeny. *PLoS one,* 2: e296.

Jenkins, C. N., Pimm, S. L., & Joppa, L. N. (2013). Global patterns of terrestrial vertebrate diversity and conservation. *Proceedings of the National Academy of Sciences*, *110*(28), E2602-E2610.

Jenkins, C. N., Alves, M. A. S., Uezu, A., & Vale, M. M. (2015). Patterns of vertebrate diversity and protection in Brazil. *PloS one*, *10*(12), e0145064.

Jetz, W., Thomas, G. H., Joy, J. B., Redding, D. W., Hartmann, K., & Mooers, A. O. (2014). Global distribution and conservation of evolutionary distinctness in birds. *Current biology*, *24*(9), 919-930.

Joppa, L. N., O'Connor, B., Visconti, P., Smith, C., Geldmann, J., Hoffmann, M., ... & Ahmed, S. E. (2016). Filling in biodiversity threat gaps. *Science*, *352*(6284), 416-418.

Kier, G., Mutke, J., Dinerstein, E., Ricketts, T. H., Küper, W., Kreft, H., & Barthlott, W. (2005). Global patterns of plant diversity and floristic knowledge. Journal of Biogeography, 32(7), 1107-1116.

Lenzen, M., Lane, A., Widmer-Cooper, A., & Williams, M. (2009). Effects of land use on threatened species. *Conservation biology*, *23*(2), 294-306.

Lenzen, M., Moran, D., Kanemoto, K., Foran, B., Lobefaro, L., & Geschke, A. (2012). International trade drives biodiversity threats in developing nations. *Nature*, 486(7401), 109-112.

Laestadius, L., Maginnis, S., Minnemeyer, S., Potapoy, P., Saint-Laurent, C., & Sizer, N. (2011). Mapping opportunities for forest landscape restoration. *Unasylva (English ed.)*, *62*(238), 47-48.

Marquardt, S. G., Guindon, M., Wilting, H. C., Steinmann, Z. J., Sim, S., Kulak, M., & Huijbregts, M. A. (2019). Consumption-based biodiversity footprints–Do different indicators yield different results?. *Ecological Indicators*, *103*, 461-470.

Martinelli, G., & Moraes, M. A. (2013). Livro vermelho da flora do Brasil. Jardim Botânico do Rio de Janeiro, Brazil: Centro Nacional de Conservação da Flora. Retrieved from https://geonode.jbrj.gov.br/layers/geonode%3Apoligonos_ameacadas_atualizado_22042015_portaria_443_2014

Midolo, G., Alkemade, R., Schipper, A. M., Benítez-López, A., Perring, M. P., & De Vries, W. (2019). Impacts of nitrogen addition on plant species richness and abundance: A global meta-analysis. *Global Ecology and Biogeography*, 28, 398– 413.

Moran, D., Petersone, M., & Verones, F. (2016). On the suitability of input–Output analysis for calculating product-specific biodiversity footprints. *Ecological Indicators*, *60*, 192-201.

Moran, D., & Kanemoto, K. (2017). Identifying species threat hotspots from global supply chains. *Nature Ecology & Evolution*, *1*(1), 1-5.

Newbold, T., Hudson, L. N., Arnell, A. P., Contu, S., De Palma, A., Ferrier, S., ... & Burton, V. J. (2016). Has land use pushed terrestrial biodiversity beyond the planetary boundary? A global assessment. *Science*, *353*(6296), 288-291.

Nunez, S., Arets, E., Alkemade, R., Verwer, C., & Leemans, R. (2019). Assessing the impacts of climate change on biodiversity: Is below 2°C enough? *Climatic Change*, 154, 351– 365.

Petchey, O. L., & Gaston, K. J. (2002). Functional diversity (FD), species richness and community composition. *Ecology letters*, *5*(3), 402-411.

Potapov, P., Hansen, M. C., Kommareddy, I., Kommareddy, A., Turubanova, S., Pickens, A., ... & Ying, Q. (2020). Landsat analysis ready data for global land cover and land cover change mapping. *Remote Sensing*, *12*(3), 426.

Redding, D.W., 2003. Incorporating genetic distinctness and reserve occupancy into a conservation priorisation approach. Masters Thesis, University Of East Anglia, Norwich, UK

Ridgely, R.S., Allnutt, T.F., Brooks, T., McNicol, D.K., Mehlman, D.W., Young, B.E., and Zook, J.R. (2003). Digital Distribution Maps of the Birds of the Western Hemisphere. Version 1.0. . (Arlington, Virginia, USA.: NatureServe).

Roelants, K., Gower, D. J., Wilkinson, M., Loader, S. P., Biju, S. D., Guillaume, K., ... & Bossuyt, F. (2007). Global patterns of diversification in the history of modern amphibians. *Proceedings of the National Academy of Sciences*, *104*(3), 887-892.

Rondinini, C., Di Marco, M., Chiozza, F., Santulli, G., Baisero, D., Visconti, P., ... & Amori, G. (2011). Global habitat suitability models of terrestrial mammals. *Philosophical Transactions of the Royal Society B: Biological Sciences*, *366*(1578), 2633-2641.

Safi, K., Cianciaruso, M.V., Loyola, R.D., Brito, D., Armour-Marshall, K. & Diniz-Filho, J.A.F. (2011). Understanding global patterns of mammalian functional and phylogenetic diversity. Philosophical Transactions of the Royal Society of London Series B, Biological Sciences, 366, 2536–2544.

Safi, K., Armour-Marshall, K., Baillie, J. E., & Isaac, N. J. (2013). Global patterns of evolutionary distinct and globally endangered amphibians and mammals. *PloS one*, *8*(5), e63582.

Schipper, A. M., Hilbers, J. P., Meijer, J. R., Antão, L. H., Benítez-López, A., de Jonge, M. M., ... & Mylius, S. (2020). Projecting terrestrial biodiversity intactness with GLOBIO 4. *Global change biology*, *26*(2), 760-771.

Scholes, R. J., & Biggs, R. (2005). A biodiversity intactness index. *Nature*, *434*(7029), 45-49.

Song, X. P., Hansen, M. C., Stehman, S. V., Potapov, P. V., Tyukavina, A., Vermote, E. F., & Townshend, J. R. (2018). Global land change from 1982 to 2016. *Nature*, *560*(7720), 639-643.

USGS. (2006). Shuttle radar topography mission 3 arc second version 2.0. Retrieved from https://on.doi.gov/31SsvqB

Van Asselen, S., & Verburg, P. H. (2013). Land cover change or land-use intensification: simulating land system change with a global-scale land change model. *Global change biology*, *19*(12), 3648-3667.

Venter, O., Sanderson, E. W., Magrach, A., Allan, J. R., Beher, J., Jones, K. R., ... & Levy, M. A. (2016). Sixteen years of change in the global terrestrial human footprint and implications for biodiversity conservation. *Nature communications*, *7*(1), 1-11.

Véron, S., Saito, V., Padilla-García, N., Forest, F., & Bertheau, Y. (2019). The use of phylogenetic diversity in conservation biology and community ecology: a common base but different approaches. *The Quarterly Review of Biology*, *94*(2), 123-148.

Verones, F., Saner, D., Pfister, S., Baisero, D., Rondinini, C., & Hellweg, S. (2013). Effects of consumptive water use on biodiversity in wetlands of international importance. *Environmental science & technology*, 47(21), 12248-12257.

Verones, F., Moran, D., Stadler, K., Kanemoto, K., & Wood, R. (2017). Resource footprints and their ecosystem consequences. *Scientific Reports*, *7*, 40743.

Vogtländer, J. G., Lindeijer, E., Witte, J. P. M., & Hendriks, C. (2004). Characterizing the change of land-use based on flora: application for EIA and LCA. *Journal of Cleaner Production*, *12*(1), 47-57.

Wilson, D. E., & Reeder, D. M. (Eds.). (2005). Mammal species of the world: a taxonomic and geographic reference (Vol. 1). *JHU Press*.

Zelený, D. (2009). Co-occurrence based assessment of species habitat specialization is affected by the size of species pool: reply to Fridley et al.(2007). *Journal of Ecology*, *97*(1), 10-17.