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Abstract

Extant global biodiversity is undergoing accelerating decline; driven by a hierarchy of anthropogenic pressures whose relative contributions remain poorly resolved at the national scale where actions to reduce their impacts must be taken. Existing assessments of global biodiversity threat contributions primarily rely on species threat prevalence counts that are globally aggregated and unable to quantify activities’ specific, localised impacts. Such limitations are restricting the translation of international decline-reduction pledges into effective targeted national action. Piloting the application of Life Cycle Assessment (LCA) methods to a collated inventory of all global annual resource use and emissions, my research reveals different nation’s biodiversity threat profiles to be highly heterogenous in composition and magnitude, identifying the prioritised importance of tailored national interventions. Comparison with a revised assessment of threat prevalence across the IUCN Red List confirmed the shared dominance of agricultural threats to global declines and revealed the strong methodological divergences of the two approaches, emphasising the importance of a multi-faceted approach when informing conservation decision making. These results provide the first empirical, globally cohesive, production-based, national threat attribution of ongoing biodiversity loss, providing the understanding necessary to translate commitments into targeted reduction strategies at a resolution matching national jurisdictional capacity.

1. Introduction

Despite our inherent dependence on ecosystem functioning for food, climate regulation, health, wellbeing, and resilience to climate change, global biodiversity is under critical anthropogenic pressure (Bridle et al., 2025; IPBES, 2019). Such declines demand transformative changes to our impacts on the natural world to avoid uncontrollable, future ecological collapse (Díaz et al., 2019; Trisos et al., 2020).

Following calls for action from the wider scientific community, policy makers have sought bold international commitments to tackle global biodiversity loss (CBD, 2010, 2022). Appreciating the need for collective effort built around national actions reflecting jurisdictional capacity, regionalised pressures, and localised biodiversity contexts, these targets outline the necessary impact reductions and ecosystem restoration required to halt and reverse biodiversity loss. However, achieving pledge

consensus on such targets and their operationalisation towards tangible action are two distinct challenges, with the latter historically proving difficult (Xu et al., 2021).

Crucially, efforts to reduce ongoing biodiversity losses are being inhibited by our limited understanding of the relative contributions of nations and their activities to global declines (CBD, 2022). Biodiversity arises from a hierarchy of drivers and threats. Acting at the highest order, indirect drivers include the systemic economic, demographic, governance, and technological pressures that spur on direct drivers; defined as the broad human activities, behaviours or natural processes that contribute to biodiversity loss (IPBES, 2019). Occasionally intersecting with direct-driver descriptors, direct threats are the final mechanism of harm, describing the immediate and localised actions, events, or pressures that degrade specific ecosystems or species (IUCN, 2025). While the relative contributions made by different drivers are well understood (Jaureguiberry et al., 2022), our ability to attribute their consequential threats to specific actors and biodiversity losses remains underdeveloped.

Existing research has often relied on globally aggregated threat-prevalence data rather than spatially resolved estimates of impact. With our predominant benchmark understanding assessing threat incidence across species on the IUCN Red List, crop farming and logging are considered the dominant threats to current biodiversity declines, followed by the clustered impacts of housing, livestock farming and invasive species (Maxwell et al., 2016). However, such approaches do not resolve the regional contexts, national actors or activity level pressures through which biodiversity impacts arise and must therefore be tackled for effective decline reductions. Additionally, previous snapshot assessments of threat prevalence fail to account for temporal relationships between threat potency and persistence, a crucial component when evaluating impact extent (Keith et al., 2014). New approaches are therefore required to complement threat-prevalence assessments with spatially-resolved, magnitude-based estimates of biodiversity impact.

Biodiversity Life Cycle Assessment (LCA) methods evaluate the negative impacts on nature exerted by a product or system throughout its relevant value chain (ISO 14040, 2006; ISO 14044, 2006). Within a predefined scope breadth and depth, this process begins with the collation of data quantifying the extent of different resource consumption and environmental emissions (termed 'elementary flows') produced over the course of the assessed entity's lifecycle (Bromwich et al., 2025). The flows of the aggregated Life Cycle Inventory (LCI) of all inputs and outputs under the defined scope is subsequently matched to a series of midpoint environmental avenues (termed 'impact pathways') (Figure 1). To evaluate the endpoint biodiversity impact of each impact pathway, a Life Cycle Impact Assessment (LCIA) metric's characterisation factors (CFs) are multiplied by the magnitude of each midpoint-matched elementary flow (Stage two to three in Figure 1.). While carrying recognised limitations in capturing biodiversity's ecological complexities and LCIA metric assumptions (Crenna et al., 2020; Damiani et al., 2023;

Koslowski et al., 2020; Martínez-Ramón et al., 2025), LCA methods provide a consistent and comparable measure of impact across disparate threats (Verones et al., 2020). With recent developments in LCIA's threat coverage and regionalisation, LCA approaches have been increasingly used as a biodiversity footprinting tool amongst organisations (Bull et al., 2022). In light of the immediate demand to understand the involvement of threats and nations to biodiversity loss at a regionalised, globally cohesive scale, LCA's methodological capacity can provide support.

This analysis uses LCA methods to quantify the relative production-based contributions of countries and threats of differing specificity to ongoing global biodiversity loss. To contextualise the findings to current understanding, the results are compared to a revised threat prevalence analysis in the IUCN Red List. Together these steps aim to identify the global and national threat priorities for effective global change.

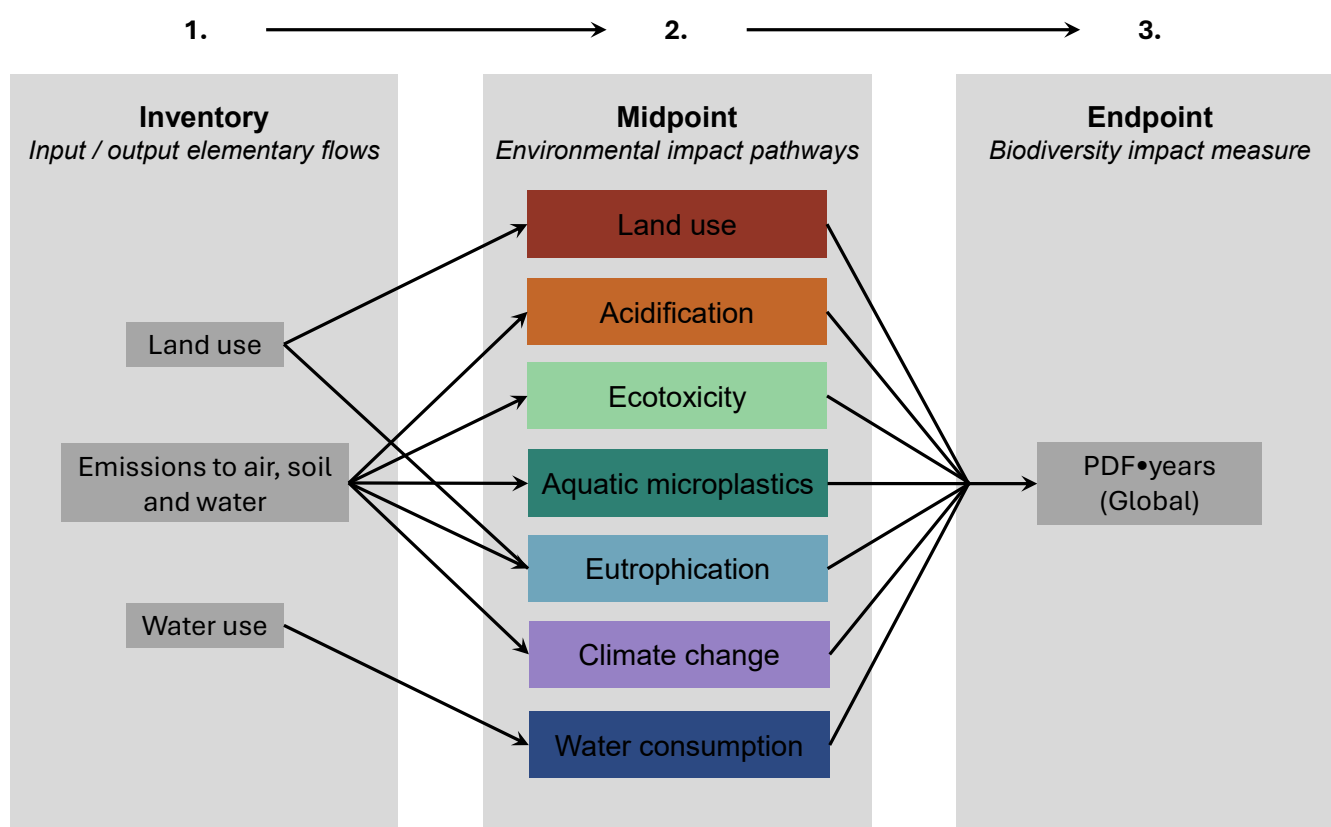


Figure 1. LCA schematic of the inputs, impact pathways and output unit used in this analysis. Visual representation of the use of Life Cycle Assessment (LCA) methods to evaluate biodiversity impacts within the context of my analysis, consisting of three steps: Collation of input output elementary flow inventories for global resource use and emissions, Conversion of inventories to midpoint pathways of impact, and Calculation of respective measures of endpoint biodiversity impact contribution. Diagram inspired by (Bromwich et al., 2025).

2. Methods

2.1. Scoping and Context

This analysis represents the first LCA with a functional unit, the reference unit quantified performance of a product or system (ISO 14040, 2006), and theoretical scope boundary defined by all anthropogenic resource extraction and emissions release occurring globally in a single year. The year 2020 was chosen due to its assessment significance marking the transition from the Aichi targets towards the KMGBF and baselining the goal-delivery of the Nature Positive initiative by 2030. Due to the exhaustive theoretical scope of my research within 2020, the in-practice, operational system boundary of this LCA was defined by the availability of elementary flow characterisation factors (CFs) within the chosen LCIA.

With the exception of land transformation's CFs, (Section 2.2.2.), I chose the Global Life cycle impact Assessment Method (GLAM) version 202410 for this analysis' LCIA metric (Life Cycle Initiative, 2024). The ecosystem quality CFs of this metric describe the per-unit, end-point biodiversity impact of resource / emission flows within environmental-midpoint impact pathway, all evaluated via the unit global Potentially Disappeared Fraction of species years (PDF•years)(Figure 1). This measure is a time integrated evaluation of the total theoretical risk to global species richness caused over a threat's lifetime, aggregated until the ecosystem returns to its reference state or over a period otherwise specified. I used this unbounded value as a proxy for biodiversity impact (Verones et al., 2022), enabling relative comparisons between actors and threats but no absolute measures of loss to be made, theoretical or observed.

I chose GLAM as the metric represented an updated consensus on LCIA methods, being the most comprehensive, globally consistent and spatially explicit framework available at the time of analysis, modelling nine independent impact pathways: Land-use, Terrestrial acidification, Freshwater and Marine eutrophication, Water consumption, Freshwater and Terrestrial ecotoxicity, Marine aquatic microplastics, and Climate change (Figure 1). Encompassing molecule releases to air, water, and soil, alongside land occupation, land transformation, and water consumption, the listed first five pathways additionally possessed regionalisation at a country resolution. Such regionalised CF's accounted for spatial variation in a threat's impact on local biodiversity dependent on where it was found. In contrast, globalised CFs applied a uniform CF irrespective of local conditions. For details on impact pathway CF modelling see (Life Cycle Initiative, 2024). With climate change affecting all three, four of GLAM's impact pathways acted within the terrestrial and freshwater ecosystems respectively and three in the marine. Paired with GLAM's extensive number of included elementary flows within each impact pathway, I judged the metrics threat coverage to be sufficiently comprehensive for investigation of my research objective's functional unit and theoretical scope boundary (Section 2.2.3.).

2.2. Life Cycle Inventory Collation

2.2.1. General Methodology

Rather than defining an elementary flow set prior to data compilation, while collating each impact pathway inventory, I considered each environmental flow equal in its importance. This step maximised the available data coverage and depth of my analysis but implicitly assumed subordinate flow significance in cases where representative data could not be subsequently collated. To mitigate this assumption, data presence was carefully noted with conclusions only being drawn relative to the coverage of the LCI.

I sourced data from secondary global or international datasets with spatially partial or regional data excluded (Table 1). Considering the spatial scope of each inventory as a single global system not a regional aggregate, I ensured any output comparisons reflected true environmental pressure rather than regional data availability. Likewise, databases representing the entirety of an elementary flow's global magnitude were selected over sources describing only a partial flow proportion, unless no alternatives were available. I adopted a preference for authoritative institutional repositories over individual peer-reviewed articles where possible. Global datasets without country disaggregation were included for completeness in the absence of alternatives.

I identified elementary flow data sources through expert consultation and literature string searches on Google Scholar and Scopus. Searched terms included specific or grouped elementary flows alongside “global” and “map”. Where exact data for 2020 were unavailable, the closest available year was either scaled or used directly, with all deviations documented (Section 2.2.3.).

Using R 4.3.2 (R Core Team, 2023) data were isolated, scaled or approximated for the year 2020 with Geographic Information System (GIS) sources being extracted at a country level resolution using national boundary vectors from the packages *exactextractr* (v. 0.10.1) and *ncdf4* (v. 1.24). All country disaggregated datapoints were then assigned ISO 3166-1 alpha-3 (ISO-3a) codes if absent to ensure consistency between database nomenclatures and enable LCIA regionalised CF matching where available. I then scaled each dataset to match to its CF input units: m² for land areas (considering occupation for a single year), kg for substance masses and m³ for water volumes. I subsequently paired the resource / emission names of the collated data to the nomenclature of their respective elementary flows, with any flow pathway descriptors appended.

All datasets were joined in completion by their substance element name, environmental pathway descriptor, and country columns, where applicable. This join prioritised the retention of all available

observations over the strict-cross country comparability of an inner join option. In doing so, my decision avoided systematically excluding impacts from nations with uneven data availability across pathways.

Data completeness was addressed consistently throughout inventory collation. Absent datapoints were implicitly treated as zero, reflecting each database's structural assumption that unqualified non-reporting equated to non-emission. Where datapoints were present but unrecorded, I propagated them as NA not zero, avoiding the conflation of lack of information with recorded absence of impact. For subsequent value aggregation steps, I excluded NA values to compute partial sums from the available data, whilst calculating the missing value proportion behind each aggregated result. In cases where the proportion of raw NA value exclusion exceeded 10% of an aggregated value's constituent elements, the aggregate was replaced with NA, ensuring subsequent results reflected only high empirical coverage values.

Impact pathway	Resource / Emission	Data source
Climate change	Methane	EDGAR Greenhouse gases (EDGAR, 2020b)
	Carbon dioxide (fossil)	
	Carbon dioxide (biogenic)	
	Nitrous oxide	
	Fluorinated gases	
Land-use: Occupation	Arable land	FAOSTAT Land-use (FAOSTAT, 2020c)
	Permanent crops	
	Permanent meadows and pastures	
	Planted Forest	
	Artificial surfaces	FAOSTAT Land cover (FAOSTAT, 2020b)
Land-use: Transformation	Arable land	HESTIA.earth (Poore, 2021)
	Permanent crops	
	Permanent meadows and pastures	
	Other land	
Water consumption	Freshwater consumption	WaterGAP v2.2e GSWP3-ERA5 (Müller Schmied et al., 2024)
Terrestrial acidification	Ammonia	EDGAR Global air pollutants (EDGAR, 2020a)
	Nitrogen oxides	
	Sulphur dioxide	
Marine eutrophication	Ammonia	EDGAR Global air pollutants (EDGAR, 2020a)
	Nitrogen oxides	
	Fertiliser nitrogen	FAOSTAT Land inputs (FAOSTAT, 2020a)
Freshwater eutrophication	Arable land	FAOSTAT Land-use (FAOSTAT, 2020c)
	Permanent crops	
	Permanent meadows and pastures	
	Fertiliser nitrogen	FAOSTAT Land inputs (FAOSTAT, 2020a)
	Fertiliser phosphorus	
Ecotoxicity	Non methane volatile organic carbons	EDGAR Global speciated NMVOC's (EDGAR, 2020a)
	Fluorinated gases	EDGAR Greenhouse gases

	Unintentional persistent organic pollutants (UPOP's)	EDGAR UPOP's (EDGAR, 2018)
	Mercury	EDGAR Global Mercury (EDGAR, 2020c)
	Pesticides	PEST-CHEMGRIDS v2.01 beta (Maggi & Tang, 2024)
	Pesticides	FAOSTAT Land inputs (FAOSTAT, 2020d)
	Antibiotics	(Ehalt Macedo et al., 2025)
Aquatic microplastics	Microplastics	Secondary data estimates

Table 1. Life Cycle Inventory data sources by impact pathway and grouped elementary flow. Data was collated across all nine of the impact pathways for which CFs were available. Land-use transformation's inventory was collated using HESTIA's 20-year land use change lookup and land cover model, see section 2.2.2. Aquatic microplastic influx into the marine environment was estimated from a synthesis of published estimates of plastics in the environment, see section 2.2.2. Emissions data were predominantly sourced from the Emissions Database for Global Atmospheric Research (EDGAR); resource use from data the United Nation's Food and Agriculture Organisation database (FAOSTAT).

2.2.2. Methodology Edits

For impact pathways or datasets found in Table 1. and not mentioned in the following section, the general methodology above was applied without modification.

Land-use: Transformation

I deemed GLAM's land transformation CFs, describing unpaired area flows from (negative CFs) or to (positive CFs) a land-use type, to be erroneous. Returning several aggregated national PDF•year values less than zero after their application, a flawed concept of negative extinction-debt-risk, I replaced GLAM's land transformation CFs for those from another LCIA, LC-IMPACT. Downloaded from v2.0 of the model (LC-IMPACT, 2026), these regionalised replacement CF's described the global PDF•year endpoint biodiversity impact of paired land-use flows from a reference state ecosystem to another land-use type, all with positive impact values.

To match the paired land flow requirements of the new characterisation factors, I collated a new inventory using HESTIA.earth, a methodologically harmonised data platform on agriculture's production practices and environmental impacts (Poore, 2021). I downloaded the region-faostatArea-UpTo20YearExpansion-lookup.csv, which calculates any changes in areas experienced by a national land-use type between a given year and its precursor state 20 years previously. Based on FAOSTAT data for the categories: Arable land, Permanent cropland, Pasture and meadows, Forest, and Other land, PAS 2050's advised 20-year lookback smooths out interannual variability to reveal any national underlying trends over time (British Standards Institute, 2011). Consistent with the GHG Protocol's Land Sector and Removals Guidelines (Greenhouse Gas Protocol, 2026), I then applied HESTIA's land coverage model to systematically pair up gains and losses of agricultural land types, Forest areas, and Other land (Poore, 2021). After the hierarchical model application, I additionally quantified any transformation flows from Forest to Other land, defined as the smaller of the absolute values of any remaining Forest loss and Other land expansion. From the calculated paired land transformation flows, Forest to: Arable land, Permanent cropland, Pastures and meadows, and Other land were considered reference state conversions. I then divided by each flow magnitude by 20 to calculate the change only attributable to 2020 (British Standards Institute, 2011), and then matched them to their respective characterisation factors. Forest land to Other land transformation flows were paired to the CF "from reference state to urban, green areas", representing the most conservative conversion impact due to an absence of described CFs matching FAOSTAT's Other land category disaggregation.

Water consumption

2020's national consumptive freshwater use, including surface and ground water sources, was extracted from WaterGAP's v2.2e GSWP3-ERA5 model representing climate forcing under a historical direct

human impacts setup (Müller Schmied et al., 2024). I assigned this data to the elementary flow descriptors “freshwater” and “Resources from water” for subsequent CF matching.

Ecotoxicity: PEST-CHEMGRIDS pesticides

2018's country-level deposition rates for 115 Pesticide Active Substances (PAS) molecules were extracted from the PEST-CHEMGRIDS v2.01 beta global maps (Maggi & Tang, 2024). To approximate 2020 values, national scaling factors were derived from FAOSTAT's proportional change in total pesticide application between 2018 and 2020 which were then applied uniformly across each countries applied compounds.

Ecotoxicity: FAOSTAT pesticide residual

Modelling the national application rates of up to 115 individual Pesticide Active Substances (PAS) across six major and four aggregated crops, PEST-CHEMGRIDS accounted for the emission of only a subset of pesticides and a partial proportion of each molecule's true national application. To estimate each nation's unaccounted pesticide application mass but with a lack of further compound-specific data, I calculated the difference between FAOSTAT's national estimates of 2020 total pesticide application and each country's total mass of the scaled and CF-matched PEST-CHEMGRIDS molecules. I used this residual mass excluded by PEST-CHEMGRIDS or the availability of the appropriate compound CFs as a pragmatic filler for the inventory of global pesticide application.

Ecotoxicity: Ehalt Macedo et al.'s Antibiotics

Using estimates of global household antibiotic excretion in 2015, the excreted global total mass of each antibiotic was multiplied by the global average environmental fate proportion, 31%, to estimate the share released to freshwater environments (Ehalt Macedo et al., 2025). Each flow was then matched to its respective CF by substance name and the descriptor "Emissions to freshwater."

Aquatic microplastics

Collation of an inventory for the marine impacts of aquatic microplastics was complicated by its CFs specificity and the substantial variability between published annual environmental plastic flux estimates. To navigate the uncertainties associated with strong methodological differences, variable environmental sink definitions, and sparse data representation of 2020, I constructed a flow diagram representing the relevant environmental sinks in which micro and macro plastic exist. I then populated this framework with published estimates of annual plastic sink masses or inter-sink flow proportions for global plastic data from and around 2020 (Full details in Section 9.1.1.). A distribution of annual marine microplastic influx was then estimated by multiplying every sink estimate by the sequential flow proportions of its viable pathways, defined as pathways describing progressive macro to micro-plastic fragmentation and

transport from terrestrial and freshwater systems into the marine environment. Flows representing reverse transport or fragmentation were excluded unless a sink's estimates had no alternative viable downstream routes. I then interpreted the produced distribution as a representative range of global annual marine microplastics influx across the literature's methodology and reference year heterogeneity.

Using the median of the produced distribution for subsequent inventory construction, I then disaggregated by polymer for fibres and non-fibres separately using published marine polymer compositions (Hoseini & Bond, 2022; Oerlikon, 2010). With a lack of size disaggregation, default-size CFs were assigned.

2.2.3. Inventory Coverage Assessment

After collation, I assessed the coverage of my LCI against the analysis' operational scope, defined by the available CFs within the chosen LCIA metric. All nine of GLAM's impact pathways were represented in the inventory with 155 unique resource / emissions flows included, indicating both strong breadth and depth with respect to the scope boundary.

The inventory's temporal representation of 2020 was strong. Only one data source required scaling using an external multiplier: PESTCHEM-GRIDS, while three were used as closest available approximations: EDGAR's Unintentional Persistent Organic Pollutants (2018), Ehalt Macedo et al.'s household antibiotic consumption (2015), and the collated estimate of annual marine microplastic mass deposition (variable). Additionally, Land transformation's 20-year annualised average described transformation attributable to 2020 rather than land-use change observed within the year.

Household antibiotic consumption (Ehalt Macedo et al., 2025), and the collated estimate of annual marine microplastic deposition were the only two datasets that lacked national resolution, contributing to global totals but not national threat profiles. Some degree of national attribution was therefore possible for all impact pathways except aquatic microplastics.

Internal coverage of each impact pathway's constituent flows and representation of each flow's global extent was considered robust but with several notable exceptions. The collated inventory of land transformation struggled to disaggregate transformation destinations other than those for agricultural purposes. Additionally, while often containing large areas of natural ecosystems and with many countries displaying high rates of transformation from Other land to alternative land-use types, FAOSTAT's 'Other land' category could not be considered a reference state ecosystem. High fluxes of Forest to Other land transformation in some nations, along with Other land's obscured constituent breakdown, meant only Forest areas were considered reference state transformation sources for which CFs were available.

Further limitations arose from partial molecular coverage in the ecotoxicity pathway. FAOSTAT's gap filling procedure on PEST-CHEMGRIDS partial coverage of global pesticide application lacked molecule-specific representation. Meanwhile PEST-CHEMGRIDS scaling from 2018 to 2020 assumed uniform proportional change across pesticides within each country. Ehalt Macedo et al.'s antibiotic data estimated global riverine release rates for the top 40 antibiotics consumed by humans, representing over 90% of human antibiotic consumption by mass, but excluding industrial, veterinary, and agricultural sources. For both pesticide and antibiotic inventories, I could not assume mass-based coverage to be proportional to ecotoxicological impact, as toxicity varies substantially among individual compounds (Douziech et al., 2024; Oginah et al., 2023; Owsianiak et al., 2023). As the antibiotic inventory could not be gap-filled, I interpreted the biodiversity impacts generated from this flow group as an underestimate of their true value.

Overall, I considered the collated inventory coverage to be sufficient to support the primary objectives of my analysis. However, the results were only interpreted within the defined operational scope of my analysis and with a strong awareness of the temporal, spatial and flow-specific caveats described above.

2.3. Life Cycle Impact Assessment Application

2.3.1. General Methodology

To calculate the endpoint biodiversity impact of each inventory data point, the collated and processed flows were paired to their respective CFs using their matched substance names and descriptors. Regionalised impact pathways were additionally paired by their national ISO-3a codes. Tracing based on these terms avoided double counting the impact of a single element through multiple flow pathways or locations.

To calculate the biodiversity impact of the collated threat inventories, I multiplied the quantity of each resource use / emission by its paired elementary flow CF with data's country disaggregation being maintained where available. Where CF upper and lower bounds existed, they were applied to calculate each impacts uncertainty range.

To aid interpretability, I then aggregated the elementary flow impacts into grouped flow categories whose boundaries reflected the reporting resolution of the collated inventory datasets, as detailed in the second column of table X. I then summarised the global-scale biodiversity impacts at two hierarchical levels: the grouped elementary flow and impact pathway stages. For impacts with country disaggregation, I repeated the same process, enabling national threat contributions and ecosystem footprint comparisons.

2.3.2. Methodology Edits

For impact pathways or datasets found in Table 1. and not mentioned in the following section, the general methodology above was applied without modification.

Land-use: Occupation

I assigned Planted forest to the `light-intensity plantation` CF, as the available data did not permit a distinction between minimal, light and intense management, warranting a middling approach.

Ecotoxicity: EDGAR NMVOC emissions

EDGAR reported non-methane volatile organic compound (NMVOC) emission masses by chemical group totals rather at a molecule-specific resolution, hindering direct substance-to-substance CF matching. To address this, I assigned each “Emissions to air” ecotoxicity flow CF, for terrestrial and freshwater impacts respectively, to their corresponding EDGAR NMVOC category, where applicable. After grouping the relevant CFs, I then calculated the median CF of each category and used these values as a representative group-level CFs to be multiplied by each NMVOC categories total emission.

Ecotoxicity: FAOSTAT pesticide residual

The biodiversity impacts of FAOSTAT’s national pesticide residuals (Section 2.2.2.) was calculated using the median of each nation’s matched PEST-CHEMGRIDS molecules CFs, serving as a representative average for the uncharacterised mass fraction.

2.4. Interpretation Analysis

Water consumption’s biodiversity impacts were excluded from my results interpretation due to unresolved concerns regarding the magnitude of the pathway’s influence on global biodiversity declines. Returning a global impact of 47.0 PDF•years, accounting for 99.4% of freshwater’s total threat, the pathway results exceeded the combined total of the terrestrial and marine ecosystems by ~45x. After extensive investigation into the CF methods and comparison to other literature, I excluded my collated inventory as the origin of the inflated values. I subsequently contacted the authors of the impact pathways CFs but gained limited further clarification, resulting in my consequent exclusion of the pathway results from interpretation. This exclusion should not be interpreted as evidence that water consumption lacks potentially severe biodiversity consequences but reflects unresolved uncertainty around its modelled severity in LCIA methods. The impact pathway’s top ten countries feature in the supplementary materials, section 9.2.1.

2.4.1. LCA – Red List Comparison

To compare the results of the LCA analysis and my revised threat tally shares of the IUCN Red List (Section 9.1.1.), each LCA threat pathway or elementary flow group was traced to its closest match in the IUCN's tiered threat classification list (IUCN, 2025) (Table 2). Where tier one matching was clear, but the LCA threats lacked a tier two resolution, the tier two category was left unspecified. Taking the results of my revised Red List threat prevalence assessment (Section 9.2.2.), I then isolated the tallies for only the tier one IUCN threats included in Table 2, enabling an internal share comparison.

Impact pathway	Resource / Emission	IUCN tier one threat		IUCN tier two threat
Climate change	Methane	Climate Change & Severe		NA
	Carbon dioxide	Weather		
	Nitrogen dioxide			
	Fluorinated gases			
Land-use: Occupation	Arable land	Agriculture & Aquaculture		Annual & Perennial Non-Timber Crops
	Permanent cropland			Livestock farming and ranching
	Pasture and meadows			Wood & Pulp Plantations
	Planted forests			
	Artificial areas	Residential & Commercial Development	NA	
Land-use: Transformation	Arable land	Agriculture & Aquaculture		Annual & Perennial Non-Timber Crops
	Permanent cropland			Livestock Farming & Ranching
	Pasture and meadows			
	Other land	Natural Modifications	System	Other Ecosystem Modifications
Water consumption	Freshwater	Natural Modifications	System	Dams & Water Management/Use
Terrestrial acidification	Ammonia	Pollution		Air-Borne Pollutants
	Nitrogen oxides			
	Sulphur dioxide			
Marine eutrophication	Ammonia	Pollution		Air-Borne Pollutants
	Nitrogen oxides			
	Nitrogen fertiliser			Agricultural & Forestry Effluents
Freshwater eutrophication	Arable land	Pollution		Agricultural & Forestry Effluents
	Permanent cropland			
	Pasture and meadows			
	Nitrogen fertiliser			
	Phosphate fertiliser			
Freshwater ecotoxicity	Non methane volatile organic carbons	Pollution		Air-Borne Pollutants
	Fluorinated gases			

	Persistent organic pollutants		
	Mercury		
	Pesticides		Agricultural & Forestry Effluents
	Antibiotics		Domestic & Urban Waste Water
Terrestrial ecotoxicity	Non methane volatile organic carbons	Pollution	Air-Borne Pollutants
	Persistent organic pollutants		
	Pesticides		Agricultural & Forestry Effluents
	Antibiotics		Domestic & Urban Waste Water
Aquatic microplastics	Microplastics	Pollution	Garbage & Solid Waste

Table 2. Matched LCA elementary flows and threat categories of the IUCN's Threat Classification (v3.3). Correspondence between Life Cycle Assessment (LCA) elementary flows and the IUCN Threat Classification Scheme v3.3 tier one and tier two categories, used to enable comparative analysis between LCA-derived biodiversity impact estimates and IUCN Red List threat prevalence. Where no tier two match could be resolved at the resolution of the LCA inventory, NA was denoted. Water consumption was excluded from primary results interpretation but included here for completeness.

3. Results

3.1. Global Ecosystem and Impact Pathway Contributions

Anthropogenic biodiversity impact in 2020 exhibited strong asymmetry across ecosystems and threat impact pathways. Terrestrial ecosystems emerged as the dominant contributor to global declines, ~3.2x and ~6.5x greater than freshwater and marine ecosystems respectively, suggesting impacts on land were the overwhelming proponent of losses. Within the terrestrial environment, land-use was the principal influential threat, contributing 88% of the ecosystem total followed by the diminishing contributions of acidification (11.0%), ecotoxicity (0.651%), and climate change (0.324%) (Figure 2.).

Freshwater ecosystem impacts presented a split pathway structure with eutrophication (51.0%) and climate change (43.3%) comparably dominating the ecosystem total, followed by ecotoxicity's minor involvement (5.75%) (Figure 2.).

Lowest overall in total ecosystem impact, the marine environment was similarly dominated by eutrophication but to a much greater extent (83.4%). Aquatic microplastics (11.6%) and climate change (4.97%) possessed minor influence (Figure 2.).

Climate change was the only impact represented in all three ecosystems, making highly variable contributions. Responsible for nearly half of all freshwater impacts, minor but present in the marine environment and negligible in the terrestrial ecosystem, global freshwater biodiversity was found to be uniquely sensitive to climate-mediated stressors (Figure 2.).

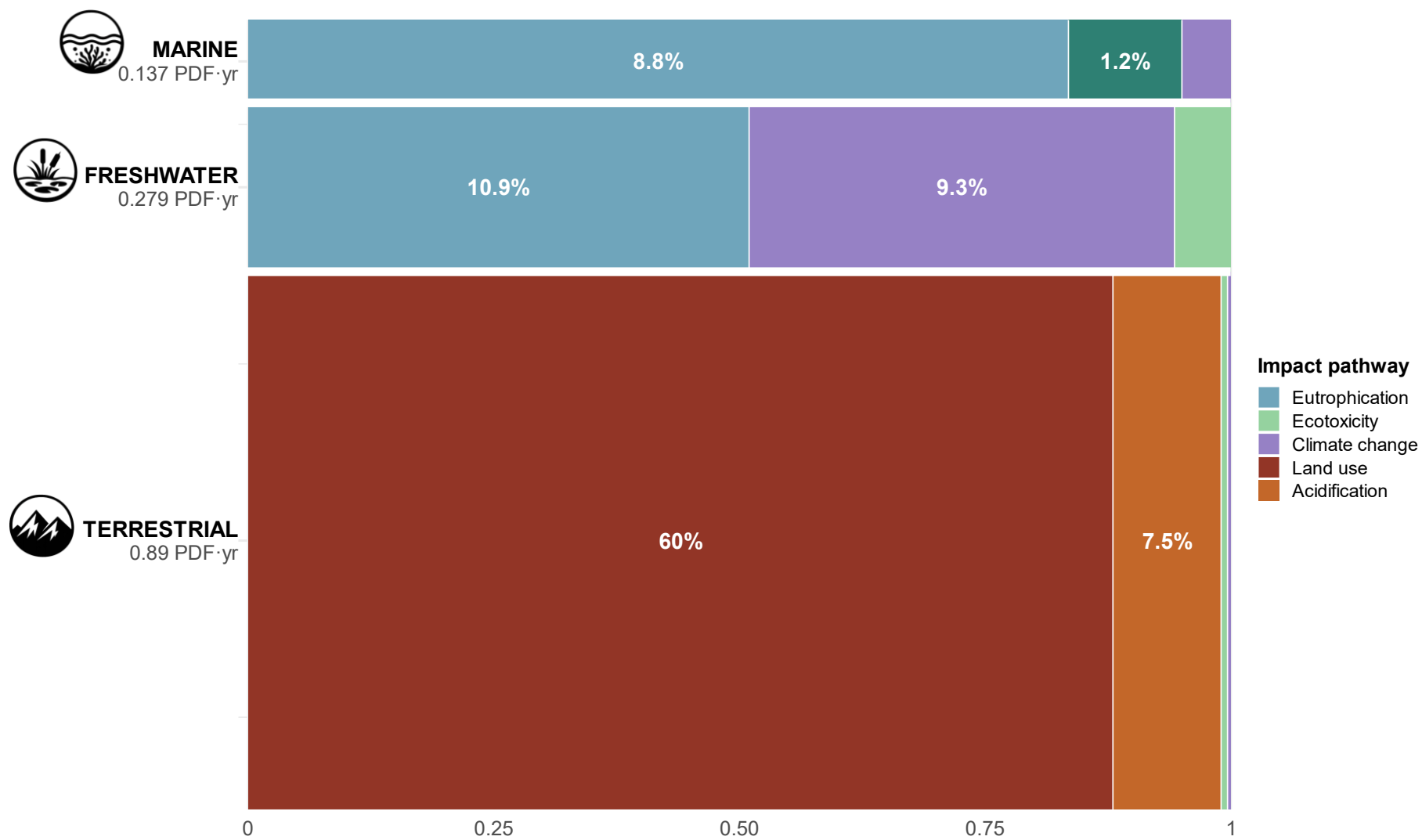


Figure 2. Impact pathway and ecosystem contributions to global biodiversity impacts. LCA relative impact assessment. X and Y axis respectively represent the proportional shares of impact pathways to ecosystem total and relative ecosystem impact magnitudes. Bar areas and percentage values indicate the contribution of each impact pathway to total global impact, finding terrestrial and land use dominance.

3.2. National Footprints

Nation's biodiversity footprints sizes varied substantially, with a small country cohort accounting for the majority of impacts across ecosystems. With a strong localisation around the equator, the top-ten national footprints contributed 74.9%, 56.9% and 59.6% of total terrestrial, freshwater and marine impact respectively (Figure 3., Figure 4.).

Terrestrial biodiversity loss was the most nationally concentrated with a high number of top-ten countries featuring from North and South America (Figure 4.). Indonesia alone, however, contributed 34.3% of the global terrestrial burden, ~3x that of Brazil in second place. Together Indonesia, Brazil and the Democratic Republic of Congo accounted for over half of the global ecosystem impact. A 92.4% decline in footprint magnitude down the top ten group strongly supported extant terrestrial biodiversity loss' high national concentration (Figure 3.).

Freshwater ecosystem impacts displayed a reduced skew amongst nation's biodiversity footprints. China was the largest contributor of freshwater impact followed by Brazil and the USA. Although impacts still declined substantially (82.3%) between first and tenth place, the lower cumulative share of the top ten indicated a larger aggregate influence of nations outside the leading group relative to terrestrial losses. Such accumulation accounted for nearly half of global impact (Figure 3.).

Interpretation of the marine pattern was constrained by the lack of country level resolution available for the aquatic microplastics inventory and low ecosystem threat coverage. Within the available data, global impacts were found to be strongly concentrated around Southern and South East Asia with India contributing the largest footprint (24.2%) followed by China and Indonesia (Figure 3., Figure 4.). Marine impacts occupied an intermediate position between the highly concentrated and more distributed terrestrial and freshwater structures respectively, with a major drop in footprint size across the group (93.2%) alongside substantial contributions still arising from countries outside the leading ten (Figure 3.).

3.3. National Threat Contributions

3.3.1. Impact Pathway Contributions

Disaggregation of global ecosystem threat proportions to a national resolution revealed major variation in biodiversity threat structures and limited correspondence between footprint magnitude and pathway composition (Figure 3.).

Within terrestrial ecosystems, globally aggregated pathway shares masked a two-group structure among the top ten largest national footprints. Indonesia, the DRC, Madagascar, Peru, Brazil and

Argentina each attributed over 95% of their national footprint to land-use impacts, exceeding the global average proportion of 88%. In contrast, acidification contributed disproportionately to the footprints of the USA, China, Mexico and Australia. This grouped structure bore no systematic relationship to footprint magnitude with acidification-elevated nations interleaved with their land-use-elevated counterparts throughout the ranking. Collectively, China, Mexico, USA and Australia accounted for 64.9% of the global acidification's impacts despite representing only 14.5% of the global terrestrial footprint. China was additionally the only country with an ecotoxicity share substantially above the global norm, contributing 17.2% of the pathways terrestrial total (Figure 3.).

Freshwater ecosystems displayed the strongest divergence between national and global threat structures with two contrasting profiles emerging. The footprints of China, India and the USA were dominated by climate change while Sri Lanka, Peru, Vietnam, Thailand, Mexico and Brazil were strongly eutrophication-dominated. The clearest expression of this contrast occurred between the two largest national footprints. China contributed 26.7% of global freshwater climate change yet only 7.7% of global eutrophication, while Brazil contributed 14.2% of global eutrophication yet only 3.7% of global climate change. The top ten countries accounted for 55.6% of global freshwater climate change, 60.1% of eutrophication and 39.5% of ecotoxicity, indicating substantial shares of freshwater pressure remained distributed beyond the leading nations (Figure 3.).

The inability to disaggregate aquatic microplastics impacts at a country resolution inflated the marine environments other apparent impact pathway shares. Nevertheless, eutrophication dominated marine impacts across all top ten countries. Cumulatively accounting for 68.9% of the pathway's global impact, India alone contributed 28.8% of global marine eutrophying effects. China was the primary structural outlier, with climate change contributing more than double the global marine average share and accounting for 26.3% of total marine climate change impact (Figure 3.).

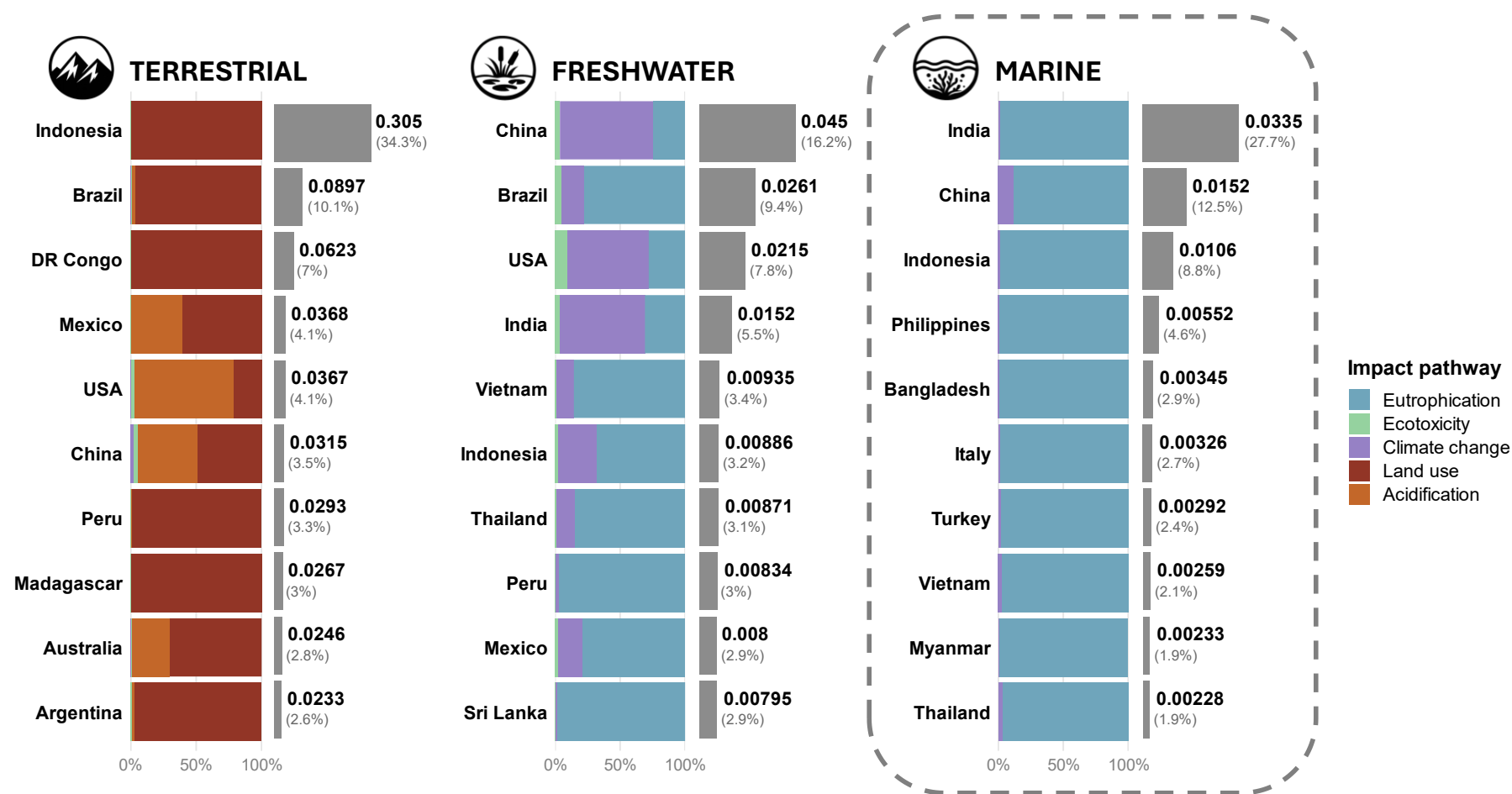


Figure 3. Top ten national ecosystem footprints to global biodiversity loss, with impact pathway breakdown. LCA relative impact assessment. Measured in global PDF-years, country footprints showed major differences in both impact composition (LHS) and footprint magnitude (RHS). Percentage values left of footprint magnitude bars indicate each nations ecosystem footprint contribution to the global ecosystem total impact for country disaggregated data, displaying varying degrees of share concentration among the top ten subset of each ecosystem. Marine isolation box indicates the ecosystem's poor threat representation.

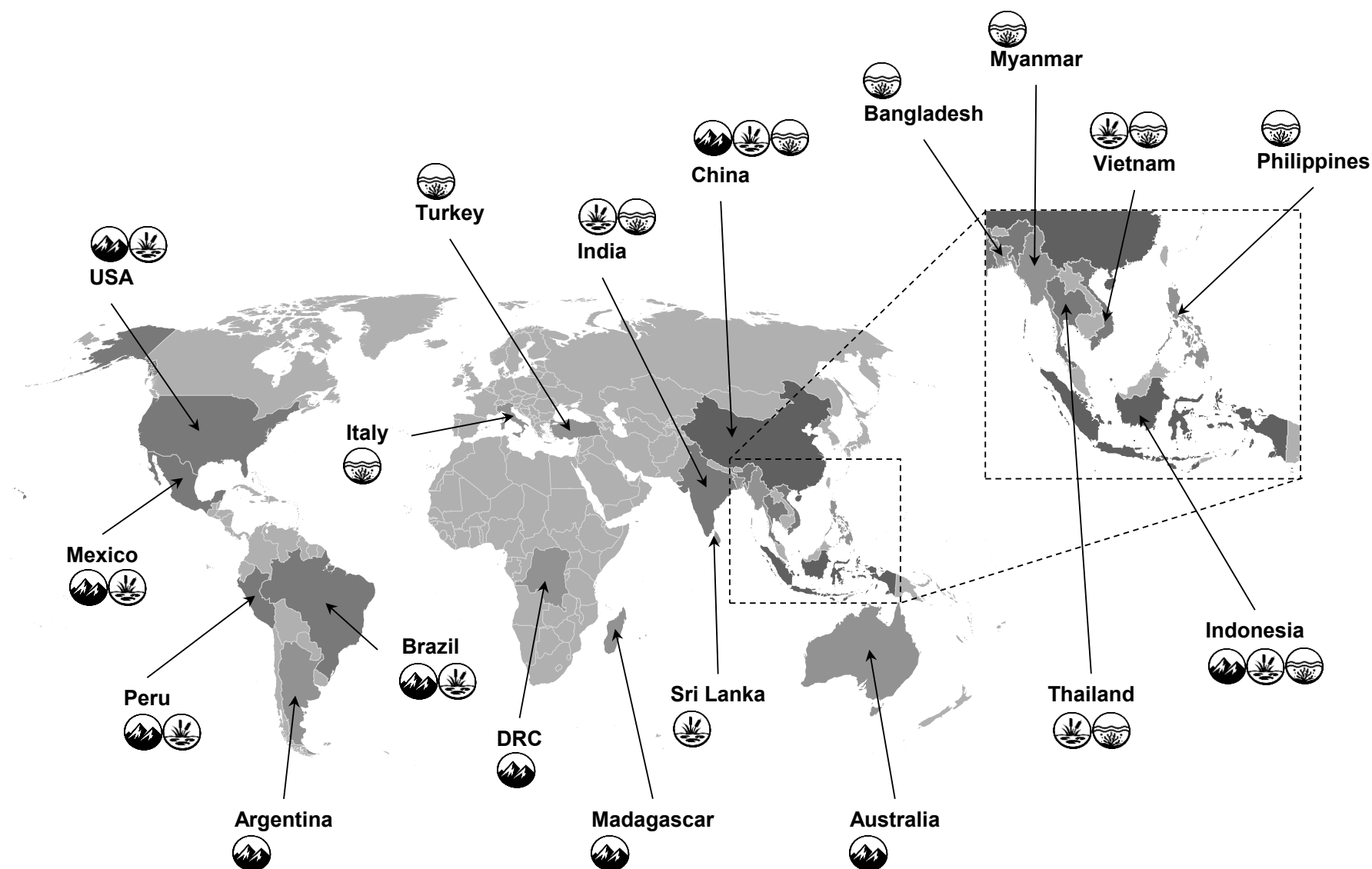


Figure 4. Locations of the Ecosystem Top Ten National Footprints. Grey shading intensity correlates with the number of ecosystem top ten each nation features in, finding high but individually variable overlap between nation's ecosystem impacts. Southeast Asia inset enables clearer visualisation of its high country density and marine impact concentration. Map constructed using a Robinson projection.

3.3.2. Elementary Flow Contributions

Analysis of the top ten country-disaggregated elementary flows to each ecosystem's global impact revealed further national profile differences and biodiversity pressure concentration within a small threat subset (Figure 5.).

The top ten country disaggregated terrestrial elementary flows accounted for 0.515 PDF•years, contributing to 57.9% of the global total. Indonesia's land transformation to permanent cropland was the largest single flow across all ecosystems, contributing to 32.9% of the global terrestrial total and almost the entirety of its national terrestrial footprint. Combined, Indonesia's cropland transformation, Brazil's transformation to 'Other land', and the DRC's transformation to arable land accounted for 45.8% of global ecosystem impact. Madagascar's and Australia's were the only top ten flows associated with land occupation not transformation, both driven by pasture and meadow areas (Figure 5.). The USA's nitrogen oxide and ammonia acidification flows were the only non-land-use entries, reinforcing the nations disproportionate contribution to global terrestrial acidification identified at a pathway level (Figure 3.).

Substantial divergence was observed between terrestrial footprint- and flow-level rankings. Tanzania appeared within the flow top ten despite not ranking amongst the largest national footprints, reflecting a highly concentrated individual pressure. In contrast China, Mexico, Malaysia, Myanmar and Thailand, all present in the footprint top ten, contributed no individually globally significant flow, revealing diffuse impact profiles requiring a multi-pronged approach to impact reductions (Figure 3., Figure 5.).

Totalling to 0.0900 PDF•years and 32.2% of the global freshwater total, the top ten freshwater flows contributed the lowest flow-level concentration of any ecosystem. Flow composition closely mirrored the bifurcated pathway structure identified previously with four climate change and six eutrophication flows represented. China's carbon dioxide emissions were the single largest freshwater flow globally, contributing 9.9% of total freshwater impact, followed by Brazil's phosphate fertiliser emissions and the USA's carbon dioxide emissions. China and Brazil each appeared twice within the top ten flows, with China spanning both climate change and eutrophication pathways, while Brazil was represented entirely through eutrophication-related flows. Sri Lanka's eutrophying fertiliser emissions represented the most concentrated national flow profile across the top ten of all ecosystems, accounting for 98.4% of the country's freshwater footprint (Figure 5.).

Matching the terrestrial ecosystem, freshwater flow and footprint rankings diverged. Russia and the DRC appeared in the flow top ten despite not ranking in overall footprint magnitude. Meanwhile Vietnam, Thailand, Mexico and Indonesia generated no individually significant flows despite their footprint

rankings, reflecting diffuse impact structures inconsistent with single flow level target interventions (Figure 3., Figure 5.).

The top ten national marine flows contributed to 0.0607 PDF•years and 44.3% of global marine impact. All ten flows were associated with marine eutrophication, very likely reflecting the lack of country disaggregation of aquatic microplastics. Despite this pathway uniformity, countries varied in their dominant elementary flow types including ammonia emissions to air, nitrogen fertiliser emissions to soil, and nitrogen oxide emissions to air. India dominated the marine flow rankings, contributing three of the top ten flows, collectively accounting for 27% of total marine impact and 98% of India's marine footprint. China also contributed three top-ranked flows spanning all three eutrophication-related flow types (Figure 5.).

Unlike terrestrial and freshwater ecosystems, all countries represented within the marine flow top ten were also present within the marine footprint leaders, indicating greater correspondence between the two hierarchies. However, countries including Turkey, Myanmar, Malaysia, and Vietnam possessed relatively large marine footprints but no individually dominant flow, revealing comparatively diffuse profiles (Figure 3., Figure 5.).

For full national flow breakdown see (Section 9.2.3.)

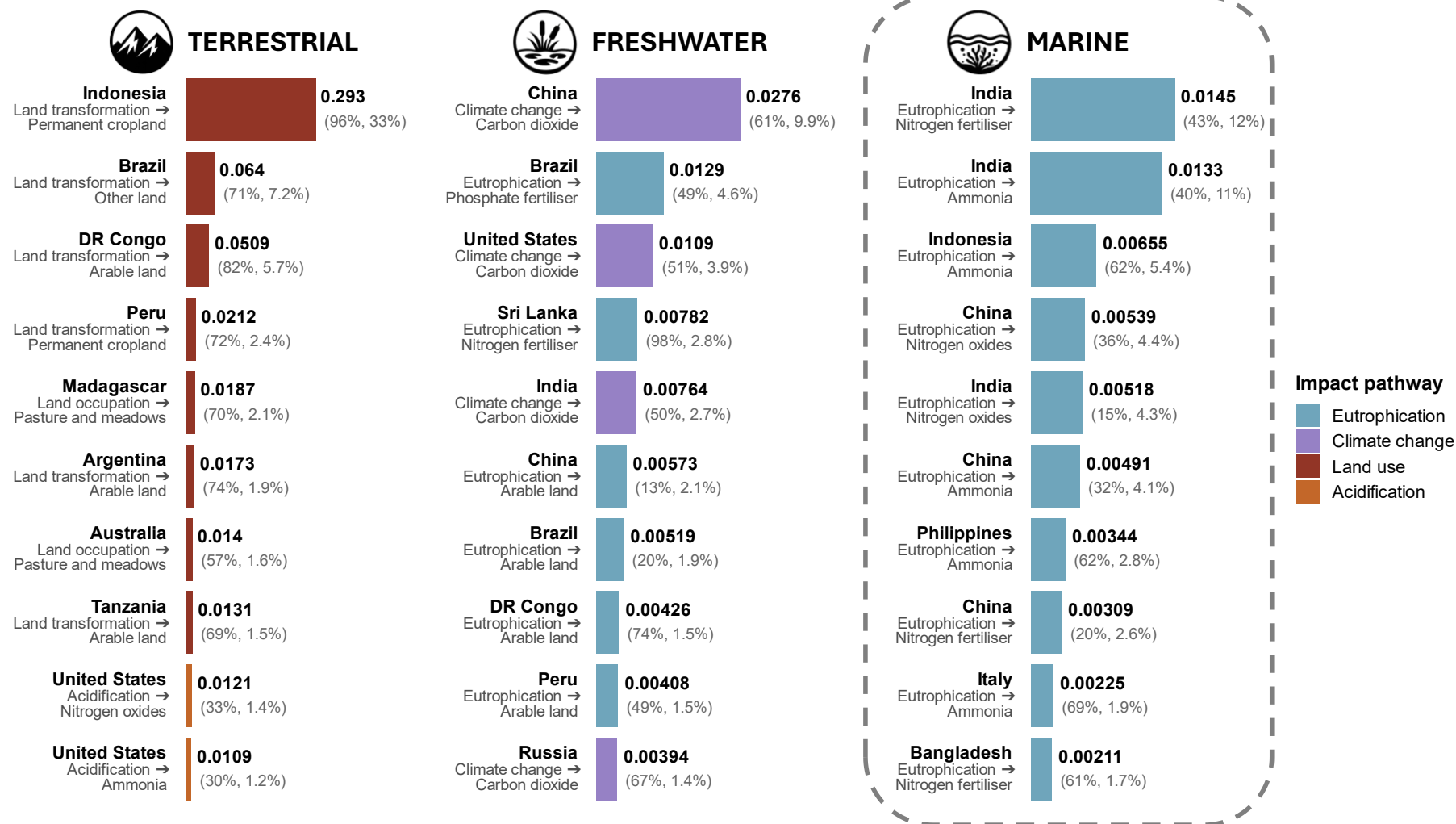


Figure 5. Ecosystems top ten national individual elementary flows to global biodiversity impact. LCA relative impact assessment. Measured in global PDF-years the top ten national flows revealed major national variability below impact pathway composition. With the paired percentage values representing each national flow's impact contribution to its country-specific ecosystem footprint and global ecosystem total respectively, national impact pathway contributions were found to vary significantly in their internal flow compositions and concentrations. Marine isolation box indicates the ecosystems poor threat representation.

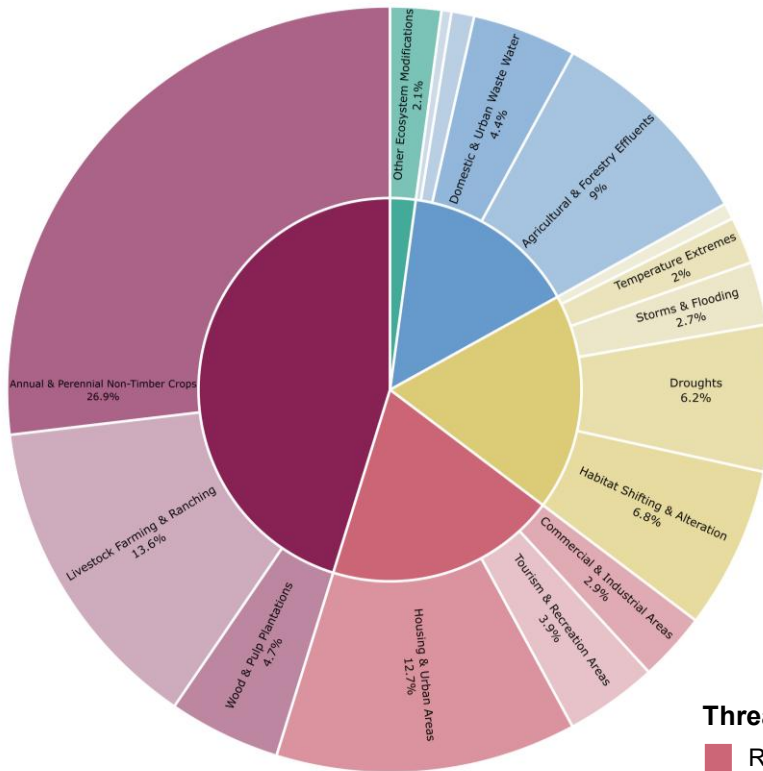
3.4. LCA Red List Comparison

Between my revised IUCN Red List threat prevalence and cross-walked LCA results, both approaches identified Agriculture & Aquaculture as the dominant tier one threat and aligned in their tier two importances of Annual & Perennial Non-Timber Crops, Livestock Farming & Ranching, and Wood & Pulp Plantations respectively. Beyond this shared dominance, however, the two methods displayed limited correspondence.

Residential & Commercial Development and Pollution represented the largest threat divergences between the two approaches. While the former ranked second and accounted for 19.5% of threat prevalence in the Red List, it contributed negligibly to the LCA results. In contrast, Pollution accounted for approximately 30% of LCA biodiversity impact, ~2x its Red List assessment contribution. Within the LCA pollution category, Air-Borne Pollutants and Agricultural & Forestry Effluents contributed similar shares, whereas Red List pollution prevalence was more strongly associated with Agricultural & Forestry Effluents.

Climate Change & Severe Weather ranked third in both assessments, but displayed a lower proportional contribution in my LCA results. Conversely, Natural System Modifications were more prominent in the LCA results, than in the Red List threat-prevalence assessment. Overall, the comparison suggests that the Red List's threat-prevalence patterns do not translate directly into magnitude-based biodiversity impact estimates, particularly amongst certain pathways.

Red List tallied threats



Threat category

- Residential & Commercial Development
- Climate Change & Severe Weather
- Agriculture & Aquaculture
- Natural System Modifications
- Pollution

LCA threat proportions

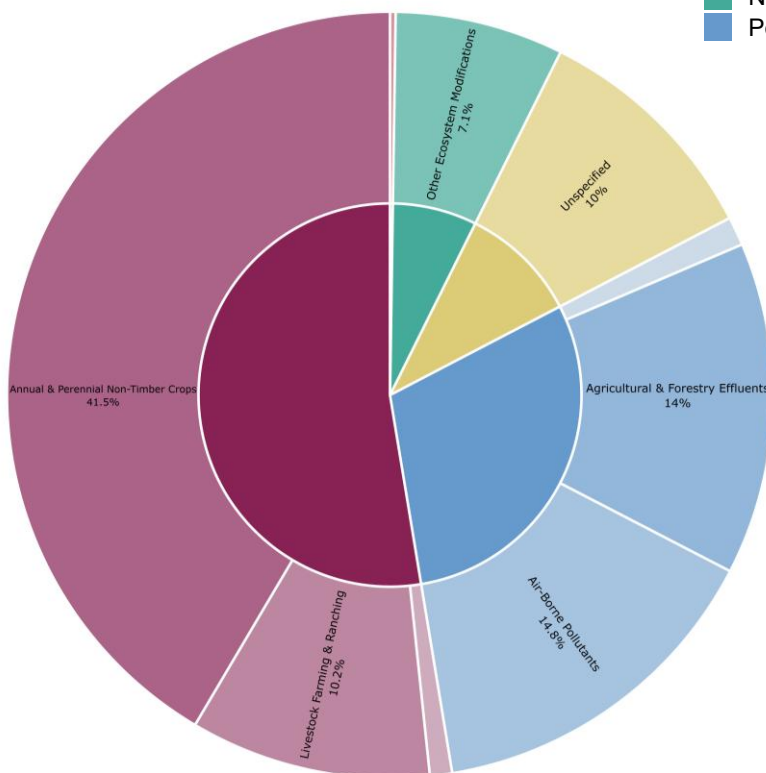


Figure 6. Comparison of threat proportions between revised IUCN Red List tally and LCA biodiversity impact estimates. Comparison of tallied threat prevalence across species considered “Near-threatened” or “Threatened” on the IUCN Red List and LCA threat impacts matched to their corresponding IUCN classified threats where possible. Pie chart inner rings represent tier one threat category proportions and outer rings showing the tier two breakdown within each tier one group. The two approaches strongly supported the importance of agricultural threats in global biodiversity losses but lacked further correspondence. Percentage values represent each segments share of the respective assessment total with segment labels omitted below 2% for clarity.

4. Discussion

4.1. Overview

Assessing the biodiversity impacts of 38,692 country disaggregated resource use / emission flows, 9967 of which belonged to regionalised impact pathways with country-localised CF's, I was able to provide a comprehensive global evaluation of our contemporary impacts on biodiversity focussed on a production based framing.

4.2. Assumptions and Limitations

The year 2020 coincided with the COVID-19 pandemic which resulted in anomalous shifts in societal behaviour compared to adjacent years. Nation's annual resource use / emissions profiles were therefore distinct relative to predicted trends based on historical annual data, producing potentially uncharacteristic biodiversity impact profiles for informing contemporary reductions (Liu et al., 2020). However, due to my analysis' heavy reliance on synthetic data, calculated using broad, multi-year trends, the results' sensitivity to the pandemic anomaly were considered limited.

Due to the extensive but not exhaustive coverage of my research, this analysis provides a conservative estimate of threat and national contributions to global biodiversity loss, allowing only relative internal comparisons. Due to the coverage gaps between my collated LCI and operational scope boundary, combined with missing threat CFs, this analysis was not comprehensive in its representation of all threats to extant global biodiversity. Operating at multiple scales, such gaps underestimated and introduced structured bias into specific results comparisons, with threats possessing higher data and CF representation appearing disproportionately impactful relative to those with partial coverage. Interpretation of my results should therefore be supported by a rigorous understanding of each impact's data representation.

Effective quantification of the uncertainty around and sensitivity of my impact results was strongly restricted by a near-universal absence of upper and lower bound estimates across both the inventory datasets and LCIA CFs. Except from the distribution of annual marine microplastic influx, and the CFs of Climate change and Water consumption, both components in my analysis suffered from a systemic absence of uncertainty integration. This absence must crucially be addressed in further research to improve LCA reporting accuracy (Bromwich et al., 2025; Igos et al., 2019; Rosenbaum et al., 2018).

Global PDF•years evaluates impact based on biodiversity characteristics with lower marine ecosystem incidence. The unit quantifies the risk of local threats producing global species extinctions as a fraction of total species richness (Verones et al., 2022), assigning high impacts in areas characterised by small species ranges, high isolation and endemism. Although the metric accounts for ecosystem differences in absolute species richness (Román-Palacios et al., 2022), these characteristics are typically more frequent in terrestrial and freshwater environments due to their stronger barriers to migration, range expansion, and recolonisation (Pinheiro et al., 2017). The metric structure therefore evaluates lower relative impacts in the marine environment, compounding its already poor threat representation (Stanford-Clark et al., 2024). This finding does not mean that marine biodiversity pressures are necessarily less severe but that inter-ecosystem comparisons are sensitive to the chosen endpoint metric. Future research should integrate alternative biodiversity characteristics into LCA methods to avoid the impacts of such biases.

4.3. Global Biodiversity Loss Ecosystem Priorities

Terrestrial impacts dominated their freshwater and marine counterparts, a finding that likely combines the influence of genuine ecological reality and structured methodological biases. Already the dominant impact pathway, I anticipate global terrestrial land-use impacts to be conservative due to land transformation's inventory partiality (Section 2.2.3). This terrestrial weight strongly suggests impacts on land are the major force driving global biodiversity declines, a finding well-supported by wider literature (IPBES, 2019; Jaureguiberry et al., 2022). However, considering the marine ecosystem's prior-mentioned coverage underrepresentation, global PDF•year bias, and the increasing discovery of terrestrial ecosystem bias extents in conservation (Caldwell et al., 2024), inter-ecosystem comparisons should be treated with caution. Inferences made for policy interventions and decision making should treat ecosystem impacts independently until further research addresses the inter-ecosystem differences of LCA methods.

4.4. National Threat Profiles

Countries varied strongly in their impact pathway footprint proportions alongside the identities and impact concentration of their contributory elementary flows. Such differences were broadly consistent

with wider literature describing the geographically heterogeneous nature of extant biodiversity and nation's disparate activity inventories. Across all ecosystems, the majority of global impact was located around the equator, reflecting the intersection between biodiversity's latitudinal gradient (Gaston, 2000), and those countries experiencing high economic development (Moran & Kanemoto, 2017; Wiebe & Wilcove, 2025). Marine ecosystem impacts additionally experienced further localisation within Southern and Southeast Asia, a previously observed trend (Moran & Kanemoto, 2017). The dominant national elementary flows of global land transformation strongly aligned with the Global Forestry Watch's documentation of the proponents of national forestry loss (Global Forest Watch, 2026). Meanwhile, the strong variability of flow identity in driving national freshwater eutrophication matched regional variability in molecular emission release quantities, environmental fate, and impacted biodiversity (Jwaideh et al., 2022). This multiscale variability – across nations and threats – indicates the need for national disaggregation of the activities most effective at minimising ongoing biodiversity losses.

4.5. Approach Comparisons

The strong divergence between my LCA and revised assessment of Red List threat prevalence primarily reflects fundamental methodological differences not factual contradiction. LCA's poor representation of 'Residential & Commercial Development' threats can be attributed to the inability to disaggregate FAOSTAT's 'Other land' category, conservative CF pairing, and "Other Natural Systems Modifications" assignment. Meanwhile, the Red List is documented to underestimate the influences of slow or diffuse impacts (Keith et al., 2014), and carry taxonomic biases (Humphries et al., 2026). Considering this evaluation, the results of these approaches should be considered complementary, not competitive, and emphasise the importance of a multifaceted approach in informing effective biodiversity reduction decisions. Despite these differences, the shared dominance of agricultural threats emphasises its immediate attention demand, widely documented as a crucial priority (Boakes et al., 2024; Poore & Nemecek, 2018), especially in the face of projected expansion and intensification (Zabel et al., 2019).

4.6. Policy Maker Implications

Within its scope, my research enables countries to now pursue tailored impact reduction roadmaps and deliver coordinated global efforts considering their immediate demand. The identification of dominant, country-specific elementary flows, such as Indonesia's Forest to permanent cropland transformation or Sri Lanka's nitrogen fertiliser releases, present isolated interventions for significant reductions. Nations with more diffuse flow impacts, meanwhile, can now identify the portfolio of actions required to achieve notable footprint reductions. I identify countries with high inter-ecosystem impacts, notably Indonesia, China, Brazil, and India, as requiring integrated ecosystem reduction strategies rather than siloed approaches. These results could be integrated into National Biodiversity Strategy and Action Plan

(NBSAP) reporting (CBD, 2022), against which nations could baseline and track future impact reductions, aided by my analysis' repetition on future data.

4.7. Future Research

Beyond the addressed limitations, the methodological gaps of this analysis present the most immediate future research priorities. Resolution of GLAM's water consumption and land transformation CF validity transformation through further LCIA comparisons and CF developer discussion would resolve a significant gap in my analysis. Efforts to integrate existing CFs representing marine overexploitation would also address the current threat coverage gap around the ecosystem (Stanford-Clark et al., 2024).

Improvements in the regionalisation of CFs to match ecoregion resolution would increase the biological relevance of LCA methods. With many nations possessing high internal ecological variability with specific vulnerabilities, regionalisation resolutions matching both jurisdictional capacity and ecological relevance would significantly improve LCA results' ability to inform effective impact reductions.

PDF•years is a useful relative comparison metric but is unable to convey measures of absolute biodiversity impact, impairing its communicability to policy audiences and risking misinterpretation (Kuipers et al., 2021). With the imminent need for understanding and action around ongoing biodiversity loss reductions, future LCA development should link its outputs to direct ecological outcomes, theoretical or observed. This could potentially involve a reconsideration of the independence of risk propagation between years used in current modelling approaches.

Building on the production-based impacts of this research, future investigation should expand upstream to identify the indirect, embodied involvement of globalised economic actors (Lenzen et al., 2012). Pairing my inventory-endpoint analysis with a global Environmentally Extended Multi-Regional Input-Output (EE-MRIO) analysis, evaluating the involvement of parties and monetary flows in inventory activities and midpoint impacts, could attribute funding responsibility for the threat impacts of ongoing biodiversity loss identified by my research.

5. Conclusion

This analysis presents the first bottom-up LCA assessment of the relative biodiversity impacts of global resource use and emissions. Resolving the contributions of national activities to ongoing declines, my results reveal the strong variability in both the magnitudes and threat composition of countries', production-based biodiversity footprints previously obscured by globally aggregated approaches. While the limitations of LCA methods require addressing and the findings should be supported by other information sources, my research represents an empirical step towards closing the implementation gap

between pledged international commitments and effective, globally coordinated action. For further policy applicability, future research should extend this framework to incorporate economic actor attribution across supply chains and improved spatial precision of impact characterisation.

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8. Management Report

Throughout my project I met with my supervisors for 30 minutes each week. They also provided me with written input in the writing up phase.

Over the course of the project, I encountered and largely overcame several methodological and data-related roadblocks. At the outset, I had planned to use LC-IMPACT as the Life Cycle Impact Assessment method for evaluating the biodiversity impacts of my global resource-use and emissions inventory. However, during the summer preceding this academic year, GLAM was released. As it offered broader threat coverage and was partly developed in response to known limitations of earlier LCIA methods, my supervisors and I decided that GLAM was better suited to the objectives of the project.

This change improved the relevance of the analysis but introduced an unexpected challenge. Because the most recent version of GLAM was newly released, it was not accompanied by a single methodological document explaining the full mechanics of the framework or the integration of characterisation factors across impact pathways. Instead, the framework primarily cited the underlying papers for each pathway. This meant that I had access to the final characterisation factors and their source literature, but limited explanation of how the independent pathway methods had been harmonised into a single LCIA framework. As a result, the early stages of the project were slowed by the need to work backwards from the cited literature to understand GLAM's assumptions, structure and limitations. For future users, a cohesive user manual accompanying the GLAM characterisation factors would be valuable, both to improve confidence in the method and to make its assumptions and limitations more transparent.

A second major challenge was the construction of the global Life Cycle Inventory. Although this occupies only a limited portion of the written methods, identifying, evaluating and harmonising suitable datasets for global resource use and emissions took a substantial amount of project time. Many candidate datasets ultimately proved unsuitable because they lacked global coverage, country-level resolution, 2020 representation, or compatibility with GLAM's elementary-flow requirements. The marine microplastics inventory was particularly time intensive, requiring extensive literature searches and filtering of published estimates to populate the flow diagram used to estimate annual marine microplastic influx. Similarly, the decision to replace GLAM's land transformation characterisation factors with those from LC-IMPACT required the construction of an additional paired land-transformation inventory, creating an unanticipated methodological setback.

A final challenge concerned the interpretation of water consumption impacts. This pathway returned values that were much larger than expected relative to the other ecosystems and impact pathways. Investigating whether these values arose from inventory construction, characterisation factor behaviour,

or methodological assumptions required substantial additional work, including correspondence with the characterisation factor authors. In part, the impact pathways final exclusion from my results was a product of running out of time to investigate its values further.

Overall, the project involved more methodological troubleshooting than initially expected, particularly around LCIA method selection, inventory construction and interpretation of uncertain pathway outputs. However, these challenges also improved my final analysis, forcing clearer documentation of the research's assumptions, stronger data coverage scrutiny, and a greater caution when interpreting my results. I am pleased with how I resolved the issues that could be addressed within the project timeframe, and how the unresolved challenges now provide clear priorities for future research.

9. Supplementary Information

9.1. Methods

9.1.1 Aquatic Microplastic Inventory

Below lies the data sources and estimates used in the aggregated marine microplastic influx estimation described in section 2.2.2. All values are measured in Mega tonnes (Mt). Published estimates were resolved to their primary literature sources where possible to avoid repetition of the occurrence of certain values. For published sink or flow proportion estimates presented with an uncertainty, I used the central or midpoint estimate to populate my flow diagram. Published sink and flow proportion estimates were combined across years followed by the combination of all viable pathways by each estimate to calculate a distribution of total annual marine microplastic influx. This final estimation includes both primary and secondary sources of microplastics describing plastic pieces smaller than 5mm in size originating from direct production or macroplastic fragmentation respectively.

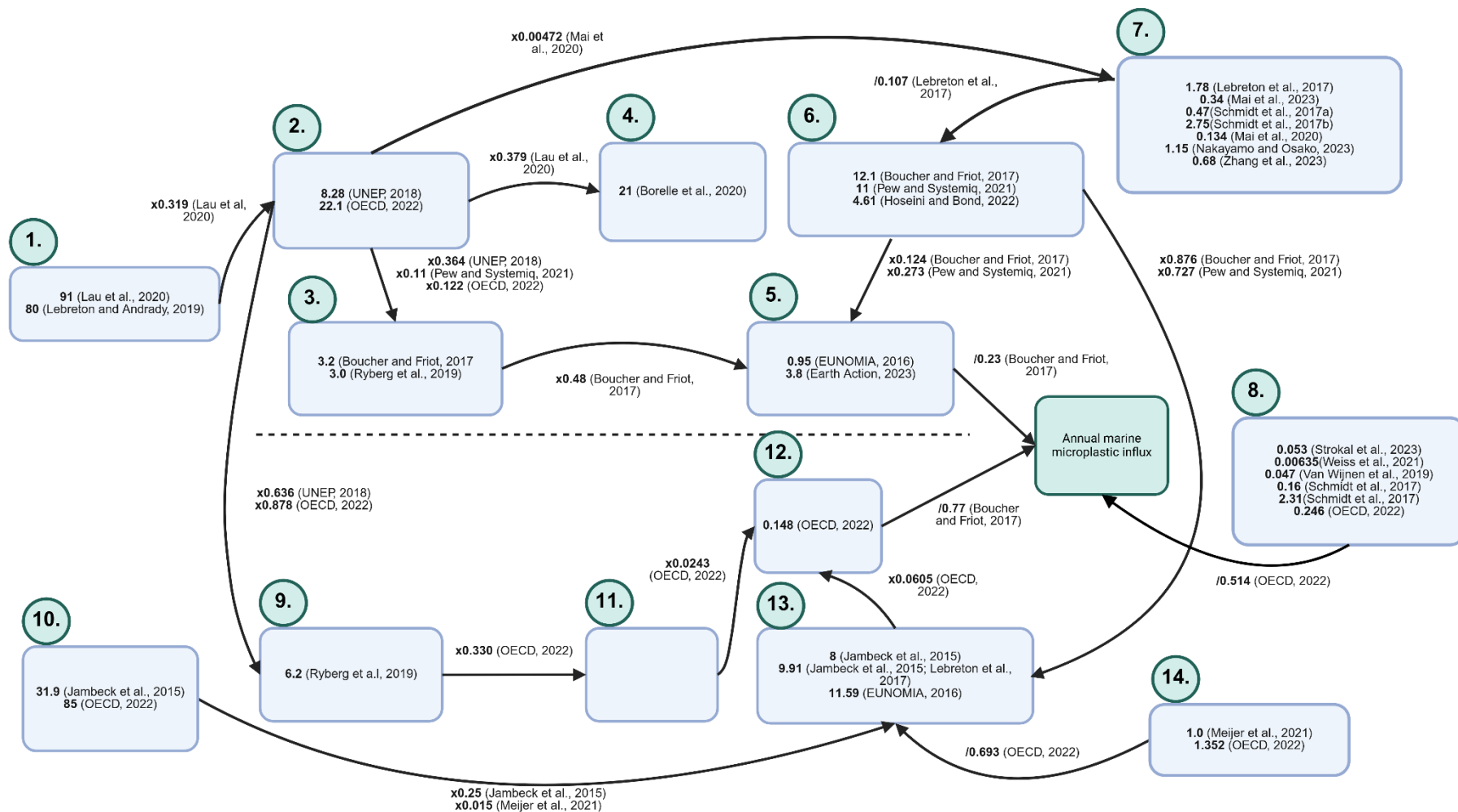


Figure 7. Environmental plastic sink estimates and viable pathway flow diagram. 1 = All plastic mismanaged waste, 2 = All plastics into environment, 3 = Primary microplastics into environment, 4 = All plastics into aquatic environment, 5 = Primary microplastics into marine environment, 6 = All plastics into marine environment, 7 = All plastics from rivers into marine environment, 8 = All microplastics from rivers into marine environment, 9 = Macroplastics into environment, 10 = Macroplastics mismanaged waste, 11 = Macroplastics into aquatic environment, 12 = Secondary microplastics released into marine environment, 13 = Macroplastics into marine environment, 14 = Macroplastics from rivers into marine environment. All values measured in Mt (mega tonnes). Figure created in Biorender.

9.1.1. Revised assessment of threat prevalence in IUCN Red List

As a comparator to the global threat analysis produced from the LCA method, a new contemporary assessment of the threat prevalence in the IUCN Red List was performed to account for the high number of species additions since Maxwell et al analysis nearly a decade ago. To estimate the relative contributions of the IUCN's classified threats to global biodiversity loss, the number of Red List species affected by each respective level one and two categorised threat were tallied. The species included in the tally were only taken from taxonomic groups with coverage of 70% or more, removing poorly assessed groups to avoid potentially systematically skewing the results towards well documented threats rather than those globally prolific. The approach follows the methodology used by Maxwell et al. (2016) but was revised to address limitations in the original coverage estimation procedure.

A subset of the IUCN Red List was first identified for which threat data was available. The Red List presents its own coverage estimates calculating the proportion of Red List classified species relative to the estimated true total number of species within a group. Used by Maxwell et al, these proportions, however, do not necessarily reflect the proportion of species for which categorised threat data are available. As a species can be Red List certified with no resolution of the threats to its existence, conventional coverage estimates risked inflating the apparent suitability of certain groups to a threat analysis while carrying underlying biases in their threat information. To calculate a revised coverage estimate the Red List was filtered for only species for which threat data was available. To define this subset, the global red list was filtered to exclude species possessing no classified threats and flagged for requiring threat research. The resulting subset, across all population trends and Red List statuses bar those data deficient, included species with no threats or research requirement and those with IUCN classified threats. This species subset was amenable to the potential a species may have no threats and did not exclude all species requiring research into their threats but instead prioritised the use of available knowledge with respect to species with at least some classified threats. Although introducing a source of potential bias, this approach was considered preferable to discarding all partially

characterised species, reflecting a broader demand for conservation to work in the immediacy with what information is available.

The taxonomic completeness of the Red List subset was then assessed by comparison to the Catalogue of Life (CoL), the most complete benchmark of taxonomic diversity documenting the names and taxonomies of all known species. As the Red List and CoL employ different taxonomic rank hierarchies, a harmonisation methodology was developed to ensure consistent match up. Flattened hierarchical sequences were constructed for both datasets by concatenating the taxonomic terms of each species into a word string. In the case of the IUCN species these sequences spanned the seven core ranks: Kingdom, Phylum, Class, Order, Family, Genus, Species. Meanwhile the CoL sequences additionally incorporated a series of intermediate ranks, reflecting its finer granularity. Flattening the taxonomic ranks into a sequence reconciled these structural differences without requiring a direct rank to rank alignment specific to each species. Species names were then matched between the two datasets. For each matched species, the taxonomic terms present in the IUCN sequence were compared against those in the corresponding CoL sequence. Any CoL term found within the IUCN sequence was assigned to the rank label it occupied in the IUCN rank hierarchy. Applied iteratively across all species matches to construct a comprehensive term-to-rank lookup table, this process captured the cases where CoL intermediate ranks corresponded functionally to one of the five core IUCN ranks. This lookup was then applied across all CoL species to reclassify each record into the five core IUCN rank fields. Where a CoL term, regardless of its original rank position, was identified in the lookup table as corresponding to an IUCN rank, it was reassigned accordingly across the CoL dataset. For terms that still did not match between the core ranks of the reassigned CoL and IUCN taxonomies, due to having different terms entirely, the rank IUCN term overwrote the CoL counterpart for all instances of the latter's occurrence. This step was only performed for species that had at least one term to rank lookup match up, from the previous step, that was downstream and more specific of the CoL term being renamed. Renaming the CoL terms with their IUCN rank counterpart assumed taxonomic synonymy between the two terms, therefore carrying a potential risk of underestimating the coverage of certain taxonomic groups if the CoL term was higher order, and therefore described a larger taxonomic group, than its IUCN counterpart. However, because this process only risked producing a more conservative estimate of the taxonomic coverage of certain groups, the method was retained.

The taxonomic coverage of the IUCN Red List was then calculated as the proportion of species it shared out of the harmonized CoL dataset. After calculating the coverage of all taxonomic groups defined by the IUCN red list, a hierarchical top-down screening procedure was applied to identify the taxonomic groups that met a pre-defined coverage threshold of 70%. This threshold is slightly lower than the 80% used by the IUCN and Maxwell et al, reflecting both the often-higher total species counts recorded by

the Catalogue of Life relative to those used in IUCN's own estimates, and the decided value of the retained threat information from using a slightly less conservative delimiter. Screening for sufficiently covered groups proceeded from the broadest taxonomic rank downwards through kingdom, phylum, class, order and family. Coverage was not estimated below the family level to avoid matched groups being too specific and carrying potentially biased threat information. Species already assigned to higher-rank groups with qualifying coverage were subsequently excluded from consideration at finer resolution ranks, preventing double counting and ensuring that coverage qualification was attributed at the most parsimonious level.

From the taxonomic groups with qualifying coverage, the threat information of their contained species was then tallied using a Red List v4 API. To assess the threats involved in biodiversity decline, only species with Near Threatened, Vulnerable, Endangered or Critically Endangered Red List status were selected. Using the IUCN Threat Classification scheme v3.3, the threat timings to be extracted included those ongoing, past likely to return, future and unknown, excluding past threats unlikely to return. These choices were to reflect current threats and those anticipated to occur due to the persistence of current activities, alike to the LCA's extinction risk estimate of PDF•years. The scope choices excluded threats with negligible impact. Additionally, the chosen severities of the selected threats excluded those that caused negligible or no declines. If the timing, scope or severity of the threats was unknown they were included in the analysis for completeness.

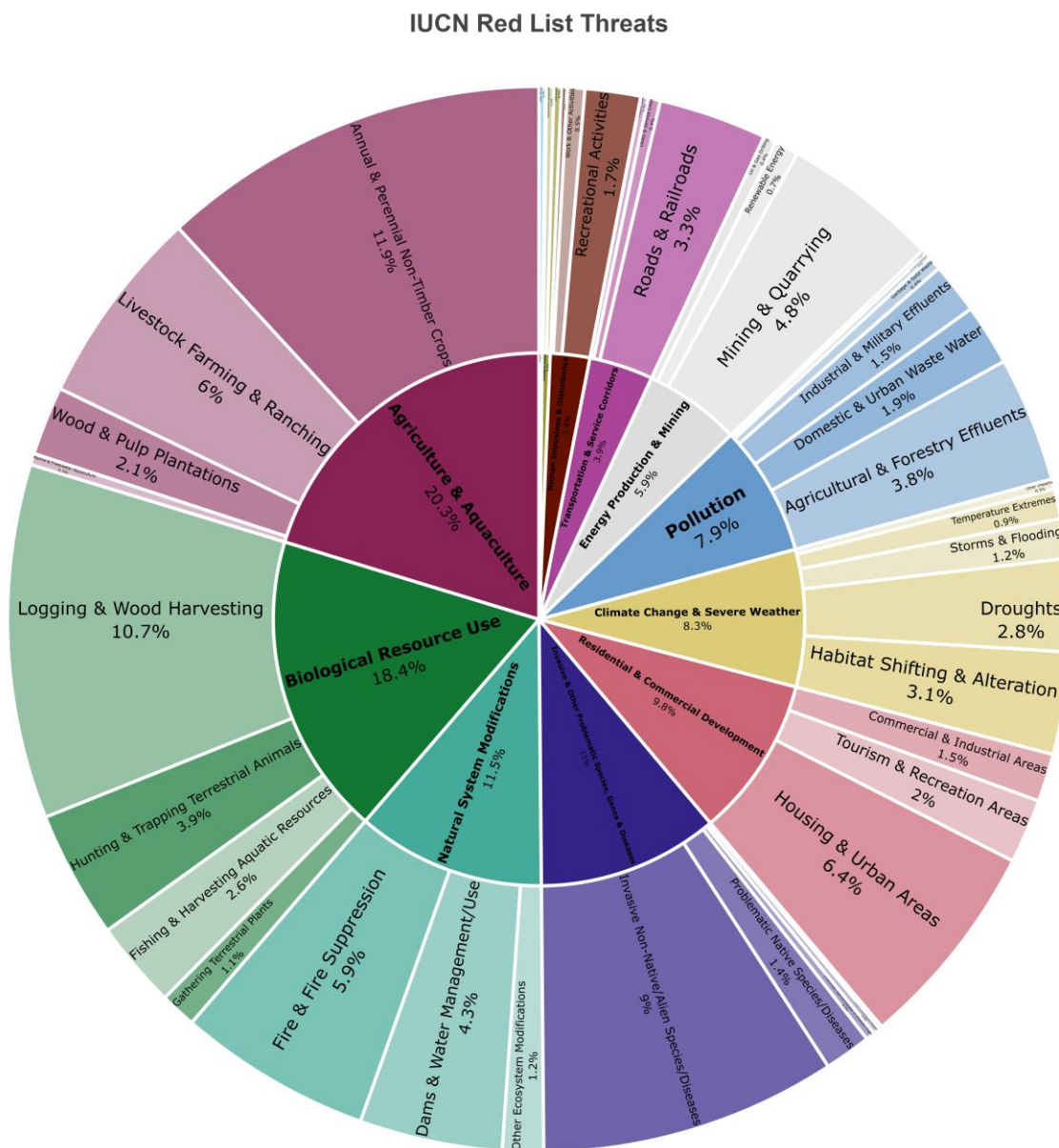
For those selected threats, the number of unique species included in each individual tier one and tier two category was then totalled. Alike to Maxwell et al, threats against the same species were therefore given equal weighting when comparing between tier two categories, but these were not double counted in the tier one total. The analysis output produced a tally of the threats to near threatened and threatened species from groups with 70% or greater coverage in the IUCN red list with respect to species with available information on the threats to their survival.

9.2. Results

9.2.1. Water consumption

Considered independently, water consumption's top ten national footprints included, in decreasing size: Egypt, Mexico, Australia, USA, India, Iran, Libya, Saudi Arabia, Spain and Peru. These top ten countries contributed a cumulative impact of 33.4 PDF•years, accounting for of the total threat impact pathway global footprint and 70.6% of the ecosystem total, if included. Within this country cohort, individual national impacts ranged from 18.0 to 1.32, displaying a 92.7% drop in footprint magnitude.

9.2.2. Revised assessment of threat prevalence in IUCN Red List



Threat category

- Residential & Commercial Development
- Agriculture & Aquaculture
- Energy Production & Mining
- Transportation & Service Corridors
- Biological Resource Use
- Human Intrusions & Disturbance
- Natural System Modifications
- Invasive Species, Genes & Diseases
- Pollution
- Geological Events
- Climate Change & Severe Weather
- Other Options

Figure 8. Revised IUCN Red List threat prevalence proportions. Number of species considered “Near-threatened” or “Threatened” on the IUCN Red List and recorded as impacted by a threat were tallied for each tier one and tier two threat respectively. At a tier one level, agricultural threats were found to be the primary driver of losses followed by the influence of Biological resource use and Natural System Modifications. At a tier two level, Annual & Perennial Non-Timber Crops were found to be the most influential threat followed by Logging & Wood Harvesting then Invasive Non-Native / Alien Species / Diseases. Percentage values represent global total share.

9.2.3. National footprint grouped-flow data

Below lies a link to every nation’s grouped flow impact contributions calculated in my analysis. Each flow’s percentage contributions to the total country ecosystem impact and global ecosystem impact are included along with any calculated upper and lower bounds arising from the availability of such CFs. Water consumptions impact pathway flows are excluded.

[National Grouped-Flow Threat Contributions.xlsx](#)