Consumption-based biodiversity footprints – do different indicators yield different results?

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This document is the unedited Author’s version of a Submitted Work that was subsequently accepted for publication in Ecological Indicators, Copyright © 2019 Elsevier Ltd. after peer review. To access the final edited and published work see https://doi.org/10.1016/j.ecolind.2019.04.022
ABSTRACT

Land use related to human consumption patterns leads to significant loss of biodiversity. Here, the implications of using different indicators in the calculation of biodiversity footprints caused by land use were analyzed. Footprints refer to the impacts related to the net consumption in a region. We calculated biodiversity footprints for 140 regions in the world with an environmentally-extended multi-regional input-output (EEMRIO) model. The EEMRIO links economic activities from the Global Trade Analysis Project (GTAP) database with land use and four indicators of biodiversity loss. We included three alpha diversity indicators (loss of mean species abundance, relative abundance and relative species richness) and one indicator of gamma diversity (vulnerability-weighted relative species richness loss). While the three alpha diversity indicators reflect local diversity within a site, the gamma diversity indicator captures global diversity by weighting regional species richness with species’ extinction vulnerability in a region. We found that the three alpha diversity footprints show close alignment ($r_S > 0.93$), while there was limited convergence between alpha and gamma diversity footprints ($r_S < 0.22$). The alpha diversity indicators identified a diverse set of regions with high per capita consumption-based biodiversity footprints across the globe, while the gamma diversity indicator emphasized human consumption patterns threatening particularly tropical biodiversity. Although all footprints are positively related to rising household expenditure, this relationship was weaker and highly uncertain for the gamma diversity footprints. The alpha-based footprints also showed a negative relationship with population density, while the gamma-based footprint was not related to population density. Our results highlight the relevance of including both alpha and gamma diversity indicators in land-based biodiversity footprint calculations.

Keywords (max 6): Biodiversity footprint; Multi-regional input-output analysis; Gamma diversity; Alpha diversity; Consumption; GTAP

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1. Introduction

Biodiversity ultimately supports and stabilizes the provisioning of ecosystem services that are necessary for maintaining the production of food and fiber and regulating earth systems such as climate and freshwater (Cardinale et al., 2012; Isbell et al., 2017; Tilman et al., 2014). The impacts of human consumption on biodiversity can be assessed with multi-regional input-output (MRIO) analysis in which global industry transactions are translated into final demand for goods and services in the global economy (Miller and Blair, 2009). The economic relationships can be linked to environmental impacts to derive environmentally-extended (EE)MRIO models and compute production-based and/or consumption-based environmental footprints (e.g. Hertwich and Peters, 2009; Kitzes et al., 2016; Steen-Olsen et al., 2012; Weinzettel et al., 2013).

While several biodiversity footprinting studies have been published, they have typically focused on one dimension of biodiversity, such as number or composition of species (Chaudhary et al., 2016a; Chaudhary and Kastner, 2016; Chaudhary and Brooks, 2017; Lenzen et al., 2012; Moran et al., 2016; Moran and Kanemoto, 2017; Verones et al., 2017; Wilting et al., 2017). Comprehensive assessments of biodiversity require consideration of different dimensions of biodiversity and different spatial scales (Isbell et al., 2017; Marques et al., 2018; Purvis and Hector, 2000; Santini et al., 2017, Schipper et al., 2016b). Although examples of comparing different biodiversity indicators for specific products exist (Nishijima et al., 2016), systematic evaluation of whether different biodiversity indicators provide additional insights in a global footprint context covering all economic flows is currently lacking. Indicators reflecting different biodiversity dimensions provide different insights: alpha diversity captures local biodiversity within a site; beta diversity reflects structural differences between sites and gamma diversity is the total species diversity in a landscape (Whittaker 1972).

In this study, we quantified and compared different biodiversity indicators to derive consumption-based footprints of nations. We focused on land use as one of the key pressures on biodiversity (Murphy and Romanuk, 2014). To this end, we linked an MRIO model, based on the Global Trade Analysis Project (GTAP) database, with areas of land (forestry, pasture, cropland and urban) and the intensity of its use (low, medium, high). Land use was subsequently linked to three indicators of alpha diversity: loss of mean species abundance (Alkemade et al., 2009; Schipper et al., 2016a), loss of relative abundance (Newbold et al., 2016, 2015) and loss of relative species richness (Newbold et al., 2016, 2015) and one indicator of gamma diversity: loss of vulnerability-weighted global relative species richness (Chaudhary et al., 2016a, 2016b, 2015). All the chosen biodiversity indicators reflect long-term biodiversity effects of a specific land use type relative to a reference land use state.
Rising incomes, as an indicator of increasing prosperity, typically result in increased levels of consumption and thus consumption expenditure (Varian 2006). To understand how the four biodiversity footprints were linked to levels of prosperity, we tested the responsiveness of each of the per capita biodiversity footprints to per capita household expenditure. With increasing population density, less land is available for resource use thus driving technological development for improved resource use efficiency (Wiedmann et al., 2015; Wilting et al., 2017). To test for a systematic relationship between population density and per capita biodiversity footprints, we also included population density as a second explanatory variable.

2. Methods

2.1. Biodiversity footprint

We calculated the biodiversity footprints following the approach employed by Wilting et al. (2017). The biodiversity footprint $B^j$ of region $j$ in the multi-regional context was defined as:

$$B^j = i(M°D)(I - A)^{-1}y^j + m^jd^j$$

with $i$ being a vector of ones needed for the summation over all land use categories to arrive at the biodiversity footprint $B$ of region $j$. $M$ corresponds to the matrix of biodiversity loss factors (in percent of biodiversity loss per land use) per region and sector, and is linked to land use intensities, $D$, differentiated per region and sector, and land use category employed in this analysis. Both matrices, $M$ and $D$, are defined for all regions and sectors per land use category; elementwise multiplication of matrix components is indicated by the matrix operator $°$. $(I-A)^{-1}$ is the standard Leontief inverse matrix depicting information on industry use of imported and domestic intermediate inputs (Leontief, 1936). Vector $y$ depicts the final demand for goods and services in region $j$ from domestic and foreign origin. The Leontief inverse and final demand vector $y$ were derived using the procedure described by Peters et al. (2011) to construct an MRIO table from the GTAP database. To account for the direct linkage of land use to final demand the product $m^jd^j$ is added. $m$ corresponds to the vector of biodiversity loss factors linked to land use in region $j$ and vector $d$ to the direct land use pressures for all land use categories by final consumers in region $j$.

2.1.1 Biodiversity indicators

To link biodiversity indicators to the MRIO framework, the indicators need to be applicable at the global scale and have sufficient detail on the definition of the underlying land use categories. This limited the range of potential indicators to three alpha diversity indicators (loss of mean species abundance, relative abundance at the local scale and relative within-sample species richness) and one indicator of gamma diversity (vulnerability-weighted relative species richness...
Table 1 provides an overview on the definition, diversity classification (following Whittaker, 1972), and characteristics of the respective biodiversity indicators.

<table>
<thead>
<tr>
<th>Indicator</th>
<th>Diversity classification / Description</th>
<th>Characteristics and limitations</th>
<th>Source</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Mean species abundance (MSA) loss</strong></td>
<td><strong>Classification:</strong> Alpha (local within-site diversity)</td>
<td>Characteristics: Generic factors for 16 land use categories</td>
<td>Methodology: Alkemade et al. (2009) and Schipper et al. (2016a)</td>
</tr>
<tr>
<td><strong>Description:</strong> The mean original species abundance (A) in disturbed conditions relative to their presence in undisturbed conditions (A_ref):</td>
<td>Factors truncated at 1 (representing undisturbed habitat)</td>
<td>Included taxa: mammals, birds, reptiles, amphibians, terrestrial invertebrates, vascular plants</td>
<td></td>
</tr>
<tr>
<td>$MSA_{loss} = 1 - \frac{1}{n_i} \sum_i A_i A_{ref,i}$</td>
<td><strong>Limitations:</strong> Does not capture</td>
<td>- among site differences - species vulnerability</td>
<td></td>
</tr>
<tr>
<td>based on n species ($n_i$)</td>
<td></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Relative abundance (RA) loss</strong></td>
<td><strong>Classification:</strong> Alpha (local within-site diversity)</td>
<td>Characteristics: Generic factors for 13 land use categories</td>
<td>Methodology: Newbold et al. (2015, 2016)²</td>
</tr>
<tr>
<td><strong>Description:</strong> Sum of the measures of abundance of all taxa at a site relative to abundance in undisturbed conditions.</td>
<td>Factors not truncated at 1 (allowing for biodiversity gains compared to the undisturbed habitat)</td>
<td>Included taxa: mammals, birds, amphibians, reptiles, anthropods, plants</td>
<td></td>
</tr>
<tr>
<td>$RA_{loss} = 1 - \frac{\sum_i A_i}{\sum_i A_{ref,i}}$</td>
<td><strong>Limitations:</strong> Does not capture</td>
<td>- among site differences - species vulnerability</td>
<td></td>
</tr>
<tr>
<td><strong>Relative within-sample species richness (RWSR) loss</strong></td>
<td><strong>Classification:</strong> Alpha (local within-site diversity)</td>
<td>Characteristics: Generic factors for 13 land use categories</td>
<td>Methodology: Newbold et al. (2015, 2016)</td>
</tr>
<tr>
<td><strong>Description:</strong> Number of taxa at a given site in a standardized sampling unit (S) relative to the number of taxa in an undisturbed habitat (S_ref).</td>
<td>Included taxa: mammals, birds, amphibians, reptiles, anthropods, plants</td>
<td><strong>Limitations:</strong> Does not capture</td>
<td></td>
</tr>
<tr>
<td>$RWSR_{loss} = 1 - \frac{S}{S_{ref}}$</td>
<td>- among site differences - species vulnerability - changes in species composition</td>
<td></td>
<td></td>
</tr>
</tbody>
</table>
### Vulnerability-weighted global relative species (VGSR) loss

**Classification:**
Gamma (global across-site diversity)

**Description:**
Loss in global relative species richness associated with land use type (i) in country (c) per taxon (t). $S_{\text{loss}}$ is the land use and country-specific species loss, $S_{w,t}$ is the global number of species of taxon t summed over all land use types and countries, $V_{C,t}^5$ is the country-specific vulnerability for global extinction based on IUCN$^6$ and $V_{S,w,t}$ the world average vulnerability score of taxon t.

$$VGSR_{\text{loss},i,c,t} = \frac{S_{\text{loss},i,c,t}}{S_{w,t}} \cdot \frac{V_{C,t}}{V_{S,w,t}}$$

**Characteristics:**
- Ecoregion-specific factors for six land use categories$^7$
- Included taxa: mammals, birds, reptiles, amphibians, vascular plants

**Limitations:**
- Does not capture changes in species composition

### Methodology:
Chaudhary et al. (2015, 2016a, 2016b)

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**Notes:**
1Following Whittaker (1972): alpha diversity captures biodiversity within a site and gamma diversity reflects the total diversity.
2We obtained the exact coefficients in log-transformed format through personal communication with Tim Newbold in June 2017.
3Calculated based on methodology in Gotelli and Colwell (2001)
4The vulnerability-weighted relative species richness loss (expressed in potentially disappeared fraction (PDF) per square meter) is obtained by a weighted average of the taxon-specific VGSR$_{\text{loss}}$ over all taxa giving equal weighting to plants and animal taxa and equal weighting within the animal taxa.
5Through vulnerability-weighting, actual species richness loss (in number of species lost) was weighted by the vulnerability-weighted global species richness to arrive at a fraction of species lost (dimensionless). Consequently, the gamma diversity indicator differs between countries due to (i) differences in species richness between ecoregions and (ii) differences in vulnerability of the species occurring in different ecoregions. This does not alter the spatial scale of the indicator but allows for inter-country comparisons regarding country’s contributions to global extinction. See Chaudhary et al. (2015, 2016b) for a more detailed description of the calculation procedure.
6IUCN - International Union for Conservation of Nature.
7Factors are available at an ecoregion or country level and for five taxa. We used the country level factors in our analysis. As our regional classification also includes aggregates composed of several countries, there were cases where we needed to aggregate the supplied loss factors. This was done in compliance with Chaudhary et al.’s (2015) geographical aggregation formula by computing area-weighted loss factors (equation S8).

Consequently, there is, by definition, a high correlation between RWSR-based footprints versus MSA- and RA-based footprints. For this reason, we chose to show the MSA- and RA-based footprints in the main text and the RWSR-based footprints in the supporting information.

### 2.2. Data compilation

#### 2.2.1. Specification of land use classes and derivation of region-specific land use areas

We harmonized the land use categorization from the different data sources to allow for a consistent application of the biodiversity indicators. The land use categories reflect the type (e.g.
cropland) and intensity (e.g. low-input farming) or production system (e.g. reduced impact logging) of the land use. Table A1 (Supplementary information) provides a detailed overview of the 19 different land use classes after harmonization, as well as corresponding nomenclature in the different original sources.

Information on land use served as the link between biodiversity loss and global economic relationships. To derive hectare values for land use differentiated according to our 19 land use categories, we primarily used the country-specific land use data from the Food and Agriculture Organization (FAO) database (FAO, 2017). As the FAO does not provide details about the intensity of cropland or forest land use or stocking densities on pasture; we disaggregated the FAO data according to other data sources. The Supplementary information (Section A2) provides a detailed explanation of the individual steps associated with this data processing. These steps are summarized below.

We used FAO data to derive arable land areas per crop and country. We then distinguished arable land area per production system and crop based on country-specific relative shares. Relative shares differentiate between the production systems ‘irrigated high inputs’, ‘rain-fed high input’, ‘rain-fed low input’ and ‘rain-fed subsistence’ per crop and are based on the Spatial Production Allocation Model (SPAM) (You et al., 2014).

Our pasture land use categories were derived using stocking densities and type of vegetation as the main defining elements. FAO pasture areas were disaggregated using animal density information contained in the Gridded Livestock of the World maps (Robinson et al., 2014) and maps on global biomes (Olson et al., 2001).

For a differentiation between the different forest production systems, ‘plantation forest’, ‘clear-cut forest’, ‘selectively logged forest’ and ‘reduced impact logging (RIL) forest’, we used area shares of these production systems as identified by Arets et al. (2011). As the FAO does not provide explicit area information for urban areas, we chose to use values provided by the ESA Climate Change Initiative (ESA CCI, 2017).

2.2.2. Allocation of region-specific land use areas per land use class to economic sectors

The GTAP databases represent the world economy for a single year, valued in US dollars. They are based on the harmonization of national input-output tables, bilateral trade, macroeconomic and protection data (Narayanan et al., 2015). The databases are typically used to project the effects of economic shocks on the global economy using computable general equilibrium (CGE) analysis; however, the databases can also be transformed into an MRIO table.
We used the GTAP Power Database, which is an extension to the standard GTAP database with more detail in the energy sectors (Peters, 2016).

To construct an MRIO table using the GTAP Power-Database, we followed the methods of Peters et al. (2011). The output was an MRIO table for 2011 with 140 regions (individual countries and aggregate regions) and 68 economic sectors. Compared to other databases (e.g. World Input-Output Database (WIOD) (Timmer et al., 2015), Eora (Lenzen et al., 2012) and Exiobase (Wood et al., 2014)), GTAP provides higher regional detail for all continents and, compared to WIOD and the harmonized Eora, a higher resolution in agricultural sectors (14 sectors in total, including eight crop sectors). Furthermore, the GTAP database is periodically updated and expanded to include more regions and/or more sectors.

The GTAP database provides less regional and sectoral detail than the FAO statistics. Therefore, we aggregated the relevant FAO crop-specific areas to the eight GTAP crop sectors (Supplementary information, Table A3). As GTAP livestock sectors include different types of livestock, pasture areas were allocated to the three livestock sectors using each sector’s share of land value-added. Following the approach by Wilting et al. (2017), we allocated urban areas to final consumers (see Supplementary information Section A2 for further details).

2.3. Footprint analysis and comparison

2.3.1. Biodiversity footprint comparison

We calculated the biodiversity footprints according to Eq. 1. Subsequently, we compared the ranking of the 140 GTAP-regions’ alpha and gamma footprints using spearman rank correlations. A high spearman rank correlation between two biodiversity footprints implies low added value of including these two indicators separately; low correlation shows that the two indicators provide additional regional insights for a biodiversity assessment.

Additionally, testing for correlation between the generic alpha diversity loss factors revealed high correlation between each of the abundance-based alpha diversity loss factors (r = 0.88 for MSA and r = 0.8 for RA) and the species richness-based alpha diversity loss factors (RWSR); correlation between the abundance-based factors is, however, limited (r = 0.62) (compare Supplementary information, Section A4.2). For this reason, we show the results of the MSA- and RA-based footprints in the main text and the RWSR-based footprints in the supporting information.
2.3.2. Prosperity and population density as drivers of biodiversity footprints

We tested the responsiveness of each of the per capita footprints to per capita household expenditure and population density allowing for linear and quadratic terms. The quadratic terms in the regression account for the possibility of a non-linear relationship with expenditure and/or population density and were only included if the linear term of the variable was retained in the final model. Values for 2011 household expenditure (in purchasing power parity (PPP) corrected US dollars) and population were taken from the World Bank World Development Indicators database (World Bank, 2018). The corrected Akaike Information Criterion (AICc) was used to select the best model among all possible combinations (see Section A5).

Following Wilting et al. (2017), we calculated the sensitivity towards changes in expenditure and population density for each biodiversity footprint. The sensitivity was summarized by the relative difference $d$, calculated as:

$$d = \left| \frac{B_1 - B_2}{\frac{B_1 + B_2}{2}} \right|$$

With $B_1$ and $B_2$ corresponding to the biodiversity footprints calculated using the minimum and maximum, respectively, of the explanatory variable of interest and the mean of the remaining explanatory variable in the regression equation.

2.3.3. Uncertainty analysis

To test the variation in our footprint results due to uncertainty in biodiversity loss factors, we conducted a Monte Carlo simulation (10,000 iterations). The uncertainty in the alpha loss factors was reflected by a normal distribution, as derived from Newbold et al. (2016) for RA and RWSR loss and Alkemade et al. (2009) for MSA loss. The uncertainty in the gamma loss factors was reflected by a beta pert distribution, as derived from Chaudhary et al. (2016b). Further details of deriving the uncertainty distributions are described in the Supplementary information, Section A4.4.

2.3.4 Comparison with land footprint

Finally, we tested the added value of biodiversity footprints compared to land footprints (Supplementary information, Section A4.3). Land footprints represent the total amount of land area required for per capita consumption in a country without considering biodiversity loss factors. These were calculated using Eq. 1 without including the biodiversity loss factors.

We compared the biodiversity and land footprint ranking of the 140 GTAP-regions with spearman rank correlation. A high spearman rank correlation between biodiversity and land footprint indicators implies low added value of including biodiversity as a separate indicator, while low correlation shows that biodiversity indicators indeed provide additional regional insights.
3. Results

3.1. Footprints of nations

Alpha diversity-based results showed close regional alignment (Fig. 1). Australia, Botswana, Canada and Russia ranked among the top ten countries, while India, China, Bangladesh had the lowest per capita biodiversity footprints. Note that among the alpha diversity footprints, MSA-based footprints of Uruguay and Paraguay were relatively low compared to RA-based footprints (Fig. 2A). For Kazakhstan the situation was reversed. Compared to loss factors for RA, loss factors for MSA are relatively high for cropland compared to pasture (compare Supplementary information, Table A4). This explains why Kazakhstan, with a relatively high crop consumption, has a relatively high MSA-based biodiversity footprint. The average uncertainty was +/- 20% for MSA footprints, +/- 40% for RA footprints and +/- 16% for RWSR footprints (for country-specific values see Supplementary data, Tables B1-B3).

Contrastingly, the gamma diversity results identified primarily tropical regions, such as Madagascar, the Caribbean and Brazil, as having high per capita footprints (Fig. 1; Fig. 2B, C). Pakistan, Mongolia and Bangladesh were among the countries with the lowest per capita gamma diversity footprints. The average uncertainty was -60 to +85% (for country-specific values see Supplementary data, Tables B4).
Fig. 1. Region-specific differences (in %) in biodiversity footprints per capita compared to the average per capita footprint for (A) mean species abundance loss, (B) relative abundance loss, and (C) vulnerability-weighted global relative species richness loss. PDF = potentially disappeared fraction of species.
3.2. Comparison of biodiversity footprints

Fig. 2 indicates high (Spearman rank) correlations between the alpha diversity footprints ($r_S > 0.93$), while the (Spearman rank) correlation between the gamma and the alpha diversity footprints was relatively low ($r_S < 0.22$). Alpha diversity loss factors do not depend on the regional context, while regional differences are prominent in gamma diversity loss factors. Consequently, we found limited convergence of the gamma diversity footprints with any of the alpha diversity footprints. The same findings were obtained for individual consumption categories (see Supplementary information, Table A7a).
Fig. 2. Pairwise comparison of consumption-based per capita biodiversity footprints (A) relative abundance (RA) and mean species abundance (MSA) footprints, (B) vulnerability-weighted global relative species richness (VGSR) and mean species abundance footprints, (C) vulnerability-weighted global relative species richness and relative abundance footprints. PDF = potentially disappeared fraction of species, $r_S =$ Spearman rank correlation.

3.3. Footprints and trade

Alpha diversity footprints showed high shares of imported biodiversity loss for developed and densely populated regions (e.g. Europe, Japan, South Korea) or regions with natural conditions limiting the potential for agricultural land use (e.g. Saudi Arabia). In contrast, the gamma diversity-based footprints were largely influenced by the initial threat of species’ extinction, as captured by the specific loss factors of the country in question, or the relevance of trade relationships with countries with a high threat level (Fig. 3.; Supplementary data, Tables B1-B4). For instance, the gamma diversity footprints also indicated high imported biodiversity loss shares for countries such as Russia (68% for gamma diversity vs 9% for alpha diversity footprints), the US (71% for gamma diversity vs 33% for alpha diversity footprints) and Canada (88% for gamma diversity vs 24% for alpha diversity footprints).
Fig. 3. Shares of imported biodiversity loss (A) mean species abundance, (B) relative abundance, (C) vulnerability-weighted global relative species richness.
3.4. Footprints, prosperity and population density

Household expenditure and population density explain 52% to 55% of the variance for the alpha diversity footprints and considerably less for the gamma diversity footprints with an explained variance of 5%. The alpha diversity-based footprints showed a distinct positive relationship with household expenditure and negative relationship with population density (Fig. 4). For these relationships, the alpha based footprints were less sensitive to household expenditure \( (d = 1.10-1.37) \) compared to population density \( (d = 1.42-1.50) \). The gamma diversity footprint showed a relatively weak responsiveness to household expenditure \( (d = 0.87) \) and no relationship for population density, as population density was not selected as variable in the best model (Supplementary information, Section A5).
Fig. 4. Partial response plots of per capita biodiversity footprints related to per capita household (HH) expenditure (A) mean species abundance, (B) relative abundance, (C) vulnerability-weighted global relative species richness; and related to population density (D) mean species abundance, (E) relative abundance, (F) vulnerability-weighted global relative species richness.
Relative differences, $d$, were calculated according to equation (3). PDF = potentially disappeared fraction of species.

3.5. Comparison with land footprints

Comparing the alpha diversity footprints with land footprints showed close alignment ($r_S = 0.69 – 0.82$) implying low added value of alpha biodiversity indicators compared to a simple summation of land requirements. There are, however, noteworthy outliers (Supplementary information, Section A4.3). Countries, such as Mongolia and Botswana, have large shares of low-intensity grazing areas and consequently large land footprints. These areas have – according to the definition of the alpha biodiversity loss factors (Supplementary information, Table A4) – no biodiversity impacts. Thus, using a land footprint assessment as a proxy for alpha diversity footprints could overestimate countries’ biodiversity impacts. For gamma footprints we found only a limited relationship to land footprints ($r_S = 0.16$) showing that land footprints cannot be used as a proxy for gamma diversity.

4. Discussion

4.1. Interpretation

Our novel inter-indicator comparison of linking a common land use and MRIO framework with different biodiversity indicators, shows that employing alpha diversity indicators results in a different selection of countries with relatively high biodiversity footprints compared to the gamma diversity indicator. For alpha diversity footprints, regional differences were partly driven by the generic loss factors allocated to different land use types (compare Supporting information, Table A4). For gamma diversity, loss factors are given by region as well as land use types, giving more emphasis to the location of biodiversity loss. The regional component reflects threat levels to global biodiversity, as per the IUCN red list classification (IUCN 2018) (see Supplementary information, Section A7). Compared to a purely land based footprint assessment, biodiversity footprints capture the quality of biodiversity. While there was close alignment between countries’ ranking of alpha footprints and land footprints, the identified outliers showed the additional insights gained from incorporating alpha diversity indicators for some countries. Land footprints treat land areas equally and would thus overestimate the biodiversity impact of countries with large shares of low-intensity grazing areas, such as Mongolia and Botswana. Furthermore, as indicated by our findings, land footprints are not able to serve as a proxy for gamma diversity footprints.

There is close agreement between our alpha diversity-based (particularly MSA) results and those of Wilting et al. (2017), who employed an EEMRIO based on the WIOD economic database to link land use, greenhouse gas (GHG) emissions and MSA. For example, both studies showed
relatively high per capita biodiversity footprints for Australia and Russia, as well as North American and European countries. Wilting et al. (2017) identified food consumption as contributing 50% of global land-related biodiversity loss; we report an aggregated contribution of 59% for the consumption of ‘grains, other crops’, ‘meat, dairy, fish’ and ‘processed foods, beverages, tobacco’ for our MSA-based assessment (see Supplementary information, Table A7a). The land-related biodiversity footprint in Wilting et al. (2017) also includes biodiversity losses from infrastructure and encroachment that are not directly caused by the consumption of food. Furthermore, Wilting et al. (2017) have a limited representation of developing nations, particularly in Africa. Our results show high biodiversity footprints for several African countries (e.g. Botswana, Namibia), illustrating the importance of greater regional detail for comprehensive analysis of consumption-based biodiversity footprints.

Our relatively high per capita biodiversity footprints of Australia, Botswana and Kazakhstan are in line with the analysis of Kitzes et al. (2016). They employed the GTAP database and used the same methodology as Peters et al. (2011) for their MRIO model construction. To assess biodiversity impacts, they related land use impacts to bird loss (measured as 'missing individual birds'). Thus, by focusing on one taxon, they employed a narrower focus of the implications of biodiversity loss, which possibly causes the comparatively low relevance of Europe and Central America in their analysis. Kitzes et al. (2016) also identified food consumption as the largest cause of biodiversity loss and attributed a lesser relevance to sectors with limited connection to land use (such as 'transport, communication' and 'services').

Comparing analyses by Lenzen et al. (2012) and Chaudhary and Kastner (2016) to our gamma diversity results, we find a similar emphasis on losses in tropical biodiversity. Lenzen et al. (2012) used an MRIO model based on the Eora database (Lenzen et al., 2013) and directly linked its sectors to IUCN red-list species, establishing a focus on globally endangered species. Using IUCN species information to reflect global biodiversity impacts is also intrinsic to the gamma indicator used in our analysis. Based on the IUCN data, species extinction threat levels are particularly high in tropical regions. Similar to our findings, Lenzen et al. (2013) identified North American and European countries and Japan as having high imported shares of biodiversity loss; countries in tropical regions with endangered biodiversity, (e.g. Madagascar) were primary exporters of biodiversity loss. Chaudhary and Kastner (2016) did not employ an EEMRIO, but linked land use maps with physical trade data from the FAO and biodiversity loss factors to analyze global biodiversity footprints. Countries in Central America and the Caribbean were shown to have high per capita footprints. They also found high shares of imported biodiversity loss for developed and small countries, such as European countries, Bahrain and Qatar.
The relationship between biodiversity footprints and household expenditure levels and population density observed for our alpha diversity indicators was also found by Wilting et al. (2017). However, in our study, the relationship between gamma diversity footprints and household expenditure was much weaker and the relationship between gamma diversity footprints and population density is not statistically significant. Thus, the strength of the link between the biodiversity loss drivers, household expenditure levels and population density, and biodiversity impacts is influenced by the choice of biodiversity indicator.

4.2. Limitations

By connecting various biodiversity indicators to land use information, we provide a method to calculate consumption-based biodiversity footprints globally. However, this approach also has several limitations and constraints.

Although using the GTAP database allows for a greater level of regional detail, our method does not overcome key weaknesses of using MRIO in biodiversity footprint assessments, namely the high level of geographic aggregation (country-level) and the reliance on monetary flows to capture global dynamics (for further discussion of MRIO weaknesses in the biodiversity context see Kjaer et al. (2015) and Kitzes et al. (2016)). Biodiversity contributes to local life-supporting functions and thus assessment based on country-level aggregation might obscure threats to local ecosystem function.

Furthermore, our assessment is limited to biodiversity loss related to land use. Excluding other drivers, such as climate change, clearly results in an underestimation of biodiversity footprints for consumption categories that are less reliant on land use, such as ‘transport, communication’. For this consumption category, our MSA-based assessment indicates a contribution of 2% to overall biodiversity footprints, whereas Wilting et al. (2017) report a contribution of 11% (47% of which resulted from GHG emissions).

Other constraining factors are that only a limited number of biodiversity indicators have sufficient global coverage to be linked to our calculations and the potential influence of the underlying land use classification scheme on the results. In the present analysis we were restricted to using biodiversity indicators that can be used in global assessments, have a well-documented methodological basis and which employ data that is publicly available. The indicators’ methodology needed to be documented such that it enabled easy aggregation and provided sufficient detail on the definition of the underlying land use categories, to allow for a mapping with our country and land use classification. For land use classification, we faced the challenge of harmonizing aggregate classification schemes (e.g. Chaudhary et al. (2015, 2016a,
2016b) rely on six categories) and relatively disaggregated schemes (Newbold et al. (2016) and Schipper et al. (2016a) that rely on 13 and 16 categories, respectively) to facilitate allocation of physical areas from the FAO without losing information contained in the biodiversity loss factors. Furthermore, the choice of land use areas included in the assessment can influence the list of countries identified as having high biodiversity footprints (see Supplementary information, Section A8 for an extensive analysis). For instance, setting the loss factors connected to the land use category ‘other forest’ to zero, substantially lowered the per capita footprints for several developing countries (e.g. Botswana, Namibia, Zambia) and developed nations (e.g. Finland, Russia, Australia) (Supplementary information, Fig. A12). The (Spearman rank) correlation analysis, however, still showed high correlations between alpha diversity indicators and limited convergence between alpha and gamma diversity indicators (compare Supplementary information, Table A7a and Table A7b).

4.3. Implications – relevance and outlook

Our methodology allows for a comprehensive assessment of the main consumption patterns causing biodiversity loss. We demonstrate that using different biodiversity indicators (alpha vs. gamma) has implications on the countries and regions identified as key contributors to global biodiversity loss. Assessing and mitigating global environmental impacts requires targeted action by producers and changes in consumption patterns (Poore and Nemecek, 2018). Biodiversity footprinting can facilitate decision-makers to assess the implications of behavior change, ranging from changes in diets to shifts towards low impact agricultural production (see Wilting et al. (2017) for an extensive list). By extending these analyses across different dimensions of biodiversity, the scope of results can be broadened. Alpha diversity footprints are particularly linked to ecosystems’ capacity to provide local ecosystem services (Newbold et al., 2015). Gamma diversity footprints compliment alpha diversity footprints, by capturing implications of consumption on, for example, endangered tropical diversity. According to our comparison, no single indicator would have been able to capture both aspects. Comprehensive biodiversity assessment should also include functional or structural aspects of biodiversity (beta diversity) (Balvanera et al., 2014; Isbell et al., 2017; Marques et al., 2018). However, there is currently no indicator capturing these features of biodiversity with a regional and sectoral coverage and connection to land use that could be linked to our EEMRIO framework. The flexibility of our EEMRIO structure allows for a future widening of the scope of analyses, should relevant indicators become available.

Our work also provides the basis for future scenario analyses. With these analyses, public and private sector decision-makers could gain additional insights into the biodiversity implications...
of future global production and consumption patterns – e.g. cross-industry changes in product composition or raw material sourcing strategies, shifts in dietary preferences, conservation activities and changes in policy environments. By employing at least a two-dimensional view on biodiversity, future actions can be designed that safeguard against a loss of diversity with high risks of species extinction (gamma diversity) as well as losses that are relevant for local ecosystem functioning (alpha diversity).
Acknowledgments

We would like to thank Tim Newbold for sharing relevant data used as input information in our analysis and answering important questions about his methodology. We would like to thank Rebecca Chaplin-Kramer for her comments during the drafting of this paper. This work was supported by the European Union’s Horizon 2020 research and innovation program under the Marie Sklodowska-Curie grant agreement No 641456 (RELIEF).

Appendix A. Supplementary information (DOCX file)

Appendix B. Supplementary data (XLS file)


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