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# Quantifying Land Use Impacts on Biodiversity: Combining Species–Area Models and Vulnerability Indicators

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S Supporting Information

ABSTRACT: Habitat degradation and subsequent biodiversity damage often take place far from the place of consumption because of globalization and the increasing level of international trade. Informing consumers and policy makers about the biodiversity impacts "hidden" in the life cycle of imported products is an important step toward achieving sustainable consumption patterns. Spatially explicit methods are needed in life cycle assessment to accurately quantify biodiversity impacts of products and processes. We use the Countryside species–area relationship (SAR) to quantify regional species loss due to land occupation and transformation for five taxa and six land use types in 804 terrestrial ecoregions. Further, we calculate vulnerability scores for each ecoregion based on the fraction of each species' geographic range (endemic richness) hosted by the ecoregion and the IUCN assigned threat level of each species. Vulnerability scores are multiplied with SAR-predicted regional species loss to estimate potential global extinctions per unit of land use. As a case study, we assess the land use biodiversity impacts of 1 kg of bioethanol produced using six different feed stocks in different parts of the world. Results show that the regions with highest biodiversity impacts differed markedly when the vulnerability of species was included.

$$S_i = c_i \left(\sum_{j=1}^{m} h_{i,j} A_j \right)^{z_i}$$

6 land use types · 5 taxa; 804 ecoregions
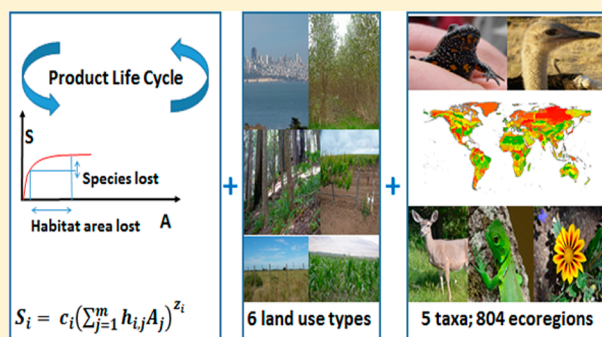
INTRODUCTION

There is an increasing demand for environmental information about the products and services provided in the global market. Life cycle assessment (LCA) is a comprehensive method for assessing environmental impacts caused by products, services, and processes.[1] Although land use is a main driver of global biodiversity loss,[2] methods of quantifying impacts of land use on biodiversity within LCA are still in early stages of development. For forestry- and agriculture-based products, neglecting these impacts can result in significant underestimation of their total environmental impacts. Even simple products like milk can imply globally distributed land use impacts through production of the concentrate feed for cows in various world regions.[3] Also for many products, such as biofuels, LCA studies have traditionally focused on greenhouse gas emissions as the only indicator, while neglecting the impact on biodiversity due to the land use and land use change during the cultivation of feedstock.[4−6]

Biodiversity loss has been studied at different spatial scales (local, regional, and global). While avoiding global species extinctions is important for preserving the evolutionary and genetic diversity of life on earth, preventing local and regional biodiversity loss is also important for long-term, resilient delivery of ecosystems services and thus to human well-being.[7−9]

The estimates of local biodiversity loss are typically obtained from plot-scale biodiversity monitoring surveys comparing diversity metrics (such as species richness or abundance) between the disturbed site (e.g., agricultural and urban land) and the natural, undisturbed habitat (reference site) of the same region.[10−12] Such spatial comparisons assume that human pressures have caused the biodiversity differences between otherwise similar sites.[13] For predicting regional and global biodiversity loss due to land use, the models describing species–area relationships (SARs) have often been employed.[14−17]

The classic SAR model[18] is the model most commonly used to describe species–area curves. It defines species richness as a power function, $S = cA^z$, where S is the number of species, A is the area, and c and z are parameters depending on the taxonomic group and region under study and on the sampling regime and sampling scale, respectively.[19] However, the classic model may fail to capture biodiversity change and has been recently criticized for overestimating[20] or underestimating[21] extinctions. Another limitation is that the classic SAR model assumes that all natural areas converted to human-dominated areas, such as agriculture and forestry, become completely hostile to biodiversity.[22] There is a growing recognition that species often face habitat change instead of habitat loss; i.e., many species are not constrained only to their native habitat, and human-modified habitats (i.e., the

land use matrix) can also play an important role in hosting biodiversity.[23,24] Moreover, the classic SAR model also fails to capture the individual differences in the responses of species to land use changes. As reported in several studies,[25−27] some species are highly sensitive to habitat loss and live in only native habitats, while other species show partial or total tolerance to human-modified habitats; still other species even benefit from the conditions found in human-modified habitats.

Models that account for habitat heterogeneity have been proposed to assess patterns of species richness in multihabitat landscapes. The Matrix SAR model[28] is one such example in which the matrix effects (i.e., the habitat provided by human-modified land) are incorporated into the SAR and account for taxon-specific responses to each component of a heterogeneous landscape. However, the Matrix SAR model predicts 100% species loss if no natural habitat remains within a region, which might be unrealistic for some species. An alternative to the Matrix SAR is the Countryside SAR model,[29] which accounts for the differential use of habitats by species and predicts that species adapted to human-modified habitats also survive in the absence of their natural habitat. Pereira et al.[30] showed that for predicting tropical bird extinctions, the Countryside SAR model outperforms both the Matrix and classic SARs. While the classic SAR has already been used for land use impact assessment within LCA,[31−33] the use of SARs that account for habitat heterogeneity and taxa sensitivity has only recently attracted attention. de Baan et al.[34] proposed a spatially explicit approach to predicting regional species loss of five taxa caused by occupation (land use) and transformation (land use change) in a product's life cycle using the Matrix SAR model.

However, the characterization factors (CFs, i.e., the factors indicating biodiversity damage per unit area of land use) of de Baan et al.[34] suffer from four shortcomings. First, they consider only four broad land use types (managed forests, agriculture, pasture, and urban) and do not differentiate between land use management intensity. Second, the estimates of taxon sensitivity to the converted habitat that were fed into the Matrix SAR model were based on data[35] from before 2009 and thus need to be updated.[34] Third, they applied the Matrix SAR model, which provides unrealistic results (100% species loss) for regions where all natural habitat has been converted. Finally, their approach treats all species equally, whether the species present in an ecoregion are critically threatened or common.

In this paper, we address these four shortcomings and provide an updated impact assessment approach and characterization factors for regional (CF regional) and global biodiversity loss (CF global) using the Countryside SAR. We illustrate the application of the new CFs to estimate the species loss due to agricultural land use associated with the production of 1 kg of bioethanol.

MATERIALS AND METHODS

This section is structured as follows. We first derive expressions for the regional CFs that quantify the regional species loss per unit of land use/land use change using the Countryside SAR. Next, we describe the approach to estimate global species loss (extinctions), i.e., global CFs, by including vulnerability of species along with regional loss. Afterward, we explain the data sources and assumed uncertainty distributions for SAR model input parameters.

Characterization Factors for Regional Species Loss. The Countryside SAR model[30] predicts the number of species lost ($S_{\text{lost},g,j}$) of taxa g due to cumulative land use in region j as

$$S_{\text{lost},g,j,\text{regional}} = S_{\text{org},g,j}\left[1 - \left(\frac{A_{\text{new},j} + \sum_{i=1}^{n} h_{g,i,j}A_{i,j}}{A_{\text{org},j}}\right)^{z_j}\right] \tag{1}$$

where $S_{\text{org},g,j}$ is the original number of species occurring in the natural habitat area ($A_{\text{org},j}$), $A_{\text{new},j}$ is the remaining natural habitat area in the region, $A_{i,j}$ is the current area of land use type i, z_j is the constant from the classic SAR model for the region, and $h_{g,i,j}$ is the affinity of the taxonomic group g for land use type i in region j. While the taxon affinity for the natural habitat is assumed to be equal to 1, $h_{g,i,j}$ for other land use types is calculated as follows:[30]

$$h_{g,i,j} = (1 - \text{CF}_{\text{loc},g,ij})^{1/z_j} \tag{2}$$

where $\text{CF}_{\text{loc},g,ij}$, within LCA, is the local land occupation characterization factor[12] and equals the relative difference between the plot-scale species richness in land use type i ($S_{g,i,j}$) and the natural reference area of the same biogeographic region j ($S_{\text{nat},g,j}$):

$$\text{CF}_{\text{loc},g,ij} = 1 - \frac{S_{g,i,j}}{S_{\text{nat},g,j}} \tag{3}$$

Outside LCA, the term $1 - \text{CF}_{\text{loc},g,ij}$ is better known as the response ratio.[11] $\text{CF}_{\text{loc},i}$ therefore represents the sensitivity[28] of the taxon to a particular land use type i and provides a measure of local species loss.[12,13] If the transformed land use type is completely hostile and cannot host any species of the taxon, the $\text{CF}_{\text{loc},i}$ value equals 1 (i.e., $h_i = 0$), and if the converted land use is as benign as the original habitat, $\text{CF}_{\text{loc},i} = 0$ (see Supporting Information-1 for further details).[12]

While eq 1 calculates the total number of species lost after conversion of the natural pristine habitat to the current land use mix (average assessment), LCA practitioners are mostly interested in the impact caused by one additional square meter of land converted from the current land use mix for the production of a product (marginal assessment). The marginal damage function for SAR models is given by the first derivative of their respective average damage function by the area lost ($A_{\text{lost}} = A_{\text{org}} - A_{\text{new}}$):[34]

$$\frac{\partial S_{\text{lost},g,j}}{\partial A_{\text{lost},g,j}} = \frac{S_{\text{org},g,j}}{A_{\text{org},j}} \times z_j \left(\frac{A_{\text{new},j} + \sum_{i=1}^{n} h_{g,i,j}A_{i,j}}{A_{\text{org},j}}\right)^{z_j - 1} \tag{4}$$

This regional damage is then allocated to the different land use types i according to their relative area share ($p_{i,j}$) in the total converted land area (A_{lost}) and their sensitivity ($\text{CF}_{\text{loc},g,i,j}$). The allocation factor ($a_{i,j}$) is calculated for each land use type i as follows:[34]

$$a_{i,j} = \frac{p_{i,j}\text{CF}_{\text{loc},g,i,j}}{\sum_{i=1}^{n} p_{i,j}\text{CF}_{\text{loc},g,i,j}} \tag{5}$$

The regional land occupation CFs are then calculated as a marginal species loss due to a marginal increase in human used area ($\partial A_{\text{lost},g,j} = 1 m^2$). The unit of CF is regional species lost per square meter.

$$\text{CF}_{\text{regional},\text{occ},g,i,j} = \frac{\partial S_{\text{lost},g,j}a_{i,j}}{\partial A_{\text{lost},g,j}p_{i,j}} \tag{6}$$

Table 1. Uncertainty Distribution of the Model Parameters and Their Sources[a]

model parameter	distribution	data source	details
$CF_{loc,g,i,j}$ (local characterization factor)	nonparametric kernel density	de Baan et al.,[12] Elshout et al.,[44] Aronson et al.[45]	independent variables for each taxon ($n = 5$), biome ($n = 14$), and land use ($n = 6$)
$S_{org,g,j}$ (species richness per ecoregion)	plants, $\sim T(a,b,c)$[b]	Kier et al.[50]	independent variables for each ecoregion ($n = 804$) and taxon ($n = 5$)
	other taxa, no uncertainty	WWF Wildfinder database[51]	
$A_{org,j}$ (original natural habitat area)	$\sim T(a,b,c)$[b]	LADA[52]	$A_{org,j}$, $A_{new,j}$, independent variables for each ecoregion ($n = 804$)
$A_{new,j}$ (remaining natural habitat area)		Ellis and Ramankutty[53]	$A_{i,j}$, independent variables for each land use type ($n = 6$) and ecoregion ($n = 804$)
$A_{i,j}$ (area per land use type)		FAO-FRA[54]	
		FAOSTAT[55]	
z_j (z value)	$\sim T(a,b,c)$[b]	Drakare et al.[56]	independent variables for each habitat type ($n = 3$; islands, forest, and nonforest ecoregions)
$t_{reg,g,i,j}$ (regeneration time)	$\sim \ln(a,b)$[c]	Curran et al.[57]	520 different regeneration times, based on all combinations of realm × biome ($n = 65$), land use intensity ($n = 2$), and taxon ($n = 5$)
$VS_{g,j}$ (vulnerability score)	none	IUCN,[43] Birdlife International[46]	independent variables for each ecoregion ($n = 804$) and taxon ($n = 4$)[d]

[a]See also Supporting Information-1 for data processing details and Excel file Supporting Information-2 for raw data. [b]The term $\sim T(a,b,c)$ denotes the triangular ditribution based on minimum (a), median (b), and maximum (c) values. [c]The term $\sim \ln(a,b)$ denotes a log normally distibuted variable with a mean and standard deviation equal to a and b, respectively. [d]For plants, only regional CFs were calculated, as the data for species range taxon and threat level were not available for calculating the VS and hence the global CFs.

Regional CFs for land transformation are calculated as a multiplication of $CF_{reg,occ,g,i,j}$ with half the regeneration time.[34,36] Here, the unit is regional species lost·year per square meter.

$$CF_{regional,trans,g,i,j} = 0.5 t_{reg,g,i,j} CF_{reg,occ,g,i,j} \quad (7)$$

In LCA, the CF_{occ} terms are multiplied by the inventory flow of occupation, that is, the land requirements of a product given in square meters·year. The CF_{trans} values are multiplied by the inventory flow of transformation, that is, the amount of land use change per product in square meters. The two impacts can be summed to determine the total impacts in units of regional species lost·year for each taxonomic group g.[34,36,37]

The regional CFs were obtained for six land use types ("intensive forestry", "extensive forestry", "annual crops", "permanent crops", "pasture", and "urban"),[38] five taxa (mammals, birds, reptiles, amphibians, and vascular plants), and 804 terrestrial ecoregions.[39] Ecoregions are chosen as spatial units because they contain distinct communities of species, and their boundaries approximate the original extent of natural ecosystems prior to major land use change.[39] Hereafter in this paper, we refer to the new CFs calculated using eqs 1–7 as regional CFs. We also calculated the CFs for the land use types mentioned above using the Matrix SAR to provide an update to the CFs calculated by de Baan et al.[34] using improved input data. The corresponding equations are provided in Supporting Information-1.

Characterization Factors for Global Species Loss. The regional CFs derived in the preceding section (eqs 1–7) give an estimate of regional species loss per unit of land use and land use change. However, if the species are endemic to the ecoregion, their loss will translate into global species loss (extinction). To determine an estimate of the permanent global (irreversible) species loss, the regional CFs for each taxon g per ecoregion j are multiplied by a vulnerability score ($VS_{g,j}$) of that taxon in that ecoregion.

For the VS, we first calculate "endemic richness ($ER_{g,j}$)" of each taxon g per ecoregion j using the definition of Kier et al.[40,41]

by summing the range fractions of all species within the ecoregion:

$$ER_{g,j} = \sum_{k=1}^{m} \frac{GR_{k,g,j}}{GR_{k,g}} \quad (8)$$

where $m = S_{org,g,j}$ is the total number of species of taxa g found within ecoregion j, $GR_{k,g,j}$ (in square kilometers) is the portion of geographic range of species k inside ecoregion j, and $GR_{k,g}$ is the total (global) geographic range of species k (in square kilometers). The endemic richness of a region can be interpreted as the specific contribution of the region to global biodiversity.[41]

Following Verones et al.,[42] we then multiplied the range fraction of each species with its IUCN[43] assigned threat level (TL) to calculate the "threatened endemic richness (TER)" per taxa in each ecoregion. The vulnerability score (VS) is now defined as the ratio of "threatened endemic richness ($TER_{g,j}$)" to total species richness:

$$VS_{g,j} = \frac{TER_{g,j}}{S_{org,g,j}} = \frac{\sum_{k=1}^{m} TL_{k,g} ER_{k,g,j}}{S_{org,g,j}} = \frac{\sum_{k=1}^{m} \frac{TL_{k,g} GR_{k,g,j}}{GR_{k,g}}}{S_{org,g,j}} \quad (9)$$

The CFs giving a measure of global species loss (called global CFs hereafter) are then calculated by simply multiplying regional CFs by the VS of the corresponding taxon and ecoregion:

$$CF_{global,g,i,j} = CF_{regional,g,i,j} VS_{g,j} \quad (10)$$

Note that multiplying VS with regional CF as above is equivalent to replacing the "species richness" ($S_{org,g,j}$) in eq 1 by the threatened endemic richness ($TER_{g,j}$):

$$S_{lost,g,j,global} = TER_{g,j} \left[1 - \left(\frac{A_{new,j} + \sum_{i=1}^{n} h_{g,i,j} A_{i,j}}{A_{org,j}} \right)^{z_j} \right] \quad (11)$$

The ER per ecoregion was obtained from range maps of species available at IUCN,[43] and the TL was obtained by linearly
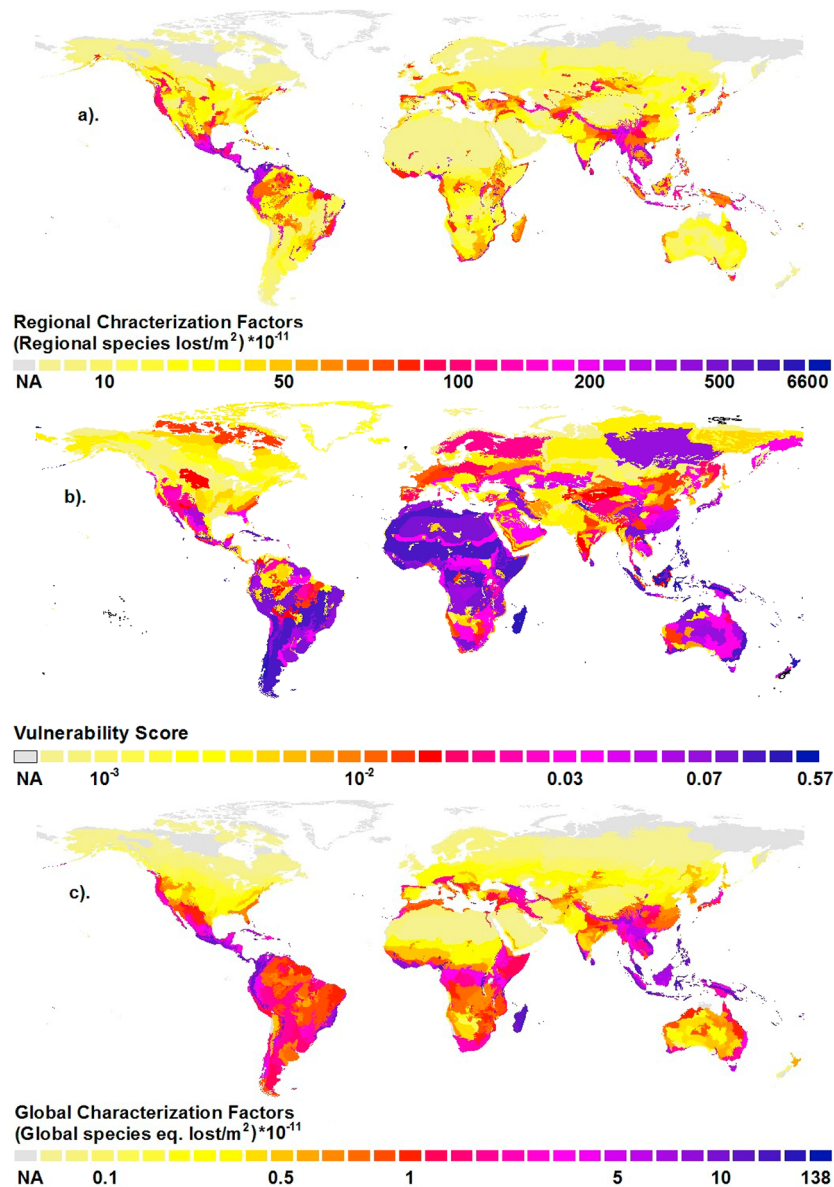
Figure 1. (a) Median regional occupation characterization factors (CFs) per ecoregion for mammals and the land use type "annual crops" calculated using the Countryside SAR from eq 1. (b) Vulnerability scores (VS) of mammals per ecoregion calculated using eq 9. (c) Median global CFs for mammals and the land use type "annual crops" per ecoregion calculated using eq 10. NA means no data available. See Excel file Supporting Information-2 for a full list of CFs and VS.

rescaling the categories defined by the IUCN Red List of threatened species from 0.2 to 1 (least concern, 0.2; near threatened, 0.4; vulnerable, 0.6; endangered, 0.8; and critically endangered, 1). Global CF calculation using a geometric numerical scale for TL is discussed in Supporting Information-1.

The VS value reaches 1 if all species within a region have 100% of their range inside it (i.e., strictly endemic) and are assigned a "critically endangered" category by the IUCN red list. Also, via calculation of the VS according to eq 9, the unit of global CF given by eq 10 is now threatened endemic richness lost per unit of land use/land use change. Hereafter, we refer to it as global species-eq lost. The global CFs thus give a measure of potential global extinctions for product comparison purposes rather than exact species extinction numbers.

Model Input Parameters. Table 1 shows the data sources and the assumed probability distributions of all eight model input parameters.

The CF_{loc} data set was updated with recently published survey studies (see Excel file Supporting Information-2 for raw data used).[44,45] Using ArcGIS version 10.2,[48] we overlaid global land cover maps, LADA[52] and Anthromes[53] (both available at 5 arc minute resolution), with ecoregion shape files to derive the current share of natural habitat ($A_{new,j}$) and each of the six anthropogenic land use types ($A_{i,j}$) per ecoregion j (see Supporting Information-1 and de Baan et al.[34] for processing details). Values of the SAR exponent (z values)[56] and regeneration times[57] were kept the same as those used by de Baan et al.[34] To calculate the vulnerability scores, the geographic range maps for 5386 mammals, 6251 amphibians, 3384 reptiles, and 10104 bird species were obtained from IUCN[43] and Birdlife.[46] As the range maps of individual plant species are not available from IUCN, the global CFs could not be calculated for them.
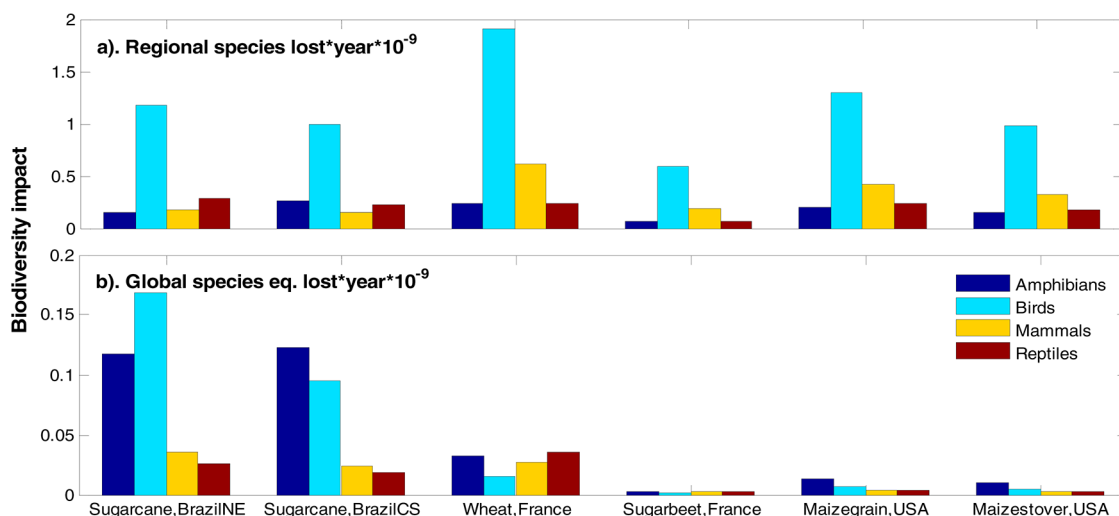
Figure 2. Total biodiversity impact due to land use (occupation and transformation) associated with the feedstock production of 1 kg of bioethanol calculated using (a) regional CFs and (b) global CFs. Land use inventory data are provided in Table S2 and detailed results in Supporting Information-2.

Further, we calculated the country and world average CFs for land use flows of unknown origin and also the CFs aggregated across five taxa (see Supporting Information-1 for equations).[47] Parameter uncertainty was propagated into the CFs using Monte Carlo simulation (1000 iterations), and median values along with 95% confidence intervals were calculated. To assess the influence of each parameter on the uncertainty of the CFs, their contribution to variance (CTV)[34] was calculated (Supporting Information-1). All calculations were performed in MATLAB.[49]

RESULTS

Both regional and global characterization factors (CFs) for land occupation and transformation varied by ~4 orders of magnitude across 804 ecoregions (Excel files Supporting Information-2 and Supporting Information-3). Ecoregions in tropical biomes had in general higher CFs, primarily because of existing species richness per unit area values that were higher than those in temperate and boreal biomes (e.g., Table S3 in Supporting Information-1). Regions that had been heavily converted in the past, i.e., with small remaining natural habitat areas ($A_{new,j}$, eq 1), have CFs generally higher than those of the regions with large shares of undisturbed habitat. Annual crops and urban land use had in general the highest CFs, reflecting the relatively low affinity ($h_{g,i,j}$, eq 2) of species to them as alternative habitats compared to forestry, pasture, or permanent crops. CFs for some land use types in certain ecoregions could not be calculated (displayed as "NaN" in Excel files Supporting Information-2 and Supporting Information-3) because the land use type did not exist in that ecoregion ($p_{i,j} = 0$; eq 5).

For a given taxon, ANOVA and Kruskal–Wallis tests showed that both the regional and global CFs differed significantly across all six land use types but were within 1 order of magnitude for most ecoregions. CFs for a given land use type across five taxa varied by ~2 orders of magnitude. Transformation CFs were ~2 orders of magnitude higher than occupation CFs because the average regeneration time for biodiversity recovery stood at ~350 years (eq 7).[57] Regeneration times were highest for boreal ecoregions followed by temperate ecoregions, while tropical ecoregions had the shortest regeneration times.[57]

With regard to habitat type, island ecoregions had the highest global CFs, followed by forest and then nonforest ecoregions. This is because the island and forest ecoregions have SAR exponents (z values) higher than those of nonforest ecoregions.[56] Also, despite the fact that forest ecoregions had z values marginally higher than those of island ecoregions, we found that global CFs were higher for the latter. This is because island ecoregions host relatively more range-restricted (endemic) and threatened species, resulting in high vulnerability scores (VS, eq 9) compared to those of both forest and nonforest ecoregions (see also Table S4 and Figure S1).

The relative order of CFs differed significantly depending upon whether regional or global extinctions are considered (Figure 1). For example, the island ecoregion "Sao Tome and Principe moist lowland forests (ecocode AT0127)" in West Africa has the second highest global CF among all 804 ecoregions for mammals (1.38×10^{-9} species equivalents lost per square meter of land occupation) and for the land use type "annual crops" (Excel file Supporting Information-2). However, it ranks 85th on the corresponding list for regional CFs. On the other hand, the forest ecoregion "Chimalapas montane forests (NT0114)" in Mexico ranks 253rd on the global CF list of mammals and annual crops but second for regional CFs. This is because the VS of mammals in the Sao Tome ecoregion is 0.23 as compared to 0.0004 for the Chimalapas ecoregion. Three of the 10 total mammal species found in the Sao Tome ecoregion are strictly endemic to it and are found nowhere else (and hence have a high VS and global CF).[51] On the other hand, each of the 145 mammal species found in Chimalapas montane forests has only a small fraction of their range inside that ecoregion. The endemic richness (ER) and threatened endemic richness (TER) of this ecoregion are therefore 0.26 and 0.06, respectively, thus leading to its low VS and global CF.

The regional CFs for each land use type were in general highest for most species rich taxa plants, followed by birds, mammals, and amphibians, and lowest for reptiles, which had low species richness per ecoregion ($S_{org,g,j}$, eq 1). However, the relative order changed for global CF, as can be illustrated in the case of the island ecoregion "Halmahera rain forests (AA0106)" in Indonesia. This ecoregion hosts 50 mammal species, of which 7 are endemic and 15 amphibian species of which 6 are endemic.[51] The calculated VS for amphibians (0.32) in this ecoregion is therefore much higher than that for mammals (0.05). Consequently, while the regional CFs for mammals are

∼3 times higher than for amphibians, the global CFs turned out to be higher for amphibians by a factor of ∼2.

Additional Analyses. The regional and global CFs calculated using the Matrix SAR model are presented in Excel file Supporting Information-3. For all of the ecoregions in which the natural habitat accounts for >18% of total land area (eq 1; A_{new}/A_{org} > 0.18), the Countryside model predicted greater biodiversity damage. On the other hand, CFs from the matrix SAR were generally a factor of ∼2 higher than those from the Countryside SAR in ecoregions that have <10% of the natural habitat remaining (i.e., A_{new}/A_{org} < 0.1).

Global CFs were also calculated using an alternative geometric numerical scale for TL, which draws a strong contrast between successive threat categories (see Supporting Information-1). The correlations between CFs from linear and geometric scales were high for mammals and birds ($\rho \sim 0.90$) and moderate for amphibians and reptiles ($\rho = 0.60-0.80$).

Application Example. The projected increase in global biofuel production has raised concerns about increased land use pressure and associated biodiversity loss.[58,59] The newly calculated CFs in this study were used to assess the global species loss due to land use flows associated with the cultivation of six different feedstocks for the production of 1 kg of bioethanol in different world regions. The land use inventory data were taken from ref 59. The methods are described in further detail in Supporting Information-1.

Figure 2b shows that for amphibians, birds, and mammals, the global CFs predicted highest species equivalent loss from sugar cane production in Brazil's northeast (NE) region. For reptiles, wheat production in France caused the greatest species loss. Sugar beet production in France as well as maize grain and maize stover production in the United States resulted in lower species loss in general because of the absence of land transformation and relatively low land occupation requirements per functional unit (see Table S2). Although land requirements for sugar cane in Brazil and wheat in France were similar, impacts in Brazil were greater because of the high global CFs of its ecoregions.

As shown in Figure 2a, the regional CFs predicted a different order of impacts, with wheat production in France causing the greatest species loss for birds and mammals. The difference in regional and global CF results is caused by the relatively high vulnerability scores of species in Brazilian ecoregions compared to those in France and the United States. Similarly, the taxa-aggregated regional CFs predicted wheat from France to be most damaging, but the global aggregated CFs showed that sugar cane from Brazil causes a higher fraction of species to disappear (Supporting Information-2).

■ DISCUSSION

Methodological Approach. This study is the first to derive characterization factors (CFs) for global scale, land use impact assessment using the countryside SAR model, which has been shown to perform better in predicting species extinction than the classic or Matrix SAR model.[30] Previous studies have applied the Countryside SAR for specific world regions only.[16,17,30] We collected the empirical data for model parameters from the latest published literature to allow the calculation of land use type and taxon-specific CFs for 804 terrestrial ecoregions. The study also provides, for the first time, vulnerability scores (VS) for each ecoregion per taxon using species-specific threat level and geographic range data. Combining the SAR model with VS allowed the quantification of potential global extinction of species due to land use. The study marks a significant

improvement over existing land use biodiversity impact assessment methods within LCA, which previously relied on local or regional species loss metrics.[12,31,60]

Earlier approaches in land use impact assessment within LCA have also proposed to include vulnerability indicators at different levels. Weidema and Lindeijer[61] based their ecosystem vulnerability on the remaining natural habitat of an ecosystem. Michelsen[62] proposed translating the conservation status of an ecoregion given by WWF[51] into a three-grade ordinal scale into a numerical scale (values of 0.1 for intact ecoregions, 0.5 for vulnerable ones, and 1.0 for critical ones). Mueller et al.[63] proposed to use three indices to quantify the biodiversity value of each ecoregion—total species richness, the total number of strict endemics, and the conservation risk index, i.e., the ratio of already converted area to protected area in an ecoregion.[64] However, none of these authors considered the threat status and global habitat range of individual species inhabiting a region.

In this study, vulnerability is considered at two levels: the ecosystem level and the species level. The SAR model includes aspects of ecosystem vulnerability (i.e., how much an ecosystem is already affected by land use pressures), and the VS account for the vulnerability of species inhabiting an ecoregion. We defined the vulnerability of an ecoregion as the ratio of the total threatened endemic richness (TER) to the total species richness it hosts (eq 9). The endemic richness[41] part of the TER ensures that the global CFs are higher for ecoregions hosting biodiversity that is unique and endemic to them and is found nowhere else. Conversely, global CFs are lower for the ecoregions that contain only tiny fractions of species' range (mostly range edges). The threat level (TL) part of the VS then further accounts for the species facing higher extinction risk due to factors other than their endemism or small range (e.g., low and decreasing population).[65] Incorporating TL into the VS implicitly assumes that any land use or land use change will create additional pressure and negatively affect the species that are already listed as threatened by IUCN. For two ecoregions hosting equal endemic richness, the global CFs will be higher for ecoregions containing more threatened species than for those containing non-threatened species. Recently, Waldron et al.[66] also used TER to rank different countries according to the mammal biodiversity they host. Instead of TER, they called it the threatened global biodiversity fraction. Other researchers have used the number of strict endemics (the species that have 100% of their range inside a region) as an input to the SAR model to calculate the global extinctions.[28,67]

Global CFs calculated by combining the SAR model with VS give particular weight to impacts on range-restricted and threatened species that are near extinction and whose loss can result in permanent loss of unique evolutionary history associated with them. Global CFs therefore can help trace products with high land use impacts on species that require immediate conservation attention.

The results showed that CF rankings changed significantly depending upon whether regional or global species loss is considered. The use of threatened endemic richness as an input to the SAR resulted in different ecoregion rankings than when using total species richness. Previous researchers have also pointed out that different hotspots of biodiversity emerge depending upon the metric used (i.e., hotspots of endemism, species richness, and extinction threat rarely coincide).[68,69] The bioethanol case study also highlighted the discrepancy between the results obtained using regional and global CFs and the implications for product comparison purposes. Not considering

the vulnerability of species can therefore lead to environmentally undesirable products being rated as better than relatively benign ones.

The relative order of CFs also differed remarkably depending upon the taxa considered. For example, the ecoregion "Socotra Island Xeric Shrublands (ecocode AT1318)" in Yemen has the highest global CF among all 804 ecoregions for land use type annual crops and reptiles. Nineteen of 28 reptile species found there are strictly endemic to it. However, this ecoregion contains no amphibians and ranks 624th and 30th in the corresponding global CF list of mammals and birds, respectively. The results thus highlight the noncongruence of hotspots defined by different taxa, a fact also found by previous researchers.[68] Therefore, land use biodiversity impact assessment must include multiple taxa to understand the overall magnitude of damage.[70]

Comparison of Matrix and Countryside SAR CFs shows that Matrix SAR predicts smaller species loss for ecoregions with considerable intact natural forests (Supporting Information-3). For ecoregions with negligible remaining natural forests, Matrix SAR predicts that all species are lost (eq S3 in Supporting Information-1). This is unrealistic for many species that also survive in disturbed habitats. The Countryside SAR accounts for this scenario and predicts that some species still survive even after the natural forest area in a region is completely gone ($S_{lost} \neq S_{org}$ when $A_{new} = 0$; eq 1), as long as the remaining land use types offer some habitat quality (i.e., $h_{g,i,j} \neq 0$). With regard to the issue of converting IUCN categories to a numerical scale, both the linear and geometric scales have their pros and cons, and more research is needed in the future to validate and choose the appropriate scale (see Supporting Information-1 for further discussion).

The use of SAR-based methods to quantify biodiversity loss is not without limitations. One of them, as pointed out by Fattorini and Borges,[21] is that SARs do not take into account the "indirect biodiversity impacts" caused by habitat loss or degradation and therefore might underestimate actual land use impacts. For example, the number of roads and trails associated with forest management increases a forest's accessibility to hunters, which in turn leads to further intensification of species loss. Methods to incorporate such impacts by adjusting the z value of SAR have started to appear only recently.[17]

Input Parameters, Data Availability, and Uncertainty. Although using the latest published data for input parameters, the characterization factors (CFs) still have considerable uncertainty and range from positive to negative (i.e., beneficial impact on biodiversity). The contribution to variance analysis (Tables S5 and S6) revealed that the parameter dominating the uncertainty of the CFs was the local CFs (CF$_{loc}$).

CF$_{loc}$ values per taxon, region, and land use type were compiled from the studies comparing biodiversity in human-modified land with natural/undisturbed land. Such data were not available uniformly across the globe, and therefore, the CF$_{loc}$ of a taxon for a particular land use type had to be aggregated across larger spatial units (e.g., biomes or globally). Although we considerably expanded the CF$_{loc}$ data set in this study, more data about region-specific taxon sensitivity to different land use types are needed to reduce uncertainties. Data for amphibians and reptiles were less complete than for plants, mammals, and birds. As new data on these or additional species groups emerge, the presented CFs should be updated. With regard to biomes, tropical and temperate broadleaf forests, boreal forests/taiga, and montane grasslands were relatively well studied. All other biomes should become a global priority in conducting biodiversity surveys for different land use types.

Area parameters (A_{new} and A_{ij}) also contributed to the uncertainty of CFs. We could calculate the area share of only six land use types per ecoregion. These six classes are still a broad classification, and each of them contains a range of management intensity levels. For a particular land use type, different management practices result in different biodiversity impacts as shown by Mueller et al.[63] for agriculture (organic vs conventional), Gibson et al.[10] for forestry (selective logging vs clearcut), and Aronson et al.[45] for urban areas (dense urban vs vegetated urban). Therefore, more detailed global land use classification maps differentiating between management practices are needed to calculate more accurate CFs.

Taxonomic Coverage. Because of the lack of species richness and geographic range data in the WWF[51] and IUCN[43] databases, characterization factors (CFs) for other species groups, such as arthropods, could not be calculated. Arthropods make up an estimated 65% of the total global species richness and perform several important ecological functions, such as pollination.[71] Similarly, species groups such as bacteria and fungi (7 and 11% of global species richness, respectively) that fulfill critical ecosystem functions could not be included in the analysis because of a lack of necessary input data for models. Mora et al.[72] predicted that some 86% of the approximately 7 million terrestrial species on the earth have not yet been described. There are concerns that we might be losing species even before they are discovered[73] (the so-called Linnean extinction).[74] Significant efforts in exploration and taxonomy are required to fill the gaps in our knowledge of life on earth.[72]

Alternative Indicators for Biodiversity Damage. In this study, relative species richness was chosen as a measure of the local response of taxa to land use change. It was used to calculate the SAR model parameter h_i (eq 2). However, relative species richness provides information about only a small aspect of biodiversity, and the biodiversity damage caused by the complex changes in abundance, composition, and community structure that can take place following land use change remains unaccounted for.[75] The indicators that compare exclusively the composition or abundance of species between a reference and land use situation, e.g., Sørensen's similarity index[76] and mean species abundance,[35] are found to be more sensitive to land use impacts than species richness.[12] Therefore, our results could underestimate the impact of land use on native biodiversity. However, these indicators require data that are rarely reported on a global scale.

Application. Apart from conservation efforts such as setting aside land areas, environmentally conscious decisions by producers and consumers can go a long way in halting biodiversity decline and meet international targets.[77] Schemes such as the United Kingdom's Carbon Reduction Label, which requires quantification of a product's full carbon footprint, can be extended to include its biodiversity impacts, as well.[78] This study is a step in this direction and aims to allow quantification of such impacts both within and outside the LCA framework. The new CFs can be used by decision makers to quantify, compare, and potentially reduce the biodiversity footprint of products with complex supply chains and globally distributed land use flows.

■ ASSOCIATED CONTENT

Ⓢ Supporting Information

The Supporting Information is available free of charge on the ACS Publications website at DOI: 10.1021/acs.est.5b02507.

Additional methods and results (PDF)

Raw data used and the CFs from the Countryside SAR (XLSX)

Matrix SAR CFs (XLSX)

Country-specific CFs (XLSX)

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Notes

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