

Land use impacts on biodiversity in LCA: a global approach

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Abstract

Purpose Land use is a main driver of global biodiversity loss and its environmental relevance is widely recognized in research on life cycle assessment (LCA). The inherent spatial heterogeneity of biodiversity and its non-uniform response to land use requires a regionalized assessment, whereas many LCA applications with globally distributed value chains require a global scale. This paper presents a first approach to quantify land use impacts on biodiversity across different world regions and highlights uncertainties and research needs. **Methods** The study is based on the United Nations Environment Programme (UNEP)/Society of Environmental Toxicology and Chemistry (SETAC) land use assessment framework and focuses on occupation impacts, quantified as a biodiversity damage potential (BDP). Species richness of

different land use types was compared to a (semi-)natural regional reference situation to calculate relative changes in species richness. Data on multiple species groups were derived from a global quantitative literature review and national biodiversity monitoring data from Switzerland. Differences across land use types, biogeographic regions (i.e., biomes), species groups and data source were statistically analyzed. For a data subset from the biome (sub-)tropical moist broadleaf forest, different species-based biodiversity indicators were calculated and the results compared.

Results and discussion An overall negative land use impact was found for all analyzed land use types, but results varied considerably. Different land use impacts across biogeographic regions and taxonomic groups explained some of the variability. The choice of indicator also strongly influenced the results. Relative species richness was less sensitive to land use than indicators that considered similarity of species of the reference and the land use situation. Possible sources of uncertainty, such as choice of indicators and taxonomic groups, land use classification and regionalization are critically discussed and further improvements are suggested. Data on land use impacts were very unevenly distributed across the globe and considerable knowledge gaps on cause–effect chains remain.

Conclusions The presented approach allows for a first rough quantification of land use impact on biodiversity in LCA on a global scale. As biodiversity is inherently heterogeneous and data availability is limited, uncertainty of the results is considerable. The presented characterization factors for BDP can approximate land use impacts on biodiversity in LCA studies that are not intended to directly support decision-making on land management practices. For such studies, more detailed and site-dependent assessments are required. To assess overall land use impacts, transformation impacts should additionally be quantified. Therefore, more accurate and regionalized data on regeneration times of ecosystems are needed.

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1 Introduction

During the last decades, global biodiversity loss has become a major environmental concern. One of the main drivers of current and projected future biodiversity loss is habitat change or land use (Alkemade et al. 2009; Millennium Ecosystem Assessment 2005; Pereira et al. 2010; Sala et al. 2000). Within research on life cycle impact assessment (LCIA), attempts have been made to quantify the impacts of land use and other important drivers of biodiversity loss, such as climate change and pollution (for a review, see Curran et al. 2011). Several approaches on how to quantify land use-related biodiversity impacts have been proposed (Achten et al. 2008; Geyer et al. 2010; Kyläkorpi et al. 2005; Koellner 2000; Koellner et al. 2004; Koellner and Scholz 2007; Lindeijer 2000a, b; Michelsen 2008; Müller-Wenk 1998; Penman et al. 2010; Schenck 2001; Schmidt 2008; De Schryver et al. 2010; van der Voet 2001; Vogtlander et al. 2004; Weidema and Lindeijer 2001), of which some have been operationalized in life cycle assessment (LCA) software for broad use by LCA practitioners (e.g., Goedkoop and Spriensma 1999; Goedkoop et al. 2008).

Although the environmental relevance of assessing land use impacts on biodiversity in LCIA is widely recognized, the task remains difficult. Biodiversity is a complex and multifaceted concept, involving several hierarchical levels (i.e., genes, species, ecosystems), biological attributes (i.e., composition, structure, function; Noss 1990) and a multitude of temporal and spatial dynamics (see, e.g., Rosenzweig 1995). Biodiversity assessments therefore have to simplify this complexity into a few facets, which are quantifiable with current knowledge and data. Existing land use LCIA methods were mainly developed for one specific region (often Europe) using species richness of vascular plants as an indicator (e.g., Koellner and Scholz 2008; De Schryver et al. 2010). Weidema and Lindeijer (2001) proposed a first approach to assess land use impacts on biodiversity on a global scale, quantifying the biodiversity value of reference habitat of different biomes based on vascular plant species richness, ecosystem scarcity, and ecosystem vulnerability. However, the reduction of the biodiversity value of different land use types was estimated based on assumption by the authors and was not supported by empirical data (see Weidema and Lindeijer 2001, p. 37). To quantify land use impacts across global value chains more accurately, a regionalized global method is needed, based on a broader taxonomic coverage. This is required due to the spatial heterogeneity of biodiversity and due to the non-uniform and variable reactions of ecosystems and species to disturbances such as land use. Although plants are important components of terrestrial

ecosystems, they only make up an estimated 2 % of all species (Heywood and Watson 1995) and their reaction to land use is not necessarily representative for the impacts on other species groups.

In this paper, we propose a first approach to quantify biodiversity impacts in LCIA in different world regions based on empirical data, focusing on the facet of species composition. We illustrate how global quantitative analysis of peer-reviewed biodiversity surveys can be combined with national biodiversity monitoring data to assess land use impacts across multiple taxonomic groups and world regions, using a set of species-based biodiversity indicators. The indicator relative species richness is used to calculate characterization factors for occupation impacts of terrestrial ecosystems expressed as a biodiversity damage potential (BDP).

2 Methods

This study is based on the framework for LCIA of land use, developed by the United Nations Environment Programme (UNEP)/Society of Environmental Toxicology and Chemistry (SETAC) Life Cycle Initiative working group (LULCIA; Milà i Canals et al. 2007; Koellner et al. 2012b), which distinguishes three types of land use impacts: transformation impacts (caused by land use change), occupation impacts (occurring during the land use activity), and permanent impacts (i.e., irreversible impacts on ecosystems, which occur when an ecosystem cannot fully recover after disturbance). For calculating transformation and permanent impacts, reliable data on regeneration success and times of the world's ecosystems is required, which was not available for this study. Therefore, we only focused on occupation impacts and, for modeling purpose, neglected the temporal dynamics of biodiversity by assuming that we can assign a constant "biodiversity score" to occupied land (i.e., no reduction in biodiversity over time) and to a (semi)-natural reference habitat. The impact of land use on biodiversity was assessed by comparing the *relative* difference of biodiversity of a land use *i* with a (semi)-natural reference situation. Spatial aspects were considered by using a site-specific reference situation and by calculating impacts per biogeographic region. As proposed in Koellner et al. (2012a) biomes defined by the World Wide Fund for Nature (WWF; see Olson et al. 2001) were used as spatial unit for biogeographic differentiation, which represent the world's 14 major terrestrial habitat types. Land use was classified based on the UNEP/SETAC LULCIA proposal (Koellner et al. 2012a).

2.1 Calculation of characterization factors

Characterization factors of occupation impacts, CF_{Occ} , were calculated according to the UNEP/SETAC framework (Milà i Canals et al. 2007; Koellner et al. 2012b), which is

graphically illustrated in Fig. 1 of the Electronic supplementary material (ESM). CF_{Occ} are given as the difference between the ecosystem quality of a reference situation (*ref*, defined as 100 % = 1) and a land use type LU_i per region j . In this study, ecosystem quality was expressed as biodiversity, measured as relative species richness (S_{rel} ; see Section 2.4).

$$CF_{Occ,LU_{ij}} = S_{rel,ref,j} - S_{rel,LU_{ij}} = 1 - S_{rel,LU_{ij}} \quad (1)$$

The numerical value of CF_{Occ} is normally between 0 and +1 (representing a damaging impact on biodiversity), but negative values are also possible (denoting a beneficial impact). To calculate impact scores for land use occupation, CF_{Occ} is multiplied by the land use occupation flows from a life cycle inventory (given as time t_{Occ} and area A_{Occ} required for a certain land use activity).

$$\text{Occupation impact} = (A_{Occ} \times t_{Occ}) \times CF_{Occ} \quad (2)$$

Transformation impacts scores are calculated accordingly (Eq. (3)). Here, the inventory flow is given as a transformed area A_{Trans} and the characterization factor CF_{Trans} is calculated based on Eq. (4), with t_{reg} being the time required for an ecosystem to recover after a disturbance.

$$\text{Transformation impact} = A_{Trans} \times CF_{Trans} \quad (3)$$

$$CF_{Trans,LU_{ij}} = 0.5 \times (S_{rel,ref,j} - S_{rel,LU_{ij}}) \times t_{reg,LU_{ij}} \\ = 0.5 \times CF_{Occ,LU_{ij}} \times t_{reg,LU_{ij}} \quad (4)$$

As no reliable data on region and land use type-specific regeneration times of biodiversity t_{reg} was available for different world regions, CF_{Trans} were not calculated in this study.

2.2 Reference situation

Ecosystems and biodiversity are changing over time due not only to population, succession, and evolutionary dynamics, but also due to intended and unintended human impacts. To quantify land use impacts on biodiversity on a global scale, a temporal baseline or reference situation for biodiversity has to be defined, which lies either in the past, present, or future. Any choice of such a temporal reference involves different degrees of human impacts for different world regions, as the human land use history varies from region to region (see, e.g., Ramankutty and Foley 1999). Here, we chose the current, late-succession habitat stages as reference, which are widely used as target for restoration ecology and serve as a proxy for the Potential Natural Vegetation, i.e., hypothetical *future* ecosystems that would develop if all human activities would be removed at once (Chiarucci et al. 2010). Such late-succession habitat stages experienced

different degrees of natural or human disturbances in the past. In many tropical world regions, the past human influence was low, so the chosen reference is, to a large extent, undisturbed by humans; whereas in many temperate regions, few or no undisturbed habitat exists. In Europe, for example, forests currently cover 35 % of the surface (SOER Synthesis 2010), whereas the natural post-glacial forest cover (i.e., without human land use) is estimated to be 80–90 % (Stanners and Philippe 1995). Of the remaining forest area, only 5 % is considered as undisturbed forest (SOER Synthesis 2010). Thus, as the reference habitats chosen in this study do not necessarily represent prehuman, natural habitats, we use the term “(semi)-natural” to refer to the reference situation. More details on the data used for quantifying biodiversity of the reference habitat is given in the next section.

2.3 Data sources

Two data sources were combined in this study to quantify biodiversity of different land use types and reference situations for different world regions: the GLOBIO3 database, which is based on a quantitative review of literature (Alkemade et al. 2009), and national biodiversity monitoring data of Switzerland (BDM 2004). The *GLOBIO3 database* was compiled for the GLOBIO3 model, which aims at assessing impacts of multiple drivers of biodiversity loss at regional and global scales (Alkemade et al. 2009). The database contains datasets extracted from peer-reviewed empirical studies that compare biodiversity of different land use types with an undisturbed or little disturbed reference situation within the same study site. Depending on data provided in each study, the impact of land use is recorded as relative change in species richness or abundance of a range of different taxonomic groups. For each study, we additionally extracted the geographical coordinates of the study site to assign it to the corresponding WWF biome and ecoregion. A total of 195 publications providing 644 data points on different land use types and 254 data points on reference situations from a total of nine out of 14 biomes were included here, but the data was unevenly distributed. Due to publication bias and lack of undisturbed reference habitats in regions with long and intense human land use history, the database contains many studies conducted in tropical regions and less data in temperate and none in boreal zones (for geographical distribution of data, see ESM Fig. 2 and Table 1). We therefore complemented our analysis with *National Biodiversity Monitoring Data of Switzerland* (BDM 2004) used in earlier land use LCIA methods (Koellner and Scholz 2008). The used BDM indicator “species diversity in habitats (Z9)” is based on a grid of 1,600 sampling points evenly distributed over Switzerland, covering two biomes (temperate broadleaf and mixed forests and temperate coniferous forests). In each of the 10 m² sampling points, species richness

of vascular plants, moss, and mollusks and the corresponding land use type are recorded. To make this dataset comparable to the GLOBIO3 data, we first reclassified the land use type of each sampling point based on Koellner and Scholz (2008) into broader land use classes (see ESM Table 6). We then grouped all sampling points into ecologically similar regions to define regional (semi-)natural reference situations. We split the ten biogeographic regions of Switzerland defined in BDM (2004) into three altitudinal zones (colline, below 800 m asl; montane, 800–1,300 m; subalpine, 1,300–2,000 m; see Baltisberger 2009) and excluded the high-elevation plots (alpine and nival, above 2,000 m). This resulted in 26 regions j across Switzerland, as not all altitudinal zones occur in every biogeographic region. For each of the 26 regions and for each of the three sampled species groups, the average species richness of all sampling points per land use type was calculated, resulting in totally 186 averaged data points for different land use types (see also ESM Table 1). All sampling points in (semi-)natural habitats (forests, grasslands, wetlands, bare areas, and water bodies) were assigned as regional reference situation (for more details, see ESM Table 6). As for the land use types, the average species richness per region and species group was calculated for the reference, resulting in 72 data points for the reference. To test the sensitivity of choice of reference situations, results were recalculated using an alternative reference habitat containing only forest sampling points.

2.4 Indicator selection and calculation

As a primary indicator for biodiversity impacts, we chose *relative* changes in observed species richness S_{rel} between a (semi-)natural reference and a specific land use type i . For each taxonomic group g and region j , the species richness of each land use type i , S_{LU_i} was divided by the species richness of the reference situation (S_{ref}) (Eq. (5)). For the BDM dataset, the regionally averaged species richness of

the land use types and the reference were used for calculating the relative species richness.

$$S_{rel,LU_i,j,g} = \frac{S_{LU_i,j,g}}{S_{ref,j,g}} \quad (5)$$

The selected indicator species richness is a simple and widely applied indicator recording the number of species in a habitat (also referred to as α -diversity or within habitat diversity; Hayek and Buzas 2010) and data availability is rather high compared to other biodiversity indicators. The disadvantage of using species richness as a proxy for biodiversity is that it only contains limited information on the many facets of biodiversity. It only records the presence or absence of species within a sampling area and gives equal weight to all species recorded in a sample, no matter how abundant or biologically distinct they are (i.e., 10 individuals of an endemic species and one individual of an invasive species are both recorded as one species). Species richness neither provides information on between-habitat diversity, i.e., species turnover or β -diversity (see Koellner et al. 2004). This indicator is in addition affected by undersampling: the species richness of an ecosystem is often underestimated as the number of species recorded highly depends on sampling efforts.

Besides species richness, a wide range of diversity measures have been developed, each quantifying other aspects of biodiversity (see, e.g., Hayek and Buzas 2010; Purvis and Hector 2000). To analyze the influence of choice of indicator on the results, we calculated four additional, commonly used species-based biodiversity indicators: Fisher's α , Shannon's entropy H , Sørensen's S_s , and mean species abundance of original species (MSA; see formulas in Table 1). Fisher's α (1943) is an indicator that corrects for incomplete sampling: it estimates "true" species richness from a sample, fitting the observed values of species richness (S_{obs}) and total number of individuals (N_{obs}) to a theoretical (empirically derived) relationship between "true" species richness S and "true" number of

Table 1 Biodiversity indicators calculated for a subset of studies from the biome (sub-)tropical moist broadleaf forest

Indicator type	Name and reference	Data requirement	Formula
Alpha diversity	Species richness S^a	Species numbers	n.a.
Sampling corrected alpha diversity	Fisher's α (Fisher et al. 1943) ^a	Species numbers and total number of individuals	$\frac{N}{S} = \frac{(e^{\frac{S}{\alpha}} - 1)}{\frac{S}{\alpha}}$
Diversity measure	Shannon's entropy H (Shannon 1948) ^a	List of species and their relative abundance	$H = - \sum p_k \times \ln p_k$
Abundance measure	Mean species abundance of original species (MSA) (Alkemade et al. 2009)	List of species, original species and their relative abundance	$MSA = \frac{1}{S_{ref}} \sum_k \frac{n_{k,LU_i}}{n_{k,ref}}$, for all species $k \in ref^b$
Dissimilarity measure	Sørensen's S_s (Sørensen 1948)	List of species	$S_s = \frac{2c}{S_{LU_i} + S_{ref}}$

LU_i land use type i , ref (semi-)natural reference, S number of species, c number of shared species between two land use types, N total number of individuals, n_k number of individuals of species k , $p_k = n_k/N =$ relative abundance of species k

^a The presented formulas are for calculating the *absolute* indicator values. *Relative* values are derived from Eq. (5)

^b If abundance in land use type i was higher than in the reference habitat, MSA values were truncated at 1 (see Alkemade et al. 2009)

individuals N . Shannon's entropy H (1948) combines information on species abundance and richness in one number and reaches a maximum when all species occurring in a sample are equally abundant. Sørensen's S_s (1948) and MSA (Alkemade et al. 2009) both compare the species composition of two samples (here, the reference and land use type i). Sørensen's S_s reports how many reference-habitat species occur in the land use type i and reaches a maximum value of 1 if all of them occur in the land use type i and a minimum value of 0 if none of the reference-habitat species occur in the land use type i . MSA, which has been developed for the GLOBIO3 model (Alkemade et al. 2009), assesses changes in abundance of each reference-habitat species and thus reports changes in species composition earlier than Sørensen's S_s , which only indicates a complete absence of a species from a site.

Besides the number of species S , these indicators all require additional information such as species identity (i.e., checklist of species present) and/or abundance (number of individual organisms n_k , per species k or total individual organisms N per sample). This additional information complicates the process of data collection and was only available in parts of the studies in the GLOBIO3 database. We therefore performed this indicator comparison with a subset of the data: we chose all those studies from the biome (sub)tropical moist broadleaf forest (i.e., "tropical rain forest") in which a full species list indicating the abundance of each species in different land use types and a (semi-)natural reference was provided. The species abundance lists of these studies were extracted to Microsoft Excel to calculate the selected biodiversity indicators (see Table 1). Two indicators (MSA and S_s) directly calculate the relative change between a land use type i and a reference, for the other three indicators (species richness, Shannon's H , and Fisher's α), the relative values per land use type LU_i and taxonomic group g within each study j were calculated as follows:

$$I_{\text{rel}, LU_{i,j,g}} = \frac{I_{LU_{i,j,g}}}{I_{\text{ref},j,g}} \quad (6)$$

The numerical values range from 0 to 1 for the two indicators MSA and Sørensen's S_s , whereas I_{rel} of the other three indicators species richness, Shannon's H , and Fisher's α allow values above 1. For studies containing data from several reference situations, relative indicators were calculated for all possible combinations of references and land use types and also within references, giving an additional estimate of uncertainty. Hence, the reference situation was not fixed at 1 as was the case for the data on S_{rel} from the full dataset (BDM and GLOBIO3 database), where multiple reference plots per study site were averaged before the calculation of the relative indicator. This resulted in a final number of 168 (pairwise) data points for the reference and a total of 337 for all land use types.

2.5 Statistical analysis

Analysis of variance (ANOVA) was used to analyze the differences in mean relative species richness S_{rel} , depending on the four factors land use type (LU), taxonomic group (taxa), biogeographic region (biome), and data source (i.e., GLOBIO or BDM; data), including the interaction of factors (see Eq. (7)).

$$S_{\text{rel}} = f(\text{LU; biome; taxa; data; LU} \times \text{biome; LU} \times \text{taxa; biome} \times \text{taxa; LU} \times \text{data; biome} \times \text{data; taxa} \times \text{data; LU} \times \text{biome} \times \text{taxa; LU} \times \text{biome} \times \text{data; LU} \times \text{taxa} \times \text{data}) \quad (7)$$

As the data did not follow the assumption of normal distribution, we additionally applied the Kruskal–Wallis test to test the difference of medians of S_{rel} of the four factors (without interaction). Mann–Whitney U test was conducted for pairwise comparison of median S_{rel} of different land use types.

For each of the five indicators I_{rel} (see Table 1 and Eq. (6)) calculated for a subset of data, the differences in means for the three factors LU, taxa, and biogeographic region (realm) and their interactions were assessed with ANOVA (see Eq. (8)).

$$I_{\text{rel}} = f(\text{LU; taxa; realm; LU} \times \text{taxa; LU} \times \text{realm; taxa} \times \text{realm; LU} \times \text{taxa} \times \text{realm}) \quad (8)$$

As with the total dataset, robustness of results was assessed with nonparametric Kruskal–Wallis tests and Mann–Whitney U tests. In addition, Pearson's correlation between indicators was calculated. All data analysis was carried out using R statistical package v2.11 (R Development Core Team 2011).

3 Results

3.1 Land use impacts on biodiversity

Characterization factors of land occupation CF_{occ} for BDP were calculated according to Eq. (1) and are shown in Table 2 and in the Online Resource (see ESM Table 1). For easier interpretation of results, the biodiversity indicator S_{rel} is chosen for graphical display (Figs. 1, 2, and 3). The characterization factors (CF) can be derived by subtracting the median S_{rel} from 1 (see Eq. 1).

Averaged across all regions and taxa, S_{rel} of all land use types was significantly lower than in the reference, but results varied strongly from negative impacts ($S_{\text{rel}} < 1$) to positive impacts ($S_{\text{rel}} > 1$; see Fig. 1). The strongest negative

impact was found in annual crops, where S_{rel} was reduced by 60 %, followed by permanent crops and artificial areas (40 % decreased S_{rel}). In pastures, the reduction of S_{rel} was around 30 %, in secondary vegetation, used forests and agroforestry around 20 %. A pairwise comparison of the difference of median S_{rel} of different land use types is given in ESM Table 2.

A significant effect on S_{rel} of LU, taxa, and biome, and a nonsignificant effect of the source of data (GLOBIO or BDM) were found for the full dataset both in ANOVA (Table 3) and Kruskal–Wallis test (results not shown). In the ANOVA, land use effects on S_{rel} differed significantly between biomes (LU × region) and taxa (LU × taxa), but not between data source (LU × data). The latter was supported by Mann–Whitney U tests, which did not show any significant difference ($p < 0.05$) in S_{rel} between the two data sources for any land use type (results not shown).

3.2 Regionalization

Data from nine biomes were included in the analysis, but the majority of studies provide data on land use of biome (sub-)tropical moist broadleaf forests (ESM Table 1). For many combinations of land use types and biomes, no or too little

data was available to draw conclusions. Due to the inclusion of Swiss BDM data, the number of data points for two temperate biomes (broadleaf and mixed forests and coniferous forests) was considerably improved. The relative species richness of the four biomes with the highest data availability is displayed in Fig. 2. A significantly different land use impact across biomes was only found for three land use types (secondary vegetation, used forest, and pasture; Kruskal–Wallis test, $p < 0.05$). All land use types in all biomes showed a median negative land use impact ($S_{rel} < 1$), with one exception. Pastures in the biome deserts and xeric shrublands showed a slight positive median land use impact (S_{rel} increased by 8 %, ESM Table 1), but the small number of data points ($n = 5$) and the large variation in data does not allow for strong conclusions here. In general, large within-biome variations were observed.

3.3 Indicator comparison

3.3.1 Comparing impacts across taxonomic groups

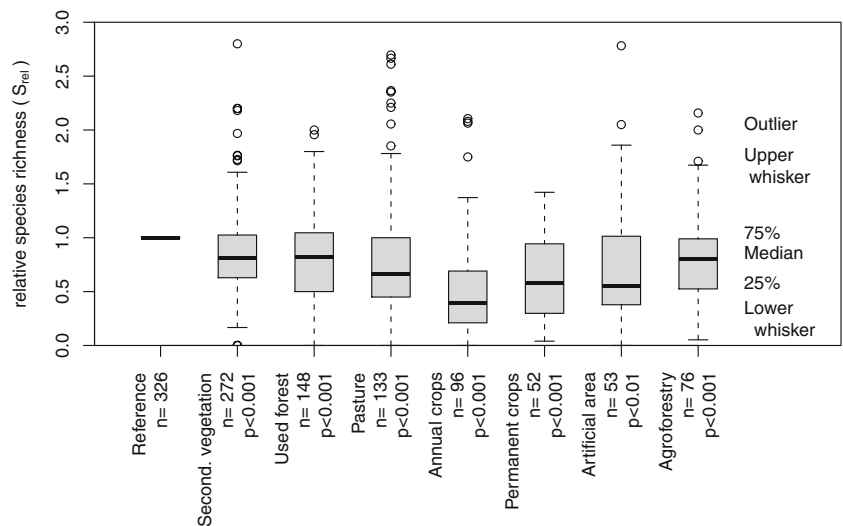
Data on different species were aggregated into broad taxonomic groups to get enough data points per group and land use type. The global dataset from GLOBIO3 contains a broad range of

Table 2 World average and regionalized characterization factors CF (median) and their uncertainties (1. and 3. quartiles) for biodiversity damage potential (BDP) per land use type

		Forest, not used	Secondary vegetation	Forest, used	Pasture/meadow	Annual crops	Permanent crops	Agroforestry	Artificial areas
Total world average	Median	0	0.18	0.18	0.33	0.60	0.42	0.20	0.44
	1. quartile	0	−0.03	−0.05	0.00	0.31	0.06	0.01	−0.01
	3. quartile	0	0.37	0.50	0.55	0.79	0.70	0.48	0.62
	n	326	272	148	133	96	52	76	53
Biome 1 (Sub-)tropical moist broadleaf forest	Median	0	0.22	0.13	0.45	0.54	0.42	0.18	–
	1. quartile	0	0.00	−0.09	0.31	0.36	0.18	−0.02	–
	3. quartile	0	0.43	0.45	0.75	0.72	0.70	0.44	–
	n	173	172	79	26	46	40	70	1
Biome 4 Temperate broadleaf forest	Median	0	0.08	0.22	0.52	0.76	0.02	–	0.40
	1. quartile	0	−0.26	−0.09	−0.35	0.46	−0.11	–	−0.10
	3. quartile	0	0.33	0.43	0.67	0.86	0.69	–	0.58
	n	46	20	35	33	24	9	0	24
Biome 5 Temperate coniferous forest	Median	0	0.17	0.15	0.24	0.54	–	–	0.50
	1. quartile	0	−0.22	0.02	−0.64	−0.15	–	–	−0.05
	3. quartile	0	0.30	0.33	0.38	0.87	–	–	0.71
	n	45	15	7	27	8	3	0	21
Biome 7 (Sub-)tropical grassland and savannah	Median	0	0.00	0.01	0.12	0.65	–	–	–
	1. quartile	0	−0.17	0.00	0.02	0.02	–	–	–
	3. quartile	0	0.15	0.06	0.27	0.80	–	–	–
	n	21	27	6	8	9	0	0	0

CF of four selected biomes are displayed, a full list of CF per biomes and taxonomic groups can be found in ESM Table 1. For land use types with less than 5 data points (n), no CF is provided

Fig. 1 Box and whisker plot of relative species richness per land use type, number of data points n per land use type, and test statistics (one-sided Mann–Whitney U test) of pairwise comparison of each land use with the reference for the full dataset (global averages across all biomes and taxonomic groups)



taxonomic groups, whereas the Swiss BDM dataset only contains data on plants (vascular plants and moss) and invertebrates (mollusks, see ESM Table 5). To achieve more or less globally averaged results, we further aggregated groups that were mainly consisting of data from the Swiss BDM. Finally, four classes of taxonomic groups were distinguished: plants, arthropods, other invertebrates and vertebrates. A significantly different ($p < 0.001$) land use impact across taxonomic groups was found in the full dataset for agroforestry and a slight difference ($p < 0.1$) for used forest (see Fig. 3). Overall, plants and invertebrates (excluding arthropods) showed a slightly stronger land use effect than arthropods and vertebrates, but this pattern was not found across all land use types. The variation within taxonomic group was considerable. Therefore, we further separated two groups, neglecting the over-representation of the Swiss data: plants were split into moss and vascular plants and vertebrates were split into birds and other vertebrates, resulting in a total of six taxonomic groups (ESM Fig. 3 and Table 1). With this finer-scaled

classification, significantly different ($p < 0.05$) land use impacts across taxonomic groups were found for all land use types except for secondary vegetation, where only a slight difference ($p < 0.1$) between taxonomic groups was found (ESM Fig. 3). Here, other invertebrates and moss showed the strongest land use impacts, with roughly a 50–90 % median reduction in S_{rel} in pasture, annual crops, and artificial area. A strong positive land use impact (42 % increased S_{rel}) on vascular plants was found in artificial areas. The underlying data ($n = 16$) was purely based on the Swiss BDM, and data from very heterogeneous land use types were included (from dump sites to urban green areas). Therefore, we further split the land use type artificial area in the Swiss BDM data into low and high intensity (ESM Fig. 4). However, no significant differences in S_{rel} between the high- and low-intensity artificial areas were found for the BDM data with a Mann–Whitney U test. Within the Swiss BDM data, vascular plants were generally less affected by land use than moss and mollusks (ESM Fig. 4), and showed an increased median relative species richness in pasture, permanent

Fig. 2 Box and whisker plot of relative species richness per land use type and four selected biomes and test statistics of Kruskal–Wallis test ($S_{rel} = f(LU \times \text{biome})$) for (a) displayed biomes and (b) all biome in full dataset. *ns* Not significant, *na* not applicable (just one biome per land use type), *TropMBF* (sub-)tropical moist broadleaf forest, *TropGL* (sub-)tropical grassland, savannas, and shrublands, *TempBLF* temperate broadleaf and mixed forest, *TempCF* temperate coniferous forest

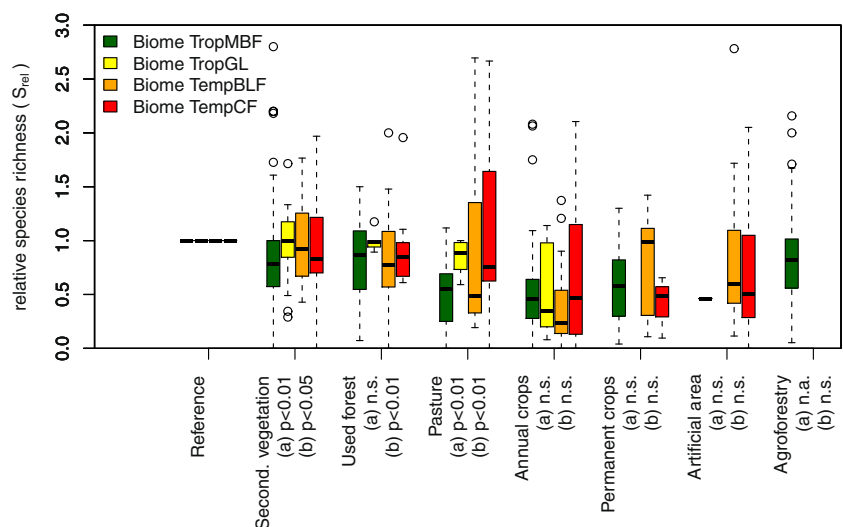
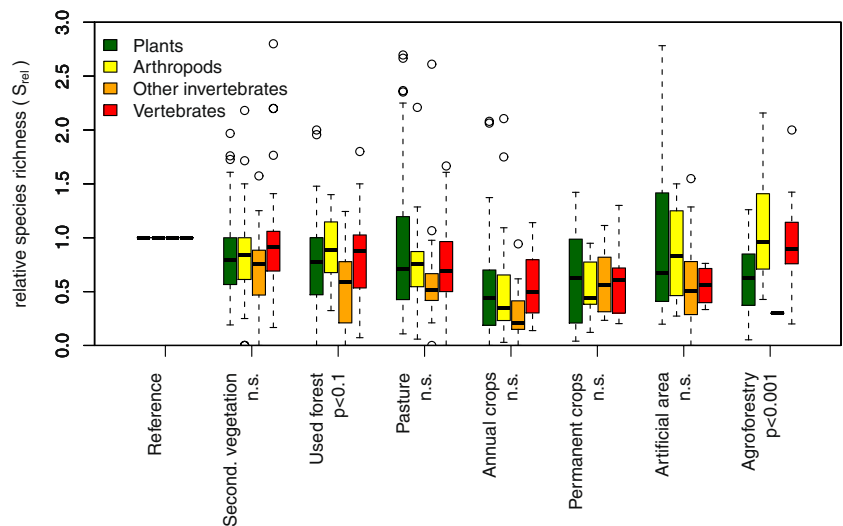


Fig. 3 Box and whisker plot of relative species richness per land use type and taxonomic group and test statistics of Kruskal–Wallis test ($S_{rel} = f(LU \times \text{taxa})$ for full dataset. *ns* Not significant



crops, and artificial areas. Moss and mollusks showed a decreased relative species richness in all land use types.

3.3.2 Comparing impacts across biodiversity indicator

For a subset of data from the biome (sub-)tropical moist broadleaf forest, four additional indicators were calculated: Fisher’s α , Shannon’s H , Sørensen’s S_s , and MSA (see Table 1). For all land use types, the impacts varied

significantly across indicator (Fig. 4). Relative species richness was highly correlated with relative Shannon’s H (Pearson’s $r=0.79$) and relative Fisher’s α (Pearson’s $r=0.83$, see also ESM Table 3). This group of indicators showed less negative (or even positive) land use impacts compared to a second group of indicators, Sørensen’s S_s and MSA, which were also highly correlated (Pearson’s $r=0.81$). In Fig. 4, the reference situation shows a considerable within-study variation, calculated as the relative difference in biodiversity

Table 3 Results of ANOVA testing the difference in mean S_{rel} of the full dataset depending on land use type (LU), taxonomic group (taxa), biogeographic region (region = biome or realm) and data sources (data) and their interactions

	Full dataset		GLOBIO data		BDM data		Subset: biome (sub-)tropical moist broadleaf forest data					
	<i>df</i>	S_{rel}	<i>df</i>	S_{rel}	<i>df</i>	S_{rel}	<i>df</i>	S_{rel}	MSA	Sørensen	Shannon (rel)	Fisher’s α (rel)
LU	7	***	7	***	6	***	7	***	***	***	***	***
Region ^a	8	***	8	***	1	<i>ns</i>	4	***	***	***	***	***
Taxa ^b	3	***	3	***	2	***	2	**	***	***	*	**
Data	1	<i>ns</i>	–	–	–	–	–	–	–	–	–	–
LU × region	38	***	33	***	6	**	20	***	***	***	**	***
LU × taxa	20	***	19	***	12	***	11	*	***	***	<i>ns</i>	<i>ns</i>
Region × taxa	17	*	16	***	2	<i>ns</i>	5	<i>ns</i>	<i>ns</i>	<i>ns</i>	<i>ns</i>	<i>ns</i>
LU × data	4	<i>ns</i>	–	–	–	–	–	–	–	–	–	–
Region × data	1	*	–	–	–	–	–	–	–	–	–	–
Taxa × data	1	<i>ns</i>	–	–	–	–	–	–	–	–	–	–
LU × region × taxa	45	*	34	**	12	<i>ns</i>	8	<i>ns</i>	<i>ns</i>	<i>ns</i>	<i>ns</i>	<i>ns</i>
LU × region × data	1	<i>ns</i>	–	–	–	–	–	–	–	–	–	–
LU × taxa × data	2	<i>ns</i>	–	–	–	–	–	–	–	–	–	–

Model of full dataset, see Eq. (7); model for subsets (GLOBIO, BDM and tropical data), see Eq. (8)

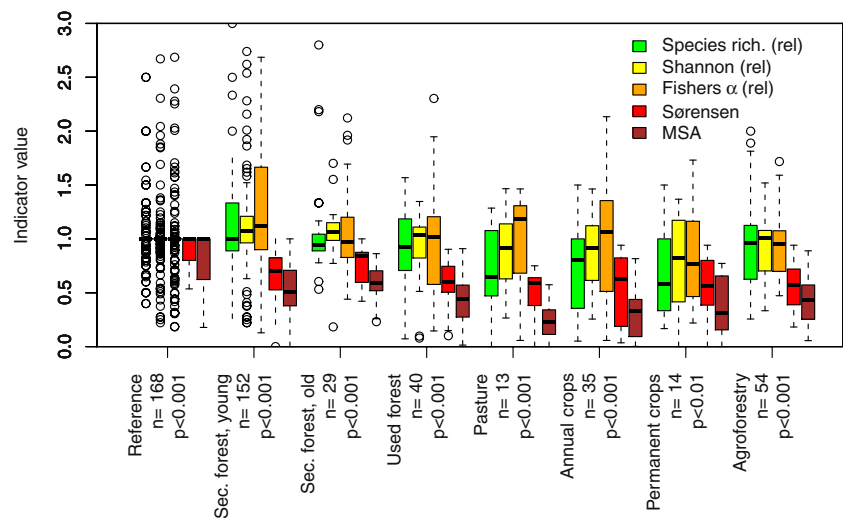
df degrees of freedom

* $p<0.1$, ** $p<0.05$, *** $p<0.01$, *ns* not significant

^a Biomes were used as the factor for testing regional differences for all datasets, except for the subset of data from the biome (sub-)tropical moist broadleaf forest, where biogeographic realms (i.e., continents) were used for regionalization

^b For BDM data, the factor levels of taxa were vascular plants, moss and mollusks. For the other datasets, the levels were plants, vertebrates, arthropods, and other invertebrates

Fig. 4 Box and whisker plot of different indicators per land use type and test statistics of Kruskal–Wallis test ($I_{rel} = f(LU \times \text{indicator})$) for a subset of data from biome (sub-)tropical moist broadleaf forest. Secondary forest was divided into young (<30 years) and old growth forest (>30 years). n Number of data points (pairwise comparisons) per land use type and indicator



indicators of multiple reference situations given for individual studies. This variation was not calculated for the full dataset (see Figs. 1, 2, and 3), where the *averages* of multiple references were used to calculate relative changes in species richness.

4 Discussion

Biodiversity is a multifaceted concept and it is difficult to express product-related impacts of land use in a single indicator value. Our analysis illustrated the variability of results, ranging from positive to negative impacts of land use, but we also found an overall negative median impact on relative species richness across all analyzed land use types. Land use impacts differed significantly across taxonomic groups and biogeographic regions, but could not be determined for all world regions due to data limitations. The choice of indicator also strongly influenced the outcome, where relative species richness was less sensitive to land use impacts than MSA or Sørensen's S_s . In the following sections, we want to highlight the uncertainties, limitations, and opportunities for improvements of this first attempt to quantify land use impacts on biodiversity in LCIA on a global scale based on empirical data. We discuss the suitability of different indicators for use in land use LCIA, appropriate coverage and classification of taxonomic groups, land use types and biogeographic regions, and finally address general uncertainties of the presented approach.

4.1 Choice of indicator

From a practical point of view, *species richness* might be the indicator of choice for biodiversity assessments on species level: data is relatively readily availability, as the data requirements are low compared with other indicators, which need additional information on abundance and/or species

composition. However, from a theoretical point of view, the indicator species richness has many shortcomings. Here, we discuss four alternative indicators analyzed in this study which partly overcome some of the disadvantages of species richness, such as (1) high dependence on sampling effort, (2) missing information on abundance, (3) no link to conservation targets, and (4) missing information on species turnover.

First, species richness is highly dependent on sampling size, whereby a nonlinear relationship between area sampled and species richness has been observed (due to a species sampling and a species area relationship; Arrhenius 1921; Dengler 2009). To compare absolute species numbers of different land use types, species richness has to be standardized to the same sampling effort (Koellner and Scholz 2008; Schmidt 2008). This proves to be difficult or even impossible when dealing with different taxonomic groups that are surveyed with very different sampling methods (e.g., visual observations of birds along 50 m transects, 20 pitfall traps of arthropods, or plant counts on 10 m² plots). Therefore, we divided absolute species numbers of each taxon of every land use type i by the absolute species numbers of a regional reference to obtain *relative* species richness (given that both absolute numbers were obtained with a similar sampling effort). This approach partly circumvents effects of sampling bias. However, a bias remains in cases where the land use type i and the reference show very different species turnover (e.g., homogeneous species composition of arable field vs. heterogeneous rain forest). In such cases, the *relative* land use impact is underestimated with small sample size, as most species of the arable field are captured, but only a small share of the species richness of the rain forest is recorded.

Several biodiversity indicators have been developed that correct for incomplete sampling (see, e.g., Beck and Schwanghart 2010). In our analysis, we applied *Fisher's alpha* (Fisher et al. 1943, see formula in Table 1) and found a high

correlation between land use impacts measured as relative species richness and as relative Fisher's α (see Fig. 4). This finding is supported by the empirical study of Kessler et al. (2009), which did not find a strong influence of sampling incompleteness on land use impacts. This indicates that correcting for undersampling might not be the most important aspect to reduce overall uncertainty of biodiversity-related land use LCIA.

A second shortcoming of species richness is the missing information on abundance. *Shannon's H*, derived from information theory, expresses abundance and richness in one number (see formula in Table 1) and reaches a maximum value when all species occur equally abundant. As in our study, relative Shannon's entropy *H* was highly correlated with relative species richness (see Fig. 4), the latter might be preferred as indicator, as it is easier to communicate to LCA users or the general public.

MSA, an indicator developed for the GLOBIO3 model (Alkemade et al. 2009), is correcting the second and third shortcoming of species richness as it includes abundance and is linked to conservation targets. *MSA* compares the abundance of "original" species occurring in natural, undisturbed habitats, in their primary "original" habitat with their abundance in secondary habitats (i.e., on the land use type *i*). As expected, our results showed that land use impacts were stronger when measured with *MSA* than with S_{rel} (see Fig. 4), indicating that the original species adapted to undisturbed habitats are more susceptible to land use changes than species adapted to disturbance. *MSA* is therefore suitable to report land use impacts in regions, where conservation targets are mainly focusing on protection of primary habitats. In areas such as central Europe, where conservation is mainly targeting at protecting species adapted to traditional land use practices, the definition of "original" species needs to be extended to these species. To base future land use LCIA methods on *MSA*, the habitats or species relevant for conservation have to be defined for all world regions, whereby the value choices unavoidably involved in this definition need to be critically reflected.

Similar to *MSA*, *Sørensen's S_s* can measure the similarity of the species composition of a land use type and a reference situation but without considering abundance. As they were calculated in this study, both *MSA* and *Sørensen's S_s* reached a maximum value of 1, when the land use type had a *maximum* similarity (i.e., the same species composition as the reference) and the two indicators were therefore highly correlated (see Fig. 4). As expected, the land use impacts measured with *Sørensen's S_s* were smaller than with *MSA*, as *MSA* already reports a decreasing abundance of species, whereas *Sørensen's S_s* only reports if a species is not present anymore. *Sørensen's S_s* can also be used to calculate similarity of species composition *within* a land use type or reference, i.e., giving information of species

turnover (or β -diversity). In that case, a maximum β -diversity score would be reached within a land use class or reference with *minimum* average similarity between samples, indicating high rates of turnover. This would require data on species composition of multiple plots of the same land use and multiple plots of a reference within one study site—or studies directly reporting β -diversity. As β -diversity can play a key role in biodiversity conservation (Gardner et al. 2010), this information is increasingly available and might open the way to use this indicator in future biodiversity LCIA.

Biodiversity impacts can be assessed in relative or absolute terms, which finally represent different value choices: if we assess absolute impacts, all species are equally weighted, if we assess relative impacts, all ecosystems get equal weight. The indicators calculated in this study all assess relative impacts. As explained above, this was required to standardize the data from a multitude of studies with different sampling design and species groups. As a consequence, a 40 % decrease of relative species richness in a species rich ecosystem (e.g., with 100 species) and in a more species poor ecosystem (e.g., 10 species) are weighed evenly, although the absolute reduction in species richness is much higher in the species rich ecosystem (40 vs. 4 species). To account for regional differences in absolute species richness, a weighing system of land use could be applied as suggested by Weidema and Lindeijer (2001). Global conservation priorities could help to develop such a weighing scheme, using weighing factors such as regional species richness, irreplaceability, and vulnerability of ecosystems (Brooks et al. 2006).

To conclude, we think that—in view of current data availability—relative species richness, as an indicator for α -diversity, is a suitable indicator for biodiversity-related land use LCIA. If future research progress allows quantifying land use-related impacts on β -diversity or changes in abundance of species important for conservation, indicators such as *MSA* or *Sørensen's S_s* should be preferred. To also account for regional differences of *absolute* species richness, a weighing of the presented CFs is required. Here, only a few facets of biodiversity were considered, with a focus on species composition. Including other facets, for example, land use impacts on ecosystem functioning (see, e.g., Michelsen 2008; Wagendorp et al. 2000) or on ecosystem services (Müller-Wenk and Brandão 2010; Saad et al. 2011; Brandão and Milà i Canals 2012), would be an important complement of this method.

4.2 Taxonomic coverage

Attractive species groups, such as mammals, birds, or butterflies are often used as indicator taxa in biodiversity assessments, with the underlying hope "that the known biodiversity is a good surrogate for the unknown" (Rodrigues and Brooks

2007, p. 714). Data availability is therefore biased towards some well-studied species groups. Existing land use LCIA mostly focused on vascular plant species richness as an indicator (e.g., Koellner and Scholz 2008; Schmidt 2008; De Schryver et al. 2010). This makes a method very transparent, but the potential to generalize results from one well-studied species group to biodiversity as whole is questionable (Purvis and Hector 2000). Empirical studies from different world regions found little predictive power of one species group for other species groups (e.g., Billeter et al. 2008; Kessler et al. 2009; Wolters et al. 2006).

In this study, we combined data from global literature review, covering a range of taxonomic groups (see ESM Table 5), with data from Swiss biodiversity monitoring BDM, containing data on vascular plants, moss, and mollusks. Although being more representative than previous LCIA studies, a publication bias towards some well-studied species groups remained. If we compare the share of species groups in our analysis with their estimated global species richness (Heywood and Watson 1995; see ESM Table 4), we find that vertebrates (26 % of data) and plants (43 %) were strongly overrepresented, as they only make up 0.4 and 2 %, respectively, of estimated global species richness. With 20 % of data points, arthropods were underrepresented in this study as they make up an estimated 65 % of global species richness. Some species groups, such as bacteria (7 % of estimated global species richness) or fungi (11 %) were not at all represented in the used dataset.

Ideally, the impact of different land use types on each target species group in each biogeographic region should be separately assessed. This could later be aggregated into characterization factors for archetypical groups of species, regions, and land use types showing similar land use effects. In this study, we present one possible classification, but due to limited data availability, we could not make a thorough analysis of different classification options nor recommend an optimal classification, where the variation within each characterization factors is minimized (i.e., representing a homogeneous group). We first divided data into four very broad taxonomic groups (plants, arthropods, other invertebrates and vertebrates), and then further subdivided plants into moss and vascular plants and vertebrates into birds and other vertebrates. A further subdivision was not possible, as too little data points were then given for each land use type. Especially for plants, the separation into moss and vascular plants revealed very diverging impacts of these subgroups (ESM Table 1 and Fig. 3), suggesting that these groups should be assessed separately. However, it is unclear to which extent this conclusion is valid for other world regions, as for many land use types the data on moss is purely derived from the Swiss BDM (see ESM Table 5).

Here, we chose a classification based on phylogenetic relationship, but closely related species not necessarily show

homogeneous reactions to land use (see, e.g., Attwood et al. 2008; Blaum et al. 2009; Anand et al. 2010). To find an optimal representation of impacts across species groups other classification criteria, such as functional traits (e.g., morphological, ecophysiological, and life history characteristics, see, e.g., Vandewalle et al. 2010) or feeding guilds (see, e.g., Scherber et al. 2010) should be tested as alternative grouping factor for species groups.

As data on all species will probably never be available, we need to find the optimal taxonomic coverage for land use LCIA. This requires a clear definition of the target of land use LCIA (i.e., why we want to conserve biodiversity; see also Michelsen 2011). If we aim at conserving biodiversity due to its intrinsic value or due to its potential future economic value (e.g., as medicine), threatened species should get higher weights and species groups selected for LCIA should be proportional to their total richness. If the target is to sustain ecosystem services, we need to conserve functional diversity (and assess land use impacts on important species of ecosystems). However, this requires a more sound understanding of the underlying ecosystem processes, e.g., on how ecosystems react if a certain species occurs more or less abundantly. In addition, better knowledge on vulnerability and potential tipping points of ecosystems (i.e., non-linear reactions of ecosystems after certain levels of accumulated multiple disturbances, see, e.g., Holling 2001; Scholz 2011) is required. Resolving the important normative question of setting appropriate targets for biodiversity assessments within LCA and of finding the right proxy for it remains a challenge for future research.

4.3 Land use classification and regionalization

As outlined above, characterization factors ideally should represent archetypical land use impacts on species groups, but also of land use classes and regions showing similar impacts. In our study, very broad land use types were classified showing considerable within-class variation of effects. Including further data points would allow to separate intensive and extensive land use (e.g., for agriculture) and could potentially reduce this variation and improve the validity of the characterization factors. However, in the case of artificial area in Switzerland, no significant differences between high- and low-intensive artificial areas were found (ESM Fig. 4). Caution should be taken with extrapolating the findings for artificial area, which are largely based on the Swiss BDM data, to other world regions.

The question of appropriate classification also applies to regionalization. Here, we chose WWF biomes as spatial units as a coarse regionalization scale with ecologically distinct regions. Due to limited data availability, it was not possible to have a more fine-scaled regionalization of *relative* impacts. However, a weighing of these relative impacts,

as suggested above, could be done on ecoregion level, using for example data on species richness of different taxa (see data of Olson et al. 2001; Kier et al. 2005). As significant differences in land use impacts were not only found across biomes (full dataset), but also across biogeographic realms (subset (sub-)tropical moist broadleaf forest, see Table 3), a further distinction of biomes across realms might better reflect differences in relative impacts. The analysis of the Swiss BDM data, covering two biomes, showed no significant difference between their reactions to land use. This suggests that not only the broad ecosystem type is important to determine land use impacts, but also the geographical proximity or similarity of land use history. Of course, aspects of practicality also need to be considered when choosing an optimal scale of regionalization. To finally assess land use impacts in LCA, not only the characterization factors have to be regionalized, but also the inventory data. How the presented CFs can be applied is illustrated in a case study on margarine by Milà i Canals et al. (2012).

As for taxonomic groups, data availability of land use impacts on biodiversity is biased towards some biogeographic regions, with data dominantly derived from a few well-studied research stations in tropical regions (see Gardner et al. 2009, 2010). In addition, some ecosystem types, such as grassy ecosystems, received less attention of researchers than forest ecosystems (Bond and Parr 2010). The uneven regional distribution is also visualized in the data distribution of this study (see ESM Fig. 2). Very little or no data was available for five out of 14 biomes: (sub-)tropical coniferous forests, boreal forests/taiga, flooded grasslands and savannas, tundra, and mangroves (see ESM Table 1 and Fig. 2). For three biomes, enough data was only provided for pastures (temperate grassland and savannah, Mediterranean forests, woodlands and scrub, and deserts and xeric shrublands). For permanent crops, agroforestry and artificial areas, data was only available from two biomes. In general, the biome (sub-)tropical moist broadleaf forest had the highest data availability. The two temperate biomes mixed and broadleaf forest and coniferous forest also showed a reasonable amount of data, but as this was mainly derived from Swiss BDM data, results are highly biased towards the European context. To which extent these results are valid for temperate forest biomes in other world regions remains a question for future research.

4.4 Data limitations and uncertainties

In this study, we combined global literature data with national biodiversity monitoring data. Both datasets have different sources of uncertainties. Summarizing data from multiple studies involves consideration of within- and between-study variance (Gurevitch and Hedges 1999). As

it was beyond the scope of this study to perform a full statistical meta-analysis, only between-study variation was considered. Therefore, the overall assessment on relative species richness suggests no variation of the reference habitat (see Figs. 1, 2, and 3), which does not reflect reality. For the subset of data used to compare biodiversity indicators, the within-study variance was included when studies reported data on multiple reference habitats. The considerable variation of indicator values of reference habitats observed in the subset of data (see Fig. 4) suggests that variation of results (including within-study variance) of the full dataset was underestimated.

For the Swiss BDM data, the main sources of uncertainties are the definition of ecologically similar regions (see Section 2.3) and the definition of reference habitat. It was beyond the scope of this study to test the sensitivity of results to choice of boundary of regions. However, for the definition of reference habitat per region, the sensitivity of results to selection of two different reference situations was tested. We compared the outcomes for using (1) a combination of all potential natural habitats ($n=305$ monitored sampling points in forests, grasslands, wetlands, bare areas and water bodies) and (2) only forest sampling points ($n=221$). No significantly different result of any land use type was found between the two alternative reference situations. Although there is a large overlap of data points between the two alternatives, it indicates that results are not very sensitive to choice of reference habitat. However, in both alternatives, the reference habitat experienced considerable past (and present) human disturbance, as no pristine areas exist in Switzerland, whereas more pristine reference habitat was included for other biomes in the GLOBIO3 database. However, this inconsistency is unavoidable when a globally valid reference situation has to be defined, as different world regions show different land use history.

In our study, we found a median reduced relative species richness across all globally averaged land use types. However, we cannot rule out that other factors, such as changes in overall landscape composition or pollution might also have contributed to the result. A meta-study across multiple taxonomic groups in the Western Ghats, India, for example found no significant effect of land use on species richness, but a significant effect of native forest cover within the landscape (Anand et al. 2010). Besides the necessity to understand cause–effect chains of biodiversity loss, this illustrates the importance of spatial context of land use (i.e., in what landscape a land use occurs). Despite their importance, it was beyond the scope of this study to include spatial and temporal effects. To improve the assessment of biodiversity loss related to land use or other drivers of biodiversity loss, better concepts including these temporal and spatial aspects are required for LCIA (see also Curran et al. 2011).

5 Conclusions and recommendations

Although uncertainties and data and knowledge gaps are considerable, human impacts on biodiversity are ongoing. Decisions how to adapt production towards being less harmful for biodiversity need to be taken urgently, and cannot wait until all data and knowledge gaps are filled. Based on empirical data, this study provides a first attempt to quantify land use impacts on biodiversity within LCA across world regions to support such decisions. Due to the mentioned challenges to quantify biodiversity impacts, the presented CF should be used with caution and remaining uncertainties should be considered when LCA results are interpreted and communicated. In LCA studies, where the “user may not directly decide on the land management practices” (Milà i Canals et al. 2007, p. 13), our CF can serve as a first screening of potential land use impacts across global value chains. For LCA studies aiming to support decisions of specific land management, a more detailed, site-dependent assessment, including additional region- or site-specific data, is indispensable (see, e.g., Geyer et al. 2010).

In this paper, occupation impacts of a range of land use types in many world regions could be assessed, but some data gaps remain. Research priorities should be set to first close data gaps for environmentally important land use activities (such as agri- and silviculture, construction, mining, and land filling) in economically important world regions (e.g., by using regionalized global inventories such as the inventory of global crop production from Pfister et al. 2011). To assess total land use impacts on biodiversity, we need to complement the presented CF of occupation with regionalized global estimates of transformation impacts. This requires more reliable information on regeneration times of ecosystems across the world, as transformation impacts (calculated according to the UNEP/SETAC framework; Milà i Canals et al. 2007; Koellner et al. 2012b) are highly sensitive to this parameter and currently available estimates vary considerably (Schmidt 2008). Estimates of regeneration times should ideally be based on empirical data, for example derived through meta-analysis of ecosystem regeneration studies.

In view of current data availability, the applied indicator relative species richness is suitable for biodiversity-related global land use LCIA. As ecological research evolves, LCIA methods should be complemented with indicators measuring other facets of biodiversity, such as conservation value, species abundance, or turnover. This applies not only to land use impacts, but also to other drivers of biodiversity loss, such as climate change, eutrophication, acidification, or ecotoxicity. To inform decision-makers about potential trade-offs of different drivers of biodiversity loss along the life cycle, indicators need to be comparable across impact pathways (see also Curran et al. 2011). Finding a measure to

quantify impacts of concurrent multiple drivers of biodiversity loss in a globally applicable and spatially differentiated way will be a challenge for future LCA research. As the importance of halting global biodiversity loss is increasingly recognized in research, industry, and policy (e.g., formulated as the 2020 targets of the Convention on Biological Diversity; CBD 2010), increased research efforts are made to close some of the mentioned knowledge and data gaps. This will also open the way to improve the accuracy of biodiversity assessments within LCA and allow for more robust and credible decision support.

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