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Toward Meaningful End Points of Biodiversity in Life Cycle Assessment[†]

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Halting current rates of biodiversity loss will be a defining challenge of the 21st century. To assess the effectiveness of strategies to achieve this goal, indicators and tools are required that monitor the driving forces of biodiversity loss, the changing state of biodiversity, and evaluate the effectiveness of policy responses. Here, we review the use of indicators and approaches to model biodiversity loss in Life Cycle Assessment (LCA), a methodology used to evaluate the cradle-to-grave environmental impacts of products. We find serious conceptual shortcomings in the way models are constructed, with scale considerations largely absent. Further, there is a disproportionate focus on indicators that reflect changes in compositional aspects of biodiversity, mainly changes in species richness. Functional and structural attributes of biodiversity are largely neglected. Taxonomic and geographic coverage remains problematic, with the majority of models restricted to one or a few taxonomic groups and geographic regions. On a more general level, three of the five drivers of biodiversity loss as identified by the Millennium Ecosystem Assessment are represented in current impact categories (habitat change, climate change and pollution), while two are missing (invasive species and overexploitation). However, methods across all drivers can be greatly improved. We discuss these issues and make recommendations for future research to better reflect biodiversity loss in LCA.

Introduction

The planet is undergoing extensive changes induced by human appropriation of natural resources. Among the most critical consequences is the stark decline in biological diversity documented over the past decades (*1−4*). The Millennium Ecosystem Assessment (MA) (*2*) recently documented a widespread decline in the quality of global ecosystems and biodiversity, stimulating the rapid development of indicators to measure the changing state of nature, the driving pressures behind, and evaluate the effectiveness of policy responses. The MA identified a number of direct drivers of biodiversity loss, of which the most important are i) terrestrial and aquatic habitat change, ii) invasive species, iii) overexploitation of wild populations, iv) pollution, and v) climate change (*2*).

The development and use of assessment tools to track hot-spots of environmental damages in production systems has been of growing interest among industry, the public sector, and nongovernmental organizations. One such method of environmental assessment at the product level is Life Cycle Assessment (LCA). LCA is used to quantify the potential environmental impacts throughout a product's life cycle from raw material acquisition, production, use, and finally disposal (*5*). The "impact assessment" stage of LCA models impacts along mostly linear, deterministic, cause-effect chains by linking inventory items to so-called *midpoint* impact categories, such as global warming potential, ecotoxicity, and land use. In an optional second step, the cause-effect chain is extended to final *end points*, which express impacts on three areas of protection: natural resources, human health, and ecosystem quality.

The development and inclusion of potential end points for biodiversity in LCA has been ongoing for more than a decade (*6−10*). Yet many methods in LCA are still in the early stages of development (*11−19*). Particular difficulties are posed by the methodological framework of LCA itself, which traditionally required impacts to be generic in space, summed across time horizons, strongly linked to a functional unit, and free of interactions between impact pathways (see ref *20*). These restrictions are only beginning to be addressed by recent LCA research. If LCA is to be truly informative to decision makers about biodiversity loss, it is important to assess whether current methods are reflecting i) the major drivers of biodiversity loss as identified by the MA and ii) whether they capture the concept of biodiversity adequately both in its inherent variation and its nonuniform distribution across the planet.

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TABLE 1. Biodiversity Indicators Across Hierarchical Components (Gene, Species, Community, and Ecosystem) and Biological Attributes (Compositional, Structural, and Functional)[a]

hierarchical components	biological attributes			assessment tools and methods
	composition	structure	function	
genes (biotic)	heterozygosity, allelic diversity, % polymorphic loci, genetic variance, phylogenetic diversity	chromosomal or phenotypic polymorphisms, physical genetic distance, effective population size, generation overlap, heritability	mutational diversity, mutation rate, duplication rate, selection intensity, rate of genetic drift, gene flow	visible polymorphisms, molecular markers (protein electrophoresis), DNA markers (microsatellites, DNA sequencing), parent-offspring regression, sibling analysis
species (biotic)	(meta)population size and number, absolute or relative abundance, frequency, biomass, cover, intactness, density	size, morphological variability, physiognomy, population structure, home range size and distribution in space, dispersal patterns, habitat requirements	metapopulation dynamics (drift, bottle necks, inbreeding, outbreeding trends) demographic processes (growth, reproductive, feeding, nesting, dispersal rate)	population censuses, time series analysis, remote sensing and GIS, habitat suitability index, species-habitat modeling, population viability analysis, species distribution modeling
communities (biotic, abiotic)	species richness, relative abundance, higher taxon diversity, phylogenetic diversity, number of endemics, invasive, threatened or focal species, similarity and turnover of species assemblages	habitat structural complexity, foliage physiognomy and layering, habitat density, gap density, volume, surface area, slope, aspect, rugosity index, nearest neighbor distance	nutrient turnover and cascades, functional group or guild diversity, number and strength of interspecific interactions (predator−prey, parasite-host), biomass production, extinction, colonization rates	remote sensing and GIS, aerial photographs, time series analysis, physical habitat measures, observation habitat descriptions, multispecies, local sampling techniques, multivariate integrative indices (Shannon−Wiener index, dispersion, layering, biotic integrity)
ecosystems and landscapes (abiotic)	patch diversity, richness, composition, number of ecosystems, relative or absolute area, area of seminatural vegetation in agriculture, emergent patterns in species distribution (richness, endemism)	patch shape and configuration (fragmentation, isolation, connectivity, spatial linkage), patch size frequency distribution, topography, river and shoreline profile	disturbance patterns and regimes (frequency, extent, intensity, seasonality), pattern metrics (patch turnover), erosion potential, geomorphic and hydrologic processes, land use patterns and trends	remote sensing and GIS, aerial photographs, time series analysis, spatial statistics, mathematical indices (pattern, connectivity, heterogeneity, layering, edge extent, diversity, fractal measures and autocorrelation)

[a] The final column on the right illustrates possible assessment methods (adapted from refs *21* and *22*).

This review article synthesizes how biodiversity indicators are currently employed in LCA during end point cause-effect modeling, and how this could be improved in the future by drawing on available methods in biodiversity research. We begin by describing a framework for characterizing biodiversity indicators. We then assess the coverage of biodiversity in relevant impact categories of LCA in light of this framework. We highlight research gaps and offer suggestions for improvement based on a review of a wide range of methods employed in the biodiversity assessment literature, including a comparison of LCA with recent biodiversity assessments such as the MA (Supporting Information VII).

Biodiversity Indicators

Framework. We adopt the definition of biodiversity provided in the Convention on Biological Diversity (CBD) (*1*), as a nested hierarchy of *components* defined by the level of scale and complexity (*21*). We separate components into four broad levels: gene, species, community, and ecosystem (*21, 22* differing slightly from the CBD). At each level, components may be characterized in terms of *attributes*, which reflect composition, the quantity and variety of elements; function, the ecological and evolutionary process acting among elements; and structure, the physical organization of elements (*22*). Indicators used to measure biodiversity can be correspondingly described by attribute and component. Table 1 illustrates the indicator framework adopted for this review.

Genetic Indicators. At the genetic level, indicators reflect intraspecific (within-species) or interspecific (between species) diversity (Supporting Information I). Intraspecific indicators include heterozygosity, allelic richness, nucleotide

diversity, genetic variance, and heritability (*23*). Interspecific variation is quantified using phylogenetic indicators (*24*), including phylogenetic diversity (*25*).

Species-Based Indicators. Species level indicators describe trends in the abundance or attributes of individual species (Supporting Information II). These include the focal species approach (*26*) and species intactness indices (*27*). Methods in modeling species distributions, habitat suitability, and sensitivity to environmental stress may take a deductive approach, using expert opinion and meta-analysis to derive cause-effect relationships, or an inductive approach, extracting patterns from empirical data via multivariate statistics with no proposed *a priori* cause-effect mechanism (*28*).

Community Indices. Community level indices describe the emergent patterns in biodiversity resulting from the overlap of individual species ranges (Supporting Information III). They characterize the number and relative abundance of species in a community in a single value. The value of a diversity index may be totally dominated by the number of species in a community (i.e., species richness) or conversely by only the relative abundance of species (i.e., pure evenness indicators). Intermediate points represent well-known indices such as the Shannon−Wiener index and Simpson's concentration (*29*). Community indices such as the Bray−Curtis index or ordination measures also represent beta diversity changes (turnover) between samples or locations. Recent work has focused on modeling emergent community patterns in biodiversity such as richness, turnover, and endemism as a substitute for data-demanding species level approaches (*30*) (Supporting Information IV). Indices of functional

diversity may be derived by grouping species into functional groups or calculating continuous distance in functional trait space (*31*).

Ecosystem and Landscape Indicators. Indicators of ecosystem diversity are split into those of *pattern* and *process* (*32*) (Supporting Information V). Landscape pattern indicators represent human-perceived patterns in a landscape (diversity, patch size, and configuration of habitat). Their link with biological processes, such as dispersal and persistence of species, is not fully understood (*33*). However, key pattern metrics such as area of native habitat and summed anthropogenic edge length often correlate with processes and patterns in emergent biodiversity (*34*). Variables derived from remote sensing, such as the Normalized Difference Vegetation Index (NDVI), can illustrate disturbance regimes, measure vegetation cover, and chart phenological changes (*35*).

Assessing Biodiversity Loss in LCA

In the LCA framework, end point impacts on biodiversity resulting from an environmental intervention (e.g., emission of acidifying substances, conversion or occupation of land) have been developed in the impact categories of land use, water use, climate change, acidification and eutrophication, and ecotoxicity. This covers three of the five principal drivers of biodiversity loss as identified by the MA (Table 2). End point models generally include three components: i) **fate factor**, which models the spatial distribution and intensity of pressures induced by an intervention; ii) **impact factor** (also known as damage or effect factor), which relates the intensity of a unit of pressure to a quantified loss in biodiversity, frequently expressed as the unit-less indicator of "*potentially disappeared fraction (PDF) of species*" (*6*); and iii) **characterization factor**, which multiplies impact factors (intensity of the intervention) by fate factor (size and duration of the intervention) to give an end point of PDF*m^x*yr, where the power term, *x*, equals 2 (for area fate models) and 3 (for volume fate models). Below we briefly summarize the history and state of art of end point modeling in each impact category.

Land Use. The conversion of natural habitat to human use has been the most important driver of biodiversity loss over the past century (*2*). Methods to characterize land use impacts to biodiversity in LCA have mainly used compositional indicators at the level of the local community, primarily species richness (*6, 7, 11, 12, 36, 37, 86*). Koellner and Scholz (*11*) additionally used the number of threatened species as an indirect indicator of ecosystem diversity and land use value. Some studies have included ecosystem level indicators directly, using the relative area of ecosystems (*8, 38–40*), or by predicting the effect of ecosystem level changes on the regional pool of species (*12, 36*). Genetic indicators are absent, but Weidema and Lindeijer (*8*) proposed calculating the change in community phylogenetic diversity due to land use change.

A first attempt to incorporate the effects of fragmentation at the midpoint level was made by Jordaan et al. (*41*). Schenck (*42*) presented a range of indicators including the protection of habitats/species, connectivity of habitats, invasive species, and percentage of native-dominated vegetation but proposed no means to integrate these into an operational framework. Michelson (*43*) included a limited set of local indicators of ecosystem function. Net primary productivity (NPP) was proposed early on as a functional indicator (*7–9*). Other approaches used the concept of hemeroby - naturalness of ecosystems - to characterize land use types on a scale of 0, purely artificial, to 1, no human influence (*44–46*).

Vascular plant species richness has been the core taxa for land use assessments, mainly because of data availability and the close associations to specific land uses (*6, 7, 11, 12, 36*). Michelsen (*43*) suggested an integrative index, Conditions

for Maintained Biodiversity, in order to address taxonomic coverage, but this indicator requires region-specific information, not readily available for many areas or ecosystems. Koellner and Scholz (*11*) included species richness of mollusks and moss in addition to vascular plants. Geyer et al. (*86*) used the habitat affinities of vertebrate species to calculate impacts on species richness, abundance, and evenness. Mattsson et al. (*47*) recommended using richness of mammals, birds, and butterflies, but no overall assessment framework was provided. A multitaxa approach to agricultural land use and management regimes using taxon-specific impact scoring was employed in the Swiss Agricultural Life Cycle Assessment (SALCA) method (*48*).

The majority of approaches were developed for specific geographic regions, namely Northern Europe (*11, 36, 43*), North America (*49, 86*), and South-East Asia (*12*). Weidema and Lindeijer (*8*) proposed a global approach at a biome scale, but it remains of limited application because of the coarseness of the method (but see ref *49* for a regionalized adaptation). The species-area relationship (SAR) (*50*) and sample-based rarefaction (*51*) have been applied to compare the species richness of standardized sampling areas in different land classes (*11, 12, 37*). The SAR also forms the basis for regional damage calculation, estimating the increased risk of regional extinction due to land use change (*11, 12, 37*).

Water Use. Anthropogenic water use reduces regional availability, impairing the functioning and diversity of water-dependent terrestrial (*13*) and freshwater (*52*) ecosystems. The assessment of water use impacts in LCA is a relatively new development. Mila i Canals et al. (*53*) suggested an indicator, Freshwater Ecosystem Impact, to describe the damage to natural ecosystems resulting from depleted water resources via land occupation and the resulting changes in runoff quality and quantity, and abstractive use for agriculture. Pfister et al. (*13*) developed the only existing method to model the impacts of freshwater use on natural ecosystems to the end point level. In this work, impacts to terrestrial biodiversity were approximated using water-limited NPP as a functional indicator (based on ref *54*). Links to species richness were established via a correlation between NPP and vascular plant species richness at low to medium levels of species richness (*13*). It was assumed that water-limited terrestrial ecosystems, generally in arid areas, do not display high species richness. Since water availability and vulnerability of ecosystems varies as a function of space, the method of Pfister et al. (*13*) was regionalized to provide impact factors for all global watersheds.

Climate Change. Climate change, driven by anthropogenic greenhouse gas emissions, is expected to cause a large number of terrestrial extinction over the next century due to changing temperature, precipitation, and seasonality (*55, 56*). Aquatic effects include extinctions of fish species due to reduced river discharge (*52*) and mass extinctions of coral reefs due to warming sea temperature (*57*) and increased ocean acidification (*58*). Within LCA, the only operational impact assessment method for climate change was restricted to terrestrial biodiversity and is based on the increased extinction risk associated with changes in individual species' distributions under future climate scenarios (*14*). The damage factor was based on the work of Thomas et al. (*56*), which reviewed nine studies linking regional extinction risk with changing climate across a number of species groups.

The method of De Schryver et al. (*14*) included assessments of 1084 plant and animal species across five regions (in Europe, Mexico, Australia, South Africa, and Brazil). Climate envelope modeling was used to estimate range area reductions per species and the associated increase in extinction risk (*56*). Three approaches based on the SAR were

TABLE 2. Recent Methods in LCA That Model End Points of Biodiversity Loss Cover Three of the Five Drivers Identified by the MA[a]

MA driver and corresponding LCA impact category	modeling approach (data type)	indicator component	attribute	taxonomic coverage	geographic coverage
Habitat Change					
		Land Use			
Koellner 2000, 2003; Koellner and Scholz 2008; Schmidt 2008	standardized species richness; standardized number of threatened species (EDP) (sampled species occurrence data)	community	composition	vascular plants, mollusks (EDP), moss (EDP)	C. Europe, SE Asia (Schmidt 2008)
Koellner 2000, 2003; Schmidt 2008	SAR-based; proportion of LI land in region and assumed species associations (GIS vegetation/LU classes)	ecosystem	composition		
Michelsen 2008 (cf. Weidema and Lindeijer 2001)	area index for scarcity; integrative conservation index for vulnerability (WWF ecoregion data)	ecosystem	integrative	weight for IUCN threatened species	global
Michelsen 2008	Conditions for Maintain Biodiversity index; decaying wood (regional estimates), set aside land (area), invasive species (percentage community)	ecosystem	integrative	n/a (multiple proxies used)	Scandinavian and Russian taiga
		Water Use			
Pfister et al. 2009	environmental modeling; w-NPP change due to water use (remote sensing and GIS)	ecosystem	function	n/a (w-NPP proxy for vascular plant richness)	global
Climate Change					
De Schryver et al. 2009	meta-study-based impact factor; climate-envelope modeling; 3 SAR-inspired methods (species occurrence data)	species	composition	vascular plants, mammals, birds, amphibians, insects	global (extrapolated)
Pollution					
		Acidification and Eutrophication			
Van Zelm et al. 2007 (acidification)	modeled species absence as function of BS (species occurrence data); % sp. absent ≈ PDF	species	composition	vascular plants (forest species)	Europe
Goedkoop and Spriensma 2001 (acidification and eutrophication)	modeled species absence as function of nitrogen deposition (species occurrence data); % sp. absent ≈ PDF	species	composition	vascular plants, insects (butterflies)	Netherlands
Goedkoop et al. 2009 (eutrophication)	modeled genera absence as function of phosphorus conc. (genera occurrence data): % gen. absent ≈ PDF	species	composition	insects (macro-invertebrate)	N. Europe
		Ecotoxicity			
Van den Brink et al. 2002; Posthuma and de Zwart 2006	testing the PAF ≈ PDF relationship with semifield data (community composition and richness)	community	composition	cold-blooded model organisms	temperate climates
Goedkoop and Spriensma 2001	NOEC(SSD)-based PAF ≈ 0.1*PDF; laboratory species reproductive declines (species abundance data)	species	composition	cold-blooded model organisms	global (extrapolated)
Rosenbaum et al. 2008	USEtox; HC50(SSD)-based PAF; laboratory species reproductive declines (species abundance data)	species	composition		global

[a] End point modeling (second column) refers to method and data used to calculate characterization factors. Indicator component and attribute is described in the text. Taxonomic coverage lists species groups assessed. Geographic coverage refers to broad region used in analyis. PDF = potentially disappeared fraction of species; PAF = potentially affected fraction of species; SSD = species sensitivity distribution; HC50 = effect concentration for 50% of the population; NOEC = no observed effect concentration; BS = base saturation; SAR = species area relationship; w-NPP = water limited net primary productivity; EDP = Ecosystem Damage Potential, LI = low intensity; n/a = not applicable.

used to estimate predicted extinctions. Responses were tested under assumptions of dispersal and nondispersal ability and red list species and all species, respectively (56). This species level approach was used to approximate the potentially disappeared fraction of species, extrapolated to global terrestrial extent to represent a global impact factor.

Acidification and Eutrophication. Acidification and eutrophication leads to a disruption of the natural nutrient balance, altering the species composition of ecosystems, and frequently leading to a loss of biodiversity (59, 60). The effects of acidification on ecosystems quality have been included in LCA using methods that considered the sensitivity of the

receiving ecosystems (*61–66*) or effects on NPP (*67*). Species level impacts for terrestrial acidification have been modeled based on occurrence data for vascular plants (*6, 15, 68*) and butterflies (*6*). Van Zelm et al. (*15*) modeled the probability of occurrence of over 240 forest plant species in Europe. A threshold was constructed for each species as a function of the base saturation of the soil. The PDF was approximated by the percentage of species predicted to be absent because of elevated base saturation. This impact factor was multiplied by the total forest and nonforest area of Europe to approximate overall impacts to the region affected by acidifying emissions.

Freshwater eutrophication was included in the ReCiPe method (*68*) for Europe using the diversity of macroinvertebrate genera as indicators of taxonomic diversity. Environmental modeling was used to predict the absence of over 837 macro-invertebrate genera, approximating PDF, as a function of phosphorus concentration (*68*).

Taxonomic coverage for both acidification and eutrophication remains limited to species groups where pressure and occurrence data exist. Current methods are applicable to Europe, although the impact factors are likely to apply to other temperate climates, but not to tropical and subtropical regions (*69*). Impact factors for aquatic acidification and marine eutrophication are absent from any proposed method.

Ecotoxicity. Chemical emissions to aboveground biomass, air, water, and soil cause toxicity to a variety of organisms. Research on ecotoxicological impacts to biodiversity in the context of LCA has been ongoing for many years (*16*). Model species in laboratory settings are used to establish the *potentially affected fraction* (PAF) of species due to elevated concentrations of a toxin. It is defined as the percentage of species within a community or taxonomic group that is expected to be exposed above a certain effect-related threshold, such as the effect concentration for 50% of the population (EC_{50}) or the no observed effect concentration (NOEC) (*16, 70*). This uses species level indicators of abundance and reproductive decline.

The exact relationship between the PAF and species loss from a community is a topic of debate. By comparing laboratory experiments with field data, Van den Brink et al. (*71*) showed that direct effects of long-term and acute exposure are generally well reflected by species sensitivity distributions used to calculate the PAF of a community. The study assessed changes in biodiversity across a wide range of animal and plant taxa. Posthuma and de Zwart (*72*) showed that in fish species assemblages in North American streams, the observed loss of species ascribed to mixture toxicity closely matched the predicted risks based on EC_{50}. Snell and Serra (*73*) modeled reproduction effects on rotifers and showed that an EC_{50} will result in population extinction after a long exposure time. The PAF therefore may have the diagnostic properties required to assess ecological responses to ecotoxic stress.

LCA models are available that can be adapted to meet region-specific conditions but can also provide continental and global factors, such as the USEtox model (*74*). Freshwater biodiversity responses have received the most attention, and more research is necessary on the response of terrestrial and marine ecosystems. Taxonomic coverage is usually limited to low trophic position, cold-blooded species. The effects of bioaccumulation and biomagnification are only beginning to be investigated in LCA.

Limitations. End point modeling in LCA currently suffers from at least two classes of limitation, that we term "*Conceptual limitations*" and "*Data limitations*". The former relates to methodological choices during impact factor development and the constraints imposed by the overarching LCA framework. The latter relates to a general lack of knowledge on how interventions affect biodiversity and a lack of biological data for many taxa and world regions. This has invariably necessitated the adoption of numerous assumptions, some of which are listed below:

Conceptual Limitations.

1. End Point Unit. Because PDF is unit-less, characterization factors (PDF*m^x*yr) are expressed in units of area/volume loss (in m^2 or m^3) for a fixed duration (in yrs). This assumes impacts across all impact categories can be expressed as an *effective loss of habitat* for biodiversity.

2. Impact Scale. Some impact factors express local extinctions (e.g., acidification), while others express regional extinctions (e.g., climate change). It is assumed that impacts at different scales can be directly compared and aggregated.

3. Linear Damage Relationship. When characterization factors are developed for scales other than what was used for impact factor development, the relationship between species loss (overall impact) and area affected is assumed to be linear (except for the land use regional impact which applied the nonlinear SAR (*11*)).

4. Use of Indicators. Indicators used to construct impact factors may reflect various components (species, communities, and ecosystems) and attributes (compositional, functional, and structural) of biodiversity but are assumed to approximate damages to species diversity (PDF).

Data Limitations.

5. Geographic Coverage. Regionalization is incomplete for most impact factors. It is assumed that impact factors developed in certain regions (mainly Western Europe) are representative of all world regions. Furthermore, characterization factors are missing for major realms across all impact categories (e.g., marine eutrophication, terrestrial ecotoxicity, aquatic lake- and sea-bed damage).

6. Taxonomic Coverage. Only a relatively small number of taxa are used to develop impact factors. These impact factors are assumed to apply to all taxa during the construction of characterization factors.

7. Missing Drivers. Two drivers of biodiversity loss (over-exploitation and invasive species) are completely missing from LCA. Until impact pathways for these drivers are developed, their importance regarding biodiversity loss is essentially assumed to be negligible.

In the following sections, we critically examine these assumptions and highlight potential research directions that could improve biodiversity assessment in LCA. Due to space limitations, the last assumption (missing drivers) is addressed in the Supporting Information (section VIII).

End Point Unit, Scale, and Linearity

End Point Unit. End points of biodiversity in LCA are expressed across all impact categories as an *effective loss of habitat*, which converts the area/volume partially affected by an intervention (i.e., PDF < 1) to an equivalent area/volume of total loss of habitat value for biodiversity (PDF = 1). The exact proportion is dependent on the intensity of the intervention, which is given by the impact factor. This is a potentially useful approach that has been applied outside of LCA to assess land use impacts using variants of the SAR (*27, 75*) and forms the basis of the GLOBIO3 modeling framework (*3*). It has also been expanded to include freshwater impacts across a range of pressures using river section length in place of area (*76*).

Impact Scale. Current LCA impact factors estimate species extinctions, in terms of PDF, at largely undefined spatial scales. Biodiversity loss represents a concern over the potential extinction of species at broadly defined scales (subnational, national, and international (*1*)). Likewise, the scale of extinctions in LCA requires standardization at one or multiple scales (i.e., the local community, the ecosystem or landscape, the region, or the globe). Koellner (*37*) highlighted the arguable distinction between local impacts,

which reflect concerns over the loss of local ecosystem functioning, and regional impacts, which reflect conservation concerns over species loss. Both are valid impacts but convey very different messages to the end user of an LCA. This raises serious questions about the validity of current aggregative single score assessment tools where damages across impact categories, representing various geographic scales of extinction, are combined by simple summation (e.g., EcoIndicator 99 and ReCiPe 2008).

Linear Damage Relationship. Current scaling of impact factors to arrive at characterization factors assumes a simple linear damage function (PDF*area). This should be reconsidered given the importance of scale influences in ecology (77) and the presence of nonlinearity's, tipping points, and critical thresholds in biological responses to disturbance (78). The adoption of the nonlinear SAR and its variants (75, 76, 79, 80) could instead be used to take advantage of assumption one (end point unit) in order to address assumption two (impact scale) and three (linear damage relationship). This would require an extra step in characterization factor development that would consist of expressing effective habitat loss as a reduction in the species pool of the affected ecosystem(s), thereby providing the fraction of species potentially lost at the defined scale. This percentage loss could be related to absolute species losses using widespread regional checklist data for various taxa (e.g., WWF ecoregions (81)).

Use of Indicators

Indicators in LCA tend to reflect compositional changes in biodiversity, particularly at the species and community level (Table 2). Indicators that reflect changes in a variety of components (species, communities, ecosystems) and attributes (composition, structure, function) of biodiversity are also often employed to approximate species loss in terms of PDF. For example, the SAR is used to translate ecosystem indicators of habitat area change into predicted species losses. Likewise, single-species indicators are combined to approximate overall impacts across all species, either in a local community (e.g., PAF in ecotoxic impacts) or across an entire region (e.g., climate change impacts). Additionally, the functional indicator of NPP change is used as a proxy for species loss in water use impact assessment. Below we discuss the implications of this approach and the possibility of developing new impact factors to reflect additional aspects of biodiversity.

Genetic Component. Genetic indicators are absent from LCA. Developing impact factors based on phylogenetic diversity would enable interspecific genetic diversity to be approximated using existing species data (24, 25). Cadotte et al. (82) demonstrates an approach to calculate changes in phylogenetic diversity for plant communities using molecular sequence data from GeneBank (www.cnbe.nlm.nih.gov). The impact factor would express changes in the sum of branch lengths linking species from a sample of a community (25). Intraspecific (within-species) genetic variation, reflecting impacts to the genetic diversity of single species, such as population declines leading to reduced heterogeneity, will be extremely difficult to incorporate (see Supporting Information I) and is limited by data availability (83).

Species and Community Component. By definition, PDF is a multispecies index, and aggregating single-species indicators assumes that all species react to pressures in the same way as those assessed (Supporting Information IV). As the number of assessed species increases, results should be expected to converge (84, 88). In species level approaches in LCA, the number of species employed to construct impact factors is generally large (e.g., 1084 species for climate change (14); 240 species for acidification (15); 837 genera for eutrophication (68)). In ecotoxicity the use of model organisms generally does not exceed ten species per substance (85). This introduces large uncertainties and more studies are needed that test these laboratory results against field data (e.g. refs 72 and 73). Inclusion of both species and community approaches across impact categories may offer better estimates of trade-offs and uncertainties associated with different methods.

Ecosystem and Landscape Component. In LCA, ecosystem indicators used to approximate species loss at the end point have been employed only in land use and consider relatively simple effects based on the SAR (11, 12, 36, 37). Recent land use methods are including more complex models of habitat area and composition (86). Outside of LCA, the InVEST tool (87) takes a detailed approach in estimating the contribution of each habitat patch to a species' persistence in the landscape using "countryside SARs" (75). This accounts for patch size, cumulative anthropogenic habitat edge length, configuration, and the habitat requirements and dispersal ability of the assessed species (87).

The current species-level approach in climate change modeling in LCA could be expanded to employ ecosystem-level indicators by modeling ecosystem area changes and resulting species loss via the SAR. For example, the MA (88) and GLOBIO3 (3) predict biome and vegetation community expansions and contractions under IPCC scenarios using the IMAGE model (89) and relate this to species loss predicted by the SAR (3, 91). The ecosystem impact of consumptive water use is modeled to impacts on vascular plant species diversity in LCA through water-limited NPP. Additional, direct impacts of water use on fish species richness of rivers could be captured by the species-discharge relationship (92) both for water use and climate change (52). Remote sensing data could help expand this to identify terrestrial drought damages to ecosystems caused by water abstraction or climate change (see ref 35).

Ecosystem effects of acidification, eutrophication, and ecotoxicity, modeled to the end point of species loss, are lacking. Ecosystem impacts have been developed in LCA using critical nitrogen and phosphorus loading values for acidification and eutrophication (65, 66), but the consequential effects on species richness were not included. Critical loading has been extensively employed outside of LCA (e.g. refs 59 and 69). Acidification and eutrophication are covered in both the MA (88) and GLOBIO3 model (3) using meta-analyses of empirical studies documenting the relationship between exceedance of critical load and species loss (e.g. ref 93). Such a relationship could be adapted to existing LCA methods.

Biological Attributes. The majority of indicators of biodiversity in LCA measure composition (Table 2). Indicators of structure and function are largely absent. There are a range of indicators and methods to infer structural information at the local to ecosystem scale (Table 1). Impacts such as eutrophication or land use cause extensive structural alterations to habitats. A meta-analysis of published studies documenting the effect of pressures on the structural diversity of communities could potentially yield impact factors which could be used as a rough proxy for species loss (94).

On an ecosystem level, indicators were used in LCA to reflect fragmentation effects at the midpoint of land use (41), but no attempt was made to model the damage to species richness. The meta-study of Harper et al. (95) could be used to complete this process. Outside of LCA, fragmentation effects were included in the GLOBIO3 model using 6 published data sets that quantify species loss as a function of patch size (3). The BioScore tool (96) uses focal species that are sensitive to fragmentation (e.g., habitat specialists).

Changes in functional diversity are currently considered in LCA only at the ecosystem level using NPP. Abiotic indicators, such as NDVI-based metrics, hydromorphic and

geomorphic modeling, erosion potential, and disturbance indicators could further be used to model impacts to ecosystem functioning (functional diversity; Table 1). The relationship between species diversity and ecosystem function is not well enough understood to allow PDF to act as a proxy for functional diversity or vice versa (91). New methods in land use developed in the framework of the UNEP-SETAC Life Cycle Initiative will employ abiotic functional indicators to model damages to a separate functional end point for ecosystems services (97). Thuiller et al. (55) modeled climate change impacts to functional group diversity of plants at the community level. This could be incorporated into LCA directly as a new impact factor for climate change. Interestingly, Cadotte et al. (82) found phylogenetic diversity to be a better predictor of ecosystem function than functional group diversity. This might indicate how functional and genetic diversity may be incorporated into LCA using a single indicator.

Multiple Impact Factors. In order to better reflect the diverse components and attributes of biodiversity, we see the need to develop multiple impact factors for biodiversity. Currently in LCA, compositional indicators at the species, community, and ecosystem level approximate PDF. Structural indicators at the community and ecosystem level may also be expressed in terms of PDF, such as reductions in habitat complexity, increased fragmentation, and habitat patch configuration (3, 87). Genetic diversity will require a separate impact factor of phylogenetic diversity. Phylogenetic diversity may also function as a good proxy for community functional diversity; otherwise functional groups or trait-space distance could be used to create an additional impact factor. Finally, community and ecosystem functional diversity will require an independent impact factor (e.g., damages to ecosystem services (98)). Including the genetic component of function and structure and the species component of structure into LCA is not foreseeable in the near future.

Taxonomic and Geographical Coverage

Taxonomic Coverage. Methodologies for all impact categories (except climate change) were developed using very few taxonomic groups to construct impact factors (Table 2). The use of surrogate taxa to reflect the overall response of biodiversity to environmental stress is questionable (99). In a global meta-study of multiple taxon responses to disturbance, Wolters et al. (99) found a weak average correlation between taxa ($r = 0.38$). A number of factors influence this including habitat type, taxon, temporal, and spatial scale. Yet precise roles of these factors are poorly investigated and unpredictable in novel situations (99). In the context of LCA, methods should prioritize major trophic or functional groups, taxa which are sensitive to the relevant pressures, and expand coverage based on data availability and feasibility.

The use of deductive methods can aid in overcoming both taxonomic and geographic limitations. Such an approach has been employed in studies such as the BioScore tool to model the response of indicator species to a range of pressures (96); the Biodiversity Intactness Index to model the effects of land degradation (27); and the Mean Species Abundance as part of the GLOBIO3 model (3).

Geographic Coverage. The geographic coverage of methods in only two impact categories, water use and climate change, is global with respect to the terrestrial environment (Table 2). However, current climate change methods cover only 20% of the total terrestrial area across forest, arid/semiarid, and mountain regions. Vulnerable terrestrial areas, such as islands and polar areas, should be prioritized for future work. The methods in remaining impact categories were developed for use in specific regions or biomes. Detailed biodiversity data on the distribution of species across many taxa are incomplete on a global scale. Worldwide species

richness and endemism data are available in equal-area grids and likely to be relatively robust to undersampling only for birds and plants (100, 101; also see IUCN global assessments of other taxa). For other taxa, checklists of predefined terrestrial and aquatic biogeographic regions and expert opinion (e.g. refs 81 and 102−104) have been used to map and assess biodiversity (105).

Currently no methods exist to quantify aquatic habitat change in the context of land and water use. Meta-analysis or regional case-studies could guide the development of impact factors for lakebed, riverbed, and seabed habitats across regions and climates, such as that pursued by the GLOBIO3 model for aquatic and marine environments (http://www.globio.info/). Turak et al. (76) illustrates how an SAR-based approach can be adapted to freshwater habitats, using river length in place of area, to reflect a range of pressures. Global, spatially differentiated maps of pressures on marine ecosystems exist for 17 anthropogenic pressures at a grid resolution of 1 km^2 (106). For climate change, freshwater effects could be included by adopting a similar approach to Xenopolous et al. (52). For marine climate change impacts, Halpern et al. (106) provides a spatially resolved global map of climate change impacts on marine biodiversity including sea temperature rise, ocean acidification, and UV radiation. This work also provides globally mapped impacts due to pollution runoff into marine waters, information that could be used to regionalize acidification and eutrophication. Ecotoxicity requires further semifield research to verify the relationship between PAF and PDF across regions and environments (e.g. refs 72 and 73).

Research Outlook

Our review has illustrated the currently poor state of end point biodiversity modeling in LCA. The deficiencies across impact categories are not solely due to data limitations or even the inherent complexities of the element under study. They are also conceptual and methodological in nature. In order to meaningfully represent biodiversity in LCA, we present two broad recommendations for future research, presented in order of importance.

Fill the Conceptual Cracks. We see a need to first address the methodological shortcomings of current approaches. Clearly and explicitly defining PDF is an essential and urgently needed first step. Experimenting with nonlinear, potentially unifying relationships (such as the SAR) when scaling impact factors represents another promising area of research that would eliminate the need to derive new impact factors for each scale.

Challenge Data Limitations. We have highlighted a wealth of data on the distribution of pressures (the basis of fate factors), their effects on various taxa (the basis of impact factors), and the global distribution of biodiversity either through raw data, models, or surrogate indicators (the basis of characterization factors). Such data should be used to regionalize existing methods in order to capture a representative sample of the Earth's diverse terrestrial, freshwater, and marine habitats and to include a range of representative taxa. Following this, integrating new drivers and impact factors reflecting additional attributes of biodiversity could further improve the modeling of biodiversity loss in LCA.

Supporting Information Available

Expanded account of biodiversity indicators and their uses in biodiversity assessments. This material is available free of charge via the Internet at http://pubs.acs.org.

Literature Cited

(1) CBD: Convention on Biological Diversity; Rio de Janeiro, 1993 http://www.cbd.int/ (accessed July 13, 2009).

(2) MA: Millennium Ecosystem Assessment: Current state and trends 2005 http://www.millenniumassessment.org/en/index.aspx (accessed July 21, 2009).

(3) Alkemade, R.; van Oorschot, M.; Miles, L.; Nellemann, C.; Bakkenes, M.; ten Brink, B. GLOBIO3: A Framework to Investigate Options for Reducing Global Terrestrial Biodiversity Loss. *Ecosystems* **2009**, *12*, 374–390.

(4) Sala, O. E.; Chapin, F. S.; Armesto, J. J.; Berlow, E.; Bloomfield, J.; Dirzo, R.; Huber-Sanwald, E.; Huenneke, L. F.; Jackson, R. B.; Kinzig, A.; Leemans, R.; Lodge, D. M.; Mooney, H. A.; Oesterheld, M.; Poff, N. L.; Sykes, M. T.; Walker, B. H.; Walker, M.; Wall, D. H. Global Biodiversity Scenarios for the Year 2100. *Science* **2000**, *287*, 1770–1774.

(5) Finnveden, G.; Hauschild, M. Z.; Ekvall, T.; Guinée, J.; Heijungs, R.; Hellweg, S.; Koehler, A.; Pennington, D.; Suh, S. Recent developments in Life Cycle Assessment. *J. Environ. Manage.* **2009**, *91*, 1–21.

(6) Goedkoop, M. ; Spriensma, R. *Eco-indicator 99, a damage oriented method for Life Cycle Impact Assessment: methodology report,* 3rd ed.; 2001.

(7) Lindeijer, E. Biodiversity and life support impacts of land use in LCA. *J. Cleaner Prod.* **2000**, *8*, 313–319.

(8) Weidema, B. P. ; Lindeijer, E. Physical impacts of land use in product life cycle assessment. *Final report of the EURENVIRON-LCAGAPS sub-project on land use*; Department of Manufacturing Engineering and Management, Technical University of Denmark: 2001.

(9) Blonk, H.; Lindeijer, E.; Broers, J. Towards a methodology for taking physical degradation of ecosystems into account in LCA. *Int. J. Life Cycle Assess.* **1997**, *2*, 91–98.

(10) Heijungs, R.; Guinée, J.; Huppes, G. Impact categories for natural resources and land use. *CML report* **1997**, *138*.

(11) Koellner, T.; Scholz, R. W. Assessment of land use impacts on the natural environment. Part 2: Generic characterization factors for local species diversity in central europe. *Int. J. Life Cycle Assess.* **2008**, *13*, 32–48.

(12) Schmidt, J. Development of LCIA characterisation factors for land use impacts on biodiversity. *J. Cleaner Prod.* **2008**, *16*, 1929–1942.

(13) Pfister, S.; Koehler, A.; Hellweg, S. Assessing the Environmental Impacts of Freshwater Consumption in LCA. *Environ. Sci. Technol.* **2009**, *43*, 4098–4104.

(14) De Schryver, A.; Brakkee, K.; Goedkoop, M.; Huijbregts, M. Characterization Factors for Global Warming in Life Cycle Assessment Based on Damages to Humans and Ecosystems. *Environ. Sci. Technol.* **2009**, *43*, 1689–1695.

(15) van Zelm, R.; Huijbregts, M. A. J.; van Jaarsveld, H. A.; Reinds, G. J.; de Zwart, D.; Struijs, J.; van de Meent, D. Time horizon dependent characterization factors for acidification in life-cycle assessment based on forest plant species occurrence in Europe. *Environ. Sci. Technol.* **2007**, *41*.

(16) Larsen, H. F.; Hauschild, M. Evaluation of Ecotoxicity Effect Indicators for Use in LCIA (10 + 4 pp). *Int. J. Life Cycle Assess.* **2007**, *12*, 24–33.

(17) Pennington, D. W.; Payet, J.; Hauschild, M. Aquatic ecotoxicological indicators in life-cycle assessment. *Environ. Toxicol. Chem.* **2004**, *23*, 1796.

(18) Pelletier, N.; Ayer, N.; Tyedmers, P.; Kruse, S.; Flysjo, A.; Robillard, G.; Ziegler, F.; Scholz, A.; Sonesson, U. Impact categories for life cycle assessment research of seafood production systems: Review and prospectus. *Int. J. Life Cycle Assess.* **2007**, *12*, 414–421.

(19) Koellner, T.; Scholz, R. W. Assessment of Land Use Impacts on the Natural Environment Part 1: An Analytical Framework for Pure Land Occupation and Land Use Change. *Int. J. Life Cycle Assess.* **2007**, *12*, 16.

(20) Udo de Haes, H. How to approach land use in LCIA or, how to avoid the Cinderella effect. *Int. J. Life Cycle Assess.* **2006**, *11*, 219–221.

(21) Noss, R. F. Indicators for Monitoring Biodiversity: A Hierarchical Approach. *Conserv. Biol.* **1990**, *4*, 355–364.

(22) Niemi, G. J.; McDonald, M. E. Application of ecological indicators. *Annu. Rev. Ecol., Evol., Syst.* **2004**, *35*, 89–111.

(23) Hughes, A. R.; Inouye, B. D.; Johnson, M. T. J.; Underwood, N.; Vellend, M. Ecological consequences of genetic diversity. *Ecol. Lett.* **2008**, *11*, 609–623.

(24) Faith, D. P. Quantifying biodiversity: a phylogenetic perspective. *Conserv. Biol.* **2002**, *16*, 248–252.

(25) Faith, D. P.; Reid, C. A. M.; Hunter, J. Integrating phylogenetic diversity, complementarity, and endemism for conservation assessment. *Conserv. Biol.* **2004**, *18*, 255–261.

(26) Lambeck, R. J. Focal species: a multi-species umbrella for nature conservation. *Conserv. Biol.* **1997**, *11*, 849–856.

(27) Scholes, R. J.; Biggs, R. A biodiversity intactness index. *Nature* **2005**, *434*, 45–49.

(28) Corsi, F.; de Leeuw, J.; Skidmore, A. Modeling Species Distribution with GIS. *Res. Tech. Anim. Ecol.* **2000**, 389.

(29) Jost, L. Entropy and diversity. *Oikos* **2006**, *113*, 363.

(30) Ferrier, S.; Guisan, A. Spatial modelling of biodiversity at the community level. *J. Appl. Ecol.* **2006**, *43*, 393–404.

(31) Petchey, O. L.; Gaston, K. J. Functional diversity: back to basics and looking forward. *Ecol. Lett.* **2006**, *9*, 741–758.

(32) McGarigal, K. ; Marks, M. Spatial pattern analysis program for quantifying landscape structure. *Gen. Tech. Rep. PNW-GTR-351.* U.S. Department of Agriculture, Forest Service, Pacific Northwest Research Station: 1995.

(33) Turner, M. G. Landscape Ecology: What Is the State of the Science. *Annu. Rev. Ecol. Evol. Syst.* **2005**, *36*, 319–344.

(34) Fischer, J.; Lindenmayer, D. B. Landscape modification and habitat fragmentation: a synthesis. *Global Ecol. Biogeogr.* **2007**, *16*, 265–280.

(35) Foody, G. GIS: biodiversity applications. *Prog. Phys. Geogr.* **2008**, *32*, 223–235.

(36) Koellner, T. Species-pool effect potentials (SPEP) as a yardstick to evaluate land-use impacts on biodiversity. *J. Cleaner Prod.* **2000**, *8*, 293–311.

(37) Koellner, T. *Land Use in Product Life Cycles and Ecosystem Quality*; Peter Lang: Bern, Frankfurt a. M., New York. 294, 2003.

(38) Müller-Wenk, R. Land-use - The Main Threat to Species. *How to Include Land Use in LCA. IWÖ-Diskussionsbeitrag* **1998**, *64*.

(39) Vogtländer, J. G.; Lindeijer, E.; Witte, J. M.; Hendriks, C. Characterizing the change of land-use based on flora: application for EIA and LCA. *J. Cleaner Prod.* **2004**, *12*, 47–57.

(40) Kyläkorpi, K. ; Rydgren, B. ; Ellegård, A. ; Miliander, S. ; Grusell, E. *The Biotope Method 2005. A method to assess the impact of land use on biodiversity*; Vattenfall, Sweden, 2005.

(41) Jordaan, S. M.; Keith, D. W.; Stelfox, B. Quantifying land use of oil sands production: a life cycle perspective. *Environ. Res. Lett.* **2009**, *4*, 024004.

(42) Schenck, R. Land use and biodiversity indicators for life cycle impact assessment. *Int. J. Life Cycle Assess.* **2001**, *6*, 114–117.

(43) Michelsen, O. Assessment of land use impact on biodiversity. *Int. J. Life Cycle Assess.* **2008**, *13*, 22–31.

(44) Baitz, M.; Kreissig, J.; Wolf, M. Method for integrating Land Use into Life-Cycle-Assessment (LCA). *Forstwiss. Centralbl.* **2000**, *119*, 128–149.

(45) Bauer, C.; Zapp, P. Towards generic characterisation factors for land use and water consumption. *International Workshop on Life Cycle Assessment of Metals—issues and research directions.* SETAC; Pensacola, FL, 2004; pp 96−101.

(46) Brentrup, F.; Küsters, J.; Lammel, J.; Kuhlmann, H. Life Cycle Impact assessment of land use based on the hemeroby concept. *Int. J. Life Cycle Assess.* **2002**, *7*, 339–348.

(47) Mattsson, B.; Cederberg, C.; Blix, L. Agricultural land use in life cycle assessment (LCA): case studies of three vegetable oil crops. *J. Cleaner Prod.* **2000**, *8*, 283–292.

(48) Jeanneret, P.; Baumgartner, D. U.; Knuchel, R. F.; Gaillard, G. *In 6th International Conference on LCA in the Agri-Food Sector*, Zurich, November 12−14, 2008.

(49) Toffoletto, L.; Bulle, C.; Godin, J.; Reid, C.; Deschênes, L. LUCAS - A New LCIA Method Used for a Canadian-Specific Context (10 pp). *Int. J. Life Cycle Assess.* **2007**, *12*, 93–102.

(50) Rosenzweig, M. L. *Species Diversity in Space and Time*; Cambridge University Press: Cambridge, 1995.

(51) Colwell, R. K.; Mao, C. X.; Chang, J. Interpolating, extrapolating, and comparing incidence-based species accumulation curves. *Ecology* **2004**, *85*, 2717–2727.

(52) Xenopoulos, M. A.; Lodge, D. M.; Alcamo, J.; Märker, M.; Schulze, K.; Vuuren, D. P. V. Scenarios of freshwater fish extinctions from climate change and water withdrawal. *Global Change Biol.* **2005**, *11*, 1557–1564.

(53) Milà i Canals, L.; Chenoweth, J.; Chapagain, A.; Orr, S.; Antón, A.; Clift, R. Assessing freshwater use impacts in LCA: Part I—inventory modelling and characterisation factors for the main impact pathways. *Int. J. Life Cycle Assess.* **2009**, *14*, 28–42.

(54) Nemani, R. R.; Keeling, C. D.; Hashimoto, H.; Jolly, W. M.; Piper, S. C.; Tucker, C. J.; Myneni, R. B.; Running, S. W. Climate-Driven Increases in Global Terrestrial Net Primary Production from 1982 to 1999. *Science* **2003**, *300*, 1560–1563.

(55) Thuiller, W.; Lavorel, S.; Sykes, M. T.; Araújo, M. B. Using niche-based modelling to assess the impact of climate change on tree functional diversity in Europe. *Diversity Distrib.* **2006**, *12*, 49.

(56) Thomas, C. D.; Cameron, A.; Green, R. E.; Bakkenes, M.; Beaumont, L. J.; Collingham, Y. C.; Erasmus, B. F. N.; Ferreira de Siqueira, M.; Grainger, A.; Hannah, L. Extinction risk from climate change. *Nature* **2004**, *427*, 145–148.

(57) Hughes, T. P.; Baird, A. H.; Bellwood, D. R.; Card, M.; Connolly, S. R.; Folke, C.; Grosberg, R.; Hoegh-Guldberg, O.; Jackson, J. B. C.; Kleypas, J.; Lough, J. M.; Marshall, P.; Nystrom, M.; Palumbi, S. R.; Pandolfi, J. M.; Rosen, B.; Roughgarden, J. Climate Change, Human Impacts, and the Resilience of Coral Reefs. *Science* **2003**, *301*, 929–933.

(58) *CBD Scientific Synthesis of the Impacts of Ocean Acidification on Marine Biodiversity*; Technical Series No. *46*; Secretariat of the Convention on Biological Diversity: Montreal, 2009; p 61.

(59) Smith, V. H.; Tilman, G. D.; Nekola, J. C. Eutrophication: impacts of excess nutrient inputs on freshwater, marine, and terrestrial ecosystems. *Environ. Pollut.* **1999**, *100*, 179–196.

(60) Stevens, C. J.; Dise, N. B.; Mountford, J. O.; Gowing, D. J. Impact of Nitrogen Deposition on the Species Richness of Grasslands. *Science* **2004**, *303*, 1876–1879.

(61) Potting, J.; Schöpp, W.; Blok, K.; Hauschild, M. Site-dependent life-cycle impact assessment of acidification. *J. Ind. Ecol.* **1998**, *2*, 63–87.

(62) Huijbregts, M. A. J.; Schöpp, W.; Verkuijlen, E.; Heijungs, R.; Reijnders, L. Spatially explicit characterization of acidifying and eutrophying air pollution in life-cycle assessment. *J. Ind. Ecol.* **2000**, *4*, 75–92.

(63) Krewitt, W.; Trukenmüller, A.; Bachmann, T. M.; Heck, T. Country-specific damage factors for air pollutants. *Int. J. Life Cycle Assess.* **2001**, *6*, 199–210.

(64) Hauschild, M.; Potting, J. *Spatial Differentiation in Life Cycle Impact Assessment - the EDIP2003 Methodology*; The Danish Environmental Protection Agency: Copenhagen, 2005.

(65) Seppälä, J.; Posch, M.; Johansson, M.; Hettelingh, J. Country-dependent characterisation factors for acidification and ter-restrial eutrophication based on accumulated exceedance as an impact category indicator. *Int. J. Life Cycle Assess.* **2006**, *11*, 403–416.

(66) Posch, M.; Seppälä, J.; Hettelingh, J. P.; Johansson, M.; Margni, M.; Jolliet, O. The role of atmospheric dispersion models and ecosystem sensitivity in the determination of characterisation factors for acidifying and eutrophying emissions in LCIA. *Int. J. Life Cycle Assess.* **2008**, *13*, 477–486.

(67) Hayashi, K.; Okazaki, M.; Itsubo, N.; Inaba, A. Development of damage function of acidification for terrestrial ecosystems based on the effect of aluminum toxicity on net primary production. *Int. J. Life Cycle Assess.* **2004**, *9*, 13–22.

(68) Goedkoop, M.; Heijungs, R.; Huijbregts, M.; De Schryver, A.; Struijs, J.; van Zelm, R. *ReCiPe 2008. Main Report, Part 1: Characterization*, 1st ed; VROM: The Netherlands, 2009.

(69) Bobbink, R.; Hicks, K.; Galloway, J.; Spranger, T.; Alkemade, R.; Ashmore, M.; Bustamante, M.; Cinderby, S.; Davidson, E.; Dentener, F.; Emmett, B.; Erisman, J.; Fenn, M.; Gilliam, F.; Nordin, A.; Pardo, L.; De Vries, W. Global assessment of nitrogen deposition effects on terrestrial plant diversity: a synthesis. *Ecol. Appl.* **2010**, *20*, 30–59.

(70) de Zwart, D.; Posthuma, L. Complex mixture toxicity for single and multiple species: proposed methodologies. *Environ. Toxicol. Chem.* **2005**, *24*, 2665–2676.

(71) Van den Brink, P. J.; Brock, T. C. M.; Posthuma, L. The value of the species sensitivity distribution concept for predicting field effects: (Non-)confirmation of the concept using semifield experiments. *Species sensitivity distributions in ecotoxicology*; Lewis Publishers: Boca Raton, FL, USA, 2002; pp 155–193.

(72) Posthuma, L.; de Zwart, D. Predicted effects of toxicant mixtures are confirmed by changes in fish species assemblages in Ohio, USA, rivers. *Environ. Toxicol. Chem.* **2006**, *25*, 1094–1105.

(73) Snell, T. W.; Serra, M. Using probability of extinction to evaluate the ecological significance of toxicant effects. *Environ. Toxicol. Chem.* **2000**, *19*, 2357–2363.

(74) Rosenbaum, R.; Bachmann, T.; Gold, L.; Huijbregts, M.; Jolliet, O.; Juraske, R.; Koehler, A.; Larsen, H.; MacLeod, M.; Margni, M.; McKone, T.; Payet, J.; Schuhmacher, M.; van de Meent, D.; Hauschild, M. USEtox — the UNEP-SETAC toxicity model: recommended characterisation factors for human toxicity and freshwater ecotoxicity in life cycle impact assessment. *Int. J. Life Cycle Assess.* **2008**, *13*, 532–546.

(75) Pereira, H. M.; Daily, G. C. Modeling biodiversity dynamics in countryside landscapes. *Ecology* **2006**, *87*, 1877–1885.

(76) Turak, E.; Ferrier, S.; Barrett, T.; Mesley, E.; Drielsma, M.; Manion, G.; Doyle, G.; Stein, J.; Gordon, G. Planning for the persistence of river biodiversity: exploring alternative futures using process-based models. Freshwater Biology 2010, In Press.

(77) Wiens, J. A. Spatial Scaling in Ecology. *Funct. Ecol.* **1989**, *3*, 385–397.

(78) Swift, T. L.; Hannon, S. J. Critical thresholds associated with habitat loss: a review of the concepts, evidence, and applica-tions. *Biol. Rev.* **2010**, *85*, 35–53.

(79) Faith, D. P.; Ferrier, S.; Williams, K. J. Getting biodiversity intactness indices right: ensuring that 'biodiversity' reflects 'diversity'. *Global Change Biol.* **2008**, *14*, 207–217.

(80) Koh, L. P.; Ghazoul, J. A Matrix-Calibrated Species-Area Model for Predicting Biodiversity Losses Due to Land-Use Change. Conservation Biology 2010, In Press.

(81) Olson, D. M.; Dinerstein, E.; Wikramanayake, E. D.; Burgess, N. D.; Powell, G. V. N.; Underwood, E. C.; D'amico, J. A.; Itoua, I.; Strand, H. E.; Morrison, J. C.; Loucks, C. J.; Allnutt, T. F.; Ricketts, T. H.; Kura, Y.; Lamoreux, J. F.; Wettengel, W. W.; Hedao, P.; Kassem, K. R. Terrestrial ecoregions of the world: a new map of life on earth. *BioScience* **2001**, *51*, 933.

(82) Cadotte, M. W.; Cardinale, B. J.; Oakley, T. H. Evolutionary history and the effect of biodiversity on plant productivity. *Proc. Natl. Acad. Sci.* **2008**, *105*, 17012–17017.

(83) Laikre, L. Genetic diversity is overlooked in international conservation policy implementation. *Conserv. Genet.* **2010**, *11*, 349–354.

(84) Roberge, J. M.; Angelstam, P. Usefulness of the umbrella species concept as a conservation tool. *Conserv. Biol.* **2004**, *18*, 76–85.

(85) van Zelm, R.; Huijbregts, M.; Posthuma, L.; Wintersen, A.; van de Meent, D. Pesticide ecotoxicological effect factors and their uncertainties for freshwater ecosystems. *Int. J. Life Cycle Assess.* **2009**, *14*, 43–51.

(86) Geyer, R.; Lindner, J.; Stoms, D.; Davis, F.; Wittstock, B. Coupling GIS and LCA for biodiversity assessments of land use. Part 2: Impact assessment. *Int. J. Life Cycle Assess.* **2010**, *15*, 692–703.

(87) Nelson, E.; Mendoza, G.; Regetz, J.; Polasky, S.; Tallis, H.; Cameron, D.; Chan, K. M.; Daily, G. C.; Goldstein, J.; Kareiva, P. M.; Lonsdorf, E.; Naidoo, R.; Ricketts, T. H.; Shaw, M. Modeling multiple ecosystem services, biodiversity conserva-tion, commodity production, and tradeoffs at landscape scales. *Front. Ecol. Environ.* **2009**, *7*, 4–11.

(88) *MA Millennium Ecosystem Assessment, Chapter 10*; World Resource Institute: Washington, DC, 2005; pp 375–408.

(89) *MNP Integrated Modelling of Global Environmental Change: An Overview of IMAGE 2.4*; Bouwman, A. F., Kram, T. , Klein Goldewijk, K., Eds.; Netherlands Environmental Assessment Agency (MNP): Bilthoven, The Netherlands, 2006.

(90) Van Vuuren, D. P.; Sala, O. E.; Pereira, H. M. The future of vascular plant diversity under four global scenarios. *Ecol. Soc.* **2006**, *11*, 25.

(91) Hooper, D. U.; Chapin, F. S.; Ewel, J. J.; Hector, A.; Inchausti, P.; Lavorel, S.; Lawton, J. H.; Lodge, D. M.; Loreau, M.; Naeem, S.; Schmid, B.; Setälä, H.; Symstad, A. J.; Vandermeer, J.; Wardle, D. A. Effects of biodiversity on ecosystem functioning: a consensus of current knowledge. *Ecol. Monogr.* **2005**, *75*, 3–35.

(92) Oberdorff, T.; Guegan, J.; Hugueny, B. Global Scale Patterns of Fish Species Richness in Rivers. *Ecography* **1995**, *18*, 345–352.

(93) Bobbink, R. Plant species richness and the exceedance of empirical nitrogen critical loads: An inventory. Landscape Ecol. 2004.

(94) Gardner, T. A.; Barlow, J.; Sodhi, N. S.; Peres, C. A. A multi-region assessment of tropical forest biodiversity in a human-modified world. Biol. Conserv. In Press, Corrected Proof.

(95) Harper, K. A.; Macdonald, S. E.; Burton, P. J.; Chen, J.; Brosofske, K. D.; Saunders, S. C.; Euskirchen, E. S.; Roberts, D.; Jaiteh, M. S.; Esseen, P. A. Edge influence on forest structure and composition in fragmented landscapes. *Conserv. Biol.* **2005**, *19*, 768–782.

(96) Louette, G.; Maes, D.; Alkemade, J. R. M.; Boitani, L.; de Knegt, B.; Eggers, J.; Falcucci, A.; Framstad, E.; Hagemeijer, W.; Hennekens, S. M.; Maiorano, L.; Nagy, S.; Serradilla, A. N.; Ozinga, W. A.; Schaminée, J. H.; Tsiaousi, V.; van Tol, S.; Delbaere, B. BioScore-Cost-effective assessment of policy impact on biodiversity using species sensitivity scores. J. Nat. Conserv. 2010, In Press.

(97) Wittstock, B.; Koellner, T.; Muller-Wenk, R.; Brandao, M.; Margni, M.; Civit, B.; Mila i Canals, L. Tokyo, 2008.

(98) Zhang, Y.; Singh, S.; Bakshi, B. R. Accounting for Ecosystem Services in Life Cycle Assessment, Part I: A Critical Review. *Environ. Sci. Technol.* **2010**, *44*, 2232–2242.

(99) Wolters, V.; Bengtsson, J.; Zaitsev, A. S. Relationship among the species richness of different taxa. *Ecology* **2006**, *87*, 1886–1895.

(100) Orme, C. D. L.; Davies, R. G.; Olson, V. A.; Thomas, G. H.; Ding, T. S. Global patterns of geographic range size in birds. *PLoS Biol.* **2006**, *4*, e208.

(101) Kier, G.; Mutke, J.; Dinerstein, E.; Ricketts, T. H.; Küper, W.; Kreft, H.; Barthlott, W. Global patterns of plant diversity and floristic knowledge. *J. Biogeogr.* **2005**, *32*, 1107–1116.

(102) Olson, D. M.; Dinerstein, E. The Global 200: Priority Ecoregions for Global Conservation. *Ann. Mo. Bot. Gard.* **2002**, *89*, 199–224.

(103) Spalding, M. D.; Fox, H. E.; Allen, G. R.; Davidson, N.; FerdañA, Z. A.; Finlayson, M.; Halpern, B. S.; Jorge, M. A.; Lombana, A.; Lourie, S. A.; Martin, K. D.; Mcmanus, E.; Molnar, J.; Recchia, C. A.; Robertson, J. Marine ecoregions of the world: a bioregionalization of coastal and shelf areas. *BioScience* **2007**, *57*, 573.

(104) Abell, R.; Thieme, M. L.; Revenga, C.; Bryer, M.; Kottelat, M.; Bogutskaya, N.; Coad, B.; Mandrak, N.; Balderas, S. C.; Bussing, W.; Stiassny, M. L. J.; Skelton, P.; Allen, G. R.; Unmack, P.; Naseka, A.; Ng, R.; Sindorf, N.; Robertson, J.; Armijo, E.; Higgins, J. V.; Heibel, T. J.; Wikramanayake, E.; Olson, D.; López, H.; Reis, R. E.; Lundberg, J. G.; Sabaj Pérez, M. H.; Petry, P. Freshwater ecoregions of the world: a new map of biogeographic units of freshwater biodiversity conservation. *BioScience* **2008**, *58*, 403.

(105) Brooks, T. M.; Mittermeier, R. A.; da Fonseca, G. A. B.; Gerlach, J.; Hoffmann, M.; Lamoreux, J. F.; Mittermeier, C. G.; Pilgrim, J. D.; Rodrigues, A. S. L. Global Biodiversity Conservation Priorities. *Science* **2006**, *313*, 58–61.

(106) Halpern, B. S.; Walbridge, S.; Selkoe, K. A.; Kappel, C. V.; Micheli, F.; D'Agrosa, C.; Bruno, J. F.; Casey, K. S.; Ebert, C.; Fox, H. E.; Fujita, R.; Heinemann, D.; Lenihan, H. S.; Madin, E. M. P.; Perry, M. T.; Selig, E. R.; Spalding, M.; Steneck, R.; Watson, R. A Global Map of Human Impact on Marine Ecosystems. *Science* **2008**, *319*, 948–952.

ES101444K