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LC.biodiv.IA

Guideline

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Inhalt

1   Purpose of this guideline

In the project Life Cycle biodiversity Impact Assessment (LC.biodiv.IA, 2017 – 2020), Fraunhofer IBP, ifeu Heidelberg and TU Berlin developed a method that allows biodiversity to be addressed within the overarching methodology of life cycle assessment (LCA). The method is documented in German in the final report of the project (Lindner et al. 2020a), in a shorter version and in English in the journal Sustainability (Lindner et al. 2019). This guideline serves three purposes. First, it is intended to help users of the method understand how to apply it in their own LCA studies (Chapter 3). Second, to help developers of LCA data sets understand how to generate characterization factors with the method (Chapter 4). Thirdly, to help developers of LCIA models understand how models for generating characterization factors are derived from the method (Chapter 5).

2   Context of the project and methodology

LCA as a product management tool typically answers questions such as: "Is it worth accepting higher CO_2 emissions in the production of an electric vehicle if less CO_2 is emitted over the vehicle's lifetime (compared to an internal combusiton vehicle)? Also: "What is the ecological advantage of a new bioplastic for the housing of a computer compared to the established fossil plastic in the context of the production of the entire device (including the many electronic components)? And finally: "What is the influence of the temperature in a heated bioreactor compared to the influence of the rotational speed of the agitator in the same reactor? In the first case, the aim is to make visible and manageable shifts of environmental burdens. The second case is about the quantitative understanding of environmental burdens. And the third case is about singular process parameters.

With regard to established quantities such as greenhouse gas emissions, the variable depth of the analyses is common and the questions can be answered with the same impact model (the Global Warming Potential) and largely the same calculation rules. The second global ecological challenge of the 21st century is the – also anthropogenically induced – sharp decline of biological diversity (biodiversity). Up to now, LCA has been able to contribute to the topic of biodiversity only to a very limited extent, and it can contribute little to the discussion of sub-problems and solution approaches. This is changing with the recently completed project LC.biodiv.IA.

The method developed in LC.biodiv.IA – based on years of preliminary work by several research institutes – allows the use of LCA to address issues such as those outlined above: Detection of burden shifts between life cycle phases of products. Quantitative discussion of the environmental impacts of individual processes in the context of entire value chains. Comparison of the influence of individual process parameters on the process' environmental impacts.

Industrial processes are the building blocks of value chains. Value chains are the abstract structures that provide us with concrete products with which we conduct our everyday lives. In this respect, the methodology presented here is relevant both for the people who ultimately use products, for the people who organise or (further) develop value chains, and for the people who set the regulatory framework for the creation of added value.

3 Application of the method in LCA studies

The method developed in the LC.biodiv.IA project ties in with the Land Use Framework of the Life Cycle Initiative (Milà i Canals et al. 2007, Koellner et al. 2013). Shortened and simplified, the framework prescribes that a "quality" (ΔQ) of a land surface (A) that deviates from a reference condition and is maintained for a determinable period of time (Δt) is interpreted as the impact of the process. The term "quality" is used as a placeholder for valuable environmental qualities anchored on the earth's surface – including biodiversity.

As with all Life Cycle Impact Assessment methods, for a concrete LCA study, inventory data of the relevant processes must be available. In the case of land-use processes, these are data on the area (A) [m²] and the time of use (Δt) [a]. The two quantities are usually combined in process datasets to the areatime [m²a]. Many relevant inventory datasets in commercial LCA databases now also contain the area or areatime, but usually relatively highly aggregated.

For a simplified application of the method according to Lindner et al. (2019), only the areatime of a land use process has to be multiplied by the characterization factor of the land use type of the process. The characterization factor corresponds to the quality difference (ΔQ) in the Land Use Framework. A number of characterization factors were published by Fraunhofer IBP at the end of the LC.biodiv.IA project.

In LCA practice, the application of the Land Use Framework and the biodiversity impact assessment method described here is therefore not fundamentally different from established impact dimensions related to emissions (e.g. the well-known Global Warming Potential, GWP): impact is equal to inventory size multiplied by the respective characterization factor. However, it is possible that not all characterization factors required for a given LCA study are available for this new method (see Chapter 4).

4 Development of characterization factors

If a characterization factor for a specific land use process is not available, it can be estimated in various levels of detail depending on the scope of the specific LCA study. According to the Land Use Framework of the Life Cycle Initiative, the quality difference corresponds to the characterization factor. It is therefore important to determine the quality level (in terms of biodiversity as a valuable environmental quality) for a broadly described land use type or for a specific land-use process.

Lindner et al. (2019) and Lindner et al. (2020a) describe the step-by-step determination of the quality level. A rough distinction is first made between land use types: forestry, pasture, arable, and mining. Within each land use type, the land use-specific biodiversity value (BV_{LU}) is determined (see below for details). The BV_{LU} indicates the proportion of the biodiversity potential that is reached within the quality range of the respective land use type. The standardized biodiversity value (BV_{loc}) is calculated from the BV_{LU} in two further transformation steps. The BV_{loc} indicates the proportion to which the local biodiversity potential (within a specific Ecoregion) is achieved (more on Ecoregions see below).

By weighting with the Ecoregion Factor (EF), the BV_{loc} is transformed into the global biodiversity value BV_{glo}. The BV_{glo} indicates to what extent the global biodiversity potential is achieved at the location of the process in question. The BV_{glo} corresponds to the quality as defined in the Land Use Framework. The quality level in the reference state is defined as $BV_{loc} = 1$, i.e. at global level the reference quality level differs from one ecoregion to another and corresponds to the EF. The quality difference (the characterization factor) is then
$$CF = \Delta Q = EF\,(1 - BV_{norm}).$$

Two points need further explanation: the land use-specific biodiversity value BV_{LU} and the Ecoregion factor. They will be explained in the following.

The concept of Ecoregions is a concept of delineation of biogeographical units, which is also used by the WWF. Many land use-specific impact assessment methods in LCA refer to it. According to Olson et al. (2001), ecoregions are "relatively large units of land containing a distinct assemblage of natural communities and species, with boundaries that approximate the original extent of natural communities prior to major land-use change." The distinction of ecoregions with specific characteristics is used here to differentiate impacts on biodiversity.

For (almost) every Ecoregion, the LC.biodiv.IA project provides an Ecoregion Factor (EF), which describes a highly aggregated general nature conservation value of the Ecoregion in the global context (Lindner et al. 2019, Lindner et al. 2020a). Thus, if in a high-EF ecoregion the BV_{loc} reaches a level of only 0.5 (out of 1), this is a higher damage to biodiversity in the global context than if the same BV_{loc} level is reached in a low-EF ecoregion. The Ecoregion factors from Lindner et al. (2019) were updated and published in the final report at the end of the LC.biodiv.IA project (Lindner et al. 2020a).

Depending on the scope of the specific LCA study, the BV_{LU} of an area claimed by a process can be estimated as a lump value (Chapter 3.1) or calculated in detail (Chapter 3.2).

4.1 Estimating the biodiversity value

The local biodiversity value can be estimated on the basis of the concept of hemeroby (distance from nature). According to Fehrenbach et al. (2015) and with adjustments according to Lindner et al. (2020a), four rough land use types

are distinguished (see above) and a total of seven hemeroby levels are defined transversely to these types. The higher the hemeroby level, the fewer natural structures and ecosystem dynamics are found on the investigated land. The hemeroby level correlates strongly with the intensity of land use, but some land use types are inherently closer to nature than others. For orientation see Table 1. Further details can be found in Fehrenbach et al. (2015), Lindner et al. (2019) and Lindner et al. (2020a).

Table 1

Hemeroby level	Forestry	Pasture	Arable	Mining
1 natural	primary forest or long abandon-ded forest	n/a	n/a	n/a
2 close to nature	forestry very close to nature	grassland close to nature	n/a	n/a
3 partially close to nature	extensive forestry	extensively used grassland	highly diverse agroforestry	n/a
4 semi-natural	semi-intensive forestry	semi-intensively used grassland	extensive agriculture	n/a
5 partially distant from nature	intensive forestry	intensively used grassland	semi-intensive agriculture	high structural diversity
6 distant from nature	n/a	n/a	Intensive agriculture	low structural diversity
7 artificial	n/a	n/a	n/a	sealed or devastated area

The local biodiversity value BV_{loc} as a function of the hemeroby level of the area is defined in Table 2. The value intervals of the land use types in Table 1 are visualized in Figure 1.

Table 2

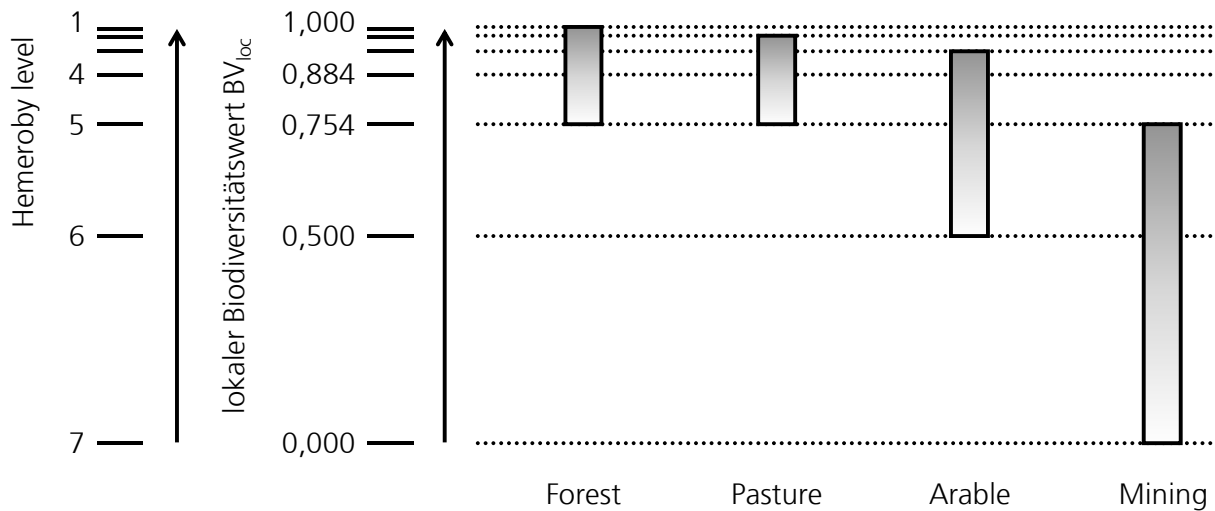| Hemeroby	1	2	3	4	5	6	7
BV_{loc}	1,000	0,983	0,950	0,884	0,754	0,500	0,000

Figure 1

A finer gradation (e.g. hemeroby 5.1 or 5.7) is not provided for in the simple estimation. A continuous classification into the hemeroby pattern is possible using the so-called potential field method.

4.2 Detailed calculation of the biodiversity value using the potential field method

For a finer determination of the biodiversity value of a specific area in the context of a concrete LCA study, the land use-specific biodiversity value BV_{LU} is not determined from tables, but is calculated from detailed input values. The biodiversity value is a function of parameters. Technically, a potential field can be defined that is spanned by the parameters. For a specific area with specific parameter values, the biodiversity value is a certain value of the field function. Therefore the method is also called the potential field method (mostly for illustration – many aspects of potential theory are not applicable to the biodiversity potential field).

Individual parameter sets were defined for the four land use types forestry, pasture, arable, and mining (whereby the parameters for pasture and arable are almost identical). The values of the parameters on the area to be evaluated are the input values for the calculation of the BV_{LU}. This is then translated into the BV_{norm}, (see below) the BV_{loc} and finally into the BV_{glo} (see chapter 4.1).

The calculation rules for processing the parameter values are set out in Lindner et al. (2020a). They are briefly repeated here.

Each parameter x is transformed into a biodiversity value contribution y(x). For this purpose, a function with a general form is used, which is adapted to the individual case.

Biodiversity contribution: $y = \gamma + \varepsilon * exp\left[-\frac{\left|(x^{\delta}-\beta)^{\alpha}\right|}{2\sigma^{\alpha}}\right]$ (1)

The function is defined through parameter-specific settings of α, σ, β, γ, δ, and ε. The range of definition of the function is the interval [0, 1], i.e. the input values must be normalized to this interval if necessary. Each biodiversity contribution function is thus completely defined by a 6-tuple (α, σ, β, γ, δ, ε). The value range of y(x) is also [0, 1]. If a biodiversity contribution function is already defined, the 6-tuple is given. The construction of new biodiversity value contribution functions is explained in chapter 5.

Several biodiversity value contributions (e.g. y_A and y_B) are aggregated into one criterion z (e.g. $z_{AB}(y_A, y_B)$). In certain cases, a criterion may contain only the biodiversity value contribution of one parameter, which is then directly adopted as the value of the criterion. Two or more biodiversity contributions are aggregated according to one of two possible functions.

AND aggregation: $z_{A...s}(x_A, ..., x_s) = 1 - \sqrt[p]{\frac{1}{s}\sum_{i=1}^{s}(1 - y_i(x))^p}$ (2)

OR aggregation: $z_{A...s}(x_A, ..., x_s) = \sqrt[p]{\frac{1}{s}\sum_{i=1}^{s}(y_i(x))^p}$ (3)

Here AND means that all parameters that constitute the criterion must contribute a high biodiversity value in order to achieve a high criterion value. OR means that one parameter with a high biodiversity value is sufficient to achieve a high criterion value. The exponent p is used to fine-tune the aggregation function. If a biodiversity potential field is already defined, the aggregation rules for biodiversity value contributions are given. The definition of new aggregation rules is explained in chapter 5.

Several criteria (e.g. z_{AB} and c_{CD}) are aggregated to the land use-specific biodiversity value BV_{LU} (e.g. $BV_{LU}(z_{AB}, z_{CD})$). For this purpose, the biodiversity value contributions of the criteria are weighted and summed, whereby the sum of the weighting factors is 1 ($\sum g = 1$). Thus, the value range of BV_{LU} lies within the interval [0, 1]. The weighting factors of the criteria values for an already defined biodiversity potential field are given; the definition of new weighting factors is explained in Chapter 5.

Land use-specific biodiversity value: $BV_{LU} = \sum_{i=1}^{n} g_i z_i$ (4)

The challenge in the development of case-specific characterization factors lies in collecting the input data (parameter values). Primary data should be used for this purpose, provided that they are documented. Many parameters are likely to be found in the corresponding management documentation if the land in question is responsibly managed.

If the parameters are not documented, they must be collected for the specific LCA study. In the course of the development of the LC.biodiv.IA project, most

of the parameters were defined in such a way that they can be collected relatively easily if they are not documented. Estimation procedures and expert judgement can also be used, as is quite common in LCA practice. If it should nevertheless be impossible to collect primary data in a specific case, literature data can be a practical substitute.

In summary, the BV_{LU} is the weighted sum of the criterion values z, which in turn are defined as aggregates of the biodiversity value contributions y, which are calculated individually from the parameters x using contribution functions: $x \rightarrow y(x) \rightarrow z(y) \rightarrow BVLU(z)$

In the next steps, the BV_{LU} is used to calculate the normalized biodiversity value BV_{norm}, the local biodiversity value BV_{loc} and finally the global biodiversity value BV_{glo}.

The BV_{LU} retains its meaning within the respective land use type. The value ranges of the biodiversity values of different land use types are brought into a common value interval (BV_{norm}). In the scale of the BV_{norm} the minimum and maximum biodiversity values are not between 0 and 1, but [0, 1] becomes the common interval of biodiversity values across all land use types (see Figure 2). The minimum and maximum possible values of BV_{loc} depending on the type of land use depend on the minimum and maximum possible hemeroby levels of the land use types. Each land use type is assigned a minimum and a maximum hemeroby level (see Table 3).
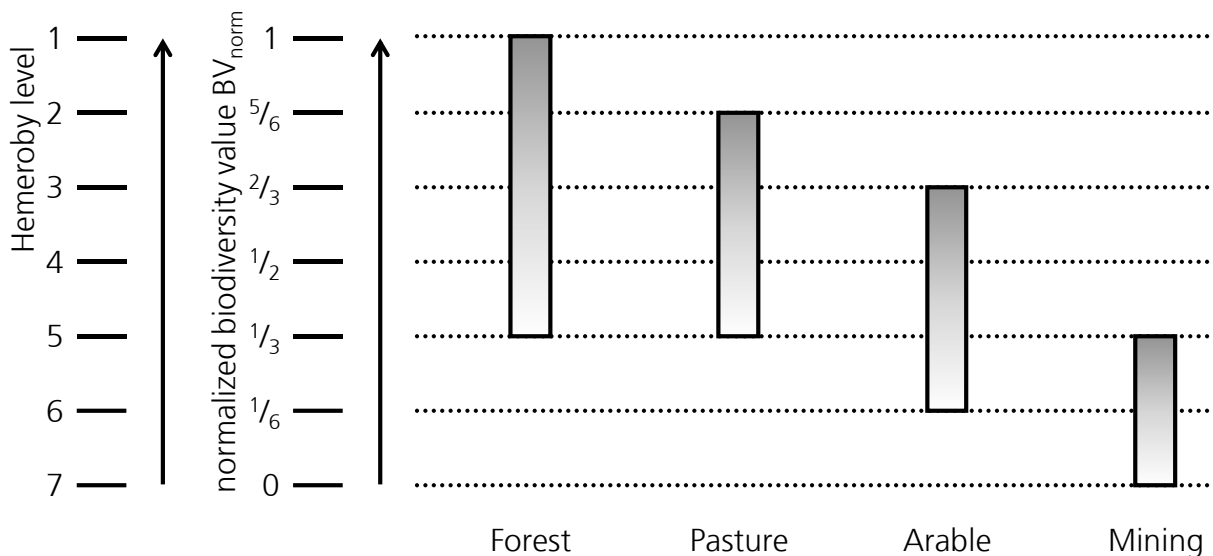

Figure 2

Normalized biodiversity value:
$$BV_{norm} = BV_{norm,j,min} + BV_{LU,j}\left(BV_{norm,j,max} - BV_{norm,j,min}\right) \tag{5}$$

The minimum and maximum values of BV_{norm} are found in the following table.

Table 3

Land use type	Forestry	Pasture	Arable	Mining
Hemeroby$_{min}$	1	2	3	5
Hemeroby$_{max}$	5	5	6	7
BV$_{norm,max}$	1.000	$5/6 = 0.833$	$2/3 = 0.667$	$1/3 = 0.333$
BV$_{norm,min}$	$1/3 = 0.333$	$1/3 = 0.333$	$1/6 = 0.167$	0.000

The local biodiversity value BV$_{loc}$ is calculated from the normalized biodiversity value BV$_{norm}$ using an exponential function.

Local biodiversity value: $BV_{loc} = a(1 - e^{-b \cdot BV_{norm}})$
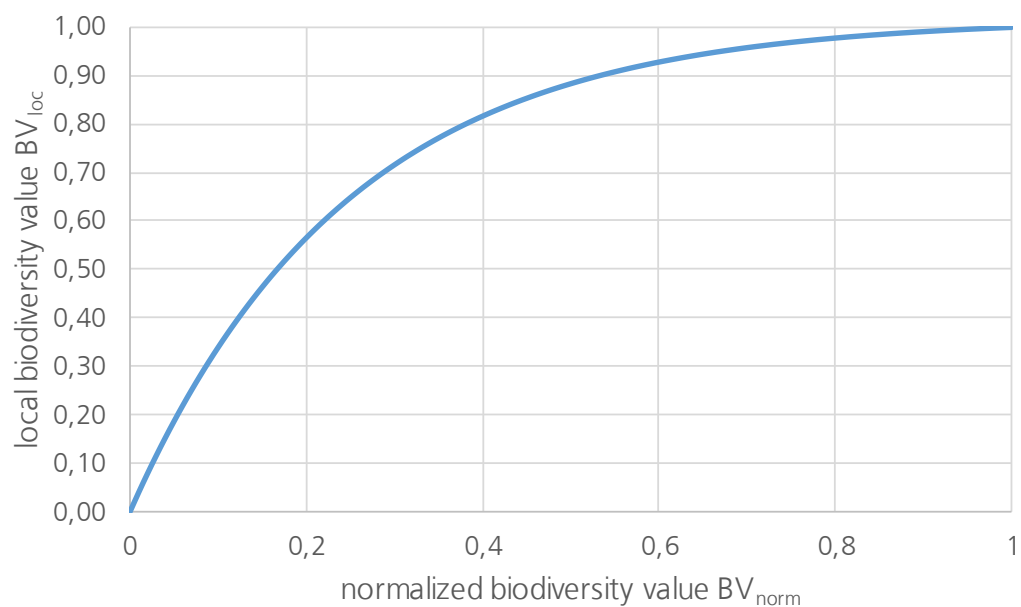with a = 1.017626088 and b = 4.055847776

(6)

Figure 3

The nonlinear conversion of BV$_{norm}$ to BV$_{loc}$ results in the unevenly distributed BV$_{loc}$ values for the hemeroby intervals per land use type in Table 2 and Figure 1.

The next steps are explained in chapter 4.1. From the BV$_{loc}$, the BV$_{glo}$ is calculated with the Ecoregion factors, which is entered as quality Q in the calculation of the impact of a land using process within a product system or LCA study.

5   Development of biodiversity potential functions

The methodology as described so far in this guide may seem static and settled. However, this only applies to the applications above. The methodology is actually modular, so that it is possible to change individual components without having to adapt the other components. In particular, an existing biodiversity potential function may turn out not to be representative. In this case, the existing function can be adapted or an entirely new one developed.

A biodiversity potential function is valid for one type of land use in a given biome. Here the definition of the 14 terrestrial biomes according to Olson et al. (2001) is used. So far, biodiversity potential functions have been developed for a total of eight combinations of land use types and biomes (see Table 4). As a pragmatic working assumption, these functions are assumed to be also valid in other biomes for the time being.

Table 4

Biome	Forestry	Pasture	Arable	Mining
Deserts and xeric shrublands			✓	
Tropical and subtropical moist broadleaf forests				
Tropical and subtropical dry broadleaf forests				
Tropical and subtropical coniferous forests				
Temperate broadleaf and mixed forests	✓	✓	✓	
Temperate Coniferous Forest				
Boreal forests / Taiga				
Tropical and subtropical grasslands, savannas and shrublands				✓
Temperate grasslands, savannas and shrublands				
Flooded grasslands and savannas				
Montane grasslands and shrublands				✓
Tundra				✓
Mediterranean Forests, woodlands and scrubs				✓
Mangroves				

The procedure described below is recommended for the development of new biodiversity potential functions.

5.1 Using existing biodiversity potential functions as a template and starting point

In order to maintain a certain consistency between the functions and to avoid multiple work, existing components of the biodiversity value calculation should be used as far as possible. Only those components that actually require revision should be changed. Functions are already available for all four land use types, so that a starting point is given. The adjustment then concerns the calculation rules within a land use type from the parameters to the land use specific bio-diversity value BV_{LU}.

5.2 Qualitative extrapolation of a parameter set to another biome

The existing input parameters should be checked for their representativeness for a new land use/biome combination. The parameter set should cover the most important threats to biodiversity and the main degrees of freedom in the land management. Overviews of the threats to biodiversity can be found in the Millennium Ecosystem Assessment (2005), the IPBES Global Assessment Report (2019), and in the regular Living Planet Reports of the WWF (latest one publis-hed 2018). Diffuse influences such as the shifting of climate zones may be neglected because the method only covers direct effects of land use on the land itself. Management options can be found in relevant recommendations which usually apply specifically to certain types of land use (e.g. Good Agricul-tural Practice, EU organic label, Forest Stewardship Coucil).

5.3 Quantitative extrapolation of a parameter set to another biome

For the parameters that are retained after the qualitative check, the value con-tribution functions $y(x)$ and the aggregation functions $z(y)$ are checked for re-presentativeness. In addition, the weighting factors g for the linear aggregation of the criteria values z to the BV_{LU} are checked. If necessary, α, σ, β, γ, δ, ε are adjusted within the functions $y(x)$, the exponent p is adjusted within the fuzzy aggregation functions $z(y)$ or, if necessary, a new aggregation type (AND, OR) is selected. When adapting the weighting factors g in the linear aggregation function $BV_{LU}(z)$, the condition $\sum g = 1$ must be observed.

5.4 Development of genuinely new biodiversity potential functions

It may be necessary to develop new value contribution functions for individual parameters – for example because some parameters relevant to a combination of land use and biome have been newly identified. The functions of the para-meter value contributions $y(x)$ and the criterion values $z(y)$ are to be understood as a system: If a value contribution cannot be represented by one parameter alone, several parameters can be used and their value contributions linked. Lindner (2016) and Lindner et al. (2020b) provide guidelines for the develop-ment of biodiversity potential functions from the literature and in interviews

with experts. The guiding questions for the development are (modified from Lindner 2016):

- What constitutes the typical biodiversity of the biome?

- Which anthropogenic activities threaten the typical biodiversity?

- By which characteristics can places and landscapes with high or low biodiversity be recognized in this biome?

- How is biodiversity qualitatively related to the anthropogenic activities in the biome and the expression of the characteristics for high/low biodiversity?

- How is biodiversity quantitatively related to the anthropogenic activities in the biome and the expression of the characteristics for high/low biodiversity?

- Are the influences of different anthropogenic activities and the descriptive characteristics independent of each other? If not, how do they interact?

- To what extent do the combinations of anthropogenic activities and descriptive characteristics influence biodiversity?

In practice, it must be possible to collect primary data with reasonable effort. Parameters that can only be collected personally by qualified personnel should be avoided (e.g. the identification and counting of specific species).

5.5   Reporting new developments

In order to maintain an overview of biodiversity potential functions in the long term, it is recommended that adjustments or new developments be reported to Jan Paul Lindner (contact details see below).

6   Summary

This guideline describes the application of the method developed in Lindner et al. (2019) and Lindner et al. (2020a) to quantify the biodiversity value of land using processes in industrial value chains. The method can be operationalized at different levels of complexity, depending on the scope of a specific LCA study.

At the simplest level, an existing characterization factor is adopted for a specific process (Chapter 2).

One level deeper, the land-use-specific biodiversity value BV_{LU} is estimated through the naturalness level of the occupied land (Chapter 4.1). This is used to

calculate the global biodiversity value BV_{glo} and from this the characterization factor.

One level deeper, the land use-specific biodiversity value BV_{LU} is calculated from several input parameters (Chapter 4.2). From this, the global biodiversity value BV_{glo} is calculated and from this the characterization factor.

Development work at the methodological basis (Chapter 5) includes checking and adapting calculation rules, which are used to calculate the land use-specific biodiversity value BV_{LU} from input parameters (the so-called biodiversity potential function). In special cases, a biodiversity potential function can be defined from scratch.

7   Contact

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Literature

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