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ABSTRACT

Biodiversity is a key component of agricultural ecosystems and belongs to one of the exceeded planetary boundaries. In the quest for innovation to mitigate impact, it is essential to have tools to assess the anthropogenic impact on biodiversity. In this study, we developed a new indicator, I-BIO that aimed to predict the impacts of management practices and the influence of the landscape on overall biodiversity at species group level. I-BIO encompassed four groups: microorganisms, vegetation, invertebrates and vertebrates. This predictive indicator was built using DEXi software that facilitates the design of hierarchical decision trees, based on input variables in the form of qualitative classes, aggregated using utility functions. I-BIO was constructed using data from a long-term platform in Scotland and then applied to two data sets in France and one in Scotland. The results showed that the lowest class is predominant for all branches especially for invertebrates and soil invertebrates. Monte Carlo sampling was used to test for sensitivity. Then, a validation step was carried out to compare I-BIO outputs with real data using data on the four groups from Scottish and French datasets. I-BIO predictions of weed and soil invertebrate abundance conformed to field data. Due to low numbers of samples, validation of microorganisms, flying invertebrates and vertebrates predictions require more data. Future developments of I-BIO will focus on predictions specifically to assess the impact of management on species richness. Avenues for improvement include a better integration of landscape features and the history of agricultural practices as they both have a great influence on biodiversity.

1. Introduction

Conservation of biodiversity as an essential element of ecosystems has been on the agenda for decision makers since the Rio Conference in 1992 (Le Guyader, 2008). It is well established that loss of biodiversity is considered as a major issue regarding sustainability of the planet, having exceeded planetary boundaries (Campbell et al., 2017). A growing number of studies highlight its major role in the supply of many ecosystem services to mankind (Sandifer et al., 2015). Nevertheless, due to the complex relation between biodiversity and ecosystem services, this contribution remains subject to investigation (Duncan et al., 2015). In spite of the growing awareness of politicians, managers and civil society and the regulations put in place, recent publications show a continued dramatic decline in biodiversity, in terms of species abundance and diversity across many ecosystems: in protected areas (Hallmann et al., 2017), in grassland and forest (Seibold et al., 2019) as well as in cropped agroecosystems (Le Roux et al., 2008). These studies addressed decline of invertebrates while others focus on birds or plants (Boatman and Brickle, 2004; Donald et al., 2001; Robinson and Sutherland, 2002; Stanton et al., 2018) and highlight the role of agricultural intensification as a cause of this decline. Intensification of agriculture has increased globally over the past 50 years through intensive use of synthetic inputs, mineral fertilizers and pesticides, and simplification of agricultural landscapes by removing semi natural habitat to increase field size, and reducing crop diversity to focus on more profitable crops (Mortensen and Smith, 2020).

In response to this tremendous transformation of agriculture, alternative approaches have been developed. Among them, organic farming has shown a clear potential to improve levels of biodiversity in farmland with an average gain of 30 % shown by several reviews and meta-analyses (Smith et al., 2020; Tuck et al., 2014). Nevertheless, other levers than minimising chemical inputs also promote biodiversity: reducing physical disturbances due to tillage (Christel et al., 2021), diversifying cropping systems (Viguier et al., 2021; Tibi et al., 2022) and landscape (Tscharntke et al., 2021), and continuous cover cropping represent the three columns of conservation agriculture, which can also reduce deleterious impact of agriculture on biodiversity (Bitew and Abera, 2019). Beyond this categorization of well-established agricultural practices, the integration of best practice management options to achieve better sustainability are key drivers in the design of innovative cropping systems supporting biodiversity conservation (Hawes et al., 2021).

Besides the question of solution, development of assessment method is a prerequisite to any action in favour of biodiversity conservation or more generally to improve agroecological sustainability. Baseline assessments of biodiversity are essential for preliminary diagnosis to orient any action plan to mitigate or restore biodiversity in agroecosystems. These may also support the design of innovative systems that promote biodiversity for ecosystem service provision. Since it is not possible to "measure" biodiversity directly, any assessment will require biodiversity indicators, which is also true when considering sustainability. To gain insights in the "indicator zoo" developed over the past 30 years, Bockstaller et al. (2015) sets out a typology based on three types of indicators: causal effect (e.g. semi-natural habitat), measured effect (e.g. number of earthworms) and predictive effect indicators (e.g. operational model). Causal or indirect indicators and measured or direct indicators are most frequently used (Bockstaller et al., 2011; Clergue et al., 2005). Relative feasibility of the former and the direct link to biodiversity state of the latter explain their popularity. Predictive effect indicators are derived from model outputs which require well documented knowledge on causal-effect relationships or statistical relationships with consequent datasets. Such indicators present a major advantage by making possible *ex ante* assessment to test innovative solutions without heavy field experiments. This modelling approach broadens remarkably the range of possibilities for exploring alternative solutions (Sadok et al., 2009a).

With regard to biodiversity, predictive indicators have been developed. While some authors use a scoring system based on scientific knowledge (Butler et al., 2009; Jeanneret et al. 2014) or decision tree using fuzzy subsets (Sattler et al., 2010), others use DEXi based models, i.e. the MASC method (Sadok et al., 2009a; Sadok et al., 2009b; Craheix et al., 2012) the DEXiPM models (Angevin et al., 2017; Pelzer et al., 2012) and more recently with DEXi-CSC (Hawes et al., 2019). DEXi software is a tool that aggregates qualitative or quantitative variables into classes according to if-then decision rules that result in a hierarchical structure with a single overall output at the top level. The various steps needed to develop this kind of model will be described in the material and method section. These methods assess the global sustainability of cropping systems integrating the biodiversity in their assessment process. However, some mechanisms are poorly considered. For example, the MASC method does not integrate the role of some vertebrates like birds, and neither the DEXiPM nor the DEXi-CSC model adequately cover soil microorganisms known for their central role in the food web and for its numerous biological functions (Bender et al., 2016; Singh, 2015; Tiemann et al., 2015). Other models mix ecosystem services and biodiversity such as in DEXiPM2 and DEXi-CSC that could bring greater complexity (Table 1). However, in these examples, little account is taken of the impact of landscape management despite the key role that landscape plays in biodiversity conservation (Tscharntke et al. 2021). Connectivity between patches of semi-natural habitats, field size or crop diversity are landscape features that could greatly increase biodiversity.

Table 1
Comparison of DEXi models assessing impacts of management and landscape on biodiversity.

Model	Output							Input management variable					Landscape input variable				
	Vertebrates	Flying invert	Soil invert	SN flora	Weeds	Microorganism	Ecosystem services	Crop rotation	Tillage	Fertilization	Pesticides	Grassland	% semi natural element	Semi natural element diversity	Landscape configuration	Filed size	Crop diversity
MASC	X	X	X	X	X	X		X	X	X	X						X
DEXiPM		X	X	X	X		X	X	X		X		X		X		X
DEXiPM2	X	X	X	X	X		X	X	X	X	X	X	X		X		X
DEXi-CSC	X	X	X	X	X		X	X	X		X		X	X	X		
I-BIO	X	X	X	X	X	X		X	X	X	X		X	X	X	X	X

The aim of this article is to present a new predictive indicator, called I-BIO, assessing the impact of cropping practices and the influence of landscape features on overall arable biodiversity. Actually, biodiversity encompasses different dimensions, structural, compositional and functional at different levels (Noss, 1990). Here we will focus mainly on the compositional, considering species diversity of organisms living above- (mammals, birds, insects, …) and below-ground (earthworms, fungi, microorganisms, etc). Starting from the biodiversity branch of the DEXi-CSC model (Hawes et al., 2019) which is the most recent version, we redesigned this branch to obtain a predictive indicator based on simple to use accounting of the surrounding landscape and the main crop management practices in arable systems. We present first the construction of the I-BIO indicator with choices of variables, classes and aggregation rules. We tested then the newly developed indicator I-BIO and validated it by comparing its outputs to measurements of biodiversity for a set of different crop production and landscape situations.

2. Materials and methods

The design of the I-BIO predictive indicator started with a preliminary step defining the situation in which the indicator can be applied, followed by the selection of input variables, their parametrization (class thresholds, weights) and aggregation rules, based on data from the Centre for Sustainable Cropping (Hawes et al., 2019). Finally, the indicator was tested and validated against datasets from East of Scotland and French sites.

2.1. Preliminary choices guiding the design

Preliminary design choices are essential to clearly identify the purpose of the indicator, the target users, the object assessed, the spatial and temporal scales, and the availability of data (Bockstaller et al. 2015). These criteria define the context which should guide the design of the indicator so that the tool is relevant to the requirements of end-users. The aim of the development of I-BIO is to help agronomists, advisers and famers working on innovative cropping systems, to gain insight into the impacts of management on biodiversity at the field level. The field includes here the cropped area and the field margins which are designated as the uncultivated herbaceous vegetation area between the cultivated strip and another patch in the landscape (e.g., ditch, hedgerow, road, field or grassland). I-BIO was developed to cover a large range of taxa covering the overall agroecosystem biodiversity, comprising four groups: microorganisms, vegetation, invertebrates and vertebrates (see section 2.2.1). While Sattler et al. (2010) addressed 3 species within 2 taxonomic groups, we worked, like most authors, on higher taxonomic groups encompassing a broader range of species. I-BIO seeks to balance the advantages of modelling specific taxonomic groups with the need to account for overall biodiversity which impacts on system functioning. Likewise, the SALCA method (Jeanneret et al., 2014) is an example of a method assessing specific taxonomic groups (11 "indicator-species group") while the IBEA method (France Nature Environnement, 2013) assesses the wild biodiversity as a whole. Last, the data for model parametrization covers common agronomic practices, organic matter inputs and landscape data (composition and configuration of semi-natural habitats, crop diversity within a 1 km radius).

2.2. Design of the indicator I-BIO

2.2.1. DEXi software

The new indicator was designed with the DEXi software (Bohanec, 2009). This software very user friendly allows the construction of hierarchical decision trees with linguistic rules which facilitate communication among non-specialists (Babuška and Verbruggen, 2003). Input indicators are characterized by their name, a description and a scale i.e. they are defined as, or transformed into, qualitative classes (e.g. low, medium, high). Those input indicators are then aggregated using utility

functions based on the "if-then" rules and weightings gathered in decision tables. These latter could be filled in the DEXi software automatically, semi automatically and by hand. For the first two options, weights for every indicator are defined by the user and only two values of aggregation are filled by hand for the automatic option and more than two values for the semi-automatic option. The software automatically fills the rest. For the option "by hand", the user fills every decision rule manually and then DEXi calculates the weight of each input indicator. This last option was implemented in the design of I-BIO. The aim is to achieve a global, qualitative assessment of the scenario tested. For further details of the DEXi tool, see Bohanec (2009) and Pelzer et al. (2012).

2.2.2. Selection and hierarchy of effect and causal indicators

The first step was to carry out a narrative review to identify and select the effect and causal indicators to be integrated in the model and their hierarchy in the decision tree. Effects indicators result from the assessment of effect of causal indicators (Bockstaller et al., 2015). To assess the impacts of a management scenario, biodiversity was split in four main groups describing overall biodiversity: microorganism, vegetation, invertebrates and vertebrates (Bar-On et al., 2018). The invertebrate group is divided into soil and flying invertebrates as organisms in these groups have different lifespan and mobility capacity and are therefore likely to show different responses to management options. Soil invertebrates spend all their life cycle in or on the soil whereas flying invertebrate' habitats vary with life cycle stages. So, if we take the example of tillage practice, the level of impact will differ between these two sub-groups (Coudrain et al., 2016; van Capelle et al., 2012). The microorganism group, the vertebrate group and the two invertebrate subgroups were described by two branches: one related to anthropogenic impacts and the other one to trophic resources. The former tackles impacts of management directly, while the latter covers indirect impacts of management. For example, a strong impact of a cropping system on invertebrates or vegetation will decrease trophic resource for vertebrates resulting in a decline in abundance. These two sub-branches were characterized by relevant indicators in each group. For example, the causal indicator "mowing" was added to the vertebrate branch in DEXi-CSC as this practice could have a great impact for ground nesting birds or young mammals like fawn (Buckingham et al., 2015; Jarnemo, 2002; Stanton et al., 2018). The vegetation group was split in two branches. The first one deals with the regional context including semi-natural flora surrounding fields and the second one describes the weed flora within the cropped area.

The whole biodiversity branch and its related effect-indicators are described by 19 causal indicators (Fig. 1). Eleven causal indicators characterize the cropping systems, such as crop sequences, crop diversity, tillage intensity and specificities of phytosanitary treatments (number of applications, pre or post emergence, weed target). Eight causal indicators are related to local context: trophic resources (soil organic matter, microorganism, vegetation and invertebrates), landscape features (field size, land cover diversity, percentage of semi-natural habitats, connectivity).

The eight effect indicators representing the taxonomic group and overall biodiversity reflect a qualitative effect on biodiversity without the need to specify the dimension such as abundance or species richness (Díaz et al., 2006).

2.2.3. Choice of qualitative state for effect and causal indicators

The second step was to select qualitative classes for simple and aggregated indicators. The biodiversity branch of DEXi-CSC had only 3 classes for all branches. The aim was to increase the tree sensitivity and to be more precise in the assessment, following guidelines of Craheix et al. (2015). For I-BIO, two classes were added at the biodiversity indicator level, one class to each group i.e. microorganism, vegetation, invertebrates, vertebrates, as well as the two subgroups soil invertebrates and flying invertebrates (invertebrates) and the indicators
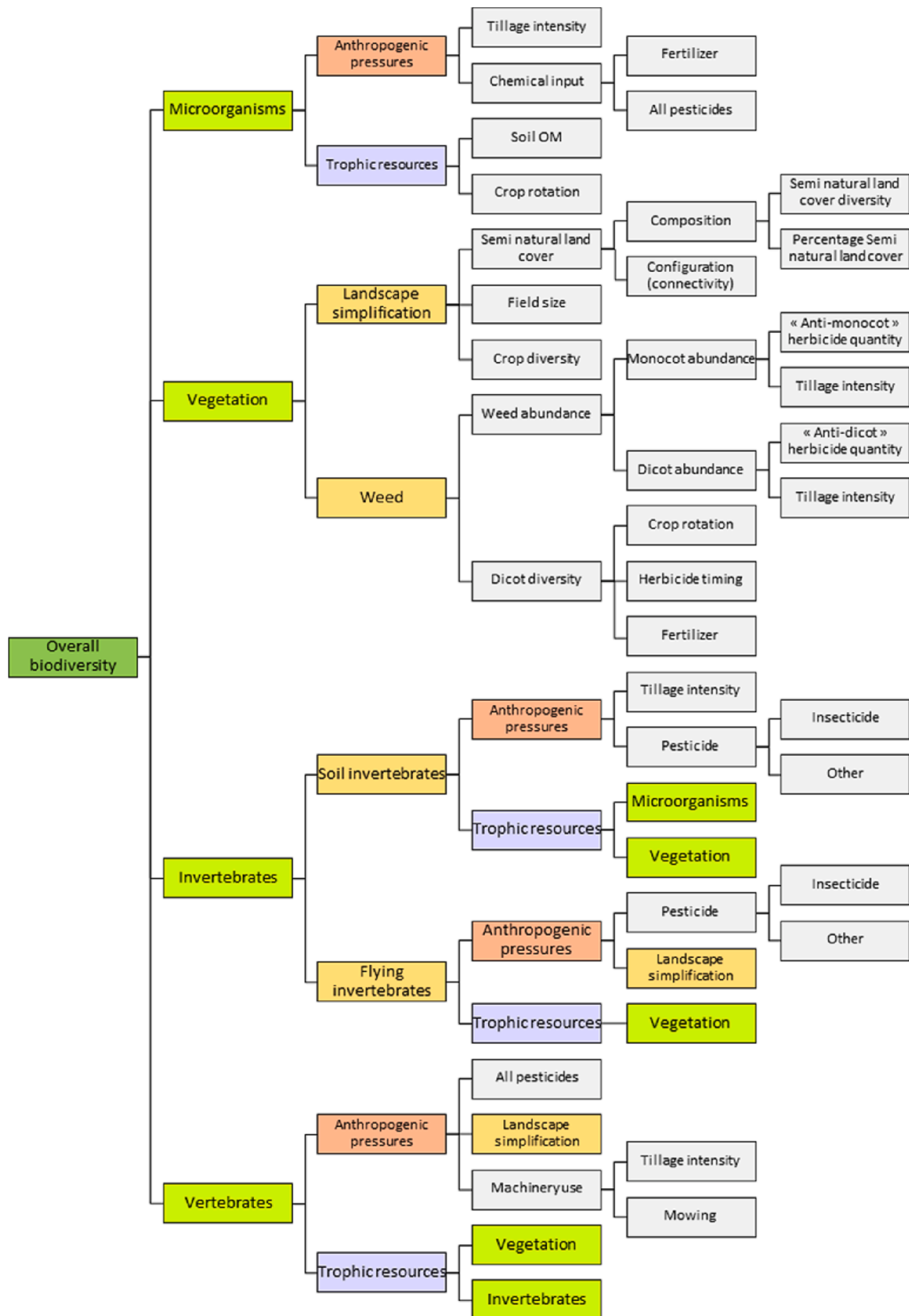
Fig. 1. Tree of I-BIO: a tool assessing the farming practices impacts on the overall biodiversity at field level. Dark green, light green and yellow indicators correspond respectively to the global indicator, the taxonomic indicators and main sub-group indicators. Red indicators correspond to "Anthropogenic pressures" sub-branches and purple indicators to "Trophic resources" sub-branches. (For interpretation of the references to colour in this figure legend, the reader is referred to the web version of this article.)

"anthropogenic pressures" and "trophic resources" (vertebrates). Thus, I-BIO (the overall biodiversity) has 5 qualitative classes: very low, low, medium, high, very high; indicators with 4 qualitative classes are categorized in: low, low to medium, medium to high, high; other indicators (the basic one) have 3 qualitative classes: low, medium, high. Thresholds of the qualitative classes are defined in Table 2. All basic indicators except two (herbicide timing and tillage intensity) are assessed quantitatively and converted to a qualitative class based on references or expert knowledge. For herbicide timing and tillage intensity, they are directly assessed qualitatively. Some indicators required an adaptation to the context of a specific case study. An example was the treatment frequency index which enables easy comparison between farms or regions (Hossard et al., 2017) but is not used in Scotland. Without this index for the CSC case study, we have defined the indicator levels based on a threshold of number of applications. All aggregated indicators are in qualitative classes based on a system of references and expertise. The eight effect indicators representing the taxonomic groups and the overall biodiversity are expressed on a qualitative performance scale (the higher, the better) without any quantitative correspondence. Indeed, a shift from a lower to a higher class means that the effect on biodiversity is less, but without defining the size of that effect.

2.2.4. Choice of aggregation rules

The third step was to define utility functions, to aggregate indicators, and their relative weight. Utility functions consist of "if – then" linguistic rules which means that the class of an aggregated indicator is set according to the class of input indicators from the lower level of aggregation. For instance, if the aggregated indicator Y has two descendant indicators X1 and X2 which have respectively low and high qualitative classes, then we apply the "if – then" rule that will be "if X1 is low and X2 high, then Y is high". Expert knowledge was used to apply the law of the

maximum i.e. keep the class with the highest impact. Utility functions could be set to automatically weight the indicators. However, this can lead to compensation effects between indicators. For example, an indicator with a low class and an indicator with a high class yields the same average class as two indicators with medium class, leading to an information loss. Furthermore, the distribution of outputs may be unbalanced causing a lack of sensitivity. To prevent this, all the utility functions in I-BIO were manually fixed in the DEXi software (Table 3). This was achieved using a function of the DEXi software to export the aggregation rules to Excel by transforming the qualitative classes in quantitative ones. The mean of the input variables was then calculated and ranked

Table 3
Part of the adaptable utility function for the indicator "Semi-natural flora" with the relative weights of each basic indicators.

Semi natural land cover[a]	Field size[a]	Crop diversity[a]	Landscape simplification[b]
Low	High	Low	High
Low	High	Medium	High
Low	High	High	Medium to high
Low	Medium	Medium	Medium to high
Medium	High	Low	High
Medium	High	Medium	Medium to high
Medium	High	High	Low to medium
Medium	Medium	High	Low
High	High	Low	Medium to high
High	High	Medium	Low to medium
High	Medium	Medium	Low to medium
High	Low	Medium	Low
Resulting weights (calculated by DEXi)			
34%	23%	43%	–

[a] Three qualitative states: Low, Medium, High.
[b] Four qualitative states: Low, Low to medium, Medium to high, High.

Table 2
Thresholds and associated references of the qualitative classes for the indicator I-BIO.

	Low	<	Medium	>=	High	Comment
Fertilisation (N units)		50		150		Graaf et al. (2019)
SOM (% C)		2		5		Roussel et al. (2000)
Land cover diversity	Majority of crops		2 types of habitats well represented (crop/edge, wood)		More than two habitat types well represented (crop, meadow, pond, hedgerow, wood, flower's strip, etc.)	Expert choice (based on the CSC database)
Semi-natural habitat (%)		1		10		Sirami et al. (2019)
Connectivity (simple method)	0 or 1 side with SNH strip (>= 3m)		At least 2		More than two and SN strips within the field spaced less than 100m	Expert choice (based on the CSC database)
Connectivity (%)		25		75		Expert choice (based on the CSC database)
Field size (ha)		2		10		Sirami et al. (2019), Martin et al. (2020)
Crop diversity		3		6		Zampieri et al. (2020), Keichinger et al. (2021)
Crop rotation		3		6		Expert choice (based on the CSC database)
AntiMono (treatment number)		1		2		Expert choice (based on the CSC database)
AntiDicot (treatment number)		1		2		Expert choice (based on the CSC database)
Herbicide timing	Preemergence or both				post emergence	Expert choice (based on the CSC database)
Insecticide		1		2		Expert choice (based on the CSC database)
Other		1		2		Expert choice (based on the CSC database)
All pesticides		3		6		Expert choice (based on the CSC database)
Tillage intensity	Direct sowing		non inversion tillage		ploughing	Muneret et al. (2022)
Mowing		2		3		Buckingham et al. (2015)

(Fig. S1). The aggregation rules were then checked and corrected if the output given automatically by DEXi did not match expert knowledge or the peer reviewed literature. DEXi then recalculated the weights according to these new qualitative classes (Fig. S2 in supplementary material).

2.3. Sensitivity analysis

Following recommendation of Bockstaller et al. (2008), we tested the sensitivity of I-BIO to assess its ability to discriminate between situation. As for quantitative models, we implemented a Monte Carlo sampling (MC sampling) approach as described by Carpani et al. (2012) for DEXi models to assess sensitivity of the main branches. According to these authors, MC sampling performs well for complex models. It is more flexible and requires less stringent assumptions than two other methods, factorial designs combined with analysis of variance and conditional probability. MC sampling is based on a random selection of combinations of input variables according to their probabilities of occurrence. In our study, 5000 samples were generated and simulated using I-BIO. By default, the same probability was attributed to each input variable, following Carpani et al. (2012). MC sampling provides a distribution of the outputs across the classes of a variable. In case of an unbalance distribution in favour of one or two classes, it can be deduced that the model may suffer from a loss of sensitivity.

Regarding landscape features, we tested the sensitivity of five variables related to landscape context: land cover diversity, percentage of semi-natural land cover, configuration of semi-natural land cover, field size and crop diversity. The sensitivity test was carried out as in (Pervanchon et al., 2002) by modifying the classes of each input variable while the remainder were held constant at the unfavourable class, the average class or the favourable class.

2.4. Case studies assessed by the indicator

I-BIO was tested on three case studies in Scotland and France, to assess the reliance of the results and the ability of the model to discriminate situations for which different results are a priori expected. For some datasets, validation was carried out by comparing measurements of abundance and/or diversity against model outputs according to Bockstaller and Girardin (2003). I-BIO outputs were compared with observed data for the four groups (microorganisms, vegetation, invertebrates and vertebrates).

2.4.1. East of Scotland farm (EOSF) dataset

This dataset was taken as part of a wider farm-scale survey of arable biodiversity, resilience and crop management conducted during 2007 at 57 farms across the east of Scotland from Mid-Lothian to Invernesshire. Farmers taking part in this survey were volunteers who followed a range of organic, integrated and conventional management practices. At each farm, two fields were selected as representative of different stages in the crop rotation (generally a break crop and a cereal crop). Information on the crop management and rotational history for each field was analysed for 27 farms contributing between them 24 conventionally managed fields, 15 integrated and 15 organic" (Hillier et al., 2009; Hawes et al., 2010). For this study, 42 fields were selected where all the management data required to implement I-BIO scenarios were available to test the vegetation branch.

2.4.2. Noé network in France

In France, I-BIO was tested on a network of wheat plots in the Noé association (https://NOE.org/). The network covers 3 regions in France (Charentes, Chalky Champagne region and the Rhône valley) with 6 different departments. Biodiversity monitoring has been carried out by the association on 50 fields since 2020. Several biodiversity indicators were evaluated: soil organic matter, microorganism biomass, earthworm, pollinators, birds abundances, etc. In our study, 36 fields were

selected to validate the microorganism, flying invertebrates and vertebrates branches.

2.4.3. ENI (nonintended effects) network database

The ENI network database (Andrade et al., 2021) is a French program launched in 2012 to assess side-effects of agricultural practices and in particular pesticide management practices on biodiversity. Several indicator groups were measured, covering abundance or/and diversity of taxonomic groups of interest for farmers (weed, earthworm, beetle and bird). 500 fields were selected across all the country to assure a gradient of landscape and pedoclimatic conditions, with 20% of fields in organic farming. Selected crops represent the main crop types in France (field crops, vineyard, market gardening crops). For several taxonomic groups, the monitoring was done in field margins: plants and beetle (Coleoptera). For our study, 60 fields were randomly selected among the 500 fields of the ENI database. They were used to test the vegetation and soil invertebrates branches.

2.5. Statistical analysis

ANOVA and Tukey tests were used to compare boxplot mean of classes and the Monte Carlo sampling approach provided a sensitivity analysis of I-BIO i.e. a random sampling with replacement among the values of each leaf variable of the model (5000 samples). Statistical analyses were carried out using RStudio version 1.3.959 and R-statistical packages: Agricolae for the ANOVA and Tukey test and XML, AlgDesign, ggtools, plotrix and genalg for the MC sampling.

3. Results

3.1. Distribution of the model outputs

Results for the overall biodiversity and main branches of I-BIO, the different taxonomic groups, for the ENI and EOSF datasets are shown in Fig. 2. Globally, the lowest class is largely predominant for overall biodiversity and for three out four taxonomic groups (microorganism, invertebrates and vertebrates). Only the vegetation and the flying invertebrates showed a more even distribution across classes. The vertebrates branch stands out, especially for the ENI dataset, as the medium to high class almost reaches 25% compared to less than 5% for the EOSF dataset. EOSF outputs were tighter around the lowest class than the ENI ones. Thus, the distribution of the invertebrates and soil invertebrates across classes was skewed to only the "Low" class. Last, soil invertebrates and flying invertebrates showed a marked difference - the lowest class of the former exceeds 75% with the ENI dataset, whereas the flying invertebrates had the first three classes around 30% and an additional fourth class "high". Flying invertebrates is the only branch with four classes although the highest remained largely underrepresented. Similarly, soil invertebrates from the EOSF dataset were all in the Low frequency category whereas the flying invertebrates have a more balanced distribution.

Fig. 3 shows example of outputs of I-BIO evaluation for the ENI and EOSF datasets for some farms as the number of assessed farms were too low to show all the results together. For instance, field 311 yield a "medium" result for the overall biodiversity, being characterised by a very low level of farm inputs (fertiliser and pesticides) and no till, while fields 423 and 424 yielded a negative result "very low", due to more agrochemical inputs and tillage for the field 423. This representation makes possible direct comparison of the most aggregated indicator, overall biodiversity, alongside the main sub-indicators with an additional level of aggregation for invertebrates. Each calculation can be traced back to utility functions to understand each aggregation result. This ensures transparency of the method, a key feature, besides simplicity and flexibility to support the future implementation by external users (Craheix et al., 2015).
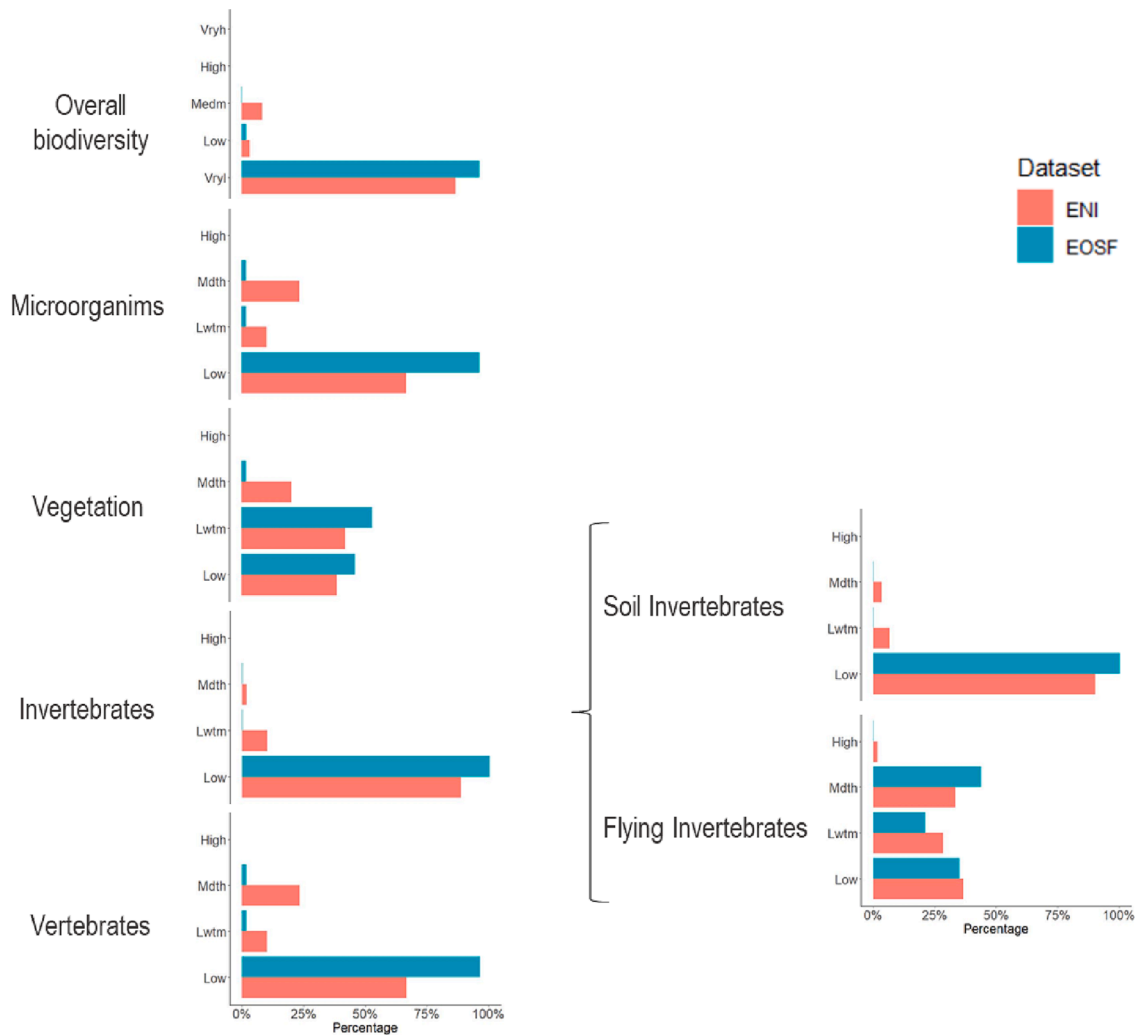
Fig. 2. Illustration of the I-BIO classes distribution with the EOSF (n = 42 fields) and the ENI (n = 60 fields) datasets for the overall biodiversity and the different taxonomic groups. Sidebars correspond to the scenario outputs.

3.2. Sensitivity analysis

The MC sampling showed an uneven frequency distribution for biodiversity indicators and the sub-indicators (Fig. 4). For overall biodiversity, the lowest category "very low" yielded the highest frequency. This unbalanced distribution in favour of "very low" can be observed for the "invertebrates" group and more precisely the soil invertebrates and to a less extent for microorganisms. However, for vertebrates and especially for vegetation, the distribution is more balanced. This uneven frequency distribution was not due to the parametrization of the final utility function of "overall biodiversity" which shows the following distribution (see Table S2 in supplementary material): for "very low" 65 rules out of 256, for "low" 71 rules out of 256, for "medium" 54 rules out of 256, for "high" 35 rules out of 256, and for "very high" 31 rules out of 256. An explanation may lie in the integration of relation between taxonomic group. The distribution shape of the microorganisms group might have influenced the soil invertebrates group and exacerbate the effect on the lowest class. This can also be observed to a lesser extent for the invertebrates group, influenced by the flying invertebrates group, which depends on vegetation. Yet this last group based on eutrophic organisms does not depend on another taxonomic group and shows a more balanced distribution, resulting in a difference in distribution between the flying invertebrates and the soil invertebrates group. Likewise, the vertebrates group depends on both the vegetation and invertebrates group, the former mitigating the effect of

the later. When combining both distributions of vegetation and invertebrates groups, the distribution of vertebrates may be understood. The uneven distribution with the overrepresentation of the lowest class in some groups seem to be amplified in the distribution of the overall biodiversity. Likewise, the slightly higher percentage in the third class relatively to the second comes from its advantage in the vegetation and vertebrates groups. However, the shape of the microorganisms group remains unexplained.

Relating to the sensitivity analysis of the landscape variables, Fig. S3 in the supplementary material indicates that the greatest effect was on vegetation and flying invertebrates for which a variation of 3 classes out of 4 could be observed. This effect is reduced to a variation of 1 or 2 classes out of 4, or even no variation, when only one or two input variables are changed. This reduction can be observed for medium and favourable scenarios while for the unfavourable scenario, the range of variation remains at 3 classes out of 4. The effect on global biodiversity was the lowest with a variation of two classes out of 5 when all variables, or combination of variables are changed, and this only occurred in the medium and favourablescenarios. Sensitivity of the vertebrates component is intermediate between the most sensitive ones, vegetation and flying invertebrates, and the least sensitive one, global biodiversity.

3.3. Validation of I-BIO

Validation of the microorganisms branch was limited as there were

Option	Id_30B	Id_33B	Id_48A	Option	Id_423	Id_424	Id_311
. Biodiversity	Very low	Very low	Low	. Biodiversity	Very low	Low	Medium
.. Microorganisms	Low	Low to medium	Low to medium	.. Microorganisms	Low	Low to medium	Medium to high
... Anthropogenic pressures	High	Medium to high	Medium to high	... Anthropogenic pressures	High	Low to medium	Low
.... Tillage intensity	High	High	High	.... Tillage intensity	High	Low	Low
.... Chemical input	High	Low	Low	.... Chemical input	Medium	Medium	Low
..... Fertilizer	High	Low	Low	..... Fertilizer	Medium	Medium	Low
..... Pesticide	Medium	Low	Low	..... Pesticide	Medium	Medium	Low
... Trophic ressources	Low to medium	Low to medium	Low to medium	... Trophic ressources	Low to medium	Low	Low to medium
.... Soil OM	Medium	Medium	Low	.... Soil OM	Medium	Medium	Medium
.... Crop rotation	Medium	Medium	Medium	.... Crop rotation	Medium	Low	Medium
.. Vegetation	Low	Low	Medium to high	.. Vegetation	Medium to high	Low to medium	Low to medium
... Regional intensification	High	High	Low to medium	... Regional intensification	Low	Medium to high	Medium to high
.... Semi natural land cover	Medium	Low	High	.... Semi natural land cover	High	High	High
..... Composition	Medium	Low	Medium	..... Composition	High	High	High
...... Land cover diversity	Medium	Low	Medium	...... Land cover diversity	High	Medium	Medium
...... Percentage Semi natural land cover	Medium	Low	Medium	...... Percentage Semi natural land cover	High	High	High
..... Configuration (Connectivity)	Low	Low	High	..... Configuration (Connectivity)	Low	Low	Low
.... Field size	High	High	Medium	.... Field size	Medium	High	Medium
.... Crop diversity	Medium	Medium	Medium	.... Crop diversity	High	Low	Low
... Weeds	Low	Low	Low to medium	... Weeds	Low	Low to medium	Medium to high
.... Weed abundance	Low	Low	Medium	.... Weed abundance	Low	High	High
..... Monocot abundance	Low	Low	Medium	..... Monocot abundance	Low	High	High
...... "Anti-monocot" herbicide quantity	High	Medium	Low	...... "Anti-monocot" herbicide quantity	Medium	Medium	Medium
...... Tillage intensity	High	High	High	...... Tillage intensity	High	Low	Low
..... Dicot abundance	Low	Low	Medium	..... Dicot abundance	Low	Medium	High
...... "Anti-dicot" herbicide quantity	Medium	Medium	Low	...... "Anti-dicot" herbicide quantity	Medium	High	Medium
...... Tillage intensity	High	High	High	...... Tillage intensity	High	Low	Low
.... Dicot diversity	Low	Low	Medium	.... Dicot diversity	Low	Low	Medium
..... Crop rotation	Medium	Medium	Medium	..... Crop rotation	Medium	Low	Medium
..... Herbicide timing	Both or pre-emergence	Both or pre-emergence	Post-emergence	..... Herbicide timing	Both or pre-emergence	Both or pre-emergence	Post-emergence
.. Invertebrates	Low	Low	Low	.. Invertebrates	Low	Low to medium	Medium to high
... Soil invertebrates	Low	Low	Low	... Soil invertebrates	Low	Medium to high	Medium to high
.... Anthropogenic pressures	High	High	High	.... Anthropogenic pressures	High	Low to medium	Low to medium
..... Tillage intensity	High	High	High	..... Tillage intensity	High	Low	Low
..... Pesticide	Low	Low	Low	..... Pesticide	Medium	Medium	Low
...... Insecticide	Low	Low	Low	...... Insecticide	High	Low	Low
...... Other	Low	Low	Low	...... Other	Low	Medium	Low
.... Trophic ressources	Low	Low	Low to medium	.... Trophic ressources	Low	Low to medium	Medium to high
..... Microorganisms	Low	Low to medium	Low to medium	..... Microorganisms	Low	Low to medium	Medium to high
..... Vegetation	Low	Low	Medium to high	..... Vegetation	Medium to high	Low to medium	Low to medium
... Flying invertebrates	Low	Low	Medium to high	... Flying invertebrates	Medium to high	Low to medium	Medium to high
.... Anthropogenic pressures	Medium to high	Medium to high	Low to medium	.... Anthropogenic pressures	Low to medium	Medium to high	Low to medium
..... Pesticide	Low	Low	Low	..... Pesticide	Medium	Medium	Low
...... Insecticide	Low	Low	Low	...... Insecticide	High	Low	Low
...... Other	Low	Low	Low	...... Other	Low	Medium	Low
..... Regional intensification	High	High	Low to medium	..... Regional intensification	Low	Medium to high	Medium to high
.... Trophic ressources	Low	Low	Medium to high	.... Trophic ressources	Medium to high	Low to medium	Low to medium
..... Vegetation	Low	Low	Medium to high	..... Vegetation	Medium to high	Low to medium	Low to medium
.. Vertebrates	Low	Low	Medium to high	.. Vertebrates	Medium to high	Low to medium	Medium to high
... Anthropogenic pressures	High	Medium to high	Low to medium	... Anthropogenic pressures	Low to medium	Medium to high	Low to medium
.... Pesticide	Medium	Low	Low	.... Pesticide	Medium	Medium	Low
.... Machinery use	Medium	Medium	Medium	.... Machinery use	Medium	Low	Low
..... Tillage intensity	High	High	High	..... Tillage intensity	High	Low	Low
..... Mowing	Low	Low	Low	..... Mowing	Low	Low	Low
.... Regional intensification	High	High	Low to medium	.... Regional intensification	Low	Medium to high	Medium to high
... Trophic ressources	Low	Low	Low to medium	... Trophic ressources	Low to medium	Low to medium	Low to medium
.... Vegetation	Low	Low	Medium to high	.... Vegetation	Medium to high	Low to medium	Low to medium
.... Invertebrates	Low	Low	Low	.... Invertebrates	Low	Low to medium	Medium to high

Fig. 3. Illustration of the I-BIO indicator outputs with the East of Scotland and ENI datasets (respectively on the left and right) and the input variables.

only 10 fields within the NOE database with microorganisms biomass data to use (Fig. 5). However, according to Chantrel-Valat et al. (2021), the measured value may correspond to a higher class than low to medium, showing that the indicator is not calibrated. The difference between the two classes "low" and "low to medium" is significant (p value = 0.0050). Comparison of I-BIO with observed data met our expectation for monocotyledon and dicotyledon abundances for the EOSF site (Fig. 6a). The difference between boxplots is significant for monocotyledons (p value = 0.0293) and for dicotyledons (p value = 0.0227). For ENI data, the trend between I-BIO outputs and observed data was the opposite to those predicted (Fig. 6b), as the high classes for both monocotyledon and dicotyledon abundances are below the other classes (p-value = 0,0419). For the EOSF weed richness, the boxplot corresponding to the "high" class is significantly higher (p value = 0.0131) than "low to medium" class (Fig. 7a). The other boxplots "low" and "low to medium" showed lower value of richness than "high" although no clear relation existed between I-BIO output and field observations. For ENI, even if we focused only on the most abundant hemerophobic

species (Fried et al., 2018) to avoid biases linked to regional features or pedoclimatic context, there was no clear trend and substantial variability between classes. (Fig. 7b).

Fig. 8a shows a straightforward relation for the soil invertebrates branch between I-BIO outputs and field observations of earthworm abundance although no significant difference between boxplots could be found (p-value = 0,622 Low-Medium to high). The comparison of the flying invertebrates branch with coleoptera abundance from the ENI dataset showed a positive trend (Fig. 8b) although it was not so clear as for earthworms and not significant. The test with observation of butterfly abundance from the Noé dataset showed a slight positive trend for abundance which is a little more pronounced for butterfly richness (Fig. 9).

Finally, it was not possible to validate the vertebrates branch, with the Farmland birds data (Fig. 10) from either the NOE or ENI datasets. This could be due to the very low number of observations and fields with "medium to high" or "high" classes (respectively 3 and 1 occurrences for the NOE dataset and 14 and 0 for the ENI dataset). Moreover, it's not
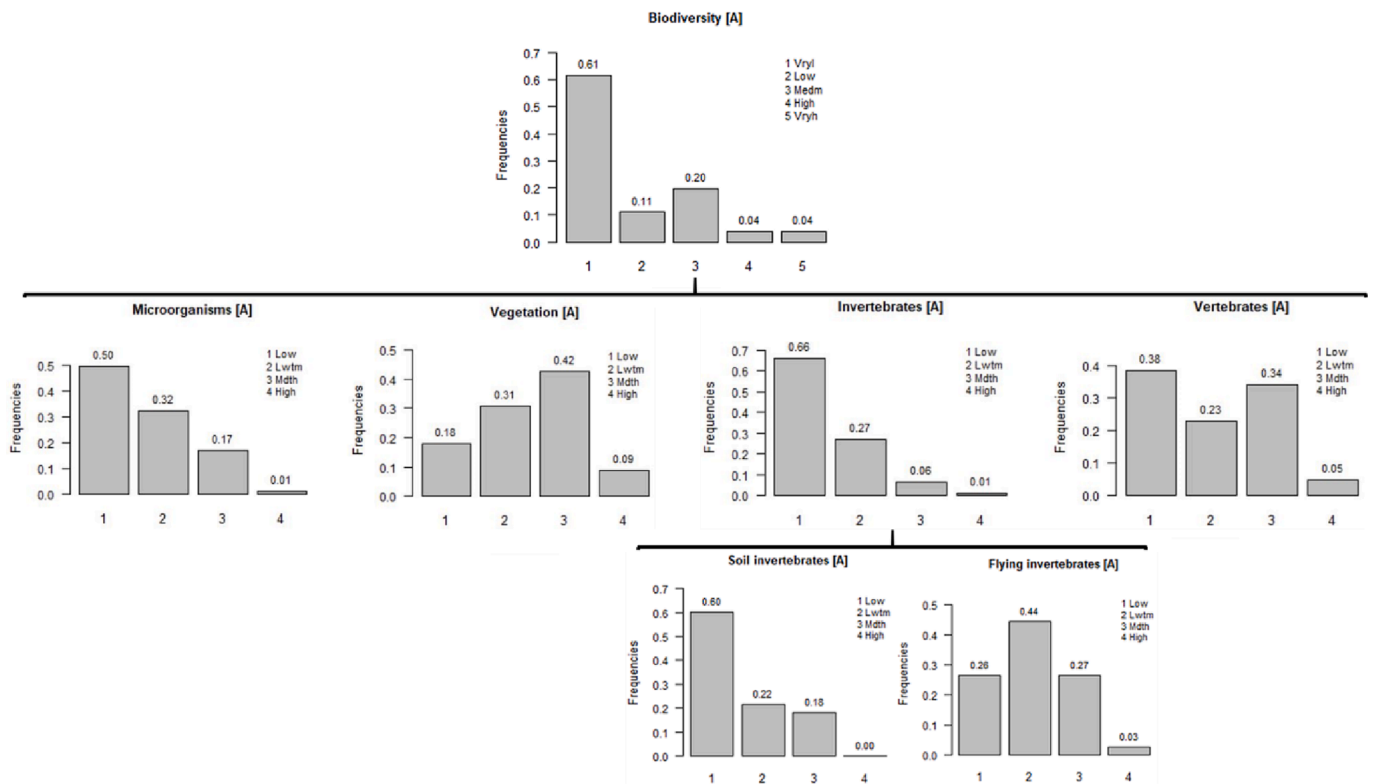
Fig. 4. Bar charts representing the distribution of the results of 5000 Monte Carlo simulations of I-BIO for the "Overall Biodiversity" and the four taxonomic groups (microorganisms, vegetation, invertebrates and vertebrates). The X-axis represents the classes of the studied variable (1 Very low, 2 Low, 3 Medium, 4 High, 5 Very high) and Y-axis gives the relative frequency of occurrence of the class (i.e. within the 5000 simulations).
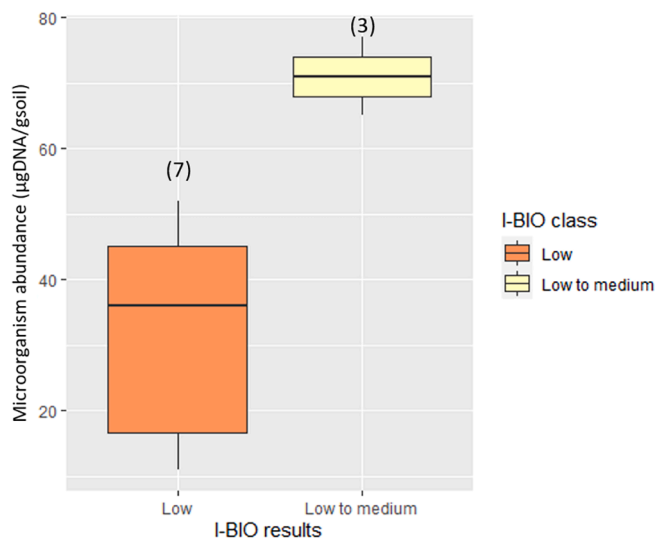

Fig. 5. Comparison of I-BIO outputs for the microorganisms branch with observed data of microorganisms biomass for the Noé dataset (n = 10, p value = 0.0050). The number of plots for each class is shown in parentheses.

surprising that birds are less impacted by local management practices compared to earthworm or coleoptera as other factors such as landscape features have a great influence on this group (Martin et al., 2019; Stanton et al., 2018).

4. Discussion

4.1. Originality of the indicator

I-BIO was designed to give a prediction of the impacts of management practices on overall biodiversity at the field level. As for every indicator design, a compromise has to be found between feasibility and integration of processes (Bockstaller et al., 2015), the former depending especially on the amount and availability of data, the latter depending on sufficient coverage of all key biodiversity components in the system Overall the I-BIO decision tree is more complex and requires more data than other predictive DEXI models: the IBEA (France Nature Environnement, 2013), the biodiversity branch of MASC 2.0 (Craheix et al., 2012) and DEXiPM1 (Pelzer et al., 2012) but less than this of DEXIPM (Demade, 2014). As a qualitative tool, it also requires less data than SALCAbd (Jeanneret et al., 2014). We did not select species groups for the different taxonomic groups like SALCA method but did not restrict to a global assessment of biodiversity as in IBEA. Like MASC 2.0 and DEXIPM 1, I-BIO addresses general taxonomic groups but, in our case, we tried to cover the whole range of groups from microorganisms to vertebrates, the former being only tackled by MASC2.0, and the latter only by SALCAbd. In comparison with DEXiPM2, I-BIO did not address ecosystem services linked to biodiversity for sake of simplicity because relation between both are complex (Duncan et al., 2015).

A major innovation in I-BIO is to consider direct impact of field and landscape management and indirect impact through trophic relation. Indeed, when a taxonomic group is impacted, for instance vegetation, higher groups in the trophic chain are also impacted by a reduction of their trophic resources, for example "flying invertebrates" (Bruun et al., 2022; Sohlenius, 1990). Another innovation in I-BIO is the integration of landscape variables. In order to better embed semi natural habitats, we created a branch for the semi natural flora which plays an important role in maintaining biodiversity (Bailey et al., 2010; Jeanneret et al., 2003;
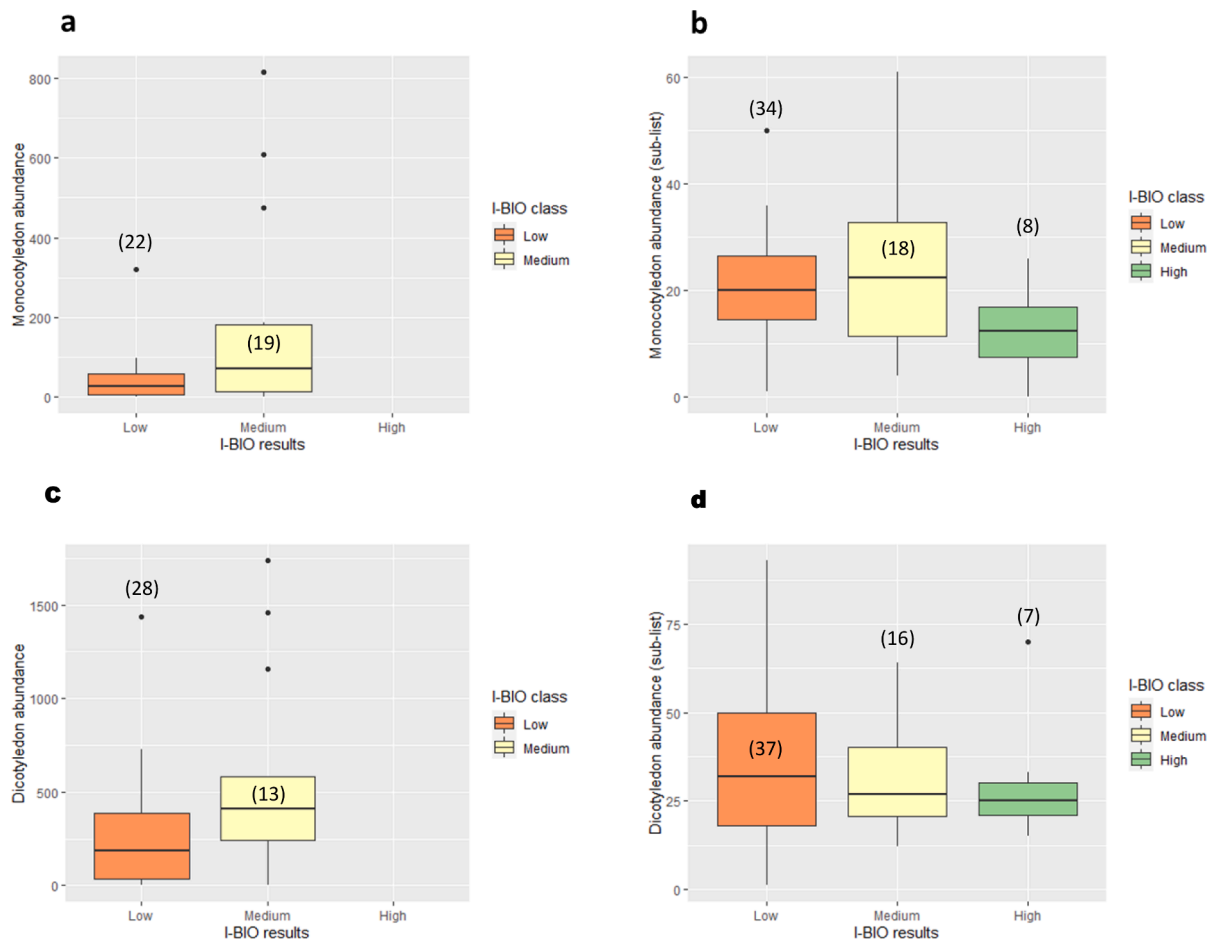
Fig. 6. Comparison of I-BIO outputs for monocotyledon abundance and dicotyledon abundance (number of individuals) with observed data: a) and c) EOSF data (n = 42, p value = 0.0293 for monocotyledon abundance and p value = 0.0227 for dicotyledon abundance), b) and d) ENI data, the sub-list encompassed the hundred most abundant species (n = 60, monocotyledon abundance Medium-High p-value = 0.0419, dicotyledon abundance Low-High p-value = 0.725). For the sake of readability, we removed two very high points for the EOSF data: the first one at 3284 for the Monocotyledon abundance and the second one at 3972 for the Dicotyledon abundance. The number of plots for each class is shown in parentheses.
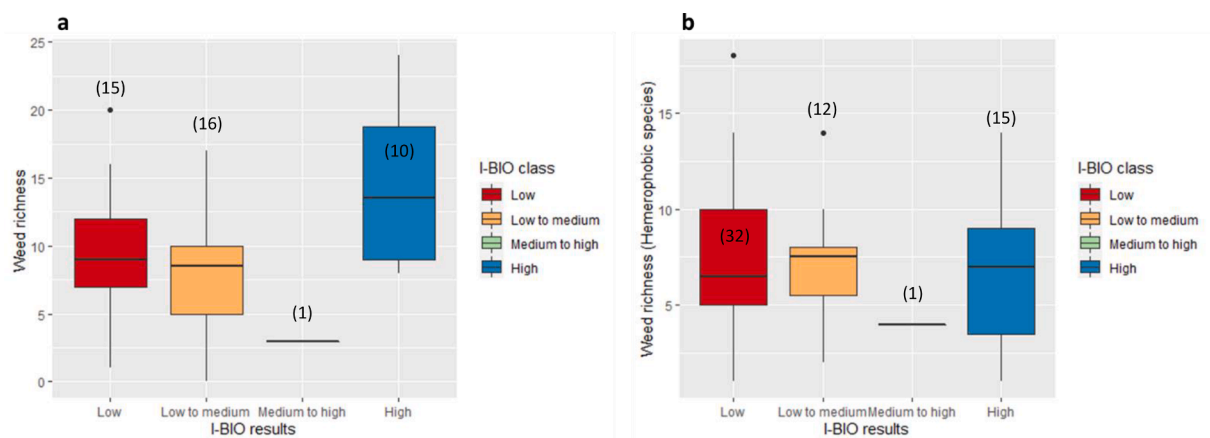
Fig. 7. Comparison of I-BIO outputs for weed richness with observed data: a) EOSF data all the species (n = 42, Low to medium-High p value = 0.0131), b) ENI data only the most abundant hemerophobic species (n = 60, Low-Medium to high p-value = 0.814). The number of plots for each class is shown in parentheses.

Martin et al., 2019; Sirami et al., 2019; Tscharntke et al., 2021). The IBEA method tackles some landscape variable like density, diversity, connectivity of landscape elements but also includes the quality of semi natural and natural habitat particularly the combination of tree species, presence of dead wood or intra-forest ponds. However, despite this example, functional aspects of landscape components remain poorly

integrated in biodiversity indicator assessment and would be a useful avenue for future work (Fahrig et al., 2011; dos Santos et al., 2021).

4.2. Sensitivity

Qualitative methods assessing agricultural systems sustainability
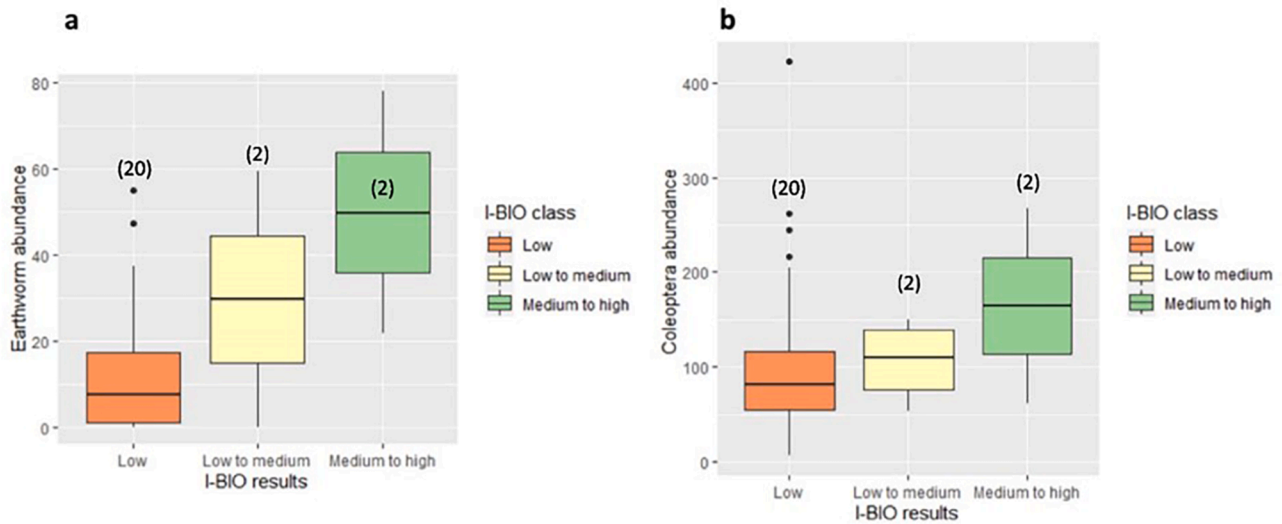
Fig. 8. Comparison of I-BIO outputs for invertebrates branch with corresponding observed data a) the soil invertebrates branch with earthworm abundances for ENI data (n = 24, Low-Medium to high p-value = 0.0622) and b) the flying invertebrates branch with coleoptera abundance for ENI data (n = 60, Low-Medium to high p-value = 0.425). The number of plots for each class is shown in parentheses.
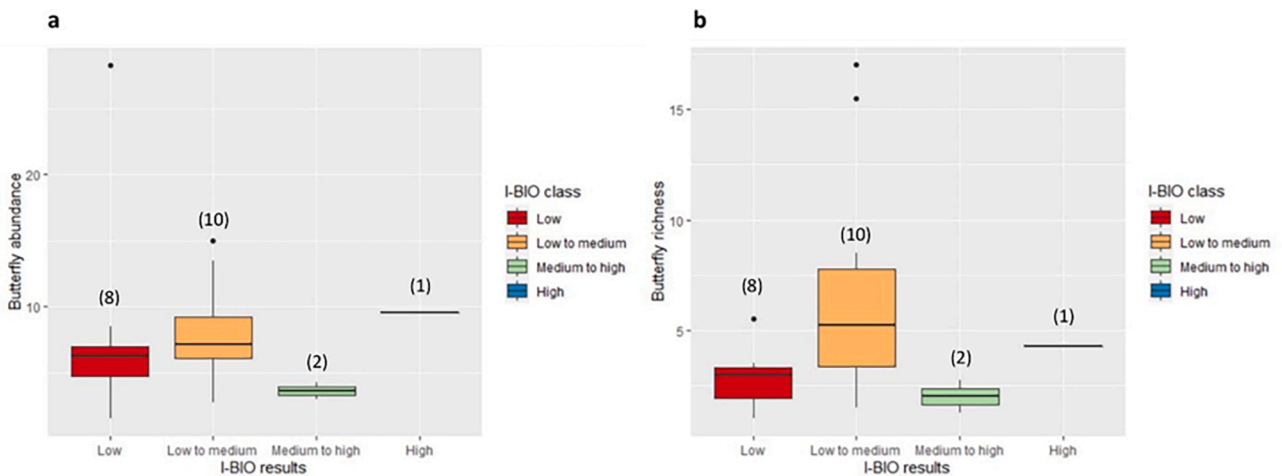

Fig. 9. Comparison of I-BIO outputs for the flying invertebrates branch with observed data for the Noé dataset (n = 21): a) Butterfly abundance (Low to medium-Medium to high p-value = 0.76), b) Butterfly richness (Low to medium-Medium to high p-value = 0.448). The number of plots for each class is shown in parentheses.
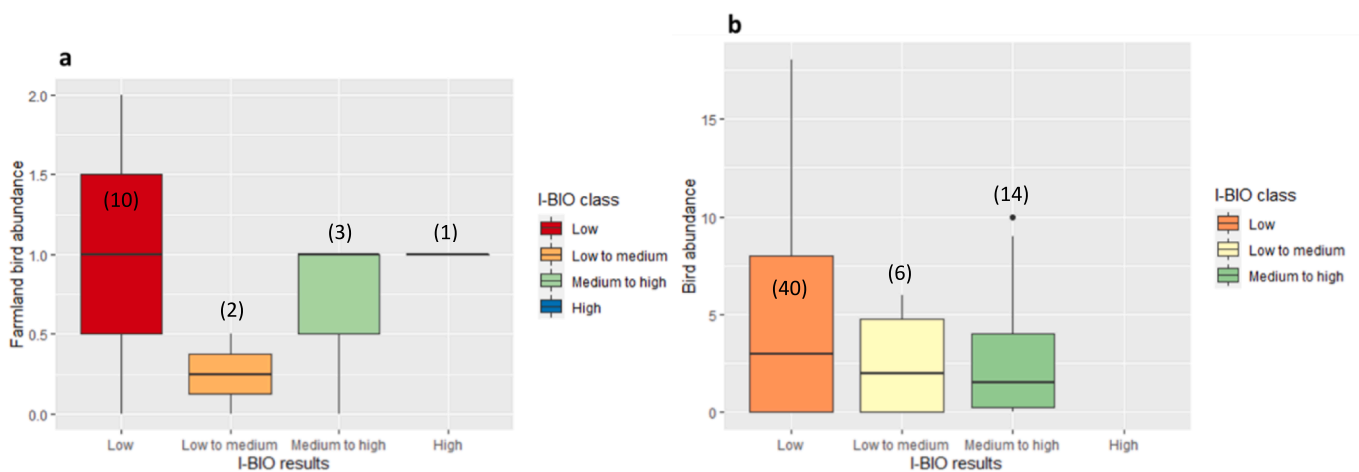

Fig. 10. Comparison of I-BIO outputs for the vertebrates branch with observed data of farmland birds: a) Noé dataset (n = 16, Low-low to medium p-value = 0.524) and b) ENI dataset (n = 60, low-medium to high p-value = 0.425). The number of plots for each class is shown in parentheses.

have shortcomings in terms of sensitivity, which due to the inherent structure of the DEXi model, are limited by the threshold effect. I-BIO attempts to mitigate this by adding more classes to some branches, but is still limited by the total number of decision rules due to combinatory explosion. I-BIO resulted in a total of 256 decision rules and although we developed a method to cope with this inflation (see section 2 and Fig. S2 of the supplementary material), it is uncertain that the method can be implemented for a higher number of rules. In any case, a trade-off has to be found between sensitivity of the tool and the problem of combinatory explosion. One possibility to resolve this sensitivity problem is to implement a quantitative method combining decision rules and fuzzy set like the CONTRA method which was tested to design an assessment method of grassland management on biodiversity (Bockstaller et al., 2017).

The results of the MC sampling approach showed an uneven distribution of I-BIO outputs for the overall biodiversity, skewed to the low class. This may be explained by the structure of the tree, although the behaviour for one branch, microorganisms remain unexplained. The results obtained may be compared with the outputs in Carpani et al. (2012) for the MASC1 model (Sadok et al., 2009b) for which extreme classes had a nil probability and always two mediums took the majority of probability. For our indicators, no nil probability was observed. If we calculated a root mean square deviation in relation to a balance distribution (probability = 0.20) it was slightly smaller than for MASC 1, a value of 21.3 for I-BIO against 22.5 for MASC 1 but not enough to conclude to a better sensitivity. Nevertheless the uneven distribution of I-BIO reflects the actual sensitivity of biodiversity to perturbations due to arable management (Coudrain et al., 2016; Martin et al., 2020).

As advised by Carpani et al. (2012), MC sampling may be completed by two other approaches: ANOVA and conditional probabilities. Unlike MC, the ANOVA makes possible the calculation of a sensitivity index for each input variable at each "node" of the tree, i.e., an output variable resulting from this aggregation of two or more variables. However, if the model is too large, there could be computational problems. The conditional probabilities method calculates a sensitivity index for all the variables along the tree i.e., at each aggregation level. Due to lack of time, it was not possible to implement both complementary approaches in this study. But for the conditional probabilities, taking into account similarity in the size of the tree and the number of aggregation level, some comparison can be made at least for basic variables.

Regarding the sensitivity analysis of landscape variables, a possible explanation for the variation across indicators could rely in the fact that flying invertebrates are the most mobile and therefore most likely to be affected by the larger scale, landscape variables. In-field organisms like soil invertebrates, with low dispersal ability, are least affected and this lessens the average, overall impact on global biodiversity.

4.3. Validation of the model

Following Bockstaller and Girardin (2003), we assessed the predictive quality of I-BIO in which is rarely shown in in publications presenting a new indicator. Jeanneret et al. (2014) is one exception, where a validation test was presented for two taxonomic groups for grasslands but not for arable plots. The validation of I-BIO covered a larger range of taxonomic groups. However, number of plots for the test remain low, especially for the "microorganisms" group. Overall, I-BIO performed well for earthworm data and better with abundance data than richness data, although even there, the predictive power remained weak which is not surprising regarding the simplified qualitative design of I-BIO. The validation results are somewhat similar to SALCAbd for which they found significant, positive relations for a slightly larger sample (n = 77) even though the correlations were weak (Spearman coefficient = 0.58 for plants and 0.39 for grasshoppers). In the case of SALCAbd, results concerned species richness and not abundance.

The poor performance of I-BIO for the vegetation branch may be due to the fact that these data were observed at the field margin and not in the centre of the field, so less influenced by agronomic practices. Landscape data are typically heterogeneous, especially for the percentage of semi natural habitats and their connectivity. Indeed, some datasets included detailed landscape features i.e. percentage of crops and semi-natural habitats within a radius of 1 km whereas others had little or no data on landscape context. Thus, I-BIO was restricted, in some instances to using the medium class or using expert opinion in the absence of appropriate data. This was especially the case for the East of Scotland farm dataset.

Improvements to the causal indicators for predicting impact on the soil invertebrates include additional information on tillage intensity and other pesticides. For the tillage intensity, the "high" class should include animated agricultural equipment such as rotative or disc harrow and lafforge spade. For the pesticides, a distinction should be made between fungicide, molluscicide and herbicide as the latter will have less impact on soil invertebrate abundance and diversity.

As recommended by Bockstaller and Girardin (2003), we compare sub-indicators dealing with one taxonomic group. For very broad groups like invertebrates, the comparison with one specific taxonomic group (e.g. earthworms) may be questionable. Ideally, it should be compared to a set of observations (earthworms, carabidae, etc.). Likewise, the measurement of microorganism biomass covers a very broad range of organisms including bacteria and fungi, and should therefore be completed by a comparison with abundance or diversity measurements of specific taxonomic groups. A multispecies indicator like this proposed by Sirami et al. (2019) could be put forward. This would even be appropriate for I-BIO at the level of overall biodiversity. But in any case, this would require on one site multi-taxonomic observations for a very large sample.

4.4. Implementation and utility

In their methodological framework on the validation of indicators, Bockstaller and Girardin also pointed out the need for end-user validation. At this stage of development of I-BIO, it was not possible to test the utility among potential users but some points may be discussed.

A first point is the relevance of the indicator for end users, i.e. whether the theme addressed by the indicator is an issue of concern for them or not (Bauler, 2012). In case of a negative answer, the probability that the indicator will be used, is expected to remain low. Farmers are more interested in taxonomic groups supporting ecosystem services like pest regulation and concerned by groups involved in disservices like pest damage to crops (Busse et al., 2021). Therefore I-BIO which does not explicitly address biodiversity in relation to ecosystem services will not be of interest to all farmers but only those involved in biodiversity conservation, like farmers working on rewilding (Corson et al., 2022). Nevertheless, Kelemen et al. (2013) showed that farmers are generally aware of the most obvious expressions of biodiversity (diverse species and varied landscape) and ethical and social values were important for all farmers. This may be due to the increasing concern over biodiversity loss by the whole society, including farmers.

According to Craheix et al. (2015), simplicity, flexibility and transparency are key characteristics to foster implementation of a tool by other users than the designer of the tool.

Simplicity is ensured by predictive indicators in form of decision tree based on linguistic rules which are easier to understand for non-specialists (Phillis and Andriantiatsaholiniaina, 2001) than quantitative models. However, some utility functions like this for the overall biodiversity with 256 rules are not so easy to understand and require some explanation. In spite of some points, the methodology and the tool are simple to use. Input data may remain qualitative, based on expertise or expert assumption. Many input data are available in farmers' traceability information system. An effort has to be made, without this being an issue for advisers and their farmers, to assess the intensity of herbicide use which is separated by target between herbicide for the control of monocotyledons (grass species) or dicotyledons. However, a

bottleneck lies in data collection of landscape variables, proportion of semi-natural elements and their connectivity. But some tools like Google may help to assess qualitatively these landscape variables or through a semi quantitative approach as proposed by Manneville et al. (2014) in the BIOTEX method. Furthermore, in arable land where these variables may be easily set to the lowest category in many locations.

The indicator is useful for relative comparison of biodiversity levels between different sites in the same dataset but it is complicated to compare sites in different datasets. I-BIO allows a relative comparison but does not provide an absolute scale. Besides, the tool is very flexible since it is very easy to change a value and to get a result. This may support discussion between stakeholders by providing quick answers to question like what can happen if I change this management practice. However, the drawbacks are the lack of sensitivity due to its qualitative form and the uneven frequency distribution on the side of the "low class". The design of a quantitative indicator based on fuzzy decision like the CONTRA method would mitigate this issue. Lastly, transparency is supported by the form in which the results are presented by the tool, where basic indicators and all the aggregated results are available and can be traced. Aggregation functions (utility functions) are also transparent even if they are not always easy to understand. But here again DEXi offers synthesis of decision rules to facilitate an overview of the rules.

5. Conclusions

With the improvements described above, I-BIO not only provides a framework for understanding arable ecosystems and comparing management practices but can be developed as a predictive tool and decision aid for farmers and their advisers, based on a greater level of detail and complexity than previously available. Indeed, I-BIO was built to assess the impact of management practices on four taxonomic groups, covering the whole range of diversity from microorganisms to vertebrates, and encompasses both field management and landscape variables (composition and configuration). A key novelty of this indicator lies in the assessment of direct impact and indirect impact on the trophic chain. The use of decision tree ensures simplicity and feasibility but the drawback is a certain lack of sensitivity for some groups. Predictive quality assessment delivered mitigated results but, in some cases, satisfactory for species abundance. This work should be continued with other datasets and for microorganisms. Last, the tool should be tested by end-users.

Declaration of Competing Interest

The authors declare that they have no known competing financial interests or personal relationships that could have appeared to influence the work reported in this paper.

Data availability

The authors do not have permission to share data.

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Appendix A. Supplementary data

Supplementary data to this article can be found online at https://doi.org/10.1016/j.ecolind.2023.110289.

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