Calculation of biodiversity level between different land-uses to improve conservation outcomes of biodiversity offsetting

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ABSTRACT

The goal of the mitigation hierarchy is to counteract the losses of biodiversity due to development projects by avoiding, reducing and as a last resort, by offsetting these losses. However, the implementation of offset measures is currently very unsatisfactory from a biodiversity perspective, and many development projects do not incorporate them. Here, we proposed a method for comparing biodiversity level between different land-uses to propose a set of alternative offset measures offering the same biodiversity outcomes. Biodiversity level (including both bird and bat communities) was calculated from the variation in biodiversity from each land-uses (fallow, grass strip, bush, grass strip with bushes, hedgerow) compared to crops (control). In order to account for local specificities of environmental assessment studies, we modulated the calculation of the biodiversity level following three examples of scenarios that differed according to the weights assigned to different species. For each scenario, hedgerow was always the land-use that generated the greatest biodiversity level, and was found to be the best alternative in terms of effect size. The advantage of this method and its weighting system is that the opinions of local stakeholders and specificities of species, such as their sensibility level to the development project or their conservation status, can be taken into account, resulting in the results being better appropriated. Thus, offset measures could be implemented more efficiently thanks to multi-taxonomic calculations and weighing possibilities, improving biodiversity outcomes. This method can also be used to compare the residual loss of biodiversity and biodiversity gains from implemented offset measures, using the same biodiversity metric.

1. Introduction

Biodiversity offsetting, the final component of the mitigation hierarchy (European Commission (EC) (2007), is currently based on a well-established conceptual framework (Arnett and May, 2016; Business and Biodiversity Offsets Programme (BBOP, 2012; Gardner et al., 2013). The goal of the mitigation hierarchy is to counteract the losses of biodiversity due to development projects by avoiding, reducing and as a last resort, offsetting the biodiversity losses, by generating biodiversity gains through management measures to achieve no net loss of biodiversity (NNL) (McKenney and Kiesecker, 2010). The implementation and evaluation of offset measures requires the use of appropriate metrics to assess the so-called ecological equivalence between biodiversity losses (i.e., residual effects after avoidance and reduction measures) and biodiversity gains (Bezombes et al., 2017; Quétier and Lavorel, 2011). This is in practice very difficult since methods for evaluating the biodiversity that may be lost may differ greatly from methods for evaluating potential gains from offset measures that have yet to be implemented (Bull et al., 2013; Bull and Brownlie, 2017). In addition, Millon et al. (2015) highlighted the potential difficulty in biodiversity offsetting for a set of species that have different ecological requirements and thus do not respond to offset measures in the same way. Thus, the implementation of offset measures and their related ecological uncertainties affect the objectives of NNL as a conservation goal (Griffiths et al., 2018).

The implementation of the mitigation hierarchy is more complex to

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implement for some types of development projects than others. Wind farm projects are a typical example of development project for which environmental assessments often fail to find satisfying mitigation measures (Lintott et al., 2016). Moreover, given impacts of wind turbine are generated after their installation and are thus difficult to predict and quantify. Little offset measures, and highly arbitrary, have so far been implemented in Europe in the context of wind farms (Peste et al., 2015, see Supplementary Material A). It is well known that wind turbines have negative impacts on biodiversity, mainly avian species (Arnett and May, 2016). Bat and bird mortality is regularly described (Arnett et al., 2016; Gibson et al., 2017), and wind turbines may be particularly harmful to species with long life spans, such as raptors and bats (Arnett et al., 2016; Garvin et al., 2011). In addition, wind turbines may cause indirect impacts such as the disturbance of migration routes, displacement and local habitat loss (Barré et al., 2018; Frick et al., 2017; Gibson et al., 2017; Gómez-Catasús et al., 2018; Masden et al., 2009; Millon et al., 2015, 2018; Zimmerling et al., 2013). Therefore, wind farm installation should require the implementation of offset measures during the entire life-cycle of the wind farm (Arnett and May, 2016). This is especially true in countries such as France, where the study was conducted, given that almost all of species affected by wind farms are juridictionally protected (all bats, most passerine birds and all birds of prey).

However, as wind turbines are mostly installed in intensive agricultural landscapes (Staid and Guikema, 2013, see Supplementary Material B), the wind farm developers can fail to find agricultural surfaces to convert to offset measures. Farmers - who can sign contracts with the order for environmental permits - do not accept biodiversity offsetting contracts as easily as those for other agri-environmental schemes (Le Coënt et al., 2017; Vaissière et al., 2018), either because offset measures are too space consuming and generate high economical losses (e.g. fallows), or because they reduce access to farming plots (e.g. hedgerows), or simply because they are too expensive (see Supplementary Material B). Moreover, setting aside agricultural land is performed in a context of its consumption due to increasing urbanization and volatility in the agricultural market (Yang et al., 2001). The market volatility in cereal prices, particularly the high prices in the stock market during the past decade (Ott, 2014), also greatly complicates the calculation of compensatory allowances (see Supplementary Material B). Thus, for wind farms development projects in agricultural landscape, there is a need that local stakeholders could be able to select among a set of equivalent measures (in term of biodiversity level) and could select the most appropriate one on the basis of local constraints. This pro-active approach could contribute to prevent the installation of wind turbines without compensatory measures because of the lack of satisfactory solution for both stakeholders and biodiversity (see Supplementary Material A). Note however that following the mitigation hierarchy, the implementation of offset measures when relevant, is a legal requirement (in France for instance with the Law n° 76–629 of the 10 July 1976 and the decree of the 19 February 2007 on the L. 411−2 article of the French environmental code). Consequently, given systematic impacts on biodiversity documented, situations where wind farms are settled without reduction and/or compensatory measures are not supposed to happen from a jurisdictional point of view.

The objective of this study was to calculate biodiversity levels between a set of offset measures, taking into account various components of biodiversity (bird and bat communities), in order to propose different measures to implement which could compensate negatives impacts of wind farms. Thus, our study did not aim to find one unique measure to offset residual losses but aimed to propose a method to find a set of offset measures and the size of those offsets according to their relative gains. Our study took place in an intensive agricultural landscape where wind turbines were set up but without compensatory measures (see Supplementary Material A). As a first step, we evaluated the variation of biodiversity (both bird and bat communities were considered) between different land-uses (that could be implemented as an offset measure) and crops (control). Then, we calculated the biodiversity level of each land-use and defined the quantity needed of each one of them to support the same biodiversity level than the others. As previous studies tested different methodological approaches to calculate offset requirements (Bull et al., 2014; Strange et al., 2002), our calculation included differential weighting of species. Using three scenarios, we evaluated the influence of these differential weighting of species on offset quantity needed. Three scenarios were tested: (i) all species weighted the same, (ii) double weight for species identified as negatively impacted by wind farms and (iii) double weight for species of interest, defined from a set of stakeholders point of view.

2. Methods

2.1. Study area

This study was conducted in Champagne-Ardenne (north-east France, see Fig. 1); where agricultural land covered 68 % of the region (calculated from Corine Land Cover data, see Supplementary Material C). The study was conducted in 2013.

2.2. Biodiversity inventory

Bird and bat communities were sampled at different land-uses (fallows, hedgerows, grass strips, bushes and grass strips with bushes) and at crops, used as a control, following the same protocol (Fig. 1). For more details on the land-uses, see Supplementary Material D.

Because biodiversity depends on the structure of the landscape as well as the land-uses, the positions of the sampling points were selected to avoid correlations between these two variables (see Supplementary Material D). In addition to the large-scale habitat structure, local field characteristics within a 100-m buffer area were also considered (mean crop height, number and type of crops in the fields, presence of farming trails and marginal strips of spontaneous herbaceous vegetation, see Supplementary Material D).

2.2.1. Breeding bird inventory

We sampled birds at 78 sites (18 control sites and 12 sites for each of the land-uses, Table 1) using the count point method according to the recommendations of the French Breeding Bird Survey (Jiguet et al., 2012). Points were placed at the perimeter of the site and separated by at least 200 m (the mean minimum distance between neighbouring points was 890 m, Fig. 1), so the number of points per site depended on its size with a maximum of five points (Table 1, see Supplementary Material D for the sizes of the sites). Counts were performed from sunrise to up to four hours after sunrise. To determine the abundance at each point, all birds seen or heard within a radius of 100 m were counted, unless they had been counted at a previously sampled point within the same site. Bird counts occurred twice over six weeks before the 24th of May and over five weeks after that date (first and second visit, respectively). In total, 340 and 337 count points, respectively, were performed by one observer. The sites first sampled at the beginning of the fieldwork were also the first sampled after the 24th of May. Each site type (land-uses and controls) was sampled early and late in the morning. This sampling design has previously been demonstrated to be appropriate for identifying the effects of farming intensity and local landscape simplification on the abundance of bird species (Filippi-Codaccioni et al., 2010).

2.2.2. Harrier inventory

Due to ation of biodiversity for each land-use per protocol. This equation was used for each land-use and each protocol. Heing at low densities and with large home ranges, such as birds of prey, we performed two other protocols (car transects and observation points) to assess the absence or presence of Montagu's harrier (*Circus pygargus*) and hen harrier (*Circus cyaneus*) in association with different crops. One of the site types (fallows, hedgerows, grass strips, bushes, grass strips with bushes or control) was assigned to each observed crop according to its

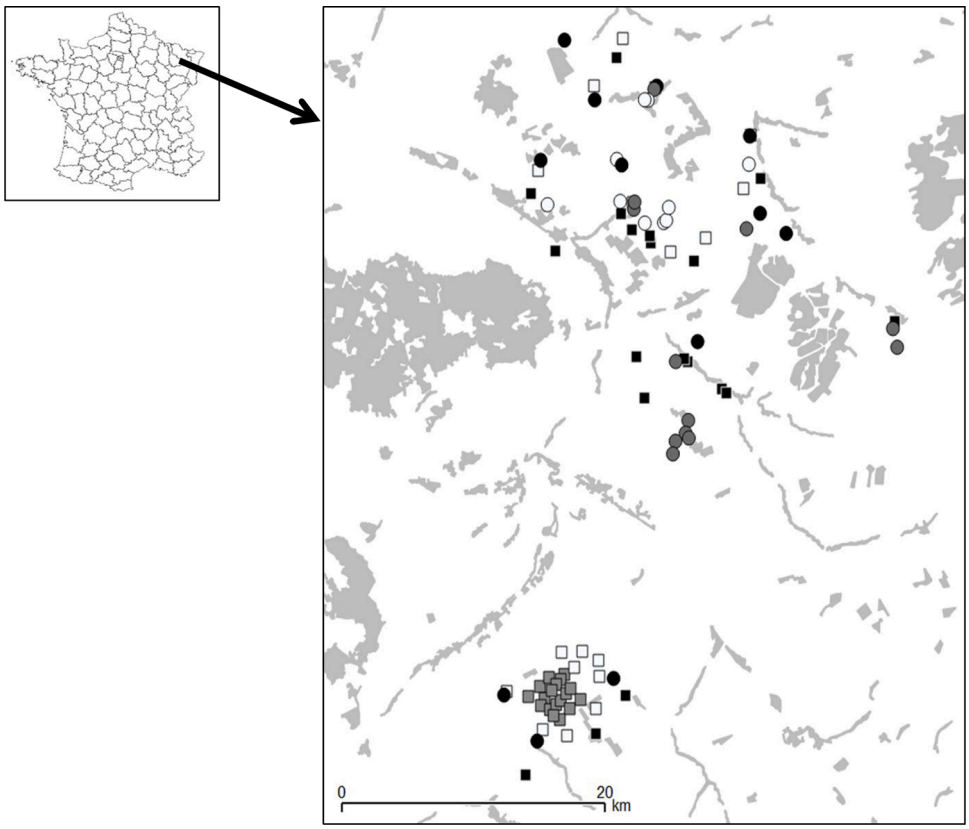


Fig. 1. Sampling design map showing the sampled sites: crops (white squares), fallows (black squares), grass strips (white circles), grass strips with bushes (grey circles), hedgerows (black circles) and crops under wind farming (grey squares). In this intensive agricultural landscape, the woodlands are indicated in grey.

Table 1
Number of sites sampled per site type for each visit. Numbers in parentheses represent the number of points per site.

Site type	Breeding bird inventory via count points	Harrier's inventory via car transects	Harrier's inventory via observation points	Bat inventory via recording echolocations at stationary points
Control				
Crops	18 (5)	≈300	≈300 (1–8)	12 (1)
Land-uses				
Fallows	12 (1–5)	11	7 (1–6)	8 (1)
Hedgerows	12 (2–5)	25	23 (1–6)	8 (1)
Grass strips	12 (2–5)	17	17 (1–4)	8 (1)
Bushes	12 (1)	35	30 (1–7)	8 (1)
Grass strips with bushes	12 (3–5)	8	7 (1–2)	8 (1)

surroundings (Table 1). Indeed, we hypothesized that crop selection by a harrier was influenced by its surroundings. Moreover, this approach prevented us from double counting the same harrier hunting above a land-use and above an adjacent crop.

The first protocol was a car transect, in which the presence or absence of harrier was noted for all crops adjacent to the track; 36 ± 5-km transects were driven at 25 km/h. The second protocol employed observation points, in which the presence or absence of harrier was noted for each crop visible with binoculars (up to 800 m away). The number of observation points, which were located along car transects at elevated locations, per day was 5.8 ± 0.6. These protocols were performed when harriers are known to be most active (6 h 30−12 h and 17 h–20 h 30) over 38 half-days between the 29th of May and the 2nd of July.

2.2.3. Bat inventory

We sampled bats by recording echolocations at stationary points. This method is known as a reliable way to assess the relationship between bat activities and habitat (Newson et al., 2015; Stahlschmidt and Brühl, 2012). The 56 sites (12 control sites and 8 sites for each of the land-uses, Table 1) were sampled twice during an entire night (from May to early July and from mid-August to late September for the first and second visit, respectively) following a protocol similar to that designed for the French Bat Monitoring Programme (see Kerbiriou et al., 2018a, b). Due to some overlap among acoustic repertoires and the difficulty of assigning exact species to all bat calls, three groups were established: *Pipistrellus* spp, *Eptesicus-Nyctalus* spp and *Plecotus-Myotis* spp. Some species within a given group may have had different ecological requirements but exhibited the same foraging behaviour and equivalent detection distances (see Millon et al., 2015). Finally, because some species were recorded at only a few sites, they were grouped together to permit statistical analysis. Bat activity, defined as the number of bat passes per night per group, was calculated for each site and each group following the approaches of Millon et al., 2015 or Barré et al., 2018.

2.2.4. Additional biodiversity inventory under wind turbines

Breeding bird and bat communities were also sampled within a wind farm. The wind farm consisted of 30 turbines with 100 m-high towers and 50 m-long blades in crop fields. (For more details on the landscape around the wind farm, see Supplementary Material D). Eighteen crops under wind turbines were sampled using the same count point method to assess breeding bird abundance, and 12 crops under wind turbines were sampled using the same echolocation recording protocol to determine bat activity. The harrier inventory was not performed at the wind farm. This additional biodiversity inventory allowed us to identify species sensible to habitat loss and thus, negatively impacted by the wind farm. Indeed, habitat loss could be perceived as a decrease in bird abundance

(Gómez-Catasús et al., 2018) or bat activity (Barré et al., 2018; Millon et al., 2015, 2018; Minderman et al., 2017).

2.3. Comparison between land-uses

2.3.1. Step one: modelling species abundance

The first step was the assessment of the differences in biodiversity between the control (crops) and each land-uses (fallows, hedgerows, grass strips, bushes and grass strips with bushes, Fig. 2). We assessed variations in bird abundance, harrier presence and bat activity (i.e., the response variable) as a function of site, land-use type, local field characteristics, weather conditions and material variables (the correlations between these explanatory variables were verified before using them in the models, see Supplementary Material D). We performed generalized linear models (GLM) with a Poisson error distribution (for the count data) or a binomial error distribution (for the presence/absence data).

Breeding bird analyses were performed for each species due to their different detection probabilities and biological requirements, and only avian species present in more than 5 % of the count points were studied at the species level (Fig. 2, see Supplementary Material E). Sylvia species other than the eurasian blackcap (Sylvia atricapilla) were grouped due to their similar biology and because their individual abundances were too low. Data from the different harrier protocols were analysed separately. The two Circus species were also grouped for the same reason as for the Sylvia species. Bird inventories (breeding birds or harriers) were repeated at similar locations, so we used generalized linear mixed models (GLMM) with the site as the random effect. The GLM for bats was performed at the group level and separately for each visit (because the different visits represented two different periods of bat activity).

We explored the data for potential spatial autocorrelations using a variogram tool (R package 'spatial', Bivand et al., 2008). When needed, we added an autocovariate (a distance-weighted function of neighbouring response values that was weighted by the square of the inverse distance; Dormann et al., 2007; Penone et al., 2013) with the autocovariate distance function in R (R package 'spdep', Roger Bivand). All analyses were performed using R statistical software v.3.0.2 (core team, 2013).

2.3.2. Step two: calculation of the variation of biodiversity for each land-use per protocol

Because of the modelling (step 1), each species or group of species had one parameter per land-use that represented the difference between the control (i.e., intercept in the modelling) and the land-use. The second step consisted of aggregating those parameters with an arithmetic mean for each inventory and each land-use (Fig. 2). According to the link (log or logit) used in the Poisson or binomial error distributions, we back-transformed these means using their inverse function (exponential or inverse logit). The difference between the exponential (or the inverse logit) of the mean and the exponential (or the inverse logit) of the intercept (crops) yielded the variation in breeding bird abundance, harrier presence or bat activity (according to the protocol) per land-use (eq. 1).Equation 1: Calculation of the variation of biodiversity for each land-use per protocol. This equation was used for each land-use and each protocol. Here, the intercept is the crops. We used the exponential function for back transformation according to the log link included in the GLM and GLMM with Poisson error distributions (for modelling with binomial error distributions, we used a similar approach but with the inverse logit function).

Equation 1.1: Example of calculating the variation in breeding bird abundance at the fallows:

$$\text{Variation}_{\text{breeding bird fallow}} = \exp((\beta_{\text{fallow sp 1}} + \beta_{\text{fallow sp 2}} + \ldots + \beta_{\text{fallow sp i}}) / i)) - \exp(\text{intercept}),$$

where β = parameter from the GLMM and i = number of breeding bird species.

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(continued on next column)

(continued)

Equation 1.2: Example of calculating the variation in breeding bird abundance at the hedgerows:

$$\text{Variation}_{\text{breeding bird}}\ \text{hedgerow} = \exp((\beta_{\text{hedgerow sp 1}} + \beta_{\text{hedgerow sp 2}} + \ldots + \beta_{\text{hedgerow sp i}}) / i) - \exp(\text{intercept}),$$

where β = parameter from the GLMM and i = number of breeding bird species.

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Equation 1.3: Example of calculating the variation in harrier presence at the fallows:

$$\text{Variation}_{\text{harriers fallow}} = \text{inverse logit}((\beta_{\text{fallow protocol 1}} + \beta_{\text{fallow protocol 2}}) / 2) - \text{inverse logit}(\text{intercept}),$$

where β = parameter from the GLMM.

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Equation 1.4: Example of calculating the variation in bat activity at the fallows:

where β = parameter from the GLM and k = number of bat groups.

$$\text{Gain}_{\text{bat fallow}} = \exp((\beta_{\text{fallow gr 1 visit 1}} + \beta_{\text{fallow gr 2 visit 1}} + \ldots + \beta_{\text{fallow gr k visit 2}}) / (k * 2)) - \exp(\text{intercept}),$$

2.3.3. Step three: scaling the variation of biodiversity according to the sampled surface

The sampled surfaces were different for each inventory (100 m radius for the breeding bird count points, 25 m radius for the bat echolocation recordings and the site size for the harrier protocols). To better apply the results, the variation of biodiversity per inventory and per land-use (from step 2) were scaled to obtain a variation of biodiversity at constant surface (1 ha). This third step was performed by two cross-multiplications. The first was to scale the surface of the intercept (i.e. crops) to 1 ha for each inventory, thus calculating the corresponding surface sampled for the other site types (eq. 2). For example, during the breeding bird inventory, the mean of the sampled surface per point was 3.14 ha for the crop and 0.6 ha for the fallow (see Supplementary Material D for details). Thus, for 1 ha of crop, the corresponding fallow surface was 0.19 ha (eq. 2.1). The second cross-multiplication scaled the variation of biodiversity for 1 ha of sampled land-use (eq. 3). We assumed a linear relationship between breeding bird abundance, harrier presence or bat activity and the surface of fallows, hedgerows, grass-strips and grass-strips with bushes at this scale of transformation. Note also that the standardized surface that was chosen in this step 3 (i.e. 1 ha) had no impact on the results. The same biodiversity level is found for all the land-use even with a different standardization surface, and in turn, the same amount of land-use to replace the fallow.

This third step was however not necessary for the bushes, as one bush was always sampled for all protocols. There was thus no need to scale their variation of biodiversity. Moreover, the linear relationship between the surface and the biodiversity could not be assumed for the bushes, which are more isolated in the landscape. They are thus expected to have an attractiveness role that do not depend on their size. Equation 2: First cross-multiplication to scale the surface of the intercept to 1 ha for each inventory:

Equation 2.1: Example of scaling the intercept of the breeding bird inventory and calculating the corresponding sampled surface of the fallow:

$$CSF = (SSF / SSC) \times 1,$$

where *CSF* is the corresponding surface of the fallow; *SSF* is the mean of the sampled surface of the fallow during the breeding bird inventory (0.6 ha in our study, see Supplementary Material D for details); and *SSC* is the sampled surface of the control (crops, i.e., $\pi \times 100^2 / 10{,}000 = 3.14$ ha) during the breeding bird inventory.

Equation 3: Second cross-multiplication to scale the variation of the biodiversity for each land-use for the same surface:

Equation 3.1: Example of scaling the variation of biodiversity from the fallow from the breeding bird inventory:

$$\text{Variation}_{\textit{breeding bird fallow standardized}} = \text{Variation}_{\textit{breeding bird fallow}} * 1 / CSF.$$

2.3.4. Step four: Calculation of the quantity of each land-use needed to support the same biodiversity level than other land-use

After all variation of biodiversity were calculated for the same land-use metric for each inventory, the means of those variations were

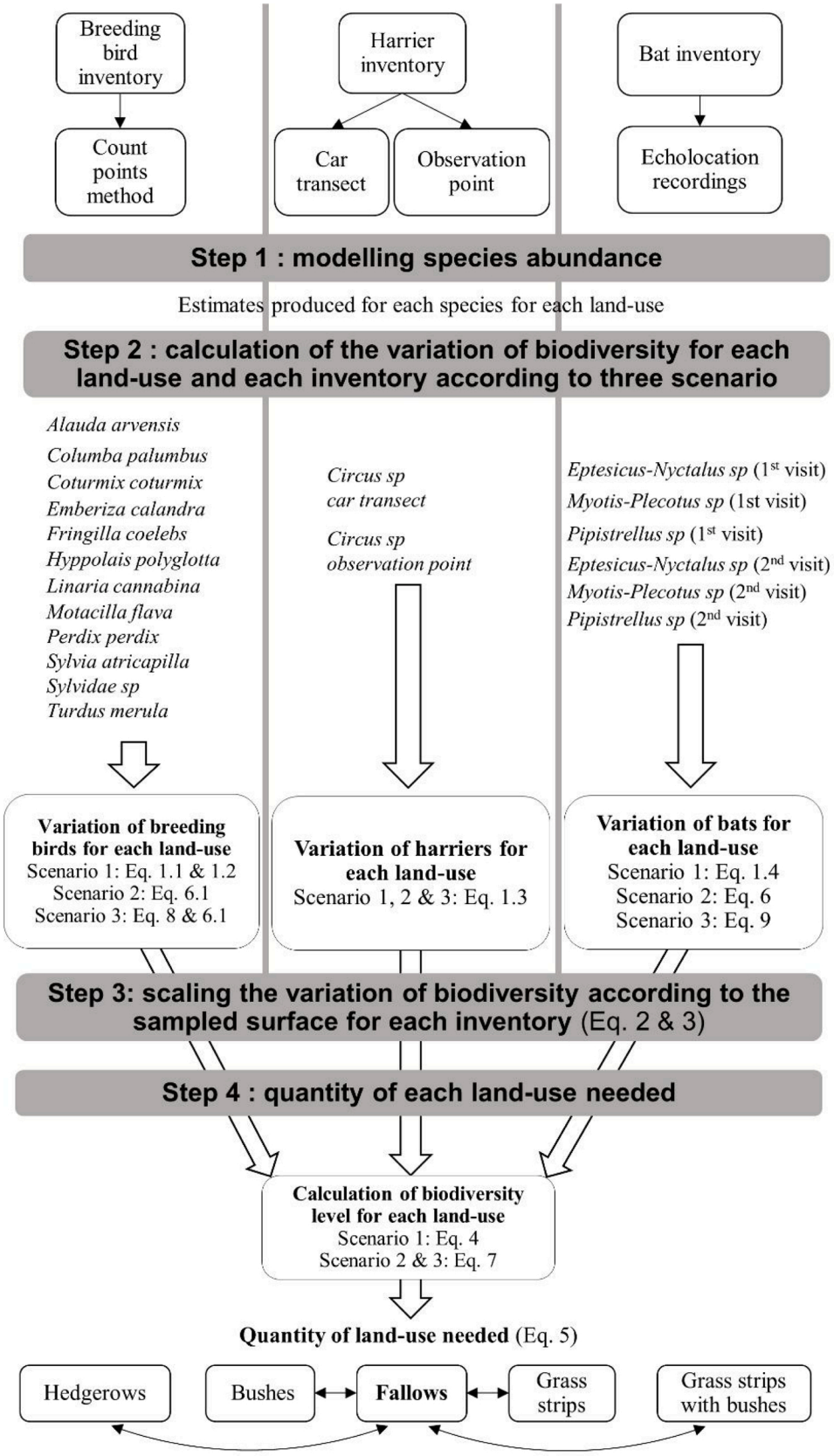


Fig. 2. Steps to calculate the quantity of the different land-uses that could replace the fallow from data on breeding birds, harriers and bat species. The exponent indicates the scenario under which the species, group of species or the mean per protocol is doubled. Eq. refers to the equations; when the scenario is not written, the equation is used for all scenarios.

calculated per land-use in order to obtain a biodiversity level per land-use. The number of species or groups of species was considered to give more weight to the inventory that included more species (Eq. 4, Fig. 2). Then, the last step determined the surface needed to support the same biodiversity level than another land-use. Taking the example of fallows as the reference, we determined the surface of hedgerows, grass strips or grass strips with bushes and the number of bushes needed to obtain the same biodiversity level as from the fallow (Eq. 5, Fig. 2). This was performed by simple cross-multiplication.Equation 4: Calculation of a biodiversity level for each land-use accounting for all inventories:

Equation 4.1: Example for the fallow:
Biodiversity level $_{all\ protocols\ fallow}$ = (Variation $_{breeding\ bird\ fallow\ standardized}$ * i + Variation $_{harrier\ fallow\ standardized}$ + Variation $_{bats\ fallow\ standardized}$ * k) / (i + k + 1),
where i= number of breeding bird species; k = number of bat groups; and the + 1 is for the harrier protocol.

Equation 5: Cross-multiplication to determine the quantity of the land-use needed to replace the fallow:

Equation 5.1: Hedgerow example:
Length $_{hedgerow}$ = Biodiversity level $_{all\ protocols\ fallow}$ / Biodiversity level $_{all\ protocols\ hedgerow}$.

2.4. Variation of this method among three weighting system scenarios

*Scenario 1:*All taxa weighted equally (Fig. 2, scenario 1). The weights in the last step referred to the number of species or groups of species in each protocol (see section 2.5.4).*Scenario 2:* Double weight for species identified as negatively impacted by the wind farms (Fig. 2, scenario 2, eq. 6 & 7). The impacted species were defined from the additional biodiversity inventory (2.3.4), and we used statistical models that compared breeding bird abundance or bat activity between crops (control) and crops under wind turbines. The abundances of the common quail (*Coturnix coturnix*), common blackbird (*Turdus merula*), common chaffinch (*Fringilla coelebs*) and eurasian blackcap (*Sylvia atricapilla*) were lower under wind turbines (see Supplementary Material F). The activity of *Eptesicus-Nyctalus spp* during the second visit was also lower under wind turbines (see Supplementary Material F, eq. 6). Although we did not have results for the harriers, we defined them as being impacted by wind farms according to the literature (Garvin et al., 2011; Gibson et al., 2017, Fig. 2, scenario 2, see eq. 7).Equation 6: Calculation of the variation of biodiversity for each land-use for the breeding bird and bat inventories accounting for taxa negatively impacted by wind farms (eq. 1 modified):

Equation 6.1: Example of calculating the variation in breeding bird abundance at the fallow with the species 1 (sp1) impacted by wind farms:
Variation $_{breeding\ bird}$ impacted $_{fallow}$ = exp (($\beta_{fallow\ sp\ 1}$ + $\beta_{fallow\ sp\ 1}$ + $\beta_{fallow\ sp\ 2}$ + … + $\beta_{fallow\ sp\ i}$) / (i + number of impacted species)) – exp (intercept),
where i is the number of breeding bird species.

Equation 7: Calculation of a biodiversity level for each land-use accounting for all protocols, with the harrier protocol being counted twice (eq. 4 modified)

Equation 7.1: Example for the fallow:
Biodiversity level $_{all\ protocols\ fallow}$ = (Variation $_{breeding\ bird\ impacted\ fallow\ standardized}$ * i + Variation $_{harrier\ fallow\ standardized}$ * 2 + Variation $_{bats\ impacted\ fallow\ standardized}$ * k) / (i + k + 2),where i
= number of breeding bird species; k = number of bat groups; and + 2 indicates counting the harrier inventory twice.

Scenario 3: Double weight for species of interest, defined from a set of stakeholders. Indeed, the participation of local stakeholders in the application of the method can be an important tool to develop their trust, as bottom-up approach is known to be useful and transparency is considered as a good practice for biodiversity offsetting (Bull et al., 2018; Voinov and Bousquet, 2010, see Supplementary Material A). In this way, a group of representative stakeholders was defined to provide an example of stakeholder-based scenario as follows: the wind farm developer (ENGIE), an environmental NGO, a local hunting association, the Regional Directorate for the Environment (RDE), Agrosolutions (the main French agricultural cooperative group in direct contact with farmers of the study area, composed of persons competent in technical aspects of agronomy) and the French National Museum of National History. The stakeholders discussed the weighting of the species according to the local specificities of the project and the area. Thus, a double weight was applied to a selection of taxa identified as species of interest from the stakeholder point of view following four criteria (Fig. 2, scenario 3).

First, as the offsetting took place in a farming landscape, priority was given to the farmland-associated bird species. According to the Species Specialisation Index (SSI, Julliard et al., 2006), the farmland species were the Eurasian skylark (*Alauda arvensis*), corn bunting (*Emberiza calandra*), common quail (*C. coturnix*), yellow wagtail (*Motacilla flava*), common linnet (*Linaria cannabina*), melodious warbler (*Hippolais polyglotta*) and grey partridge (*Perdix perdix*). Species parameters that were not considered to represent the farmland species according to the SSI were averaged together before the third step, as if there were a non-farmland species (eq. 8).

Second, the weight of the breeding bird species negatively impacted by wind farming was doubled for the same reason as described for the second scenario (Fig. 2, scenario 3, eq. 6.1). Because wind farms impact three of the five non-farmland species, the parameters of the non-farmland species were also doubled.

Third, to give more weight to the bat reproductive season, which is important for maintaining a persistent local population, the results from the first bat inventory visit were also double weighted (Fig. 2, scenario 3, eq. 9).

Finally, in the fourth step, the harrier inventory results were double weighted (Fig. 2, scenario 3, eq. 7). Indeed, both these species are impacted by wind farming (Garvin et al., 2011; Gibson et al., 2017) and are important top predators in the ecosystem (Therrien et al., 2014). Equation 8: Averaging the parameters of non-farm bird species

Equation 8.1: Example for the fallow:
$\sigma_{non\text{-}farming\ species\ fallow}$ = ($\beta_{fallow\ sp\ 1}$ + $\beta_{fallow\ sp\ 2}$ + … + $\beta_{fallow\ sp\ i}$) / $i_{non\text{-}farming\ species}$,
where β = parameter from the GLMM, and $i_{non\text{-}farming\ species}$ = number of non-farm breeding bird species.

Equation 9: Calculation of the variation of bat activity for each offset measure giving more weight to the bat reproductive season (visit 1, eq. 1.4 modified)

Equation 9.1: Example of calculating the variation in bat activity at the fallows:
Variation $_{bat\ fallow\ visit\ 1\ doubled}$ = exp (($\beta_{fallow\ gr\ 1\ visit\ 1}$ + $\beta_{fallow\ gr\ 1\ visit\ 1}$ + $\beta_{fallow\ gr\ 2\ visit\ 1}$ + … + $\beta_{fallow\ gr\ k\ visit\ 2}$) / (k* 2 + k) – exp (intercept),
where β = parameter from the GLM, and k = number of bat groups.

3. Results

3.1. Species encountered

Seventy-four bird species were identified using the count point protocol (see Supplementary Material E), but only 12 were present in more than the 5 % of the total number of count points (Fig. 2). The two harrier species were observed in low abundances (only on 157 of 1853 crops with the car transect protocol and 96 of 1456 crops with the observation point protocol). A total of 9900 bat passes were recorded: 3926 during the first visit and 5985 during the second visit. The majority was from species in the *Pipistrellus* group followed by the *Eptesicus-Nyctalus* group and the *Plecotus-Myotis* group (93 %, 4 % and 3 % of the total number of passes, respectively, see Supplementary Material E).

3.2. Results from the statistical models (step 1)

According to a slight spatial structure detected for Eurasian skylark (*A. arvensis*), common quail (*C. coturnix*), common linnet (*L. cannabina*), common chaffinch (*Fringilla coelebs*), eurasian blackcap (*S. atricapilla*), *Pipistrellus* spp (1st visit) and *Eptesicus-Nyctalus* spp (1 st visit), the autocovariate function was added to the modelling. The statistical results varied greatly from one species to another (Tables 2 and 3, Fig. 3 and Supplementary Material G). For example, some species did not significantly positively respond to any land-use, including eurasian skylark (*A. arvensis*, Fig. 3), common wood pigeon (*C. palumbus*, Fig. 3), *Pipistrellus* spp during the 1st and 2nd visits (Fig. 3, see Table 2 and 3 for more example.). Other species exhibited higher abundances or activity only at the fallow sites: *Sylvia* spp (Table 2) and *Plecotus-Myotis* spp during the 1st visit (Table 3). Melodious warbler (*H. polyglotta*), common linnet (*L. cannabina*), common blackbird (*Turdus merula*), *Circus* spp (from both protocols, Table 2, Fig. 3) and *Eptesicus-Nyctalus* spp during the 1st visit (Table 3) were significantly positively impacted by at least one land-use but not by the fallow. Finally, the last group of species significantly positively responded to the fallow and at least one other land-use: common chaffinch (*F. coelebs*) and eurasian blackcap (*S. atricapilla*, Table 2).

3.3. Results from the different scenarios

From the first scenario where all species are weighted equally, 1 ha of hedgerow resulted in the greatest biodiversity level, followed far away by grass-strip (Table 4). The biodiversity level from the fallow, the grass strip and grass strip with bushes and bushes were lower (Table 4). This resulted in a higher amount of grass strip and grass strip with bushes needed to replace 1 ha of fallow than the amount of hedgerows (Table 4).

The biodiversity level resulting from the scenario 2, where the weights of the species impacted by wind turbines were doubled, are similar concerning the fallow, hedgerow and grass strip (Table 4). The largest difference between the scenario 1 and 2 concerned the grass strip with bushes, resulting in a more than double amount of grass strip with bushes needed to replace 1 ha of fallow (Table 4).

In the scenario 3, the weight from farm-associated bird species, bird species impacted by wind turbines and the first visit of the bat inventory were doubled. The biodiversity level for all the land-uses were lower than for the scenario 1 and 2, the hedgerow still having the best biodiversity level (Table 4). Apart for the grass strip with bush, the amounts of the other land-uses needed to replace 1 ha of fallow were in the same proportion than in the scenario 1 and 2 (Table 4).

4. Discussion

In the framework of project development and offsetting measures, there is a crucial need of pragmatic methodological advances. Project developers, such as wind farms developers, can fail to find surfaces to implement specific offset measures due to potential constraints (space consuming, economical losses, implementation and maintenance costs). In this study, we argue that it is possible to develop a pragmatic workflow to calculate biodiversity levels between land-uses to find out how much of an offset measure is needed to achieve the same biodiversity gain as another. This framework goes with a robust and transparent sampling design and an explicit species-weighting concept, taking into account simultaneously bird and bat communities. We provided a set of offset measures to implement, equivalent in term of biodiversity level, and give the opportunity to the stakeholders to choose the most appropriate offset measures (or a combination of them) according to the local constraints. We are convinced that such workflow and outputs in term of biodiversity level assessment could contribute to prevent the installation of wind turbines without compensatory measures because of the lack of satisfactory solution for both stakeholders and biodiversity. Although offset measures should be used as the last resort after the implementation of the avoidance and the reduction of the negative impacts.

Biodiversity level were calculated with explicitly formulated scenarios based on the impact of wind turbines on species and their degree of specialization as follows: (i) all species weighted the same, (ii) double weight for species identified as negatively impacted by wind farms or (iii) double weight for species identified as of interest from the stakeholder point of view.

In our study, hedgerow appeared to support the highest biodiversity level we considered, whatever the scenario was, comparing to fallow, grass strip or grass strip with bushes or one bush. Those results could be used in another context than biodiversity offsetting and complete the literature available on the agri-environment context (see for example Lawer and Darkoh, 2016; Pe'Er et al., 2017; Robleño et al., 2017).

The largest difference of biodiversity level between scenario 1 and 2 concerned the grass strip with bushes. Indeed, most species or group of species that were negatively impacted by wind farm, and in turn, had a double weight in scenario 2, had a lower abundance, presence or activity at the grass strip with bushes. In the scenario 3, all biodiversity levels were lower than for scenario 1 and 2. This is mostly explained by the double weight gave to *Coturnix coturnix* which negatively responded to all land-use, and the double weight to Harriers which negatively responded to fallows, hedgerows, bushes and grass strip with bushes depending on inventory. Moreover, lower level of biodiversity in scenario 3 for grass strips was also due to the double weighting of first visit

Table 2
β parameters ± standard errors (SE) and p-values from a GLMM of species abundance for the 12 bird species and two harrier protocols. Crops (C) provided the intercept (i.e., the variable for which the parameter = 0). A positive (negative) parameter value indicated that the land-use presented a greater (lower) abundance than C.

Species	Land-use									
	Fallows		Hedgerows		Grass Strip		Bushes		Grass Strip with Bushes	
	β±SE	p-value	β±SE	p-value	β±SE	p-value	β±SE	p-value	β±SE	p-value
Alauda arvensis	−0.21 ± 0.13	0.124	**−0.59 ± 0.18**	**0.001**	−0.19 ± 0.16	0.211	−0.18 ± 0.21	0.407	−0.12 ± 0.12	0.315
Columba palumbus	2.49 ± 2.46	0.310	4.12 ± 2.28	0.072	1.55 ± 2.55	0.545	2.42 ± 2.75	0.378	0.46 ± 2.81	0.869
Coturnix coturnix	−0.39 ± 0.61	0.525	−0.35 ± 0.61	0.567	−0.25 ± 0.56	0.656	−0.02 ± 0.80	0.656	−0.76 ± 0.61	0.209
Emberiza calandra	−0.34 ± 0.47	0.471	−0.67 ± 0.50	0.181	0.24 ± 0.42	0.565	−0.84 ± 0.63	0.564	−0.79 ± 0.47	0.091
Fringilla coelebs	**1.40 ± 0.69**	**0.044**	**1.93 ± 0.69**	**0.005**	−0.37 ± 0.90	0.678	NA	NA	0.07 ± 0.77	0.923
Hyppolais polyglota	1.36 ± 0.94	0.147	**2.18 ± 0.88**	**0.013**	−0.04 ± 1.25	0.979	1.25 ± 1.14	0.272	1.06 ± 0.93	0.255
Linaria cannabina	1.81 ± 0.99	0.069	**2.62 ± 0.93**	**0.005**	**2.54 ± 0.96**	**0.008**	**2.49 ± 1.03**	**0.015**	**2.35 ± 0.93**	**0.011**
Motacilla flava	**−1.12 ± 0.35**	**0.001**	−0.41 ± 0.32	0.198	**−0.67 ± 0.31**	**0.031**	−0.17 ± 0.36	0.628	−0.35 ± 0.28	0.206
Perdix perdix	−0.64 ± 0.46	0.165	−0.73 ± 0.49	0.136	−0.86 ± 0.51	0.094	−0.75 ± 0.68	0.268	−0.008 ± 0.35	0.981
Sylvia atricapilla	**2.04 ± 0.98**	**0.037**	**2.09 ± 0.98**	**0.034**	1.25 ± 1.02	0.223	NA	NA	0.89 ± 1.03	0.387
Sylvia spp	**2.06 ± 0.84**	**0.014**	1.35 ± 0.87	0.123	−0.71 ± 1.50	0.638	0.36 ± 1.50	0.812	0.35 ± 0.97	0.719
Turdus merula	0.41 ± 0.72	0.565	**1.48 ± 0.56**	**0.008**	0.81 ± 0.61	0.192	−0.04 ± 1.20	0.972	−0.35 ± 0.79	0.657
Circus spp (transect)	0.27 ± 0.80	0.739	0.15 ± 0.35	0.672	**1.35 ± 0.35**	**<0.001**	−0.40 ± 0.36	0.265	−0.72 ± 0.67	0.281
Circus spp (point)	−0.15 ± 1.09	0.893	−0.91 ± 0.56	0.102	**1.03 ± 0.43**	**0.015**	0.16 ± 0.43	0.715	−0.72 ± 0.67	0.281

Table 3
β parameters ± standard errors (SE) and p-values from a GLM of bat activity. Crops (C) provided the intercept (i.e., the variable for which the parameter = 0). A positive (negative) parameter value indicated that the land-use presented a greater (lower) bat activity than C.

Species	Land–use									
	Fallows		*Hedgerows*		Grass Strips		Bushes		Grass Strips with Bushes	
	β±SE	p-value	β±SE	p-value	β±*SE*	p-value	β±SE	p-value	β±SE	p-value
First visit										
Pipistrellus	0.39 ± 0.52	0.452	0.82 ± 0.42	0.052	−0.10 ± 0.56	0.861	−0.94 ± 0.74	0.204	−0.26 ± 0.65	0.689
Eptesicus-Nyctalus	−0.54 ± 0.71	0.455	−0.42 ± 0.71	0.555	**1.64 ± 0.52**	**0.001**	−0.21 ± 0.97	0.827	−0.20 ± 0.75	0.792
Plecotus-Myotis	**1.18 ± 0.37**	**0.001**	0.359 ± 0.42	0.361	−1.16 ± 0.74	0.119	−0.34 ± 0.55	0.539	−0.19 ± 0.51	0.709
Second visit										
Pipistrellus	0.42 ± 0.54	0.440	−1.65 ± 1.14	0.145	−1.28 ± 0.85	0.132	0.10 ± 0.59	0.865	−1.28 ± 0.82	0.116
Eptesicus-Nyctalus	0.12 ± 0.39	0.759	−0.12 ± 0.39	0.758	0.15 ± 0.39	0.703	−0.30 ± 0.45	0.505	**−1.93 ± 0.89**	**0.031**
Plecotus-Myotis	0.86 ± 0.51	0.094	0.49 ± 0.55	0.364	0.33 ± 0.58	0.571	0.20 ± 0.63	0.751	−0.41 ± 0.74	0.577

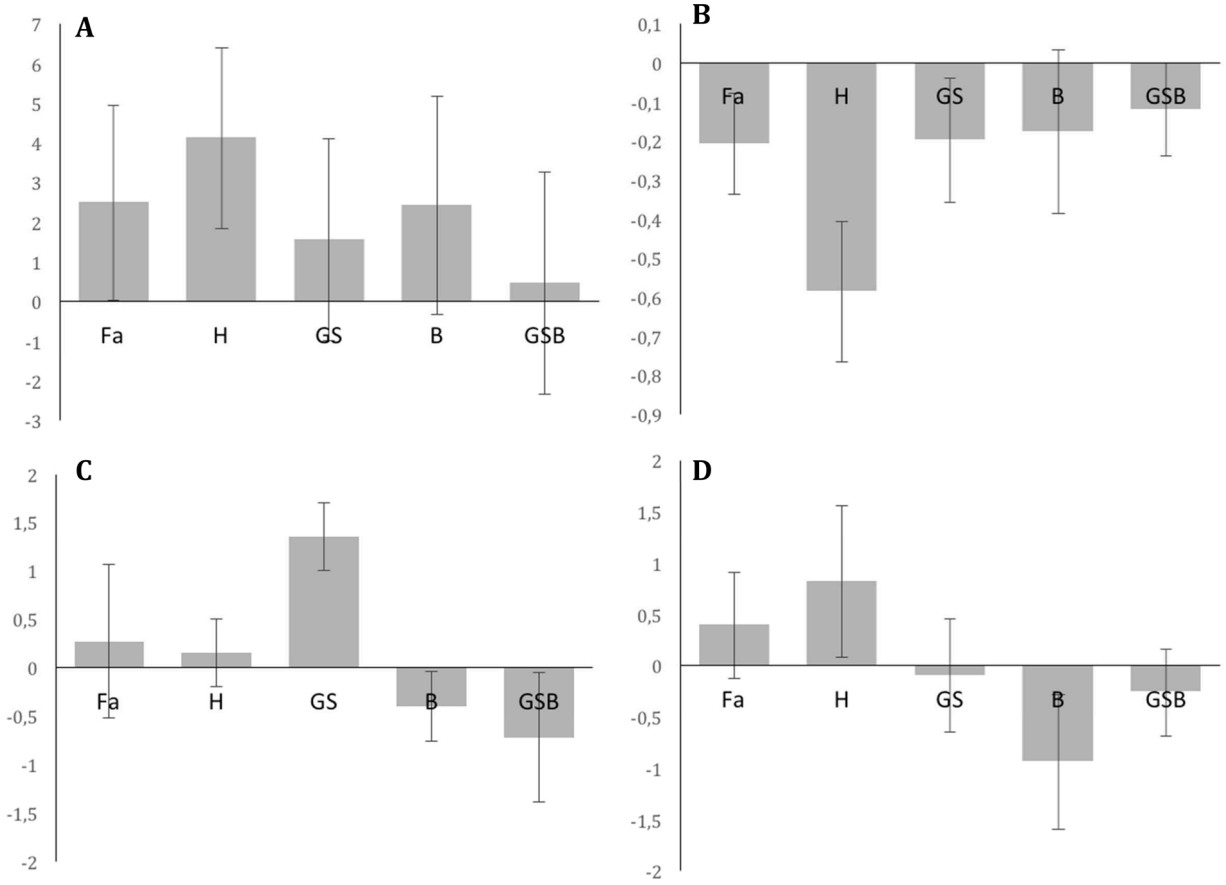


Fig. 3. Differences in relative abundance (β parameters ± standard errors) between the control (crops, intercept) and the different land-use (Fa: Fallows, H: hedgerows, GS: grass strips, B: bushes, and GSB: grass strips with bushes) for wood pigeon (Columba palumbus, A), Eurasian skylark (A. arvensis, B), Circus spp (transect, C), *Pipistrellus* spp (first visit, D). These species were selected to illustrate the different ecological requirements; the results for the other species are shown in Supplementary Material G.

in bat inventory, where *Plecotus-Myotis* was negatively associated with grass strips. The differences in biodiversity level with scenario 1 and 2 were however less pronounced for the grass strip than other land-use due strong positive relationship between harriers and grass strips. Bushes also exhibited slightly lower level of biodiversity mostly linked to its double weighted negative effects on all bat groups during the first visit.

The global, slightly negative trend of grass strip with bushes was surprising and showed that 1 ha of fallow is equal to a very large amount of grass strip with bushes (Table 4). One hypothesis is that the measured grass strips with bushes studied were not adequately managed, underlying the importance of considering management practices (Vickery et al., 2009). Another non-exclusive hypothesis is that grass strips with bushes are not suitable for hedge-nesting birds nor for ground-nesting birds. Indeed, we found that hedge-nesting birds (*Fringilla coelebs*, *Hyppolais polyglotta*, and *Sylvia atricapilla*) showed a positive response to hedgerows (Table 2), whereas ground-nesting birds (*Alauda arvensis*) were negatively impacted by hedgerows, consistent with another published study (see Bas et al., 2009). This indicates that bushes associated with grass strips do not attract hedge-nesting birds and repel ground-nesting birds. Finally, the weak attractiveness of grass strips with bushes may be linked to their age, highlighting the time lag effect. At this stage of the study, it was difficult to determine the causes of the observed weak attractiveness of grass strip with bushes; therefore, it would be desirable to conduct a study on the evolution of this attractiveness according to age.

Table 4
a) Biodiversity level for 1 ha of the different land-uses or for one bush (step 4) according to differential species weighting (scenario 1, 2 and 3). b) Example of surface of hedgerows, grass strips, grass strips with bushes and number of bushes needed to reach the biodiversity level of 1 ha of fallow.

	Land-use type	Scenario 1	Scenario 2	Scenario 3
a) Biodiversity level	Fallow	4.52	4.49	1.59
	Hedgerow	45.3	45.7	15.4
	Grass strip	7.47	8.34	4.79
	Grass strip with bushes	5.69	2.34	0.04
	Bushes	0.39	0.27	0.13
b) example of land-use quantity needed to reach biodiversity level of 1 ha of fallow	Hedgerow	0.09	0.09	0.10
	Grass strip	0.61	0.54	0.33
	Grass strip with bushes	0.79	1.92	42.6
	Bushes	12	16	12

The quantity of land-use needed to support the same biodiversity level than fallows, and in turn, the quantity of the other offset measures needed, differed among scenarios, and this result is consistent with previous studies. Bull et al. (2014) demonstrated that using different methods to calculate the required offset resulted in divergent outcomes for biodiversity, and Strange et al. (2002) also found that the design of the compensation in wetlands can vary by a factor of 3 depending on the indicator used. However, apart for the grass strip with bushes, this difference is not as important as we could expect in the scenario 3. In our case, the proposal of species weighting by the local stakeholders provided similar results in term of amount of offset measure that need to be implemented.

For all scenarios, the surface of hedgerow needed to obtain the same biodiversity level of 1 ha of fallow was lower than the surface of grass strip or grass strip with bush (0.09 or 0.10 ha of hedgerow). But in practice, farmers might choose an offset measure according to its utility (Vaissière et al., 2018) as well as consider the agricultural constraints related to different alternatives. For example, hedgerows and bushes have a greater shading impacting the yield of crops (Shively, 1997). Also, it might still be difficult to implement offset measures in general because farmers are less willing to accept constraints linked to biodiversity offsetting contracts and ask for greater payment compared to other agri-environmental schemes (Le Coënt et al., 2017; Vaissière et al., 2018). Finally, a wind farm developer would also naturally consider the monetary cost of the offset (100 m of hedgerows being 5–25 times more expensive than grass strips, BASF SE, 2018; PNRHL, 2014).

The direct application of this study is that a set of land-uses that are equivalent from a biodiversity perspective are available to implement as an offset measure.

The second application of this study is that the weighting system of the method can be changed to account for the objectives and interests of the local stakeholders – including the permitting authorities and the farmers. Note however that farmers were not included in the group of stakeholders, but were only represented by a cooperation group Agrosolutions, competent in technical aspects of agronomy. Scenarios two and three proposed here illustrated the method. Accordingly, local stakeholders may be more prone to identify sites for offset measures even within projects were the offset measures implementation was difficult, thereby improving biodiversity outcomes (Martin et al., 2016; Quétier et al., 2015; Reed, 2008). This has been demonstrated in our study area, where local stakeholders decided on their own weighting system and immediately implemented offset measures, without sparing the scientifically decisions supporting the method (Millon and Bernardin, 2020).

From a more theoretical point of view, this research tested a conceptual framework for comparing the biodiversity level of different land-uses in the context of offsets. This work was conducted to assess the possibility of aggregating numerous species that do not have the same ecological requirements (see Bas et al., 2016 for another example) and assess the influence of species weighting on the final results. While in this study, we accounted only for both bird and bat species due to their sensibility to wind turbines, other taxa of fauna and flora, or additional ecological functions, could be included in this framework in case of another kind of development project. We also showed that it is possible to use a mix of species abundance, species presence and activity data to compare biodiversity level even if it complicates the calculation (Gonçalves et al., 2015).

Although our framework did not include species conservation status (e.g. national and local population trends, red list), such information could be informative to give more weight to the species whose population dynamics are most sensitive to the project (Frick et al., 2017). Our framework did neither include uncertainty about the success of the measures and time delayed emergence of offsetting gains (Laitila et al., 2014; Bezombes et al., 2019; Kerbiriou and Laprun, 2020), for which further studies could propose improvements.

Our framework did not assess ecological equivalence between biodiversity losses induced by wind farms and biodiversity gains provided by the offsetting as this was not the objective of our study. However, the method presented here could also be used to calculate ecological equivalences between residual losses and biodiversity gains using the same biodiversity metric i.e. the species abundance. Biodiversity level should be compared between the habitat under wind turbines and a control, in order to define the residual loss. Then, instead of having the biodiversity level at one of the offset measure as a reference, the absolute value of the biodiversity level at the habitat under wind turbine should be used as a reference in order to determine the amount of offset measures needed.

Finally, wind turbines are also responsible for mortality rates that may indirectly affect the dynamics of avian species (Frick et al., 2017; Gómez-Catasús et al., 2018), and this mortality is difficult to assess and with high uncertainties on estimations (Arnett et al., 2016; Kunz et al., 2007). At this stage, our method has not been adapted to consider the mortality, and a greater challenge would be to identify a coherent approach to compensate for the mortality of migratory species. Indeed, a recent study showed that bat carcasses found under wind turbines in Germany were of various origins from nearby to Eastern Europe (Lehnert et al., 2014). Thus, it is necessary to work for these species over a larger scale and to envisage methods for assessing ecological equivalence that enable the cumulative effects resulting from several plans or projects within a region to be analysed.

The method proposed here to calculate biodiversity levels was based on the average of species responses, while most previous studies have been based on habitat area (Laitila et al., 2014; Moilanen, 2013; Parkes et al., 2004), on a selection of indicator species (Gonçalves et al., 2015; Pilgrim et al., 2013), on ecological functions (Gayet et al., 2016) or have used species richness indices (Curran et al., 2014). The aim of the method was not to find a single metric for biodiversity, but to create a new framework which help adopting an integrated ecosystems approach of the offsetting, so far little used due to the methodological difficulties we address in this study. Finally, as advocated by Quétier et al. (2014), such integrated approaches (e.g. grouping species sharing similar habitats requirements) when assessing equivalences, and even more while weighting species depending on the project and the study area, should ensure a greater effectiveness in restoring functional ecosystems through offsets.

Declaration of Competing Interest

None.

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Appendix A. Supplementary data

Supplementary material related to this article can be found, in the online version, at doi:https://doi.org/10.1016/j.landusepol.2020.105161.

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