Using total abundance as a proxy for wild bee species richness: a practical tool for non-experts

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RESEARCH ARTICLE

Using total abundance as a proxy for wild bee species richness: A practical tool for non-experts

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Abstract

1. As there is growing interest among non-specialists in participating in pollinator conservation initiatives, developing proxies for wild bee species richness that could be potentially used by non-experts can aid conservation, decision support systems for managers and policymakers, and create entry points for future taxonomists.
2. We used data from 63 independent studies in which wild bees were sampled, covering all main European habitats and climates. We tested two proxies for wild bee species richness: abundance of all wild bees (excluding the honeybee) and abundance of bumblebees. These proxies require basic taxonomic training and have the potential for routine implementation by non-experts.
3. Within-region, the abundance of wild bees was a strong predictor of wild bee species richness at the local scale, with an average correlation exceeding 0.80.

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Bumblebee abundance was a poorer proxy for total wild bee species richness (correlation coefficient of ~0.55) and was unsuitable for warm-temperate and Mediterranean climates. Observed abundance-richness correlations were consistent across climates, habitats and sampling methods, suggesting that, after a simple training, counting all bee individuals in transect walks provides a non-lethal, robust estimate of wild bee species richness. We observed a weak negative relationship between sample coverage and the strength of the abundance-richness correlation.

4. *Synthesis and applications*. The use of a simple but effective proxy could be an important starting point for the expansion of wild bee monitoring initiatives at the regional scale, particularly given the growing involvement of non-specialists. We provided here a simple implementation framework to use this proxy in rapid biodiversity assessments, such as the evaluation of payment-by-result schemes by farmers and measuring the efficacy of conservation actions in urban green areas or protected areas by citizens and site managers, respectively. It is important to stress that we are not advocating for the replacement of the urgently needed long-term monitoring of pollinator status and trends. Instead, we propose that employing an effective proxy for non-experts could enhance the evaluation of many local and regional conservation initiatives that currently lack any basic assessment schemes.

KEYWORDS
bumblebee, citizen science, indicator, non-specialist, pollinator monitoring, surrogate, taxonomy

1 | INTRODUCTION

By providing pollination services to wild plants and crops, pollinators support plant reproduction and the functioning of natural ecosystems and a steady supply of ecosystem services, such as healthy and sufficient food (Gazzea et al., 2023). Recent evidence of declines in pollinator distributions in Europe has boosted multiple conservation initiatives, such as habitat restoration or creation of protected areas, to reverse this decline and mitigate its negative impacts (Potts et al., 2016). Much emphasis has been placed on conserving highly diverse and abundant pollinator communities, as these often harbour rare species and also provide optimal pollination services to crops and wild plants (Garibaldi et al., 2011; Kleijn et al., 2015). However, despite the high priority for pollinator conservation, we often lack funding and/or expertise to assess the effects of local-scale intervention for pollinator conservation. This is particularly relevant for local projects such as citizen-science initiatives, agri-environmental schemes, and conservation and restoration actions in protected areas or urban sites, which often require snapshot comparisons of bee diversity across multiple sites.

Pollinators, and wild bees in particular, are a highly diverse group. In Europe alone, there are approximately 2000 bee species, including several taxa with challenging identification (Reverté et al., 2023). The assessment of applied conservation initiatives is often constrained by the availability of trained experts and by the difficulty of species identification (Breeze et al., 2021). In contrast to, for example, butterflies, most wild bees cannot yet be identified to the species level from photographs by experts or using AI-based approaches. In conservation practice, the costs of the analyses, incomplete reference libraries, and laboratory capacity currently constrain the identification of large samples using molecular techniques. Data collected through citizen science frameworks can provide a cost-effective means of surveying, making them an increasingly popular approach to support conservation. However, citizen science data are usually prone to serious biases originating from different levels of taxonomic expertise of volunteers, particularly for taxonomically challenging taxa such as bees (Kremen et al., 2011; Ratnieks et al., 2016). Such costs or limitations associated with species identification reduce our ability to assess the conservation effectiveness at scales relevant for conservation activities (Breeze et al., 2021; Gibbons et al., 2011), calling for indicators that are easier to measure for non-experts.

Developing a suitable set of indicators or surrogates for pollinator diversity can aid and thus improve conservation planning and decision support systems (Fraixedas et al., 2020; Larrieu et al., 2018; Tälle et al., 2023). Effective indicators should be easy to measure, cheap to monitor, usable and reliable across habitats or biogeographic regions, but should also be sensitive to environmental changes and meet user requirements (Segre et al., 2023). In the case of bees, it is particularly useful to find indicators of species-rich communities given their importance for conservation and pollination service delivery (Simpson et al., 2022). A recent meta-analysis found that floral diversity can be used to predict wild bee diversity with average correlations around 0.65 (Hyjazie & Sargent, 2022). These correlations are relatively low for a proxy (Lovell et al., 2007), and plants can also be challenging to identify for non-experts. Previous attempts to use other, more easily identified pollinator taxa such as butterflies to predict wild bee diversity were not successful (Segre et al., 2023). Using higher taxa as surrogates of species richness works well, but still requires identification skills (Báldi, 2003). However, many wild bee species depend on similar floral and nesting resources and share sensitivity to the same environmental pressures, such as pesticides and habitat degradation (Potts et al., 2016). Therefore, one would expect to find a strong cross-taxon congruence in the occurrence and abundance of different wild bee species across environmental gradients (Ganuza et al., 2022).

Although the link between the number of individuals and species richness is deeply rooted in ecological theory, little attention has been given to abundance-based measures as potential surrogates for species richness in applied ecology (Hallmann et al., 2021; Levenson et al., 2024; Magierowski & Johnson, 2006; Tälle et al., 2023). While the exact drivers and processes shaping species diversity are complex, local species richness is expected to depend on (i) the regional species pool and their relative and absolute frequencies, (ii) the spatial distribution of species at the regional scale and (iii) the total number of individuals supported by the local environment (Engel et al., 2022; McGlinn et al., 2019). If we consider wild bees, there are at least two putative proxies for species richness that could be sampled in the field: abundance of all wild bees and bumblebee abundance. First, total abundance is a relevant variable per se because it can be directly linked to flower visitation and improved pollination services (Fijen et al., 2018). The measure of bee abundance is a relatively easy task, and it requires little training for non-experts, as already demonstrated in several citizen-science projects (e.g. Burgess et al., 2017; Kremen et al., 2011). Second, in temperate regions, bumblebees (*Bombus* spp.) can be used as a potential flagship group that is more easily recognised by non-experts due to their large body size and typical habitus (Ratnieks et al., 2016). The abundance of bumblebees and their relative ease of recognition make them an attractive option to measure compared to the total wild bee abundance as a candidate proxy for non-specialists (Comont & Ashbrook, 2017; Garratt et al., 2019; Ghisbain, 2021). It remains unclear, however, whether there are differences in reliability with respect to the predictive power of wild bee versus bumblebee abundances as indicators of wild bee species richness. Similarly, it is crucial to explore the variability of the abundance–richness relationship across geographical and environmental gradients (Tsang et al., 2025) before suggesting the routine implementation of these proxies in applied conservation practice.

A key requirement for an effective indicator is the time and costs associated with its measurement. Monitoring of wild bees is usually carried out using one of two standard methodological approaches: (i) direct observations of pollinators on flowers using transect walks and (ii) passive sampling using pan-traps (or similar devices). Their pros and cons are discussed elsewhere (Klaus et al., 2024; O'Connor et al., 2019; Thompson et al., 2021; Westphal et al., 2008), but both methods currently rely on taxonomic expertise for species identification (unless genetic means for identification are used), which is the main constraining factor in implementing large-scale monitoring programmes and local scale assessments (Breeze et al., 2021). Both methods are explicitly included in the current proposal of the EU Pollinator Monitoring Scheme as being suitable for capturing differences in pollinator status, though transect walks are the preferred method (Potts et al., 2024). It is therefore highly relevant to test the performance of any potential proxy across these different sampling methods.

The overarching aim of this study was to identify proxies for wild bee species richness that could be used by non-experts to evaluate the effectiveness of local conservation interventions or to measure the impact of pressures. We collated a large dataset of published and unpublished primary data from 63 independent regional studies on wild bee communities sampled in different habitats and climates across Europe using both pan-traps and transect walks. In particular, we (i) tested whether the total abundance of wild bees and bumblebees could reliably predict the species richness of wild bees at the local scale; and (ii) quantified how sampling method, habitat type and climate modify the performance of the candidate proxies across Europe. Finally, we provided an operational framework to implement the proxy by non-experts, providing guidelines on the domain of application, field sampling techniques and data analysis. This framework can be adapted to different contexts, such as citizen-science survey programmes, assessment of payment-by-results schemes or evaluations of environmental impacts (e.g. pesticide use, management intensity and air pollution) on wild bee abundance and diversity.

2 | MATERIALS AND METHODS

2.1 | Data collection

We collated primary, unpublished and published data from different sources by contacting a large number of scientists working on wild bee conservation in Europe. We contacted scientists involved in the Safeguard, STACCATO and SHOWCASE projects and other relevant EU pollinator projects to contribute, as these initiatives include most researchers who could potentially provide suitable datasets. Building on this researcher network, we employed a snowballing approach to identify additional datasets through scientific collaborations. We did not conduct a systematic search of published studies, as the limiting factor was the availability of the raw data. Our search aimed to find studies across a diverse set of habitats and climates that represent the major European environmental gradients. The requirements to include a study were as follows: (1) a minimum of seven sites for each habitat type sampled in at least 1 year, (2) all wild bee species (Hymenoptera, Apoidea) identified at the species level or at least to morphospecies, (3) single species abundance quantified using pan-traps or transect walks and (4) study was carried out in Europe. Each study (*n* = 63) included one or more species-by-site matrices, reporting species identity and abundance, and information on the sampling method and the sampled habitat type. Often, datasets included abundance per species already pooled over multiple sampling rounds. *Apis mellifera* L., the western honeybee, was sampled in 48% of the datasets (*n* = 59). If multiple habitats and/or multiple years were sampled in a study, we created a separate matrix for each habitat and year combination and assigned a unique dataset identifier (Figure 1). Based on the original habitat description, we reclassified the habitats into the following categories: crop (both annual and perennial crops, *n* = 26 datasets), grassland (semi-natural grasslands, agricultural pastures, agricultural meadows; *n* = 39), forest (forest interior and forest openings such as clear-cuts and wind-thrown areas; *n* = 16), ecotone (field margin, hedgerow, and forest edges; *n* = 31) and urban habitat (road verges, urban green areas such gardens, brown fields, parks; *n* = 11). For each study, we classified the sampling methods into direct observations (transect walks; *n* = 60 datasets) or trapping using pan-traps (*n* = 63) and we retrieved the region where the sampling was performed. Based on the region, we extracted the dominant Köppen climate type for each dataset (Beck et al., 2018) and grouped them in three climate types: (1) Cs: Temperate with dry summer (*n* = 33), (2) Cf: Temperate oceanic climate (*n* = 26), (3) Df: Continental climate (*n* = 64). This approach led to a total of 123 datasets (i.e. habitat per study per year combination) for further analysis.

2.2 | Data analysis

2.2.1 | Total wild bee abundance and bumblebee abundance as proxies for wild bee diversity

Sampling effort was constant within single studies (e.g. number of traps, trap exposure, length or duration of transect walks); however, it largely differed between studies. Therefore, in the analyses, we always tested the predictive power of our proxies in explaining the between-site variability in species richness within the same dataset (Figure 1). We did not, however, attempt to correlate our proxies with raw species richness across different datasets, as they varied in both sampling methods and sampling effort. Where necessary, for each site in each dataset, we computed wild bee species richness by pooling species across multiple sampling rounds. Then, we estimated two putative proxies: (i) the total abundance of wild bees and (ii) the total abundance of bumblebees.

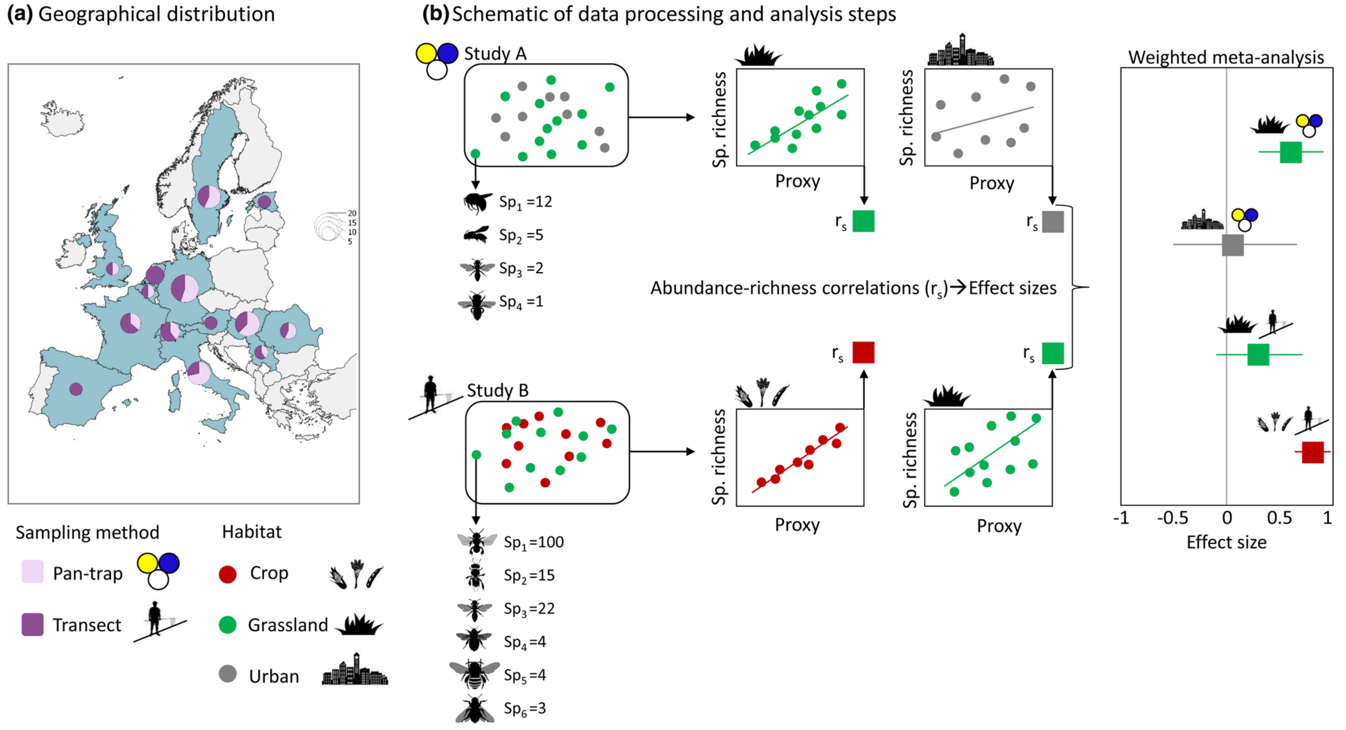


FIGURE 1 (a) Geographical distribution of the 63 published or unpublished independent studies sampling wild bees using either pan-traps or transect walks; (b) schematic of data processing and analysis steps to test the abundance-based proxies at the regional scale: Each study sampled multiple sites across one or more habitat types in one or more years. Based on the pooled species abundance across sampling rounds, we calculated abundance and species richness, and computed the correlation between our proxies and wild bee species richness within each habitat, year and region combination. Correlations were then transformed into effect sizes and analysed using a multi-level meta-analysis to test the strength of the abundance-richness relationship and how habitat type, climate, and sampling method modify this strength.

In the main analysis, *A. mellifera* L., the western honeybee, was excluded as its abundance strongly depends on the presence of managed colonies, and it was sampled only in 48% of the datasets. However, we tested the effect of the honeybee on our proxy in our sensitivity analyses, using the subset of datasets that included the honeybee (see below).

For bumblebee abundance, we removed datasets in which bumblebees comprised less than 5% of the total number of individuals. The inclusion of datasets with lower relative abundance of bumblebees (<5%) included too many zeros to compute a correlation. Using scatterplots, we visually verified that within each dataset the relationship between our proxies and species richness was positive and monotonic (i.e. as the value of the proxy increases, so does species richness). As we often observed both monotonic linear and nonlinear relationships between abundance and species richness, we ln-transformed abundance and computed the Pearson's correlation. Although Spearman correlation can capture nonlinear relationships, we opted for Pearson's correlation due to its straightforward integration into meta-analytic frameworks, where estimating variance can be systematically addressed. We estimated a correlation index between (i) total wild bee abundance versus wild bee species richness, and (ii) bumblebee abundance versus wild bee species richness. A single correlation was computed across sites belonging to the same habitat within the same dataset to ensure consistency in both sampling method and sampling effort (Figure 1).

The Pearson's coefficient (r) of each dataset was normalised using Fisher's z transformation (1):

$$z = 0.5\ \ln\left(\frac{1+r}{1-r}\right) \tag{1}$$

while the variance (υ) was estimated using the sample size (n of sites per dataset) (2) (Koricheva et al., 2013):

$$\upsilon = \frac{1}{n-3} \tag{2}$$

We used a weighted meta-analysis to compare the strength of the correlation between species richness and the two proxies across datasets. We used the correlations as effect sizes and weighted them against their precision, that is inverse variance. Some datasets contained data from multiple years or habitats, allowing us to compute more than one correlation. Therefore, we used multi-level meta-analytical models (equivalent to linear mixed-effects models) to examine the heterogeneity in effect sizes and to account for non-independence of observations (Borenstein et al., 2021). We accounted for clustered effect sizes by including the study ID as random factor (Bishop & Nakagawa, 2021). For each dataset, we tested the following moderators as fixed effects: (i) sampling method (pan-traps vs. transect counts); (ii) habitat type; (iii) climate type; (iv) sample coverage and (v) sample size (i.e. number of sites used to compute the correlation). Sample coverage was computed using the iNEXT function in R (Hsieh et al., 2016). The sample coverage of a community is the probability that a new individual will belong to one of the species already observed in the sample. We examined the significance of heterogeneity in effect sizes attributed to each moderator variable using Q_m statistics in a single model that included all moderators. We tested for potential collinearity among moderators using the GVIF from the metafor package and no collinearity issues were present. In preliminary analyses, we also tested for potential two-way interactions between sampling method, habitat type, and climate type, comparing models fitted with ML with and without one of the interactions using AIC. No interaction was supported, that is no model including interactions had a AIC difference larger than 2. To visualise model results, we displayed the mean effect alongside the 95% confidence intervals (CI) and prediction intervals (i.e. a range of values that is 95% likely to contain the value of a new observation). We back-transformed Z-scored effect sizes to Pearson correlations to help interpret the results. The statistical analyses were carried out using the R statistical environment (version 4.2.1; R Core Team, 2022). We used the package 'metafor' for the meta-analysis (Viechtbauer, 2010).

2.2.2 | Effect of honeybees

As *A. mellifera* was sampled in c. half of the studies, we could test whether including honeybees in the total abundance would negatively affect the performance of our proxy. We computed two correlations: one using species richness versus total abundance excluding honeybees (our proxy) and the second using species richness versus total abundance including honeybees. Then, we regressed one correlation against the other and tested whether the slope was different from 1 using linearHypothesis() from the car package. A slope different from 1 would indicate a systematic bias (e.g. lower correlation when abundance included the honeybee).

3 | RESULTS

We collected data from 2780 sites across 15 European countries. The sampling covered all major biogeographic regions from the Mediterranean to boreal climates (Figure 1). The average sample coverage across datasets was 0.92 (min: 0.52, max: 1.00). While the relative abundance of bumblebees did not differ significantly between the investigated habitat categories, the contribution of bumblebees to the total number of observed bees was significantly different between climate types and sampling methods. In warm temperate regions such as Spain and south Italy, the relative abundance of bumblebees was negligible, while bumblebees represented on average c. 40% of the total abundance in colder climates (Figure S1A). Irrespective of the climate and habitat, the proportion of bumblebees in the total number of observed wild bees was almost three times higher for transect walks than for pan-traps (Figure S1B), a difference that was highly significant (Table S1).

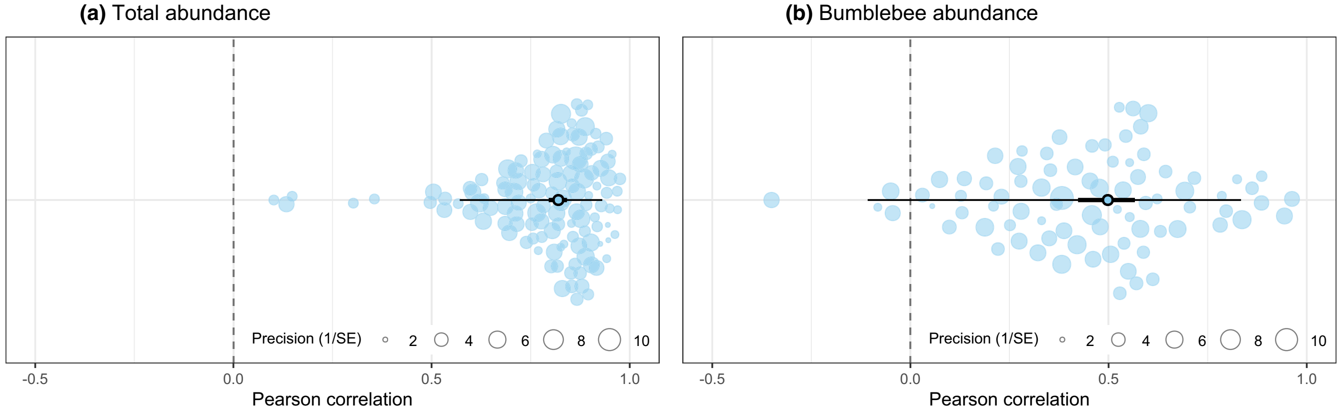


FIGURE 2 Forest plots reporting raw Pearson correlations between (a) total wild bee abundance (ln-transformed) and species richness, and (b) bumblebee abundance (ln-transformed) and species richness of wild bees. Each dot represents a dataset with dot size indicating precision (1/SE). Bold lines indicate confidence intervals and thin lines indicate prediction intervals (PIs) at 95%. PIs indicate the range of values that is 95% likely to contain the value of a new observation.

3.1 | Total abundance without honeybees

The meta-analysis showed that, across the 123 datasets (i.e. habitat per study per year combination), the total abundance of wild bees (ln-transformed) was a strong predictor of total wild bee species richness with an average correlation above 0.80 (Figure 2a). In the figure, it is also possible to see the prediction intervals, that is the lowest and highest values that will contain a future observation with a 95% confidence (low PI: 0.57–high PI: 0.93). The low end of the prediction interval indicated that the correlation between total abundance and species richness was strong across all datasets; that is, only 2.5% of future observations will have a correlation below 0.57. Climate, sampling method, habitat and size of the sampling (number of sites) did not modify the observed correlations (Table 1), indicating that the performance of the proxy was consistent under different environmental contexts. However, we found a significant negative effect of sample coverage (probability that the next individual sampled belongs to a species that has already been observed) on the correlation between abundance and species richness, that is datasets with high sample coverage tend to present a slightly weaker correlation (Figure 3). However, when the sample coverage approximated 1 (no new species expected with increasing sampling effort), the correlation was still above 0.75.

3.2 | Total abundance including honeybees

In 59 datasets, we could include honeybees in the computation of total abundance. For this subset of studies, we regressed the correlation between species richness and total abundance including honeybees (explanatory variable) versus the correlation between species richness and total abundance excluding honeybees (our proxy). We found a slope of 0.934 ($SE = 0.094$, $t = 9.93$ $p < 0.001$, $R^2 = 0.634$) that was not different from 1 ($p = 0.49$), indicating no systematic biases.

TABLE 1 Multi-level meta-analysis results of the between-group test of climate, sampling method, habitat, sample coverage and number of sites.

		df	Q_m	*p*-value
(a) ln (total wild bee abundance) vs. species richness (*n* = 123, all datasets)				
Model 1	Climate	2	2.580	0.275
	Sampling method	1	0.401	0.526
	Habitat	4	4.564	0.335
	Sample coverage	1	23.312	<0.001
	Number of sites	1	1.282	0.257
(b) ln (bumblebee abundance) vs. species richness (*n* = 80, datasets with at least 5% bumblebee individuals)				
Model 2	Climate	2	1.231	0.540
	Sampling method	1	0.185	0.667
	Habitat	4	0.901	0.924
	Sample coverage	1	1.410	0.235
	Number of sites	1	0.003	0.956

Note: Moderators were included in a single model. The table shows degrees of freedom (df), *p*-value and heterogeneity (Q_m) explained by the moderator for (a) ln (total wild bee abundance) versus species richness and (b) ln (bumblebee abundance) versus species richness. The rma.mv() model included study ID as random factor.

However, as expected, we observed a weak trend for lower correlations when the honeybee was included in the computation of the proxy (Figure 4).

3.3 | Bumblebee abundance

Out of the 123 datasets, we could use 80 datasets with more than 5% of bumblebee individuals. Using bumblebee abundance as a proxy for total wild bee species richness was also supported by our

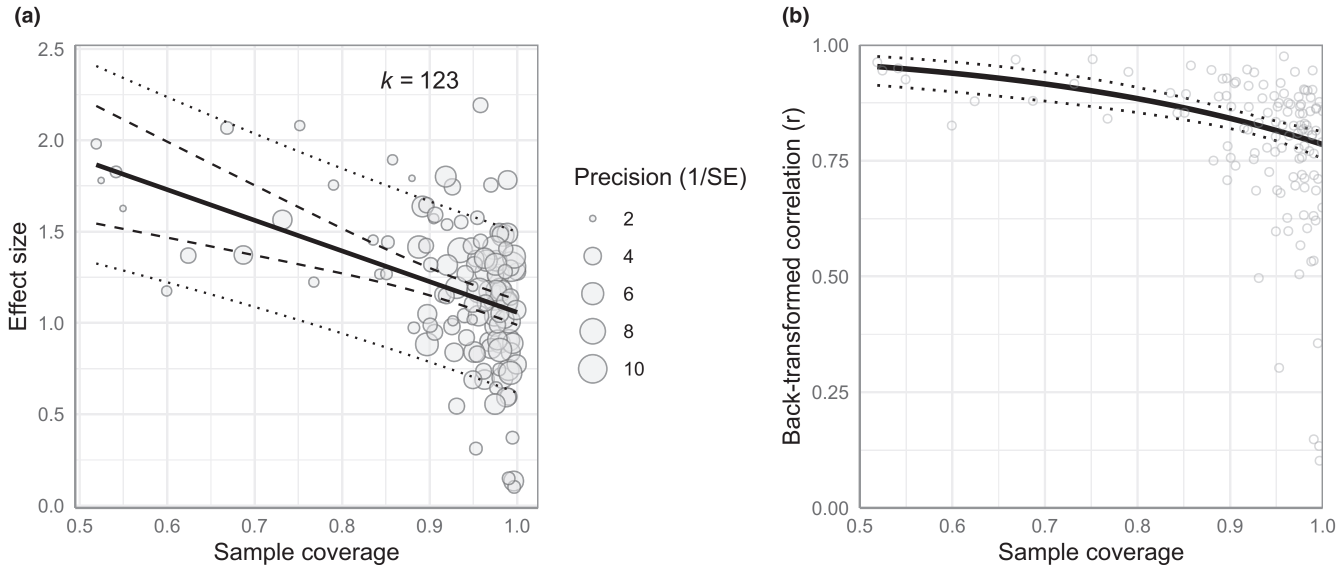


FIGURE 3 (a) Bubbleplots depicting the relationship between sample coverage and the effect size, i.e. *z*-transformed correlation between species richness and total abundance (*k* is the sample size) and (b) same effect on the back-transformed correlation. Sample coverage is the probability that a new individual will belong to one of the species already observed.

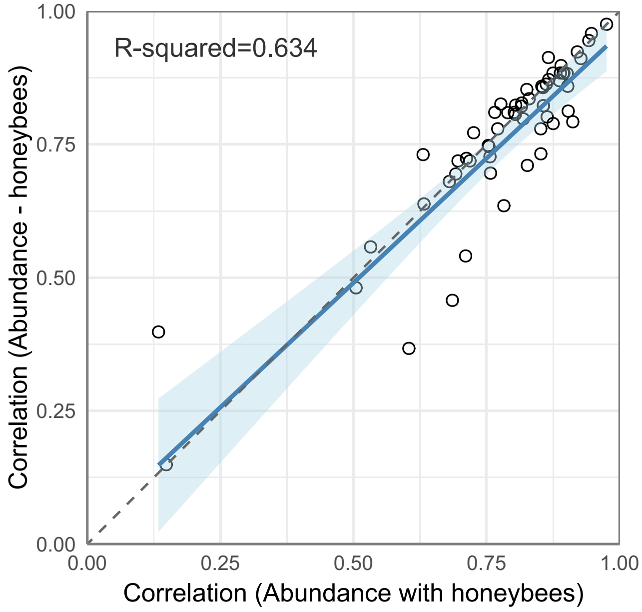


FIGURE 4 Scatterplot showing the relationship of Pearson's correlation coefficients computed between species richness and abundance computed with (*x*-axis) or without honeybees (*y*-axis) for the 59 datasets that included honeybees in the sampling. Dotted line represents a fixed slope of 1 with an intercept of 0, while the solid line represents a linear regression.

analysis, but the correlations were lower than those for total abundance (Figure 2b) (estimate: 0.498, CI: 0.42–0.57). The prediction intervals at 95% were much larger than those obtained using total abundance with the low end crossing zero (PI: −0.11-0.83). Large prediction intervals indicate high heterogeneity between datasets. For this proxy, climate, sampling method, habitat, sample coverage and sample size did not modify the observed correlations between bumblebee abundance and wild bee species richness (Table 1).

4 | DISCUSSION

There is growing interest among non-specialists in participating in wild bee conservation initiatives, including monitoring activities. The identification of simple but effective proxies for bee diversity could be an important starting point for the expansion of pollinator monitoring initiatives across Europe, particularly given the growing involvement of non-specialists and regions where funding or taxonomic expertise are lacking. Hence, finding effective, cheap and easy-to-implement proxies is urgently needed to inform management and conservation decision-making, while at the same time improving the knowledge base for wild bees through education and training for questions beyond species numbers. Here, using a large dataset of wild bees sampled across several key European habitats and climates from Mediterranean to boreal regions, we tested two proxies for wild bee species richness that require little taxonomical training and can potentially be surveyed by non-experts such as citizen scientists or farmers. Both total abundance of wild bees and of bumblebees correlated significantly with total wild bee species richness and seem promising proxies when comparing the diversity of bees across different sites. However, the total abundance of wild bees emerged as a more robust metric across disparate habitats and climatic zones, with potential to be used across European regions.

Across habitat types, climate types, and sampling methods, the total number of wild bee individuals correlated with species richness at values above 0.80. We found that high sample coverage slightly reduced the strength of the correlation that however remained above 0.75. This suggests that incomplete sampling coverage may artificially strengthen the abundance-richness correlation, as predicted by the asymptotic relationship between sampling effort and species richness (Hsieh et al., 2016). Overall, the strength of this correlation was higher than has been observed previously between wild bee and flowering plant species richness ($r=0.65$) (Hyjazie & Sargent, 2022) indicating that total wild bee abundance is a more accurate predictor of wild bee species richness. Besides its stronger predictive power, the advantages of using bee abundance over flower-based indicators are that it does not require expertise in the taxonomy of insect-pollinated plants and it provides important functional information that links directly to flower visitation and pollination services (Fijen et al., 2018). Moreover, people's willingness to protect pollinators is often linked to specific values associated with pollinators (Geppert et al., 2024). Therefore, finding indicator taxa or proxies within the target group for conservation is expected to improve public engagement and build general knowledge about pollinators, particularly as this proxy allows for non-lethal assessment, making it more suitable for non-experts.

Considering the efforts required to measure wild bee species richness, our results provide evidence-based support for using wild bee abundance as a proxy in projects where identifying species is not yet feasible due to technical or economic constraints. Current monitoring schemes running in several European countries, such as the UK pollinator monitoring schemes (O'Connor et al., 2019), have already tested the ability of citizens to distinguish wild bees from other groups of flower-visiting taxa. Typically, after a few hours of training, data are reliably collected across a diverse set of recorders (Kremen et al., 2011; Ratnieks et al., 2016). On the one hand, a recent study indicates that without specific training, non-experts often misidentify solitary bees as social wasps or hoverflies (Griffiths-Lee et al., 2023). Hence, the adoption of wild bee abundance as a proxy by non-specialists necessitates an adequate level of training but, following that, it can ensure accurate interpretation and application.

As the accuracy of distinguishing bumblebees from other groups of bees tends to be similar between researchers and citizen scientists (MacPhail et al., 2020), we also explored the relationship between the abundance of bumblebees as a proxy of wild bee species richness. We found two major limitations in the application of this proxy. First, hot European climates are not suitable for the large majority of European bumblebee species, which are adapted to temperate and cold climates (Ghisbain et al., 2024). Accordingly, in our study, ca. 30% of the datasets, all from the warmest regions, did not include sufficient numbers of bumblebees to test this proxy. This indicates that bumblebee abundance cannot reliably be used in these areas as an indicator of wild bee species richness. Second, the correlation between bumblebee abundance and wild bee species richness (on average around 0.5) was considerably lower than the correlation with total bee abundance, even in regions where bumblebees are a dominant component of wild bee communities. The literature still lacks a consensus on a minimum correlation strength to define a candidate biodiversity proxy as reliable. Some authors indicate a stringent threshold of 0.75 (Lovell et al., 2007), while others suggest more relaxed values varying between 0.3 and 0.5 (Lamoreux et al., 2006). Based on these studies, the performance of bumblebee abundance can be considered only weak to moderately good in predicting wild bee species richness.

Most surrogates and biological indicators are tested in single regions, and rarely across different ecosystems (Feld et al., 2009). Despite the differences between the two tested proxies discussed above, their performance remained constant across contrasting climates and habitats. This result indicates that both proxies could be implemented across urban, agricultural and natural/semi-natural habitats. Similarly, climate did not explain any variability in the correlation strength, with the only limitation being that the bumblebee proxy should not be used in warmer climates because of limited population abundances (Ghisbain et al., 2024). Concerning the sampling method, we also found that the performance of the two proxies was equal between transect walks and pan-traps. Altogether, these tests indicated high spatial and temporal robustness of both proxies, suggesting that they could be applied at the regional scale across different environmental conditions. Below, we provided practical guidelines for the implementation of the proxy (Figure 5).

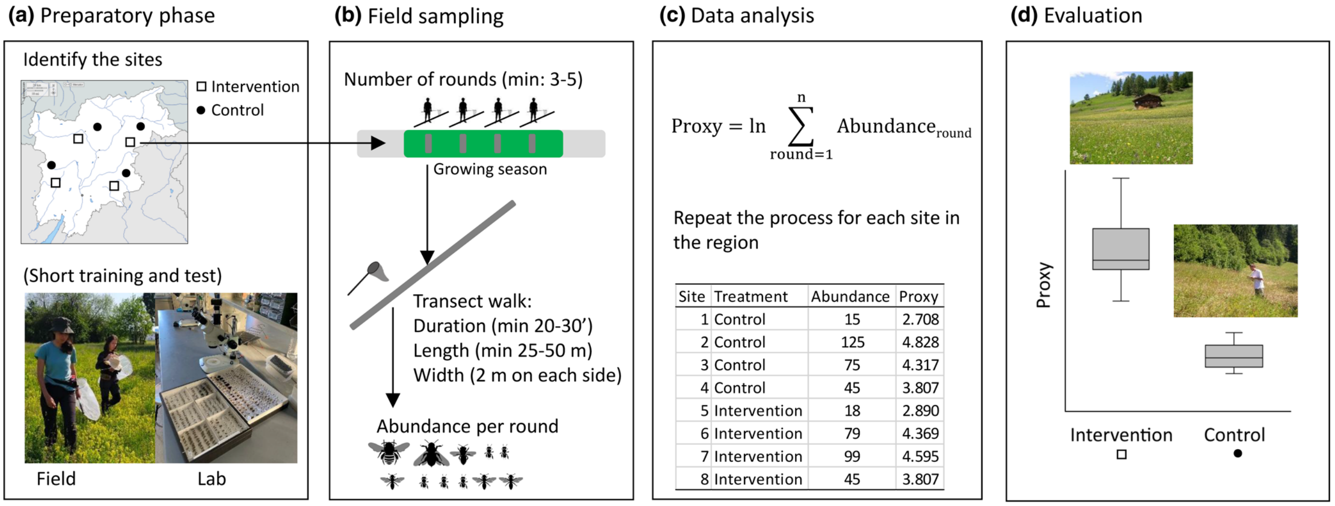
4.1 | Practical guidelines on how to implement the proxy by non-experts

4.1.1 | Domain of application and limitations

Based on our analysis, we recommend using the proxy only for comparing sites within a single region. In our pool of study areas, the size of a region varied from a few tens to hundreds of kilometres. When sampling with a more comprehensive taxonomic identification is not possible or is not the focus of the project, we suggest using wild bee abundance as a proxy for wild bee species richness to compare sites across environmental gradients within a single habitat or across multiple habitats to perform rapid biodiversity assessments of pressures or intervention effectiveness. Applying this proxy at very large spatial extents, combining data from different biogeographical regions (e.g. continental or global) would require further tests, as the abundance–richness relationships tested here might take different forms. Similarly, the use of the proxy for long-term monitoring of species richness trends cannot be recommended, since our results are only based on snapshot studies performed in the same region and year.

4.1.2 | Recorder knowledge requirements

Users should be able to identify the following groups of pollinators: wasps, bumblebees, solitary bees, hoverflies, other flies and the honeybee. Even if misidentified, other bee-looking



$$\text{Proxy} = \ln \sum_{\text{round}=1}^{n} \text{Abundance}_{\text{round}}$$

Site	Treatment	Abundance	Proxy
1	Control	15	2.708
2	Control	125	4.828
3	Control	75	4.317
4	Control	45	3.807
5	Intervention	18	2.890
6	Intervention	79	4.369
7	Intervention	99	4.595
8	Intervention	45	3.807

FIGURE 5 Main operational steps to implement the proxy for wild bee species richness by non-experts. The proxy should be used to compare sites at the regional scale (extent: from tens to hundreds of kilometres). In the preparatory phase (a), after the definition of the sampling protocol, a short taxonomic training of non-experts might be needed; (b) Total abundance of wild bees should be measured using a standardised transect walk with the same spatial and temporal sampling effort over multiple rounds (minimum 3–5 rounds depending on climate and regional species pool) during the season when bees are active (marked in green); (c) After completing the sampling in 1 year, total abundance is computed across rounds and ln-transformed to obtain the proxy; (d) The proxy values can be used to rank a number of sites from species-poor to species-rich, but no raw species richness can be estimated. Potential ecological applications include snapshot evaluations of pressures or intervention effectiveness on wild bee species richness. Based on our results, the use of the proxy for long-term monitoring of species richness trends cannot be recommended.

insects such as bee flies (Bombyliidae), some hoverflies or wasps (Vespidae) are expected to have a small impact on the proxy due to their low relative abundance in transect walks (Lanuza et al., 2025). In most cases, the application of the proxy by non-experts would require a certain degree of training and validation as wild bees are often misidentified by non-specialists (Kremen et al., 2011). We suggest carrying out small pilot studies to measure recorders' accuracy depending on their previous experience in monitoring pollinators and the diversity of the regional species pool.

4.1.3 | Field selection

In evaluating conservation interventions or pressures by non-experts, the first step involves identifying a set of reference sites that represent the ideal target for pollinator species richness in the landscape. The identification of reference sites should be done in concert with trained bee taxonomists. These sites provide a reference system to evaluate sites subjected to specific impacts and/or interventions (Hiers et al., 2012). A critical aspect to consider here is the variability in the reference sites. The higher the variability, the greater the number of reference sites that should be monitored to estimate the reference system. If an intervention is tested, in the monitoring phase, it would also be useful to include control sites, that is sites with no intervention. As pollinator communities are highly temporally dynamic and both species richness and abundance can vary considerably between and within years (Kremen et al., 2018), reference systems and sites under evaluation should always be monitored and compared within the same time frame (i.e. within a few days).

4.1.4 | Pollinator sampling

During the whole season, multiple sampling rounds should be performed using the same method and sampling effort across different sites following standard pollinator monitoring protocols (e.g. Potts et al., 2024). In most cases, 3–5 rounds represent the minimum requirement. Because the efficiency of pan traps can be influenced by the floral resources in their immediate vicinity (O'Connor et al., 2019), and conservation actions often target improvements in floral resources, we do not recommend using pan traps for studies evaluating conservation initiatives, even though the reliability of wild bee abundance as a species richness indicator was not influenced by the method. When counting only the total number of wild bees, active methods like transect walks have additional advantages over pan traps in that they do not require killing any individuals (Lövei & Ferrante, 2024) and that they are more cost- and time-efficient. We suggest a minimum of 15′–25′ active sampling time per round, but this time should be adjusted according to the local species pool diversity. The length of the transect or the size of the plot should also be adjusted depending on the sampled habitat and the species diversity expected in the area. Finally, this proxy could be implemented in easy-to-use mobile applications or video recording cameras for continuous flower monitoring. These tools could be equipped with AI-based software able to distinguish between bee and non-bee pollinators.

4.1.5 | Data analysis and interpretation of the proxy

For each site, raw abundances should be summed across sampling rounds. It is also important to stress that the correlation between abundance and species richness was computed on a log scale, and this should be considered when interpreting the abundance data measured in the field. After summing the total abundance across sampling rounds, the total abundance needs to be ln-transformed to obtain the ranking of the sites. The final use of the proxy is not to provide an absolute number of species per site but to rank them from species-poor to species-rich sites. Due to differences in the sampling effort and sampling methods across studies, our analysis cannot provide a single parameter to directly estimate raw species richness from abundance data.

4.2 | General implications for pollinator monitoring

We found strong evidence supporting the use of total wild bee abundance as a reliable proxy for wild bee species richness when comparing sites in snapshot regional studies. After receiving appropriate training, counting all bee individuals in transect walks could provide a non-lethal, effective method for estimating wild bee species richness. With the growing involvement of non-experts such as citizens, NGOs and farmers in pollinator conservation efforts (Breeze et al., 2021; Garratt et al., 2019), the use of this proxy could facilitate the expansion of pollinator monitoring initiatives across Europe, particularly where the lack of funding or taxonomic expertise is limiting factors (O'Connor et al., 2019). This versatile proxy holds promise for various applications, including the assessment of payment-by-result schemes by farmers and measures of the efficacy of conservation actions in urban green areas by citizens or in protected areas by site managers. It is important to stress that we are not advocating for the replacement of the urgently needed long-term monitoring of pollinator species status and trends. Instead, we propose that employing an effective yet simple proxy for wild bee species richness could enhance the evaluation of many local and regional conservation initiatives that currently lack basic assessment schemes. The results could contribute valuable evidence to inform the design of effective pollinator conservation interventions in different habitats and would facilitate the engagement of non-experts in pollinator monitoring, taxonomy, and conservation. When long-term trend data on species richness become available, it will be possible to test whether this proxy can also be used to evaluate temporal diversity trajectories.

AUTHOR CONTRIBUTIONS

Lorenzo Marini conceived the ideas, collated the data and led the writing. Lorenzo Marini and Elena Gazzea analysed the data. Lorenzo Marini, Elena Gazzea, Matthias Albrecht, András Báldi, Péter Batáry, Ignasi Bartomeus, Riccardo Bommarco, Hans Henrik Bruun, Andree Cappellari, Lorna J. Cole, Cristina Craioveanu, Guillaume Decocq, Imre Demeter, Martin Diekmann, Róbert Gallé, Michael P.D. Garratt, Costanza Geppert, Andrea Holzschuh, Reet Karise, Annette Kolb, Anina Knauer, Anikó Kovács-Hostyánszki, Audrey Labonté, Klara Leander Oh, Egle Liiskmann, Toshko Ljubomirov, Ola Lundin, Corina Maurer, Francisco P. Molina, Nerea Montes-Pérez, Sonja Mudri-Stojnić, Erik Öckinger, Imre Sándor Piross, Simon G. Potts, Willem Proesmans, Snežana Radenković, Chloé A. Raderschall, Jeroen Scheper, Anja Schmidt, Oliver Schweiger, Deepa Senapathi, Josef Settele, Fabien Spicher, Douglas Sponsler, Ingolf Steffan-Dewenter, Viktor Szigeti, Giovanni Tamburini, Natalia Timus, Edina Török, Adam J. Vanbergen, Elena Velado-Alonso, Kris Verheyen, Ante Vujić, Marie Winsa, Monika Wulf, Niklaus E. Zimmermann and David Kleijn provided data and contributed to the writing and results' interpretation.

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CONFLICT OF INTEREST STATEMENT

Lorenzo Marini and Péter Batáry are Associate Editors at the *Journal of Applied Ecology*, but took no part in the peer review and decision-making processes for this paper. The other authors have no conflict of interest to declare.

DATA AVAILABILITY STATEMENT

The data and code that support the findings of this study are available in Zenodo Digital Repository at https://doi.org/10.5281/zenodo.16912672 (Marini & Gazzea, 2025).

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REFERENCES

Báldi, A. (2003). Using higher taxa as surrogates of species richness: A study based on 3700 Coleoptera, Diptera, and Acari species in Central-Hungarian reserves. *Basic and Applied Ecology*, *4*, 589–593.

Beck, H. E., Zimmermann, N. E., McVicar, T. R., Vergopolan, N., Berg, A., & Wood, E. F. (2018). Present and future Köppen-Geiger climate classification maps at 1-km resolution. *Scientific Data*, *5*, 180214.

Bishop, J., & Nakagawa, S. (2021). Quantifying crop pollinator dependence and its heterogeneity using multi-level meta-analysis. *Journal of Applied Ecology*, *58*, 1030–1042.

Borenstein, M., Hedges, L. V., Higgins, J. P., & Rothstein, H. R. (2021). *Introduction to meta-analysis*. John Wiley & Sons.

Breeze, T. D., Bailey, A. P., Balcombe, K. G., Brereton, T., Comont, R., Edwards, M., Garratt, M. P., Harvey, M., Hawes, C., Isaac, N., Jitlal, M., Jones, C. M., Kunin, W. E., Lee, P., Morris, R. K. A., Musgrove, A., O'Connor, R. S., Peyton, J., Potts, S. G., … Carvell, C. (2021). Pollinator monitoring more than pays for itself. *Journal of Applied Ecology*, *58*, 44–57.

Burgess, H. K., DeBey, L. B., Froehlich, H. E., Schmidt, N., Theobald, E. J., Ettinger, A. K., HilleRisLambers, J., Tewksbury, J., & Parrish, J. K. (2017). The science of citizen science: Exploring barriers to use as a primary research tool. *Biological Conservation*, *208*, 113–120.

Comont, R. F., & Ashbrook, K. (2017). Evaluating promotional approaches for citizen science biological recording: Bumblebees as a group versus *Harmonia axyridis* as a flagship for ladybirds. *BioControl*, *62*, 309–318.

Engel, T., Blowes, S. A., McGlinn, D. J., Gotelli, N. J., McGill, B. J., & Chase, J. M. (2022). How does variation in total and relative abundance contribute to gradients of species diversity? *Ecology and Evolution*, *12*, e9196.

Feld, C. K., da Silva, P. M., Sousa, J. P., De Bello, F., Bugter, R., Grandin, U., Hering, D., Lavorel, S., Mountford, O., Pardo, I., Pärtel, M., Römbke, J., Sandin, L., Jones, K. B., & Harrison, P. (2009). Indicators of biodiversity and ecosystem services: A synthesis across ecosystems and spatial scales. *Oikos*, *118*, 1862–1871.

Fijen, T. P. M., Scheper, J. A., Boom, T. M., Janssen, N., Raemakers, I., & Kleijn, D. (2018). Insect pollination is at least as important for marketable crop yield as plant quality in a seed crop. *Ecology Letters*, *21*, 1704–1713.

Fraixedas, S., Lindén, A., Piha, M., Cabeza, M., Gregory, R., & Lehikoinen, A. (2020). A state-of-the-art review on birds as indicators of biodiversity: Advances, challenges, and future directions. *Ecological Indicators*, *118*, 106728.

Ganuza, C., Redlich, S., Uhler, J., Tobisch, C., Rojas-Botero, S., Peters, M. K., Zhang, J., Benjamin, C. S., Englmeier, J., Ewald, J., Fricke, U., Haensel, M., Kollmann, J., Riebl, R., Uphus, L., Müller, J., & Steffan-Dewenter, I. (2022). Interactive effects of climate and land use on pollinator diversity differ among taxa and scales. *Science Advances*, *8*, eabm9359.

Garibaldi, L. A., Steffan-Dewenter, I., Kremen, C., Morales, J. M., Bommarco, R., Cunningham, S. A., Carvalheiro, L. G., Chacoff, N. P., Dudenhöffer, J. H., Greenleaf, S. S., Holzschuh, A., Isaacs, R., Krewenka, K., Mandelik, Y., Mayfield, M. M., Morandin, L. A., Potts, S. G., Ricketts, T. H., Szentgyörgyi, H., … Klein, A. M. (2011). Stability of pollination services decreases with isolation from natural areas despite honey bee visits. *Ecology Letters*, *14*, 1062–1072.

Garratt, M. P. D., Potts, S. G., Banks, G., Hawes, C., Breeze, T. D., O'Connor, R. S., & Carvell, C. (2019). Capacity and willingness of farmers and citizen scientists to monitor crop pollinators and pollination services. *Global Ecology and Conservation*, *20*, e00781.

Gazzea, E., Batáry, P., & Marini, L. (2023). Global meta-analysis shows reduced quality of food crops under inadequate animal pollination. *Nature Communications*, *14*, 4463.

Geppert, C., Franceschinis, C., Fijen, T. P., Kleijn, D., Scheper, J., Steffan-Dewenter, I., Thiene, M., & Marini, L. (2024). Willingness of rural and urban citizens to undertake pollinator conservation actions across three contrasting European countries. *People and Nature*, *6*, 1502–1511.

Ghisbain, G. (2021). Are bumblebees relevant models for understanding wild bee decline? *Frontiers in Conservation Science*, *2*, 752213.

Ghisbain, G., Thiery, W., Massonnet, F., Erazo, D., Rasmont, P., Michez, D., & Dellicour, S. (2024). Projected decline in European bumblebee populations in the twenty-first century. *Nature*, *628*, 337–341.

Gibbons, J. M., Nicholson, E., Milner-Gulland, E. J., & Jones, J. P. G. (2011). Should payments for biodiversity conservation be based on action or results? *Journal of Applied Ecology*, *48*, 1218–1226.

Griffiths-Lee, J., Nicholls, E., & Goulson, D. (2023). Sow wild! Effective methods and identification bias in pollinator-focused experimental citizen science. *Citizen Science: Theory and Practice*, *8*, 23.

Hallmann, C. A., Ssymank, A., Sorg, M., de Kroon, H., & Jongejans, E. (2021). Insect biomass decline scaled to species diversity: General patterns derived from a hoverfly community. *Proceedings of the National Academy of Sciences*, *118*, e2002554117.

Hiers, J. K., Mitchell, R. J., Barnett, A., Walters, J. R., Mack, M., Williams, B., & Sutter, R. (2012). The dynamic reference concept: Measuring restoration success in a rapidly changing no-analogue future. *Ecological Restoration*, *30*, 27–36.

Hsieh, T. C., Ma, K., & Chao, A. (2016). iNEXT: An R package for rarefaction and extrapolation of species diversity (Hill numbers). *Methods in Ecology and Evolution*, *7*, 1451–1456.

Hyjazie, B. F., & Sargent, R. D. (2022). Floral resources predict the local bee community: Implications for conservation. *Biological Conservation*, *273*, 109679.

Klaus, F., Ayasse, M., Classen, A., Dauber, J., Diekötter, T., Everaars, J., Fornoff, F., Greil, H., Hendriksma, H. P., Jütte, T., Klein, A. M., Krahner, A., Leonhardt, S. D., Lüken, D. J., Paxton, R. J., Schmid-Egger, C., Steffan-Dewenter, I., Thiele, J., Tscharntke, T., … Pistorius, J. (2024). Improving wild bee monitoring, sampling methods, and conservation. *Basic and Applied Ecology*, *75*, 2–11.

Kleijn, D., Winfree, R., Bartomeus, I., Carvalheiro, L. G., Henry, M., Isaacs, R., Klein, A. M., Kremen, C., M'Gonigle, L. K., Rader, R., Ricketts, T. H., Williams, N. M., Lee Adamson, N., Ascher, J. S., Báldi, A., Batáry, P., Benjamin, F., Biesmeijer, J. C., Blitzer, E. J., … Potts, S. G. (2015). Delivery of crop pollination services is an insufficient argument for wild pollinator conservation. *Nature Communications*, *6*, 7414.

Koricheva, J., Gurevitch, J., & Mengersen, K. (Eds.). (2013). *Handbook of meta-analysis in ecology and evolution*. Princeton University Press.

Kremen, C., M'Gonigle, L. K., & Ponisio, L. C. (2018). Pollinator community assembly tracks changes in floral resources as restored hedgerows mature in agricultural landscapes. *Frontiers in Ecology and Evolution*, *6*, 170.

Kremen, C., Ullman, K. S., & Thorp, R. W. (2011). Evaluating the quality of citizen-scientist data on pollinator communities. *Conservation Biology*, *25*, 607–617.

Lamoreux, J. F., Morrison, J. C., Ricketts, T. H., Olson, D. M., Dinerstein, E., McKnight, M. W., & Shugart, H. H. (2006). Global tests of biodiversity concordance and the importance of endemism. *Nature*, *440*, 212–214.

Lanuza, J. B., Knight, T. M., Montes-Perez, N., Glenny, W., Acuña, P., Albrecht, M., Artamendi, M., Badenhausser, I., Bennett, J. M., Biella, P., Bommarco, R., Cappellari, A., Castro, S., Clough, Y., Colom, P., Costa, J., Cyrille, N., de Manincor, N., Dominguez-Lapido, P., … Bartomeus, I. (2025). EuPPollNet: A European database of plant-pollinator networks. *Global Ecology and Biogeography*, *34*, e70000.

Larrieu, L., Gosselin, F., Archaux, F., Chevalier, R., Corriol, G., Dauffy-Richard, E., Deconchat, M., Gosselin, M., Ladet, S., Savoie, J. M., Tillon, L., & Bouget, C. (2018). Cost-efficiency of cross-taxon surrogates in temperate forests. *Ecological Indicators*, *87*, 56–65.

Levenson, H. K., Metz, B. N., & Tarpy, D. R. (2024). Effects of study design parameters on estimates of bee abundance and richness in agroecosystems: A meta-analysis. *Annals of the Entomological Society of America*, *117*, 92–106.

Lövei, G. L., & Ferrante, M. (2024). The use and prospects of nonlethal methods in entomology. *Annual Review of Entomology*, *69*, 183–198.

Lovell, S., Hamer, M., Slotow, R., & Herbert, D. (2007). Assessment of congruency across invertebrate taxa and taxonomic levels to identify potential surrogates. *Biological Conservation*, *139*, 113–125.

MacPhail, V. J., Gibson, S. D., Hatfield, R., & Colla, S. R. (2020). Using Bumble Bee Watch to investigate the accuracy and perception of bumble bee (*Bombus* spp.) identification by community scientists. *PeerJ*, *8*, e9412.

Magierowski, R. H., & Johnson, C. R. (2006). Robustness of surrogates of biodiversity in marine benthic communities. *Ecological Applications*, *16*, 2264–2275.

Marini, L., & Gazzea, E. (2025). Data from: Using total abundance as a proxy for wild bee species richness: A practical tool for non-experts. *Zenodo Digital Repository*. https://doi.org/10.5281/zenodo.16912672

McGlinn, D. J., Xiao, X., May, F., Gotelli, N. J., Engel, T., Blowes, S. A., Knight, T. M., Purschke, O., Chase, J. M., & McGill, B. J. (2019). Measurement of biodiversity (MoB): A method to separate the scale dependent effects of species abundance distribution, density, and aggregation on diversity change. *Methods in Ecology and Evolution*, *10*, 258–269.

O'Connor, R. S., Kunin, W. E., Garratt, M. P. D., Potts, S. G., Roy, H. E., Andrews, C., Jones, C. M., Peyton, J. M., Savage, J., Harvey, M. C., Morris, R. K. A., Roberts, S. P. M., Wright, I., Vanbergen, A. J., & Carvell, C. (2019). Monitoring insect pollinators and flower visitation: The effectiveness and feasibility of different survey methods. *Methods in Ecology and Evolution*, *10*, 2129–2140.

Potts, S. G., Bartomeus, I., Biesmeijer, K., Breeze, T., Casino, A., Dauber, J., Dieker, P., Hochkirch, A., Høye, T., Isaac, N., Kleijn, D., Laikre, L., Mandelik, Y., Montagna, M., Montero Castaño, A., Öckinger, E., Oteman, B., Pardo Valle, A., Polce, C., … Zhang, J. (2024). *Refined proposal for an EU pollinator monitoring scheme*. Publications Office of the European Union. https://doi.org/10.2760/2005545

Potts, S. G., Imperatriz-Fonseca, V., Ngo, H. T., Aizen, M. A., Biesmeijer, J. C., Breeze, T. D., Dicks, L. V., Garibaldi, L. A., Hill, R., Settele, J., & Vanbergen, A. J. (2016). Safeguarding pollinators and their values to human well-being. *Nature*, *540*, 220–229.

R Core Team. (2022). *R: A language and environment for statistical computing*. R Foundation for Statistical Computing. https://www.R-project.org/

Ratnieks, F. L. W., Schrell, F., Sheppard, R. C., Brown, E., Bristow, O. E., & Garbuzov, M. (2016). Data reliability in citizen science: Learning curve and the effects of training method, volunteer background and experience on identification accuracy of insects visiting ivy flowers. *Methods in Ecology and Evolution*, *7*, 1226–1235.

Reverté, S., Miličić, M., Ačanski, J., Andrić, A., Aracil, A., Aubert, M., Balzan, M. V., Bartomeus, I., Bogusch, P., Bosch, J., Budrys, E., Cantú-Salazar, L., Castro, S., Cornalba, M., Demeter, I., Devalez, J., Dorchin, A., Dufrêne, E., Đorđević, A., … Vujić, A. (2023). National records of 3000 European bee and hoverfly species: A contribution to pollinator conservation. *Insect Conservation and Diversity*, *16*, 758–775.

Segre, H., Kleijn, D., Bartomeus, I., WallisDeVries, M. F., de Jong, M., van der Schee, M. F., de Jong, M., van der Frank Schee, M., Román, J., & Fijen, T. P. M. (2023). Butterflies are not a robust bioindicator for assessing pollinator communities, but floral resources offer a promising way forward. *Ecological Indicators*, *154*, 110842.

Simpson, D. T., Weinman, L. R., Genung, M. A., Roswell, M., MacLeod, M., & Winfree, R. (2022). Many bee species, including rare species, are important for function of entire plant–pollinator networks. *Proceedings of the Royal Society B: Biological Sciences*, *289*, 20212689.

Tälle, M., Ranius, T., & Öckinger, E. (2023). The usefulness of surrogates in biodiversity conservation: A synthesis. *Biological Conservation*, *288*, 110384.

Thompson, A., Frenzel, M., Schweiger, O., Musche, M., Groth, T., Roberts, S. P. M., Kuhlmann, M., & Knight, T. M. (2021). Pollinator sampling methods influence community patterns assessments by capturing species with different traits and at different abundances. *Ecological Indicators*, *132*, 108284.

Tsang, T. P. N., De Santis, A. A. A., Armas-Quiñonez, G., Ascher, J. S., Ávila-Gómez, E. S., Báldi, A., Ballare, K. M., Balzan, M. V., Banaszak-Cibicka, W., Bänsch, S., Basset, Y., Bates, A. J., Baumann, J. M., Beal-Neves, M., Bennett, A., Bezerra, A. D. M., Blochtein, B., Bommarco, R., Brosi, B., … Bonebrake, T. C. (2025). Land use change consistently reduces α but not β and γ diversity of bees. *Global Change Biology*, *31*, e70006.

Viechtbauer, W. (2010). Conducting meta-analyses in R with the metafor package. *Journal of Statistical Software*, *36*, 1–48.

Westphal, C., Bommarco, R., Carré, G., Lamborn, E., Morison, N., Petanidou, T., Potts, S. G., Roberts, S. P. M., Szentgyörgyi, H., Tscheulin, T., Vaissière, B. E., Woyciechowski, M., Biesmeijer, J. C., Kunin, W. E., Settele, J., & Steffan-Dewenter, I. (2008). Measuring bee diversity in different European habitats and biogeographical regions. *Ecological Monographs*, *78*, 653–671.

SUPPORTING INFORMATION

Additional supporting information can be found online in the Supporting Information section at the end of this article.

Table S1. Effect of climate, sampling method and habitat type on the relative abundance of bumblebees.

Figure S1. Effect of (A) climate (Cf, Temperate oceanic climate, Cs, Temperate with dry summer, Df, Continental climate) and (B) sampling method on the relative abundance of bumblebees.

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