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Manuscript Title: Integrating general and targeted biodiversity monitoring through parallel survey designs to improve indicator robustness

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Abstract

Breeding Bird Monitoring Schemes (BMS) provide large-scale, long-term data essential for biodiversity assessment and conservation decision-making. However, their multispecies design can generate species-specific detectability biases, particularly for taxa whose behavioral or ecological traits deviate from standardized count assumptions, potentially affecting abundance estimates and population indicators. We propose a structured integration framework linking general monitoring schemes with species-specific high-detection surveys through parallel designs and ecological modeling. The approach involves (1) implementing temporally matched general and targeted surveys, (2) modeling the relationship between survey outputs while incorporating ecological covariates influencing detectability differences, and (3) projecting the calibrated relationship onto broader BMS datasets to improve abundance indices and trend estimation.

We apply this framework to the Common Quail (*Coturnix coturnix*), a farmland game species with context-dependent detectability under standardized protocols. Parallel surveys revealed marked discrepancies between monitoring methods across habitat conditions. Incorporating habitat information into the calibration reduced detectability-related variability and improved the consistency of long-term trend estimates.

By formally linking general and targeted systems, this framework enhances the reliability and policy relevance of biodiversity indicators while retaining the spatial and temporal scalability of existing monitoring programs.

INTRODUCTION

Breeding bird monitoring schemes (BMS) are the cornerstone of large-scale biodiversity assessment worldwide (Gregory et al. 2005, Likens and Lindenmayer 2018). Their standardized protocols, broad spatial coverage and long-term continuity allow robust quantification of population change and ecological responses to environmental pressures through abundance-based indicators and trend indices (e.g.: Devictor et al., 2008; Rigal et al., 2023; Stephens et al., 2016). A defining feature of these schemes is their reliance on trained volunteer observers, whose coordinated effort generates large multispecies datasets that would be unfeasible through professional surveys alone (Moussy et al. 2022). By providing consistent information across extensive temporal and geographic scales, BMS programs play a key role in informing conservation policy, land-use planning and biodiversity indicators at national and international levels (Schmeller et al. 2009, Tulloch et al. 2013). Ensuring the methodological reliability and taxonomic representativeness of these schemes is therefore essential for accurately tracking environmental change (Yoccoz et al. 2001, Kissling et al. 2018).

Despite the success of BMS, their generalist and multispecies design inevitably introduces substantial variation in detection probability across species, habitats and regions (Thompson, W.L. 2002, Diefenbach et al. 2003). Species whose behavior, spatial dynamics or social organization depart from the assumptions of standard count protocols may yield biased indicators output in general monitoring schemes. Such biases may arise through missed detections, ambiguous records or potential double-counting (Guillera-Arroita et al. 2017). These issues are especially problematic for species that fall outside the core “common bird” set typically covered by BMS programs, including those that are behaviorally atypical, patchily distributed or otherwise difficult to survey using standard protocols (Nichols et al. 2007, Sardà-Palomera et al. 2012a).

Biases in detection probability can propagate through population indices, affecting abundance-based indicators, temporal trends and the ability of monitoring schemes to detect true demographic change (Kéry and Schmidt 2008). When detection is variable or inconsistent, yearly indices may become distorted, trend precision decreases and interannual variability inflates, particularly when uncertain observations are unevenly distributed across space or time (Johnson 2008, Kellner and Swihart 2014). In long-term

monitoring schemes, these effects can compromise the reliability and interpretability of populations.

As a consequence of these limitations, large-scale biodiversity indicators—such as those produced by the Pan-European Common Bird Monitoring Scheme (PECBMS, Brlík et al. 2021)—typically exclude species with low or highly variable detectability, focusing instead on widespread and consistently monitored taxa (Gregory et al. 2005, 2008, Brlík et al. 2021). This exclusion avoids introducing methodological noise into continental indicators, but it also means that many ecologically relevant or management-sensitive species remain poorly represented in general monitoring outputs. To address this gap, species-specific monitoring programs have been developed by universities, research institutes and public administrations, using tailored protocols that substantially increase detectability and provide more accurate abundance estimates for species whose behavior or ecology challenge standardized monitoring (Bibby et al. 2000).

Together, these challenges highlight the need not only for methodological comparisons between general BMS protocols and species-specific surveys (Johnson 2008), but for structured approaches that formally integrate information from both monitoring systems. Rather than treating general and targeted surveys as independent data streams, parallel implementations provide an opportunity to model systematic discrepancies and improve the robustness, consistency and comparability of abundance-based indicators derived from large-scale monitoring schemes (Kellner and Swihart 2014).

Here, we present a structured approach to integrate general and species-specific monitoring systems through parallel surveys and ecological modeling. We implement this approach by comparing indicator outputs from a general breeding bird monitoring scheme—the Catalan Common Bird Monitoring Survey (SOCC)— with those from a species-specific survey designed for the Common Quail (*Coturnix coturnix*), hereafter referred to as SEC, a farmland species whose behavioral and spatial dynamics generate highly variable detectability under standardized monitoring protocols. Using matched surveys, we (1) quantify differences in detection and abundance-based indicators between monitoring systems, (2) model how ecological conditions modulate these discrepancies, and (3) evaluate how integrating this information influences long-term population trend estimates. Through this case study, we illustrate how parallel survey

designs can strengthen the reliability and policy relevance of biodiversity indicators while retaining the spatial and temporal scalability of existing monitoring programs.

DESCRIPTION OF THE MONITORING INTEGRATION APPROACH

Conceptual structure of the integration approach

The integration approach presented here is based on the coordinated implementation of general multispecies monitoring protocols and species-specific high-detection surveys conducted under matched spatial and temporal conditions. The core premise is that systematic discrepancies between survey outputs contain information about context-dependent detection biases that can be explicitly modeled rather than treated as noise.

By structuring general and targeted monitoring as complementary components of a single analytical framework, differences in detection and abundance estimates can be quantified, related to ecological conditions, and projected onto larger monitoring datasets. This formal linkage improves indicator robustness while retaining the spatial and temporal scalability of existing monitoring infrastructures.

Parallel survey design

The proposed approach relies on the implementation of parallel surveys combining a general multispecies protocol with a species-specific high-detection survey carried out under comparable spatial and temporal conditions. Parallel sampling enables direct comparison of detection and count outputs while minimizing confounding effects of site, observer, and seasonal variation.

Surveys are conducted within the same localities and breeding period to ensure that observed discrepancies primarily reflect differences in protocol performance rather than temporal population change. When possible, synchronizing observer effort and

environmental conditions further reduces uncontrolled sources of variation. This paired design provides the empirical basis for modeling systematic differences between monitoring systems and underpins subsequent calibration and projection steps.

Modeling discrepancies between monitoring systems

Parallel surveys provide paired observations from general and species-specific monitoring protocols, enabling quantitative assessment of discrepancies in detection and abundance estimates. Rather than assuming a constant proportional difference between survey outputs, the integration approach models their relationship explicitly, allowing for non-linear responses and context-dependent variation.

Ecological covariates that may influence detectability or survey performance can be incorporated into the modeling framework to account for environmental modulation of discrepancies. This step allows differences between monitoring systems to be interpreted as structured variation rather than random error.

By statistically relating counts from general monitoring schemes to those obtained under high-detection protocols, the approach generates a predictive relationship that can be applied to broader monitoring datasets. This modeling step forms the analytical core of the integration framework.

Projection to large-scale monitoring datasets

Once the relationship between general and species-specific survey outputs has been modeled, the resulting predictive function can be applied to extended datasets generated by general monitoring schemes. This step allows discrepancies identified under paired sampling to be accounted for across wider spatial and temporal scales.

By adjusting general monitoring counts using the modeled relationship, abundance-based indicators and long-term trend estimates can be recalculated while explicitly incorporating context-dependent detectability differences. Because general monitoring programs typically provide longer time series and broader geographic coverage than

targeted surveys, this procedure enables improved inference without compromising continuity or scalability.

The projection stage thus links local calibration to large-scale indicator performance, completing the integration between general and specialized monitoring systems. To illustrate the implementation of this integration approach, we applied it to a case study focusing on the Common Quail.

CASE STUDY: COMMON QUAIL

Study species

The Common Quail is a small migratory galliform associated with open farmland in the Western Palearctic, particularly cereal crops and other herbaceous vegetation (McGowan et al. 2020). Individuals typically remain hidden within dense cover, making visual detection uncommon. Consequently, male vocalizations constitute the primary cue for detection in the field.

However, the environmental and social factors influencing calling activity remain poorly understood. Calling behavior is further shaped by a non-territorial mating system, characterized by loose and spatially dynamic male aggregations, whose calling intensity and spatial arrangement fluctuate in response to social interactions (Rodríguez-Teijeiro et al. 1992, Rodrigo-Rueda et al. 1997, Guyomarc'h et al. 1998, Sardà-Palomera et al. 2011). This behavioral complexity makes it difficult to predict when and where males will call, contributing to variable detectability across habitats and survey conditions.

In addition to these behavioral complexities, habitat quality strongly shapes the seasonal presence and abundance of the species. Quail distribution is known to shift in response to crop phenology and harvesting schedules, with individuals rapidly relocating as vegetation structure changes during spring and early summer (Rodríguez-Teijeiro et al. 2009). Complementing this, remote-sensing analyses have shown that vegetation greenness (NDVI) provides a reliable proxy for these habitat dynamics, with higher NDVI values associated with increased quail presence (Sardà-Palomera et al. 2012b).

This combination of cryptic behavior, socially mediated calling patterns and strong dependence on dynamic habitat conditions poses major challenges for general bird monitoring schemes, where detectability-related biases directly affect indicator outputs. The species is also a widely harvested game bird across much of its range and has been subject to ongoing conservation concern, increasing the policy relevance of robust population indicators. In this context, inaccuracies linked to detectability bias may have direct implications for management decisions and stakeholder discussions.

Monitoring schemes

Common Bird Monitoring Survey (SOCC)

The Catalan Common Bird Monitoring Survey (SOCC, Herrando et al. 2008) is a volunteer-based scheme in which observers conduct standardized breeding bird counts along 3-km linear walking transects. Each transect is visited twice during the breeding season (15 April–15 May and 16 May–15 June), following a common protocol regarding survey duration (2–2.5 h), time of day (first four hours after sunrise), and weather conditions (no rain, low wind and good visibility). All individual birds (including Quails) detected by song or visually within the standardized survey period are recorded.

The SOCC program was established in 2002 and currently includes 638 transects across Catalonia. In this study, we used the subset of surveys conducted between 2005 and 2025 in which the Common Quail was detected at least once (N = 205 transects; Figure 1). The starting year was selected because it coincides with the availability of spatially explicit agricultural land-use data, which allowed the identification of suitable habitat for subsequent analyses (see Section 2.3).

Common Quail Specific Survey (SEC)

The Common Quail Specific Survey (SEC; from its Catalan acronym) is a targeted monitoring protocol originally developed at the University of Barcelona to improve the

accuracy of quail counts based on behavioral research and extensive field experience with the species (Rodríguez-Teijeiro et al. 2010, Sardà-Palomera et al. 2012b). The method was designed to maximize the detection of singing males by accounting for their cryptic behavior, socially mediated calling activity and loose male aggregations. SEC surveys were conducted by trained professional personnel along predefined transects, following a structured sequence of listening stops and acoustic stimulation.

Observers moved along a fixed route and stopped at regular intervals to perform short listening sessions outside the vehicle. At each listening point, observers remained silent for 2 minutes to detect any spontaneously calling males. When spontaneous calling occurred, these males were immediately located and targeted for capture, as they provided reliable positional cues without requiring acoustic stimulation.

When no spontaneous calling was detected, observers broadcast female calls ("lure") to stimulate vocal responses from males. The playback consisted of two series of 15–20 seconds separated by short listening pauses. If males responded, their approximate locations were recorded and the observer attempted immediate capture using a hand net while continuing to use the playback device as the lure. If no response was elicited, the playback sequence was repeated 3 additional times (two series each), with 30-second listening intervals between repetitions.

At each listening point, this sequence allowed observers to: (1) activate males that were silent, (2) capture those that approached the lure, and (3) record those that continued calling but did not move toward the observer. While acoustic stimulation is intended to increase detectability and the number of males detected, capture aims to provide individual-level confirmation, allowing observers to discriminate between distinct individuals and to limit potential over-detection arising from moving individuals and repeated or socially mediated vocal responses. Captured males were held temporarily following ethical handling protocols.

At the end of the transect, all captured individuals were ringed and subsequently released at the precise point of capture. The final count for each transect consisted of the total number of males detected (captured + uncaptured), mapped at their initial detection position, with the aim of providing a high-detection reference of local abundance aligned with the behavioral characteristics of the species.

Parallel sampling design

Between 2021 and 2025, we designed and monitored 28 dedicated SOCC transects across Catalonia, spanning a wide range of quail suitable habitat types and altitudes (38–1158 m a.s.l.) and selected to represent areas where different quail densities were known or expected based on previous monitoring (Figure 1). Transects were progressively incorporated over the study period, resulting in variable annual sampling effort and partial overlap among years, with the maximum number of active transects reached in 2024 (n = 27). All surveys were carried out during the breeding season, between 1 April and 30 June. To ensure direct comparability between SOCC and SEC data, each transect was surveyed on two consecutive days: the SOCC survey was conducted first, followed the next day by the SEC survey at the same hour of the morning, under very similar weather conditions and by the same observer, and for the same duration. This standardized paired design minimized short-term temporal variation and ensured direct comparability between SOCC and SEC surveys under equivalent site, habitat, and weather conditions.

Habitat and vegetation covariates

To quantify the amount and quality of suitable breeding habitat available for Common Quails along each transect and season, we combined agricultural land-use information with remotely sensed vegetation indices. First, we identified the agricultural land-use categories considered suitable for the species based on previous studies and expert knowledge. These included cereal crops, fallows, legume crops, and herbaceous dryland mosaics, which represent the primary breeding habitats for the species in Mediterranean farmland systems. All polygons corresponding to these land-use categories were extracted from two official agricultural mapping systems: SIGPAC (the national land-parcel identification system) and DUN (the Catalan annual agricultural declaration system), both of which provide georeferenced information on crop types and field boundaries for each year between 2005 and 2025. A detailed description of the selected land-use categories is provided in Supporting Information.

For each 3-km transect and year, we quantified the amount of suitable habitat within a 300-m buffer centered on the survey route. This buffer width was selected to match the effective detection distance used in the calibration analyses. All suitable habitat polygons intersecting the buffer were merged, and the resulting area was calculated for each transect–year combination. Suitable habitat area varied substantially among transects, ranging from 45 to 171 ha, and was included as a covariate in subsequent modelling steps.

To characterize vegetation productivity and structure, we extracted the Normalized Difference Vegetation Index (NDVI) for each transect buffer using Landsat surface reflectance imagery (Landsat 5, 7, 8, and 9; 30-m resolution). NDVI was calculated for each 15-day and monthly intervals between 1 April and 30 June of each year, following cloud and shadow masking based on the QA_PIXEL band. For each interval, NDVI values were first aggregated at the pixel level using median composites, and transect-level NDVI was then obtained by spatially averaging (mean) all pixels contained within each buffered transect area. NDVI processing was conducted in Google Earth Engine (Gorelick et al. 2017). NDVI values derived from 15-day composites were unavailable for 16% of the paired surveys due to insufficient cloud-free observations, and these surveys were therefore excluded from analyses requiring habitat classification based on 15-day NDVI. In contrast, monthly NDVI metrics were available for all surveys.

To classify SOCC transects into broad habitat-quality categories, we performed a k-means clustering analysis based on three NDVI descriptors calculated for each transect: the mean NDVI during the breeding season, the within-season standard deviation, and the interannual standard deviation (see Supporting Information). These metrics respectively captured overall vegetation greenness, short-term seasonal variability, and longer-term temporal stability. All variables were standardized prior to clustering. A two-cluster solution was selected based on minimization of the within-cluster sum of squares, yielding two distinct habitat-quality groups: transects characterized by high and stable vegetation greenness (high-quality habitat) and transects with lower and/or more variable NDVI values (low-quality habitat).

Model implementation

We developed a calibration model to relate SOCC counts to SEC counts using paired survey data. For each paired SOCC–SEC survey, the SEC count was used as the reference indicator of local abundance, and its relationship with the corresponding SOCC count was modelled using a generalized linear modelling framework. SOCC counts were included as the main predictor, and both linear and quadratic forms of the SOCC term were evaluated. Habitat covariates such as suitable-habitat area and NDVI were incorporated to account for local environmental variation, and interaction terms between SOCC and NDVI were also included among the candidate formulations.

To determine the most appropriate calibration structure, we fitted a full set of candidate models combining: (1) different NDVI metrics (mean, median, and monthly or 15-day composites), (2) alternative error distributions (Poisson, negative binomial NB1 and NB2), (3) the presence or absence of zero-inflation components, (4) linear versus quadratic SOCC effects and (5) models with or without a random intercept for transect identity. Candidate models were compared using Akaike's Information Criterion (AIC), and the most parsimonious model structure was selected based on relative AIC differences. All models were inspected for residual patterns, dispersion, and potential outliers following standard diagnostic procedures. Final model performance was evaluated by assessing the agreement between predicted and observed SEC counts. In addition, the relative contribution of individual predictors was examined using ΔAIC values derived from reduced models.

After selecting the final calibration model, SOCC counts from all transects where Common Quail had been detected at least once between 2005 and 2025 were converted into SEC-equivalent abundance indicators. For each transect and year, the observed SOCC count together with the corresponding habitat covariates was entered into the calibration model, and the resulting predictions were rounded down to the nearest integer to provide calibrated abundance-based indicators reflecting SEC-level detectability.

Projection and trend estimation

We assessed long-term population trends for both the original SOCC counts and the calibrated SEC-equivalent indicators. Annual SOCC and SEC-equivalent counts were

obtained by selecting, for each transect and year, the maximum value from the two SOCC visits, following the standard procedure used by the Catalan Institute of Ornithology (ICO) for deriving official SOCC trends.

For each dataset, we fitted TRIM log-linear models with site and time effects to estimate annual population indices and impute missing values (Van Strien et al. 2004). To obtain a single overall indicator trend, we regressed the logarithm of the TRIM-imputed annual index against time using ordinary least squares; the slope of this regression provided a measure of the average annual rate of change.

To evaluate whether trends differed across habitat quality, each transect was assigned to one of the NDVI-based habitat clusters (see Supporting Information), and the TRIM and log-linear trend analyses were repeated separately for each habitat group. Differences between the original SOCC and calibrated SEC-equivalent indices within each habitat group were formally tested using linear models in which the logarithm of the TRIM-derived annual index was modelled as a function of time (covariate), data series (SOCC vs calibrated SEC-equivalent; fixed factor), and their interaction. All analyses were conducted in R (version 4.4.2) using the rtrim package (Bogaart et al. 2020).

RESULTS

Observed detection and count differences across schemes

The paired SOCC–SEC surveys revealed clear differences in detectability between the two monitoring schemes. In 32% of paired surveys where SOCC recorded no Common Quails, the SEC protocol detected at least one calling male (mean ± SD = 4 ± 3.4), whereas the opposite pattern was rare, with SOCC detecting a single individual while SEC detected none in only one case (7%), corresponding to an isolated detection of a single calling male. Overall, presence–absence detections differed significantly between methods, with a clear asymmetry favoring SEC detections in surveys where SOCC failed (McNemar's test, $p = 0.033$).

Across all surveys, the SEC generally recorded higher numbers of calling males than the SOCC. In 71% of paired surveys, SEC detected more individuals than SOCC, while

26% yielded identical counts and only 3% (one case) resulted in higher counts under SOCC.

Consistently, SEC detected significantly more Common Quail males per survey than SOCC (paired Wilcoxon signed-rank test: $p < 0.001$), with a mean difference of 3.5 individuals per survey. On average, SOCC detected approximately 2.9 calling males per survey, whereas SEC detected approximately 6.4, corresponding to more than a twofold increase under the SEC protocol (Figure 2).

Calibration model performance

Model comparison showed that the best-performing calibration model was a negative-binomial formulation (NB1) including the 15-day mean NDVI together with linear and quadratic SOCC terms and SOCC × NDVI interactions. Models using monthly NDVI metrics, or including random intercepts or zero-inflation components, all showed substantially higher AIC values.

The final calibration model (Table 1) captured a substantial proportion of the variability in SEC counts, providing a robust basis for converting SOCC-derived counts into SEC-equivalent abundance indicators (Supplementary material S3). Standard residual diagnostics indicated no relevant overdispersion, no zero inflation and no influential outliers, confirming robust model behavior.

An AIC-based assessment of predictor contributions revealed that NDVI was the most influential variable: removing NDVI together with its interactions produced by far the largest increase in AIC ($\Delta AIC = 74.3$). The linear ($\Delta AIC = 53.5$) and quadratic ($\Delta AIC = 20.0$) components of SOCC activity also contributed substantially to model fit, indicating a non-linear relationship between SOCC and SEC counts. SOCC × NDVI interactions further improved model performance ($\Delta AIC = 8.9$), showing that the strength of the SOCC–SEC relationship varied along the NDVI gradient. In contrast, available habitat surface had no detectable effect ($\Delta AIC = -1.9$). Overall, SEC counts were primarily driven by habitat greenness and SOCC activity, with NDVI modulating both the shape and magnitude of the calibration relationship.

The magnitude of the correction predicted by the calibration model varied across the SOCC–NDVI space. The largest discrepancies between SOCC and predicted SEC-equivalent indicators occurred when SOCC counts were low and NDVI values were high, whereas predicted SEC-equivalent counts and SOCC converged under conditions of low NDVI or when SOCC counts were relatively high (≥4). These patterns reflect the structure of the fitted SOCC × NDVI interactions (Figure 3).

Population trends

Applying the calibration model to the full SOCC dataset yielded SEC-equivalent abundance indicators for all transect–year combinations with available predictor information (N = 205 transects, 2005–2025).

TRIM analyses revealed minor differences in temporal patterns between the original SOCC counts and the calibrated SEC-equivalent indicator series. Across 2005–2025, the SOCC-based population index showed a slight decline (–2.1% per year), whereas the calibrated series remained approximately stable (+0.1% per year). A joint analysis of both series indicated that the difference in long-term trends was not statistically significant (time × series: $\beta = -0.028$, $p = 0.066$), providing only weak evidence for divergence, and suggesting that, when all transects were pooled, both indices described broadly comparable overall trajectories (Figure 4A).

However, analyses stratified by NDVI-based habitat clusters revealed marked habitat-dependent differences. In transects characterized by habitat with high and stable NDVI values, the interaction between time and data series was statistically significant ($\beta = -0.047$, $p = 0.0079$). In these greener habitats, SOCC-based indices showed a clear decline (–4.51% per year), whereas the calibrated SEC-equivalent indicator series remained stable (+0.15% per year), indicating diverging temporal trajectories between the two approaches (Figure 4B).

In contrast, in transects with habitat with low or highly variable NDVI, the interaction was not statistically significant ($\beta = -0.016$, $p = 0.306$), and both SOCC and calibrated series produced similar long-term indicator trends (SOCC: –1.36% per year; SEC-equivalent: +0.29% per year). In these habitats, the two monitoring approaches yielded

broadly comparable temporal patterns, with limited divergence across the study period (Figure 4C).

DISCUSSION

Integrating general and species-specific monitoring systems provides a structured mechanism to address context-dependent detectability biases that can affect abundance-based indicators in multispecies monitoring schemes. Our results show that parallel survey designs allow systematic discrepancies between monitoring protocols to be quantified and modeled, improving the consistency and interpretability of indicator outputs.

The Common Quail represents a clear example of a broader class of species whose behavioral and ecological traits generate high variability in detectability across space and time (Thompson, W.L. 2002, Diefenbach et al. 2003, Guillera-Arroita et al. 2017). By incorporating a species-specific monitoring protocol and conducting parallel surveys, we quantified how these biological traits influence detection and indicator performance, and developed a habitat-informed calibration capable of reducing these discrepancies within a broad-scale monitoring framework.

Differences between the two methodologies were evident not only in abundance-based indicators but also in basic presence–absence detection, highlighting that detectability itself is a major source of divergence. Poor agreement in low-count situations suggests that many individuals remain undetected when spontaneous calling activity is low, a pattern common to species whose vocal behavior varies over short temporal scales (Bibby et al. 2000, Sutherland 2006). Under these conditions, passive multispecies surveys may fail to register a substantial fraction of individuals, whereas targeted protocols using acoustic stimulation can reveal a larger proportion of the population (De Rosa et al. 2022). This contrast illustrates how protocol-specific detection processes can generate systematic discrepancies in indicator outputs and underscores the value of explicitly modeling these differences within an integration framework.

NDVI emerged as the strongest environmental predictor in the calibration model, indicating that habitat greenness and phenological state strongly modulate discrepancies

between the two monitoring schemes. Importantly, the magnitude of the correction was not constant across sites: discrepancies were greatest in high-NDVI habitat when the BMS protocol recorded low counts. Because NDVI varies considerably among regions and years (Pettorelli et al. 2005), the degree of underestimation in BMS data is inherently context-dependent. Accordingly, the calibration does not act as a uniform multiplier but as a habitat-mediated adjustment shaped by local vegetation dynamics. On the other hand, the lack of a detectable effect of suitable-habitat area is consistent with the fact that all paired transects were located in landscapes where quails are normally present and habitat extent was not limiting. Within this range of conditions, habitat quality—as captured by NDVI—clearly outweighed habitat quantity in shaping differences between monitoring outputs.

Although the calibration improves the consistency of local abundance-based indicators, it is not designed to be directly extrapolated to derive absolute population sizes at regional or higher scales without accounting for population dynamics. In highly mobile species such as the Common Quail, males frequently undertake movements across farmland landscapes during the breeding season, tracking changes in vegetation structure, harvesting schedules and social cues (Puigcerver et al. 1989, Rodríguez-Teijeiro et al. 2009, Sardà-Palomera et al. 2012b). Recent GPS-based tracking data indicate that individuals may move not only between neighboring SOCC transects but also across wider regional, and occasionally international, distances within the same breeding period (Sardà-Palomera et al. 2025, unpublished data), highlighting the highly dynamic nature of populations over short temporal windows and the importance of interpreting calibrated counts within an explicitly defined spatial and temporal framework.

Such mobility implies open populations with substantial turnover, increasing the risk of double counting when survey data are aggregated across space and time without explicitly modelling movement and availability. Under these conditions, the local relationship between general and species-specific survey counts should be interpreted as a calibration of detectability rather than as a direct estimator of regional population totals. Nevertheless, this limitation does not preclude the use of calibrated counts for assessing temporal change or informing population indicators when embedded within

appropriate analytical frameworks that explicitly consider population openness and mobility.

Additional information on movement rates, seasonal redistribution, and connectivity among breeding areas will be essential to refine such models. In the long term, integrating movement data into calibration or state-space frameworks could allow more accurate estimates at larger spatial scales. For now, however, in highly mobile species, monitoring outputs should be interpreted within narrow temporal windows and, where appropriate, at ecologically meaningful spatial units (e.g., migratory flyways) rather than at lower administrative scales.

From a temporal perspective, the calibration refines the ability of general BMS data to describe long-term indicator trends. Although the uncorrected BMS series broadly captured the overall regional trajectory, the calibrated values reduced noise associated with detectability variability and produced indices that more closely reflect underlying temporal dynamics. This is particularly relevant for species whose detectability fluctuates within and across seasons. By stabilizing detection-related variability, the integration framework addresses a central concern in multispecies monitoring: detectability biases can propagate into long-term indices and compromise the ability of BMS programs to detect true demographic change (Kéry and Schmidt 2008, Kellner and Swihart 2014). Correcting these biases therefore enhances the reliability and interpretability of trend indicators.

Despite these limitations, BMS remain an indispensable component of large-scale biodiversity monitoring, providing unparalleled temporal and geographic coverage that no species-specific program could realistically achieve. The challenge, therefore, is not to replace general monitoring schemes, but to complement them through structured integration approaches that explicitly address detectability-related bias.

Methodologically, the proposed integration framework establishes a functional bridge between general and species-specific monitoring schemes. It leverages the extensive spatial and temporal coverage of BMS programs while embedding information from targeted surveys that maximize detectability. This integration allows general schemes to retain their logistical advantages without inheriting the full extent of their detectability biases. Beyond the present case, similar bridging approaches could be explored for other

543 species facing detectability challenges that require specialized monitoring protocols
544 (e.g., *Crex crex*, *Burhinus oedicnemus*). In several taxa, dedicated monitoring programs
545 now incorporate passive acoustic recorders (Sugai, et al. 2018), thermal-imaging
546 devices (Lahoz-Monfortand Magrath, 2021) or camera-trap systems (Wearn and Glover-
547 Kapfer 2019), among others, to increase detection rates under conditions where standard
548 BMS protocols perform poorly. Although these technologies are generally too costly or
549 labor-intensive for broad implementation within BMS networks, they can provide high-
550 quality reference data that enable calibration or validation of general monitoring outputs
551 in a manner analogous to the approach demonstrated here. Such complementary use of
552 broad-scale and species-specific data provides a practical pathway to improve indicator
553 robustness for species that are poorly sampled by standard monitoring schemes, while
554 underscoring the ongoing challenge of translating detection-based information into
555 reliable abundance-based indicators for long-term trend assessment.

556 Overall, our study demonstrates that general BMS data can be partially reconciled with
557 species-specific information to improve abundance-based indicators and trend
558 interpretation for species with highly variable detectability. By developing a calibration
559 approach grounded in paired surveys and ecological context, we provide a practical
560 framework that addresses major sources of detectability-related bias while retaining
561 the extensive spatial and temporal coverage of general monitoring programs. However,
562 the relationship estimated here is necessarily context-dependent. Behavioral patterns,
563 population dynamics, and habitat phenology may vary across regions, years, or
564 management systems, potentially altering the relationship between general and
565 species-specific surveys. Consequently, applying this approach elsewhere may require
566 region-specific calibration analyses to identify the most appropriate model structure.
567 Despite this, the proposed framework offers a transferable methodological basis for
568 integrating general and specialized monitoring schemes. More broadly, our results
569 highlight the value of combining broad-scale volunteer-based programs with targeted
570 high-detection surveys to generate more robust, interpretable, and policy-relevant
571 population indicators for species whose detectability is shaped by behavioral or
572 environmental processes.

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PERSPECTIVES AND APPLICATIONS

Breeding bird monitoring schemes underpin many biodiversity indicators used in conservation policy and environmental reporting. However, species whose behavioral or ecological traits deviate from the assumptions of standardized multispecies protocols may be excluded from indicator frameworks or may generate biased abundance-based estimates. The integration approach presented here provides a structured way to diagnose and quantify such discrepancies by combining a general monitoring scheme with species-specific high-detection survey conducted under parallel sampling design.

Three main applied benefits arise from this approach. First, by explicitly modeling systematic differences between monitoring systems, the method allows detectability-related bias to be distinguished from random variation, increasing confidence in the interpretation of population indices. Second, once calibrated, the relationship between general and targeted surveys can be projected onto broader datasets, enabling long-term trend estimation that retains the spatial and temporal coverage of large-scale monitoring programs. Third, information gained from parallel surveys can inform future monitoring design, identifying ecological contexts in which general protocols are likely to underperform and guiding the strategic deployment of targeted surveys.

Although demonstrated here using a farmland game bird with context-dependent vocal behavior, the approach is applicable to other taxa for which detectability varies strongly across habitats, seasons, or behavioral states. Targeted surveys incorporating acoustic stimulation, passive acoustic recorders, thermal imaging, or other high-detection technologies can serve as reference systems for calibrating general monitoring outputs. In this way, broad-scale volunteer-based schemes can be complemented—not replaced—by strategically implemented specialized surveys.

By linking general and targeted monitoring through explicit calibration, this approach enhances the robustness and policy relevance of biodiversity indicators while preserving the logistical feasibility and long-term continuity of existing monitoring infrastructures. As biodiversity reporting frameworks and management policies increasingly rely on standardized indicators, integrating complementary monitoring systems offers a practical pathway to improve inference for species that would otherwise remain poorly represented.

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CONFLICT OF INTEREST STATEMENT

The authors declare no conflicts of interest.

DATA AVAILABILITY STATEMENT

Data and code required to reproduce the analyses presented in this study are available via a private Zenodo repository for peer review at:

https://zenodo.org/records/18773685?token=eyJhbGciOiJIUzUxMiJ9.eyJpZCI6IjE2YzMzMjA1LTlkZjEtNDJjZS1iMTNmLWMyODc3NjExNzMxNSIsImRhdGEiOnt9LCJyYW5kb20iOiI3NGQzZDg5ZmFmZjVmZWMwM2M2ZjI1MWEyMDYwOGU2ZCJ9.4mhJdHo-cnr950p70RTAqNgO8GQd5el330_YDf4Uun57Mekaikt9dOlenawysKv0y_QOx1eIp9aPTENgHQ6s0w.

The repository will be made publicly available and archived with a DOI upon acceptance of the manuscript.

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TABLES

Table 1 Summary of the negative-binomial calibration model (NB1) relating SEC counts to SOCC counts and habitat variables.

Predictor	Estimate	SE	z	p-value
Intercept	1.739	0.104	16.690	<0.001
SOCC (linear)	1.218	0.166	7.343	<0.001
$SOCC^2$ (quadratic)	–0.370	0.090	–4.125	<0.001
NDVI (15-day mean)	0.266	0.112	2.387	0.017
Habitat area (ha)	–0.034	0.087	–0.388	0.698
SOCC × NDVI	–0.499	0.146	–3.412	<0.001
$SOCC^2$ × NDVI	0.184	0.063	2.919	0.003

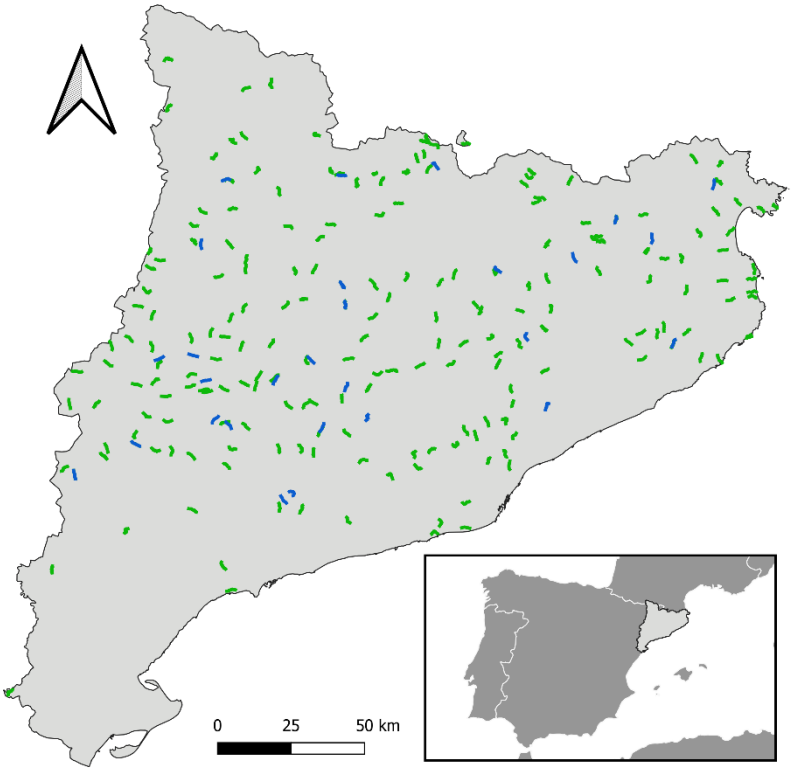
FIGURE CAPTIONS

Figure 1. Geographic distribution of transects used in this study across Catalonia. Blue lines show the 28 specifically designed SOCC transects monitored with both SOCC and SEC protocols between 2021 and 2025, which were used to calibrate the SOCC–SEC relationship. Green lines represent all SOCC transects where at least one Common Quail was detected between 2005 and 2025 (N = 205), for which the calibration model was applied to generate SEC-equivalent abundance-based indicators.

Figure 2. Mean number of Common Quail males detected per transect (± SD) by the SOCC and SEC protocols. Only transects with confirmed quail detection were included. Bars show mean values and error bars indicate standard deviation.

Figure 3. Predicted SEC-equivalent quail counts as a function of SOCC counts and 15-day mean NDVI, based on the final NB1 calibration model. The surface illustrates the combined non-linear effects of SOCC and habitat greenness, as well as their interaction.

Figure 4 Temporal dynamics of the population index derived from original SOCC counts (red) and from SEC-equivalent calibrated indicators (blue). Solid lines show annual TRIM indices and shaded areas represent standard errors. Dashed lines indicate the fitted log-linear trends, with annual percentage changes shown at the right of each panel. (A) All transects combined. (B) Transects within high and stable NDVI habitats. (C) Transects within low or highly variable NDVI habitats. * denotes a statistically significant difference between SOCC and SEC-equivalent trends (time × series interaction).



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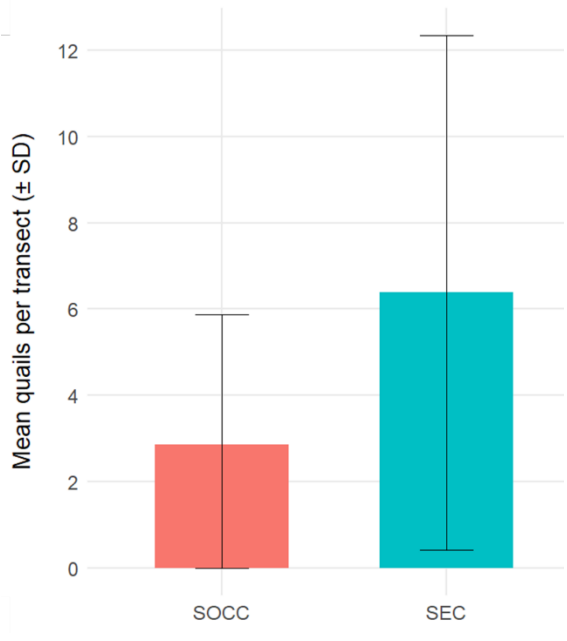
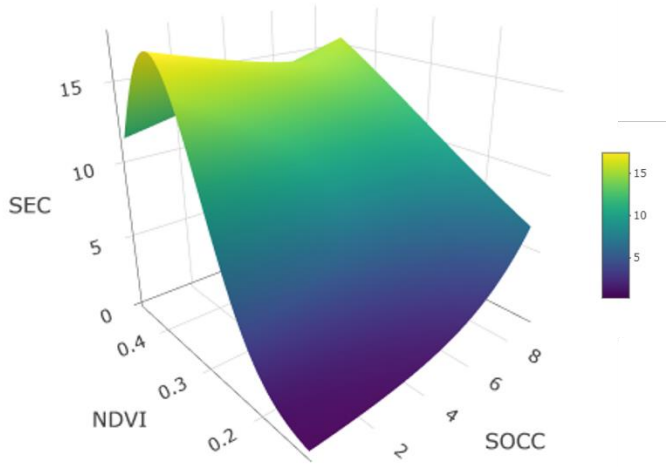


Figure 2



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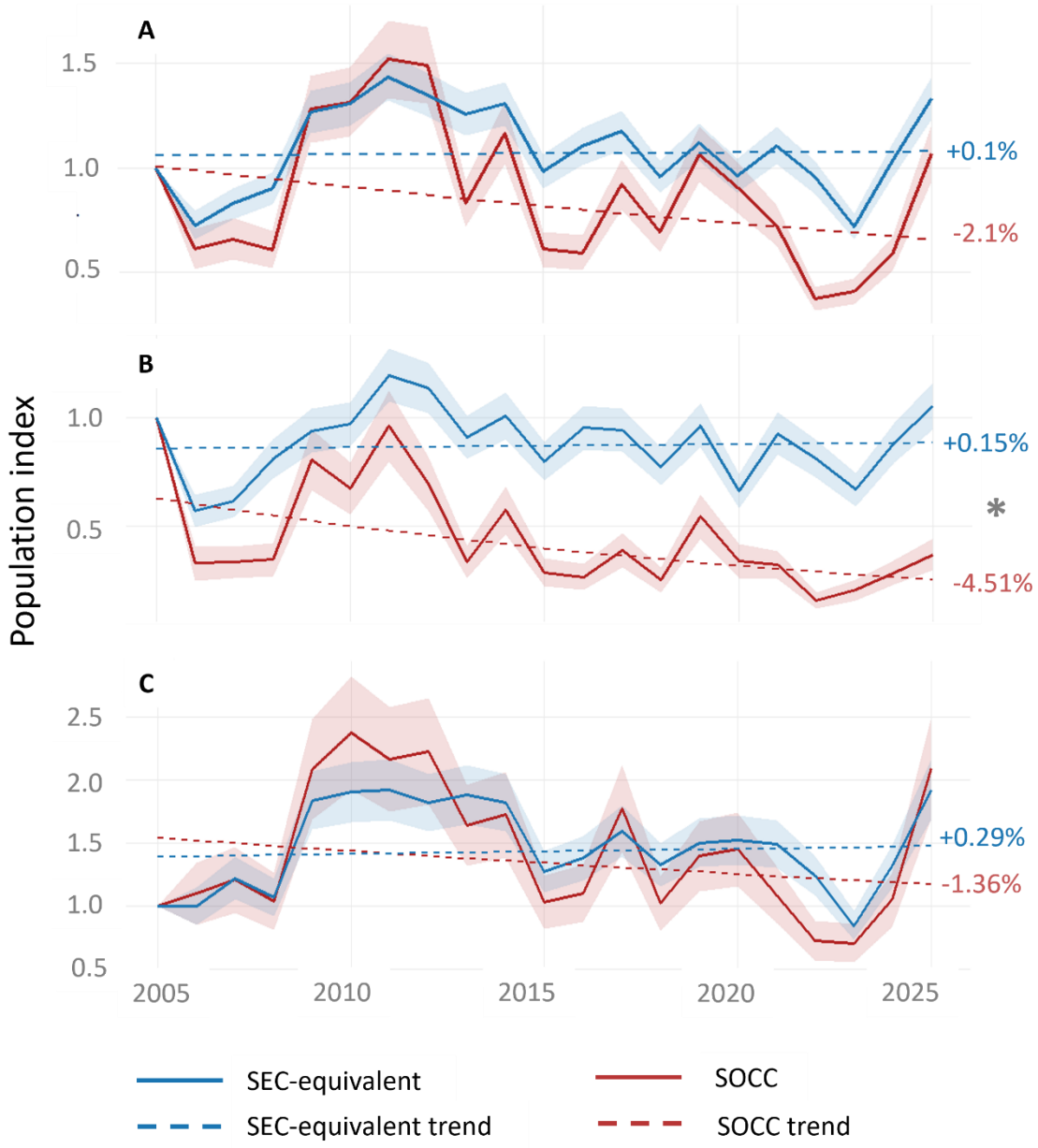

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Supporting Information S1 – Description of agricultural land-use datasets (SIGPAC and DUN) and habitat categories used in the analyses

To classify suitable agricultural habitats for the Common Quail, we relied on two official, georeferenced land-use datasets that together cover the full study period (2005–2025):

SIGPAC (2005–2014)

The *Sistema de Información Geográfica de Parcelas Agrícolas* (SIGPAC) is the Spanish Land Parcel Identification System used for the management of the EU Common Agricultural Policy. It provides annual polygon-based information on crop type and agricultural land use at field scale. For the years **2005 to 2014**, suitable quail habitat was identified by selecting all SIGPAC polygons whose *Uso* ("TA", *Tierra Arable*) and *PS* ("Pastos") codes corresponded to cereal crops, fallows, herbaceous crops or other dryland habitats consistent with quail breeding ecology.

DUN (2015–2025)

From 2015 onwards, land-use information was obtained from the *Declaració Única Agraria* (DUN), the annual agricultural declaration system used in Catalonia and derived from SIGPAC. DUN provides detailed crop information at field level and is fully harmonised with CAP reporting requirements. For each year between 2015 and 2025, we selected all DUN polygons corresponding to herbaceous crops, cereals, legumes, fallows and other dryland herbaceous habitats considered suitable for quail breeding.

Table S1 shows the correspondence between SIGPAC and DUN crop codes

Habitat classification for modelling

All selected SIGPAC and DUN land-use categories were grouped into a single set of suitable breeding habitat types.

These habitat categories were used to:

1. calculate the area of suitable habitat within a 300-m buffer around each transect, and
2. extract vegetation indices (NDVI) for modelling quail abundance and detectability.

Table S1 provides the full lists of categories and their correspondence across datasets.

Sigpac - Suitable habitat for quail	**DUN - Suitable habitat for quail (English)**	**DUN - Suitable habitat for quail (Catalan)**
TA Arable Land	Alfalfa	ALFALS
TA Arable Land	Forage mix	BARREJA FARRATGERES
TA Arable Land	Wheat	BLAT
TA Arable Land	Chard	BLEDA
TA Arable Land	Chickpea	CIGRÓ
TA Arable Land	Oat	CIVADA
TA Arable Land	Rapeseed	COLZA
TA Arable Land	Ryegrass	ERB
TA Arable Land	Spelt	ESPELTA
TA Arable Land	Fescue	FESTUCA
TA Arable Land	Sunflower	GIRA-SOL
TA Arable Land	Fallow	GUARET
TA Arable Land	Lentil	LLENTIA
TA Arable Land	Millet	MILL
TA Arable Land	Barley	ORDI
PS Pastures	Pastures < 5 years old	PASTURES DE MENYS DE 5 ANYS
TA Arable Land	Pea	PÈSOL
TA Arable Land	Quinoa	QUINOA
TA Arable Land	Ryegrass	RAIGRAS
TA Arable Land	Rye	SÈGOL
TA Arable Land	Soybean	SOIA
TA Arable Land	Sorghum	SORGO
TA Arable Land	Sainfoin	TREPADELLA
TA Arable Land	Triticale	TRITICALE
TA Arable Land	Vetch	VEÇA

Supporting Information S2. NDVI-based habitat classification

S2.1. NDVI data processing

We characterised habitat greenness for all SOCC transects with confirmed Common Quail presence using 15-day NDVI composites derived from Landsat imagery (2005–2025). For each transect and year, we computed:

1. Annual mean NDVI: average NDVI during the breeding season.
2. Intra-annual NDVI variability: standard deviation of NDVI within the breeding season for each year.

These annual summaries were then used to derive three long-term NDVI indicators per transect:

- NDVI_mean: mean annual NDVI across all sampled years.
- NDVI_SD_intra: mean intra-annual NDVI variability.
- NDVI_SD_inter: inter-annual variability, measured as the standard deviation of annual NDVI means.
- n_years: number of years with available NDVI information.

Only transects with confirmed quail detections were retained to ensure ecologically meaningful habitat summarisation.

S2.2. Clustering analysis

To classify transects according to habitat greenness and stability, we performed k-means clustering (k = 2) on the scaled values of the three NDVI indicators:

- NDVI_mean
- NDVI_SD_intra
- NDVI_SD_inter

The number of clusters (k = 2) was selected to differentiate high-quality stable habitats from low or highly variable habitats, consistent with ecological interpretations from previous NDVI-based analyses of quail occurrence.

Cluster identities were assigned based on maximum NDVI_mean in the cluster centroids. The two habitat categories were therefore defined as:

- “NDVI high and stable” — high mean NDVI, low variability.
- “NDVI low or highly variable” — low greenness and/or high temporal fluctuation.

S2.3. Principal Component Analysis (PCA)

To validate the clustering structure, we performed a PCA using the same NDVI indicators. The first two principal components explained 46.2% (PC1) and 33.0% (PC2) of the variance, respectively.

A clear separation between the two NDVI groups was observed along PC1 (Figure S2.2), confirming that the k-means clusters captured meaningful gradients of habitat greenness and stability.

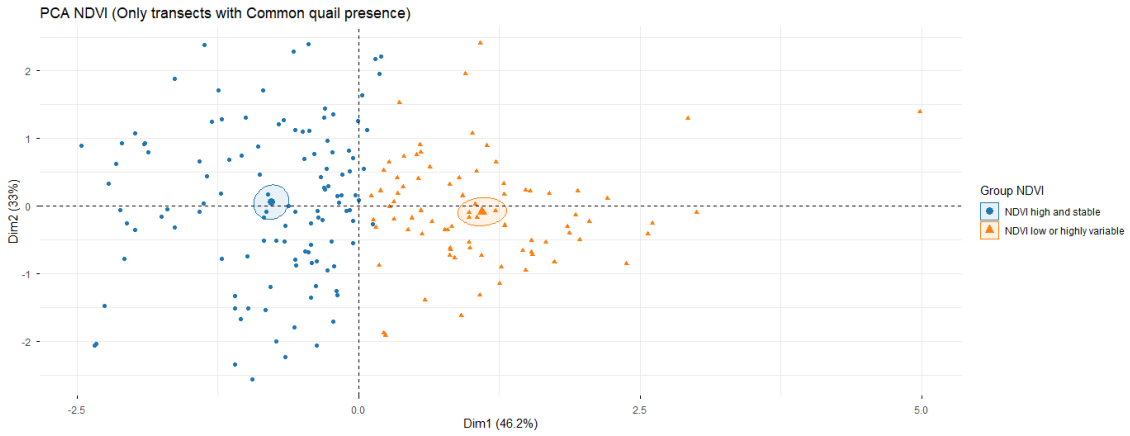

Figure S2.1. *Principal Component Analysis of NDVI indicators.* PCA of NDVI_mean, NDVI_SD_intra and NDVI_SD_inter for transects with quail presence. Colours indicate k-means habitat groups, with 95% confidence ellipses. Separation along PC1 validates the clustering structure.

S2.4. Statistical comparison of NDVI indicators between groups

To evaluate whether NDVI indicators differed significantly between habitat groups, we performed normality tests (Shapiro–Wilk) and subsequently applied either:

- Student's t-test (when both groups were normally distributed), or
- Mann–Whitney U test (for non-normal distributions).

The comparison was conducted for (Table S2.1):

- NDVI_mean
- NDVI_SD_intra
- NDVI_SD_inter

Table S2.1. Statistical comparison of NDVI indicators between habitat-quality groups. Results of parametric (t-test) and non-parametric (Mann–Whitney U) tests comparing mean NDVI, intra-annual NDVI variability and interannual NDVI variability between the two NDVI-based habitat clusters ("NDVI high and stable" vs. "NDVI low or highly variable"). Reported p-values correspond to two-tailed tests.

Variable	Test	p_value
Mean NDVI	t-test (paramètric)	< 0.001
Intra-annual NDVI SD	NDVI SD Mann–Whitney U (no paramètric)	< 0.001
Interannual NDVI SD	NDVI SD Mann–Whitney U (no paramètric)	< 0.001

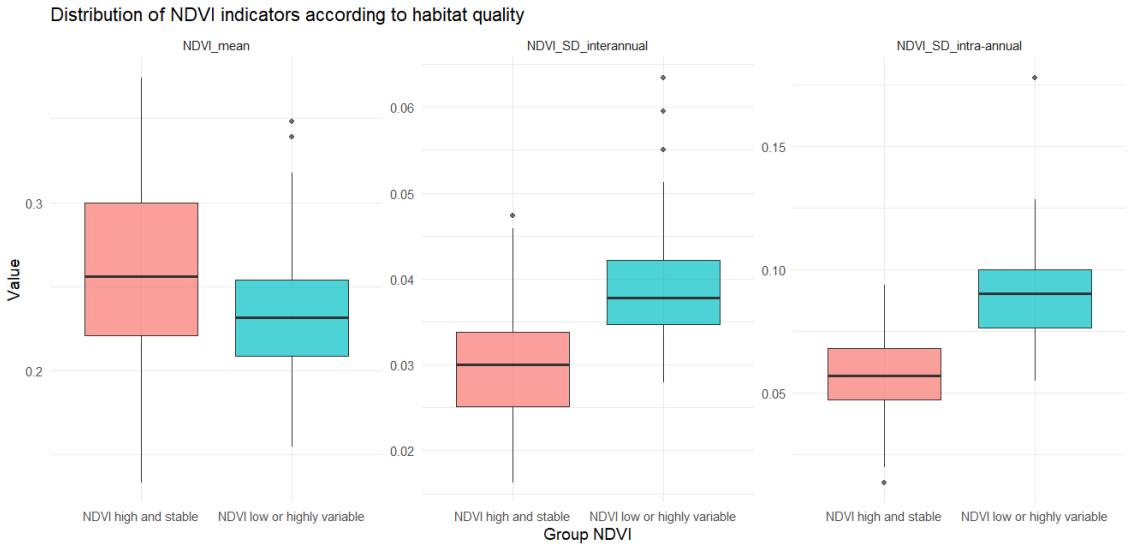

Figure S2.2. *Distribution of NDVI indicators according to habitat-quality group.* Boxplots showing (A) mean NDVI, (B) inter-annual NDVI variability, and (C) intra-annual NDVI variability for the two NDVI groups. High-NDVI stable transects show greater greenness and lower temporal variability.

Supporting Information S3 – Predictor contribution analysis

Predictor contribution was assessed by refitting reduced models on the exact training dataset used by the final calibration model (n = 58). ΔAIC values are expressed relative to the full model specification. The linear SOCC term was the most influential component (ΔAIC = 53.5), followed by the quadratic SOCC term (ΔAIC = 20.0). NDVI (including its interactions with SOCC) also contributed substantially to model support (ΔAIC = 11.9), and removing NDVI interactions alone reduced support by ΔAIC = 8.93. Suitable habitat area did not improve model support (ΔAIC = −1.85), indicating no detectable contribution of this covariate.

Table S3. Contribution of each predictor to the final calibration model based on AIC differences between the full model and models with individual terms removed.

Removed term	**df**	**AIC**	**ΔAIC**
Full model	8	282.52	0.00
NDVI_mean + interactions	5	294.45	11.93
socc (linear) + interaction	6	336.02	53.50
socc² + interaction	6	302.48	19.96
NDVI interactions only	6	291.45	8.93
Suitable habitat (ha)	7	280.67	−1.85

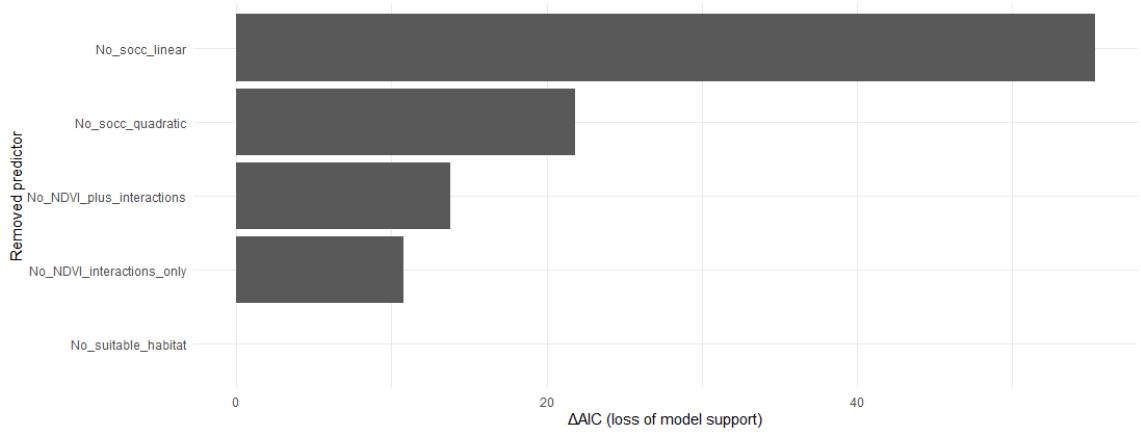

Figure S3.1. Relative importance of each predictor based on ΔAIC values obtained by removing individual terms or groups of terms from the full model. Larger ΔAIC values indicate greater loss of model support. The linear component of SOCC was the dominant predictor, followed by its quadratic component and NDVI. Suitable habitat area had no detectable influence on model performance.

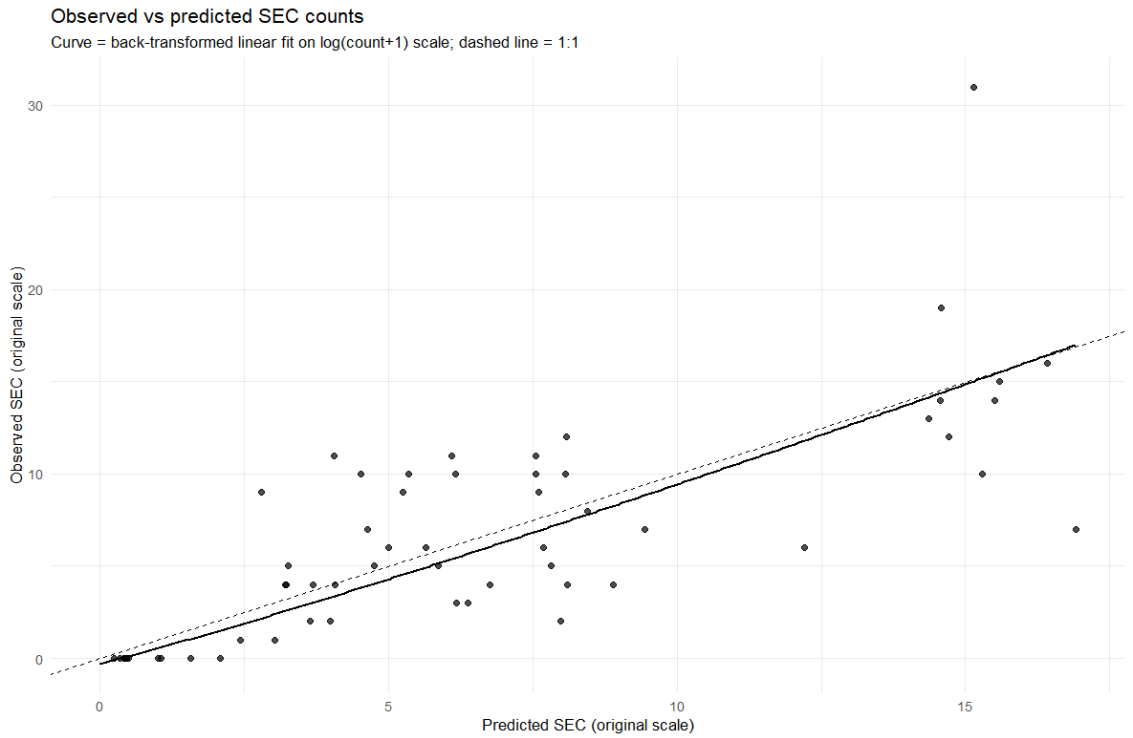

Figure S3.2. Relationship between observed and predicted SEC counts from the final calibration model (negative binomial with log link). Points are shown on the original count scale. The solid curve is the back-transformed fit from a linear regression on log(count+1), and the dashed line indicates the 1:1 relationship. Pearson correlation was computed on log(count+1) (R = 0.87).