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Multi-taxon co-located data: methods, challenges and opportunities

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Summary

We explore the potential analytical opportunities and practical challenges of using co-located multi-taxon biodiversity monitoring data. Drawing on the Tracking the Impact (TTI) project as a case study, we examine the cases in which co-location of multi-taxon biodiversity monitoring could enhance ecological insight beyond that which single-taxon or non-co-located monitoring can offer.

Co-located data more effectively supports holistic assessments of ecosystem health, the development of multi-taxon indicators, and allows for the exploration of cross-taxon relationships and shared responses to environmental pressures. It can also offer logistical efficiencies in survey planning and landowner engagement.

However, there are key analytical challenges introduced by the differences in survey protocols, spatial and temporal mismatches, pseudoreplication, and the complexity of integrating data across taxa. Potential methodological approaches to address these issues are discussed, such as model-based integration and data interpolation.

To maximise the impact of projects like TTI and ensure their data is fully harnessed, careful consideration must be given to survey design, analytical methods, and the ecological relevance of co-location. The findings presented here aim to inform future biodiversity monitoring initiatives and support the development of robust, multi-taxon ecological assessments.

Contents

1. Introduction

Citizen science biodiversity monitoring schemes offer robust and repeatable methodologies, wide geographic coverage, and long-term data for analysing trends in space and time. Sampling locations across many of the different national monitoring schemes do not overlap, as their primary aim is to describe population trends of the corresponding taxon at a national scale. However, there are several assumed benefits to surveying multiple taxa in the same location (referred to here as co-located monitoring). These benefits may relate to the scientific outputs generated from co-located data, for example identifying and exploring cross-taxa associations, or creating more holistic multi-taxon measures of ecosystem health in an area of interest (e.g. a protected landscape, or an area which has changed in its habitat quality and/or quantity). These may also be logistical, for example, by simplifying the process of getting land-owner permission for monitoring on their land.

While multi-taxon analysis using co-located biodiversity data is likely to offer benefits, it can also present significant challenges. For example, data from the UK's collection of structured terrestrial monitoring schemes (JNCC 2024) have not necessarily been collected with multi-taxon analysis in mind and may not be immediately suitable for this where surveying is co-located. Additionally, each taxon will have a different set of ideal protocols, including time of year, time of day, and survey method. Considerations must therefore be made when analysing co-located multi-taxon data, and specific methods used, to ensure that robust conclusions can be drawn and that the above benefits are realised.

Tracking The Impact (TTI) is landscape-scale monitoring initiative collecting species data across the central Chilterns. Volunteers collect these data using survey protocols from the Breeding Bird Survey (BBS), the Wider Countryside Butterfly Survey (WCBS), and the National Plant Monitoring Scheme (NPMS). These are all national monitoring schemes, used to track national-scale changes in population of specific taxa. Unlike the national schemes, which each use separate random stratified sampling approaches to decide where to survey, all of the monads within the TTI project can be surveyed by each of the included survey methods. This aims for data to be collected across multiple taxonomic groups (i.e. birds, butterflies, and plants) and to co-locate that collection at the level of the sampling monad. This approach could provide novel opportunities to answer questions at a landscape scale, informed by data from diverse taxa. The aim of this report is to identify approaches to multi-taxon analysis which could be applied to similar data to determine the challenges with, and methods available for, analysing datasets like this, and the questions such analysis could answer.

2. What insight could co-located local sampling intensification data provide?

2.1. Why might co-located data be useful?

There are a number of assumed benefits to, or potential needs for, co-location within biodiversity monitoring. Key priorities identified by UK environmental bodies, for example increased survey coverage of multiple taxa and improved spatial coverage of already well-surveyed taxa (Pocock 2018), could also be addressed by co-location. Pocock (2018) identified that co-located data could also be beneficial in the production of a “more comprehensive assessment of ecosystem health or condition”, for example by being used to create multispecies indicators. In depth knowledge and co-located monitoring of different taxonomic groups robustly support the production of indicators such as these for complex ecosystems (Blasi *et al.* 2010). Calculating metrics for multiple taxonomic groups in a given location and exploring the degree of correlation between trends for different species or for groups of species, provides greater insight into ecosystem health than equivalent analyses could do from a single taxon. For example, the Nature Index for Norway uses a composite measure derived from a number of individual indicators (principally the abundances of individual species across different taxonomic groups) to determine the state of biodiversity across different ecosystems, and across ‘thematic indices’ (Berge & Pedersen 2021). While this is applied at the national scale, a similar approach could be applied at more localised scales on appropriate co-located data. For example, the Cairngorms Nature Index is currently under development and draws inspiration from the Nature Index for Norway model to assess biodiversity at the regional level (Fraser, n.d.).

As well as a more complete overview of a specific ecosystem, co-located multi-taxon monitoring can be beneficial in overcoming some of the problems associated with indicator species. For example, singular populations not necessarily reflecting the complexity of an ecosystem or the subjective selection of indicator species (Siddig *et al.* 2016). Multi-taxon monitoring may also reduce the bias towards charismatic species or taxa (Lindenmayer *et al.* 2000). Co-located data could also help in understanding how human pressures or management at a given location influence species abundances and distributions in different ways (e.g. Zingg *et al.* 2019; Staley *et al*. 2022). Finally, co-location benefits may also be logistical, for example simplifying the process of gaining land-owner permission for biodiversity monitoring on their land, whereby only one set of permissions is needed for all surveys together, instead of permission to conduct each survey separately.

2.2. Challenges and methodological approaches to analysing co-located data

Although there are perceived benefits to co-location, integrating and analysing co-located data can present challenges. It may prove analytically challenging to compare or aggregate data from different monitoring schemes across multiple taxa and produce robust and reliable results. For example, monitoring schemes may collect data at vastly different scales, from recording species visiting a single flower (as in the Pollinator Monitoring Scheme), to recording birds across an entire 10 km square (as in the Bird Atlas). Examples such as this can be addressed during survey design and analysis by, for example, standardising the survey area across the chosen schemes, as in TTI. Other examples pose a more significant challenge and must be accounted for when interpreting results. For example, as with all monitoring data, each dataset will have its own biases associated with it. Aggregating these datasets can result in an accumulation of sampling biases, the effect of which is greater in aggregate than on each dataset individually and must be accounted for during interpretation (Ward & Siriwardena, unpublished).

Some of the challenges of aggregating co-located data can be overcome when combining and analysing the data. While the simplest way to combine multiple data sources may be to standardise protocols across monitoring schemes, this is unlikely to be practical across different taxa and does not facilitate analysis of existing datasets (Harris & Hoskins 2024). Literature focused on analysing co-located, multi-taxon data collected using different survey protocols at a localised sampling scale is relatively sparse. However, it may be possible to explore research that has conducted analysis on data aggregated from multiple sources to assess how effective these methods could be at analysing co-located data produced from a project such as TTI.

2.2.1. What can the data tell us?

Analysing co-located data from across multiple taxa is often opportunistic and uses data from multiple sources that haven't necessarily been designed to be included together in a single analysis. The available data therefore dictates what questions can be answered (Pringle & Siriwardena 2022). For example, causation is likely to be difficult to infer from available data, especially when the geographic scope is not of the appropriate scale or coverage (Henrys *et al.* 2022) or there are too many uncontrolled variables. Using BBS data, Newson *et al*. (2010a) found a statistically significant relationship between grey squirrel abundance and the population growth rates of twelve bird species. However, they could not demonstrate causation in this purely correlative study, in part due to unaccounted for environmental drivers including woodland habitat degradation. While initiatives looking to take a TTI-style approach may face similar challenges, it is worth noting that a substantial body of literature on causal inference from observational data does exist (e.g. propensity score matching, instrumental variables, structural equation modelling) (Siegel & Dee 2025). The applicability of such methods would depend on the quality, granularity, and completeness of the available data.

One approach to combining separately collected datasets would be to pool the data together. This would assume that differences between datasets are insignificant enough to ignore (Isaac *et al.* 2019). This is the simplest way of combining datasets and is likely to allow the combination of virtually all existing monitoring schemes (Henry *et al.* 2008). Alternatively, Roberts *et al.* (2007) suggest reducing each dataset down to a lowest-common denominator, so that datasets can be compared. In their study, the authors reduced multiple years of effort-corrected bird abundance data collected using mist-netting, to lists of species present in the area. These lists were used to design an analytical process that could estimate trends from data collected by schemes that only record species lists. While effective, reducing datasets to the lowest common denominator results in loss of detailed data and increases the risk of false negatives for schemes that do not emphasise recording absences when detection data is treated as occurrence data (Adams & Muths 2019). However, it is important to recognise that not all monitoring schemes are designed to draw inferences or guide decision-making. In some cases, the primary aim may be descriptive, such as documenting species presence or building biodiversity baselines, where simplified data formats may still be appropriate and informative (McShane *et al.* 2019; Wasserstein *et al.* 2019).

Alternatively, model-based integration is a powerful tool for combining datasets and could be extended to combining multi-taxon data (Mancini *et al.* 2022). By analysing data collected under different protocols – each with its own observation model – species occupancy, abundance, and trends can be accurately estimated while correcting for dataset-specific biases (Harris & Hoskins 2024; Adams & Muths 2019). This allows the retention of each dataset's strengths and, at least in part, corrects for any weaknesses. Joint species distribution models, for instance, can account for correlations not explained by available environmental predictors, such as species interactions, and missing covariates (Isaac *et al.* 2019; Wilkinson *et al.* 2021).

Another model-based approach utilised by many authors is to extend the log-linear model of inter-annual population growth rate changes developed by Freeman and Newson (2007). For a given species, this approach models change in expected abundance between consecutive years in relation to predictor variables (e.g. abundance of a potential competitor species) and can include covariates such as habitat. For example, Newson *et al.* (2010a) used this approach to combine BBS and Common Bird Census data, and Ward and Siriwardena (unpublished) used this approach to conduct three analyses which each explored the effect of Collared Dove on finch species. Although both studies focus on birds, they demonstrate the co-location and analysis of separately collected species datasets. Further examples of studies exploring multi-taxon analysis using Freeman & Newson's log-linear model are Pringle and Siriwardena (2022) who combined parakeet numbers from BBS with bat presence data from the National Bat Monitoring Programme to identify relationships between native and non-native species. The study concluded that monitoring scheme data could "provide novel insight informing the evaluation of invasive effects in a range of contexts". Similarly, Kettel *et al.* (2020) combined BBS data and data from Defra to explore impacts of badger culling on bird populations. While it concluded that there was no evidence for an impact of badger culling on breeding bird populations, this study, in combination with Pringle and Siriwardena (2022), provide examples of how national scheme surveys could be co-located to answer questions and provide novel insight.

Models can also be used to combine and analyse datasets that have been collected using different methods in a way that provides more detailed insights than when analysing an individual dataset. Adjei *et al.* (2024) demonstrates this approach by combining two different datasets from the Pollinator Monitoring Scheme (PoMS): data from pan traps (presence/absence data recorded to species level) and from FIT counts (abundance data recorded to broad taxonomic group). Authors used an Integrated Distribution Model to determine alpha community diversity for localised areas. The Integrated Distribution Model predicted alpha diversity better than the single dataset models and was more precise. While this is not combining data for more than one taxonomic group, it is an example of how co-located data could be combined to produce an improved output. This use of species-level presence/absence data, similar to those collected by metabarcoding, highlights the potential of co-locating environmental DNA with traditional scheme data to conduct multi-taxon analysis (Bohan *et al.* 2017).

2.2.2. Pseudoreplication

Another challenge arises when integrating datasets from biodiversity monitoring schemes that collect data in different ways. For example, surveys may be conducted at different temporal and spatial scales, and when these datasets are combined, sample sizes can be inflated via pseudoreplication. Pseudoreplication occurs when data points are incorrectly treated as independent, resulting in an artificially inflated sample size (Lazic *et al.* 2020). For example, spatial pseudo replication may occur when multiple 1 km^2 monads surveyed using one protocol are compared to a single 10 km^2 area surveyed by another protocol (Ward and Siriwardena, unpublished). Similarly, combining a dataset collected at a single point in time with one that is collected annually may result in temporal pseudo replication of the dataset with the lower temporal resolution. Pseudoreplication can also occur when modelled data is improperly used to fill gaps in datasets. This is as a result of modelled predictions relying on the same source information, therefore not being independent of each other (Pringle & Siriwardena 2022).

2.2.3. Degree of co-location

Many of the large-scale biological recording schemes in the UK rely on citizen scientists to collect much of their data. This makes it difficult to guarantee a high degree of co-location between schemes, with no certainty that all monads will be surveyed. In TTI for example, between 2020 and 2023, only one monad was surveyed by all three utilised recording schemes in all four years. This limitation is likely to diminish as coverage grows, and schemes become more established locally, but does mean it is unlikely that most similar projects would immediately be able to conduct analyses on their data that require sampling colocation.

2.2.3.1. Spatial co-location

Even if the survey protocols are aligned (e.g. all conducted in 1 km^2 monads), and there was a high degree of co-location in terms of the monads surveyed, the exact survey locations within the monad for each taxon are determined by the recorders themselves. In theory, this means that survey points could be at opposite corners of the 1 km^2 monad. Whether conclusions can be drawn about associations between taxa which are not surveyed in the exact same area is likely to be taxon- or species-specific. An organism's habitat is scale-dependent, with a large bird of prey likely to travel further, and have a larger range, than a small insect (Barnes *et al.* 2022). Understanding the use case for co-located data is therefore crucial when deciding whether surveys should be co-located, and how close the association between taxa needs to be.

Alongside interactions between taxa, co-located analysis using habitat data to define the species' association with a habitat can also present challenges when the habitat has not been recorded directly alongside the species. For example, Redhead *et al.* (2016) explored two butterfly monitoring schemes that collect data at the 1 km^2 scale (UK Butterfly Monitoring Scheme (UKBMS) and Butterflies for the New Millenium), to determine the habitat associations of 50 butterfly species. This was based on the proportion of broad-leaf woodland (from Land Cover Map 2007 (Morton *et al.* 2014)) within each 1 km^2 monad. Despite potential spatial mismatches between species and habitat records within these 1 km^2 monads, habitat abundance scores showed strong positive correlations with expert opinion. However, for species not considered habitat specialists, 5000 occurrence records were needed to gain an accurate estimation of habitat association. Landscape-scale data, like those produced by TTI, are likely to comprise much fewer than 5000 records per species. To draw robust conclusions on habitat association, the recorded species would need to be very strongly associated with its habitat, or sampling density much higher, where habitat data is not recorded alongside taxonomic data. The spatial and/or temporal coverage of the species sampling would also need to be ecologically relevant to the target taxa, with sufficient sample size to cover variations in presence and/or abundance of each species (Pringle & Siriwardena 2022). While this might mean a project like TTI would not be able to draw conclusions on habitat association such as these, especially if habitat information was not collected, combining data from multiple TTI-style projects may facilitate this.

2.2.3.2. Temporal co-location

Comparing datasets across different surveys which are each aimed at a different taxon can increase the likelihood of temporal mismatches. For example, the three surveys used in TTI (BBS, WCBS and NPMS) have all been designed to take place at the same spatial scale (1 km^2 monads). However, each taxon has an optimum time of the year to be surveyed, and this is reflected in their survey protocols. While there is overlap between these time periods, there is no guarantee that data collected for different taxa will be collected closely enough in time to make comparison or aggregation ecologically relevant for certain uses, even when those data were collected from the same monad and in the same year (Pringle & Siriwardena 2022). This challenge could reduce the degree of temporal co-location, and the robustness of any conclusions drawn. Depending on the question asked, this may not be a problem. Determining ecosystem health, for example, would not require data for each taxon to have been collected at exactly the same time. However, the appropriateness of an association between species (e.g. linking small numbers of butterflies with high numbers of warblers), must be considered if they were recorded at different times of year. Relevant ecological knowledge may be required to answer this question, for example on the existence of time-lags in predator-prey relationships (Newson *et al.* 2010b). In contrast, in cases where recording is due to take place at the same time, co-location could lead to logistical benefits, allowing volunteers to record more than one taxon within the same visit.

2.2.3.3. Approaches to temporal and spatial mismatches

In the case of temporal (between years) and spatial mismatches between datasets, a fourth approach to analysing co-located data is to remove any records that cannot be matched from analysis. For example, removing any monads that have only been visited by one monitoring scheme (Ward and Siriwardena, unpublished). Redhead *et al.* (2016) only used the butterfly occurrence records from the Butterflies for the New Millenium scheme with a spatial resolution of 1 km^2 or finer. This ensured that the resolution of the UK Butterfly Monitoring scheme was matched and avoided spatial pseudo replication when combining the two datasets. In TTI, many of the 1 km transects within monads were used for both WCBS and BBS surveys. While this is a relatively unique case (as WCBS was designed to align with BBS), it does present the possibility of extracting and comparing just the BBS and WCBS data to remove the risk of data not being tightly co-located. Alternatively, to avoid losing data points, monads visited by just one scheme could be matched with the nearest monad visited by another scheme. Similarly, spatial interpolation can be used to fill gaps based on surrounding monads that have been surveyed (Henry *et al.* 2008). These approaches are likely to be more robust if a covariate, such as habitat type, is used to guide the matching or interpolation. For temporal mismatches, averages across years could be calculated to fill in missing years at a site (Ward & Siriwardena, unpublished). However, these approaches rely on the assumptions that all monads contain the same or similar habitat as those nearby, and that population changes between years are consistent (i.e. not accounting for irregular increases or decreases in populations in a particular year). This may reduce the reliability of any further analysis.

2.2.4. Producing multi-taxon metrics

Challenges can arise when analysing co-located data to produce metrics which describe the ecological community overall, such as species diversity and richness. Aggregated or composite metrics are more difficult to produce when based on different units. For example, most structured schemes capture species' presence through their abundances (e.g. BBS, WCBS), some schemes capture presence through estimates of percentage ground covered by species (e.g. NPMS), while some schemes capture presence through species' activity (e.g. the National Bat Monitoring Programme). This latter example requires the use of abundance proxies (e.g. proportion of sampled nights a bat species was recorded) to calculate metrics such as Shannon diversity. Additionally, some metrics (e.g. species richness), will have to be interpreted differently for taxa with a large number of recorded species (e.g. pollinators or moths which are recorded in their hundreds) than taxa with a much smaller number of recorded species (e.g. bats with only eighteen possible species found in the UK) (Staley *et al.* 2022). The species richness at which an ecosystem is considered 'healthy' varies by taxa. Evans *et al.* (2017), for example, demonstrated the threshold values of species richness before rapid decline of temperate forest ecosystems. The species richness for each taxon (ectomycorrhizal fungi, epiphytic lichen and ground flora) at which forest dieback occurred varied significantly, demonstrating the importance of taxon-specific interpretation. This challenge becomes less significant when looking at trends, rather than at a specific point in time.

Another approach would be to avoid combining datasets collected by different recording schemes and analyse the data from each taxon separately. This approach can still explore how different taxa respond to changes in the landscape such as climate, habitat quality or quantity, or management. For example, Zinng *et al.* (2019) used data from bird and butterfly surveys conducted in Switzerland at different frequencies across sampling years, to gauge the impact of 'biodiversity promotion areas' (BPAs) (i.e. areas of land under Agri-Environment Schemes (AES)), on local bird and butterfly populations. While the datasets were not combined or analysed together, the surveys were co-located to 1 km^2 and provided a more comprehensive view of the BPAs' ecological impact due to this co-location and the larger number of species surveyed. Initiatives looking to take a TTI-style approach can therefore separately assess the response of multiple taxa to a common driver (e.g. habitat or management), potentially allowing the comparison or aggregation of the outputs.

Similarly, the 'LandSpAES' (Staley *et al.* 2022) project in the UK was set up to assess the response of mobile taxa to AES actions, beyond the boundaries of the farms in which the AES actions were undertaken. The target taxa (insect pollinators, butterflies, moths, bats and birds) were each surveyed using structured recording scheme methods which retained the data's comparability to existing national records, thereby being similar to the local sampling intensification of TTI. To help select 1 km^2 monads to survey, Staley *et al.* (2022) used an evidence review to estimate how impactful an AES intervention would be on each of the target taxa and produced separate gradient scores for four of these taxa. The taxon-specific gradient scores correlated strongly with the average gradient scores across the taxa, supporting co-location of the taxon-specific surveys. Using monitoring data from the structured scheme surveys, species richness, Shannon diversity and total abundance were calculated for each taxon overall, and trait groups within these. Correlation between these and the local and landscape AES interventions were assessed, with a small number of groups showing statistically significant positive associations. This suggests that only some taxa, or trait groups within each taxon, are positively impacted by AES management in nearby fields. The co-location in this survey helped disentangle which groups benefit from AES, and which there is less evidence for, providing more nuanced information than the literature review could.

3. Conclusions and next steps

This report has explored the analytical opportunities and challenges presented by co-located biodiversity monitoring across multiple taxa. There are clear and significant challenges, including pseudoreplication, variability in protocols and the extent of colocation, and taxon-specific data interpretation. However, when these challenges are accounted for in analysis, it is evident from the literature that co-located monitoring, similar to that used by TTI, can provide novel insight that would not be possible, or would be much less robust, using traditional single-taxon, non-co-located monitoring. These include:

- Holistic ecosystem assessment and the creation of multi-taxon composite indicators (as in Berge & Pedersen 2021).
- Identification of shared or differential responses to environmental pressures or management interventions across taxa (as in Staley *et al.* 2022 and Zinng *et al.* 2019).
- Identification of habitat associations and interactions, when sample sizes are large enough (as in Redhead *et al.* 2016).
- Identification of interactions between species (as in Pringle and Siriwardena 2022 and Newson *et al.* 2010a).
- Creation of more detailed community metrics through combining results (as in Adjei *et al.* 2024).

To maximise the impact of projects like TTI and ensure their data is fully utilised to inform decision-making and ecological understanding, we recommend:

- Project managers should determine what questions the project aims to answer, and what kind of data are needed to answer these to help design survey protocol implementation.
- Developing a clear definition of what constitutes temporal and spatial co-location, this may be project- or taxon-specific, or across multiple projects.
- Piloting TTI-style projects in other locations across the UK to facilitate comparison and combination of landscape-scale results to maximise the value of collected data.

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