Developing an interactive R Shiny app for insect biodiversity meta-analyses

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Acknowledgments

Abstract

Introduction

With regard to species richness, insects constitute the world’s most diverse taxonomic group (Homburg *et al.*, 2019; Cardoso *et al.*, 2020), representing extensive unique and overlapping functions. Pollination by Hymenoptera, Lepidoptera, and Diptera strongly influences crop yields and profits (Habel *et al.*, 2019) with around three-quarters of crop species dependent on pollination to some extent (Klein *et al.*, 2007). Additionally, insects contribute to biological pest control and organic matter recycling, as well as constituting a major link in the food web between primary producers and consumers (Sánchez-Bayo and Wyckhuys, 2019). The loss of these services threatens global ecosystem health and food security (Potts *et al.*, 2016), which is particularly apparent in the global south where reliance on insect pollinated crops is high (Dicks *et al.*, 2021).

Despite their invaluable contributions, insects are underrepresented in long-term biodiversity studies compared to vertebrates (Outhwaite *et al.*, 2020; Wagner *et al.*, 2021b). In a review by Titley *et al.* (2017) there was an even split between biodiversity papers reporting on vertebrates and invertebrates, a substantial difference to the proportions of species in existence where 95% are invertebrates. Possible reasons for this include the view of insects as pests and disease vectors (Lawton *et al.*, 1998; Miličić *et al.*, 2021), difficulty in identifying individuals to species level, as well as populations being particularly hard to monitor considering their inconspicuous nature and high annual variation (Fox *et al.*, 2019). Where insects are the focus, bees, butterflies, and moths are over-represented, limiting conclusions on the state of insects as a whole (Hallmann *et al.*, 2020). Therefore, while we may be experiencing the sixth mass extinction in evolutionary history (Dirzo *et al.*, 2014), it proves difficult to assess the extent to which insects are affected.

This underrepresentation has been somewhat rectified recently with a ten-fold increase in the number of insect decline papers between 2000 and 2010 (Eggleton, 2020), though this does not come without its drawbacks. A dearth of historical records hinders our ability to determine a baseline to which we should compare the current state of species, termed shifting baseline syndrome (Didham *et al.*, 2020). Any reported increases could be deceptively encouraging due to the possibility that the new figures are negligible compared to historical numbers. Additionally, the disparity between the one million insects described and the 5.5 million thought to exist (Stork, 2018) means studies continue to suffer from our lack of knowledge.

Although more long-term data is needed, current consensus is that insect decline is sufficient to warrant immediate further study and action (Montgomery *et al.*, 2020). Sánchez-Bayo and Wyckhuys (2019)'s speculations that 40% of insect species could go extinct in the next few decades have been prominent in bringing the issue to the forefront, though fundamental issues — particularly their biased literature search strategy, vote-counting methodology, and unjustified global extrapolation of findings — have been discussed (Simmons *et al.*, 2019; Saunders *et al.*, 2020). A similarly alarming seasonal decline of 76% of total flying insect biomass was observed in Germany (Hallmann *et al.*, 2017). Nevertheless, it is rare for a study to exclusively report declines (Saunders *et al.*, 2020); some insect populations are stable or increasing (Boyes *et al.*, 2019; Wagner *et al.*, 2021b) such as the 5.5% UK terrestrial insect occupancy increase (1970-2015) reported by Outhwaite *et al.* (2020). Crossley *et al.* (2020) conclude no overall trend in US insect abundance or diversity, though have been criticised for violating the assumption that records were collected consistently between datasets (Welti *et al.*, 2021).

A variety of reasons contribute to the contrasting results, one being geographical variation. Trends in carabids markedly differed across the UK from 50% declines in northern moorland to 50% increases in southern downland (Brooks *et al.*, 2012). Additional complexity stems from the hypothesis that areas largely surrounded by agricultural land will experience stronger rates of insect decline, possibly due to reduced dispersal ability in a fragmented habitat or increased pesticide exposure (Seibold *et al.*, 2019). Furthermore, most research to date has been restricted to human-dominated landscapes in Europe and North America. Recognising this, researchers have begun to search for population trends elsewhere including the tropics (wherein exists the highest biodiversity) (Lister and Garcia, 2018; Wagner *et al.*, 2021b) and the Arctic (Loboda *et al.*, 2018; Gillespie *et al.*, 2020).

Conflicting results may also be due to temporal or taxonomic variation. Ollerton *et al.* (2014) calculated that the highest extinction rates for British bee and flower-visiting wasps occurred in the 1920s to 1950s, likely coinciding with intensification of agricultural practise. Biesmeijer *et al.* (2006) exemplifies differences between species with bee richness decreasing in 52% of British cells, while no significant changes were observed for hoverflies. Similarly, Hallmann *et al.* (2020) reports declines in macro-moths, beetles, and caddisflies, but not true bugs and mayflies in the Netherlands. These findings indicate the difficulty of generalising research focused on specific species or timespans.

Studies that assess the status of insects at higher taxonomic levels may breach this gap, though concurrently overlook species-level trends (Wagner *et al.*, 2021b). Van Klink *et al.* (2020) found an average 9% decrease and 11% increase per decade of terrestrial and freshwater insects, respectively, but is criticised because the abundance and biomass metrics used are unable to account for changes in community structure such as the replacement of sensitive species with tolerant ones (Jähnig *et al.*, 2021), or even complete species turnover (Hillebrand *et al.*, 2018). It is also possible to observe decreases in species richness but not biomass, potentially explained by smaller species showing stronger declines than larger ones (Homburg *et al.*, 2019).

Identifying the patterns of variation in insect population trends is difficult, though it is an additional challenge to understand the drivers. The threats to insects are primarily human-caused (Eggleton, 2020) and include land-use change, climate change, habitat loss and fragmentation, pollution, and invasive species (Cardoso *et al.*, 2020). Of these, land-use — particularly agricultural expansion and intensification — has been widely discussed (Newbold *et al.*, 2014; Newbold *et al.*, 2016a; Newbold *et al.*, 2016b; Newbold *et al.*, 2018). Land-use change is associated with an increase in monoculture, which although can be a pollinator resource, the crops are often characterised by short flowering periods inadequate for pollinators with longer flight seasons (Vanbergen and Initiative, 2013). Moreover, effects are known to vary geographically and taxonomically. Millard *et al.* (2021) found pollinator species richness in non-tropical areas to be significantly higher in minimal-intensity cropland than primary vegetation, in contrast to the decrease observed in tropical regions. Land-use is thought to affect butterflies in particular with Engelhardt *et al.* (2022) observing decreases in butterfly habitat specialists, but not grasshoppers nor dragonflies. This is potentially because butterflies possess a high quantity of specialised taxa, the existence of which are associated with high quality habitats.

Climate change is also predicted to substantially impact insects with tropical species being particularly vulnerable due to their warming tolerance being roughly a fifth of that of higher latitude insects (Deutsch *et al.*, 2008). Climate change also indirectly affects insects through alteration to floral resource (Soroye *et al.*, 2020) and mismatches between symbiotic plants and pollinators. There has been conflicting evidence on the link between climate change and insect declines. Lister and Garcia (2018) report sustained biomass declines across 10 major taxa in a Puerto Rican rainforest between 1976 and 2012, concluding the findings are a result of climate warming due to average ambient temperature being a significant predictor in their model. Willig *et al.* (2019) later repeated some of these analyses and did not find evidence of declines due to climate change. The authors argue Lister and Garcia (2018) failed to account for drought or hurricanes in addition to temperature related aspects of climate change, neither did they adjust abundance data according to sampling effort. Additionally, Loboda *et al.* (2018) and Van Klink *et al.* (2020) found that most climate predictors could not explain the trends they observed.

It could be possible that climate change has more of an effect when in combination with other threats. Using PREDICTS data (Hudson *et al.*, 2017), Outhwaite *et al.* (2022) found that an increase in temperature led to larger declines in high-intensity than low-intensity agriculture when compared to primary vegetation with no warming, indicating less intensive agriculture may partially counteract the negative impacts of climate change. Nevertheless, there is still more to be understood about the drivers of insect trends, with many studies concluding that future work should focus on untangling these (Hallmann *et al.*, 2017; Habel *et al.*, 2019; Wagner *et al.*, 2021a; Wagner *et al.*, 2021b).

In addition to conducting further work to understand the drivers, it is also of paramount importance to investigate how species traits affect extinction risk. Rare species are often reported as faring worse than common ones (Powney *et al.*, 2019; Outhwaite *et al.*, 2020) though if common species are also declining, this could have stronger impacts on ecosystem functioning (Cardoso *et al.*, 2020). Declines are also more frequently reported in species which are habitat or dietary specialists (Biesmeijer *et al.*, 2006; Boyes *et al.*, 2019; Wagner *et al.*, 2021a), small (Homburg *et al.*, 2019), poor dispersers (Cardoso *et al.*, 2020), univoltine (Biesmeijer *et al.*, 2006; Wepprich *et al.*, 2019), or those that have a shorter flight season (De Palma *et al.*, 2015). Nevertheless, traits that increase survival probability may be as important to identify as those which predispose species to decline (Boyes *et al.*, 2019).

To overcome these gaps in our understanding and untangle the complex variation and drivers of insect population trends, we must synthesise information across literature to reduce the chance that scientists, media, and policy-makers place too much bearing on individual studies. A necessary step in achieving this is through collation of evidence into a database, as done by EntoGEM (Haddaway *et al.*, 2020; Grames *et al.*, 2022). This mapping of relevant literature allows easy identification of the distribution of evidence and access to additional information including the research methods.

Once sufficient data exists to answer a proposed hypothesis, there are a number of approaches available to draw conclusions across studies. These include synthetic analyses which build models based on collated primary data. Synthetic analyses are common in papers utilising data in PREDICTS (Hudson *et al.*, 2017), a database designed to explore how biodiversity reacts to land-use change (Newbold *et al.*, 2014; Gray *et al.*, 2016).

Alternatively, meta-analysis can be used to quantitatively summarise results across multiple studies (often as part of a systematic review) in a replicable process to answer pre-defined questions (Arnqvist and Wooster, 1995; Gurevitch *et al.*, 2018). Effect sizes are calculated for each primary study, weighted according to study size, and fed into a statistical model to determine overall effect size and a confidence measure. It is possible for multiple effect sizes to be extracted for a single study, and the model design must therefore take into account their relatedness. The routinely used metafor R package (Viechtbauer, 2010) is available to facilitate the process.

Building upon these methods, the natural advancement is to ensure these reviews do not remain static. This is the concept of living reviews (Elliott *et al.*, 2017) where the analytical process is repeated and the results are updated as new evidence becomes available, allowing decisions to be based upon the best current evidence. The Metadataset website and its dynamic meta-analysis R Shiny app enables users to browse for relevant data — currently in the fields of invasive species and cover crops — and meta-analyse it (Shackelford *et al.*, 2021). The infrastructure already exists for this database to be a living review, so that when new meta-analyses are conducted, results are based on the best available evidence.

Furthermore, as increasing numbers of meta-analyses are completed, we are able to perform meta-meta-analyses, adding an additional layer of complexity to analysing, visualising, and interpreting, results. We defined meta-meta-analyses as the process of analysing multiple meta-analysis studies together by combining effect sizes collected for each of these. Here, I present a new Shiny app designed to run meta-meta-analytic models on the fly and produce graphical summaries of results. The app is designed with insect population trends as the focus, though it would be possible to repurpose it for other means.

The shiny app reads in data from a living review of meta-analysis studies, rather than primary studies as used within the dynamic meta-analysis app. Using this data, the user can run a custom model based on their hypotheses and interests. Estimations of change in insect biodiversity are outputted and are specific to the threats and biodiversity metrics — and in future other variables such as location and taxonomic group — the user has chosen to investigate. As new meta-analyses are conducted, users can upload these results so the figures can reactively update to these changes.

The creation of the app is motivated by the need to make best use of existing and future data to improve our understanding of the challenging field of insect population trends and thus increase the ability of scientists to convey messages to decision and policy makers, as well as the public on how insect declines can be mitigated.

Methods

*Shiny*

The Shiny R package (Chang *et al.*, 2017) allows development of interactive web-based applications coded in R without requiring knowledge of HTML, CSS, or JavaScript languages often used for websites. Minimally, a shiny app requires a user interface describing the layout and visuals, and a server defining how the app works. Shiny apps are designed to be interactive whilst taking advantage of the analytical and graphical capabilities of R. They link to and work well with databases, as well as being easy to distribute — the user simply needs the web address of the deployed Shiny app.

The Shiny app presented here was built using the shiny R package version 1.7.1 (Chang *et al.*, 2017) within R version 4.2.0 (R Core Team, 2013). The app uses the flatly theme from the bslib package (Sievert and Cheng, 2021) and is split into the following tabs: introduction, agricultural systems / modelling, uploading data, and references. The app is prototyped using data collected by Christina Raw for the purpose of conducting a meta-meta-analysis on the effect of agricultural systems on biodiversity. This means the data is not exclusively focused on insects, but also contains data on other animals, as well as plants, fungi, and bacteria. At this stage in development, we do not view this as an issue because once sufficient insect data is available, the app is easily adjustable. The data is remotely stored within googlesheets, from which it is read into the Shiny app using the googlesheets4 package (Bryan, 2021).

The app is available at <https://r26dnk-grace-skinner.shinyapps.io/meta_meta_analysis/>, and the code is available at <https://github.com/gls21/CMEE_NHM_Project/tree/master/christina_mma/meta_meta_analysis>.

*Introduction tab*

In this tab, the user can gain background information on the app, its functionality, and the origins of the data. A table is displayed showing details of each study used within the app including the number of agricultural systems studied and total number of data points. The user is able to choose a paper for which they wish to see more details, which creates a table displaying the breakdown of agricultural systems studied. These features allow the user to gauge the size of any analyses they may conduct, and can highlight any studies that may have a potentially influential effect. For example, the app uses 122 data points from the Morales.M paper while 2 from Manik.Y and Hussain.M. If the user wants to explore a paper in depth, they can go to the references tab which provides further details enabling the original paper to be found.

Utilising the maps package (Becker *et al.*, 2021), the user is also presented with a world map layered with points indicating where the data has been collected from if this information is available. This gives the user an indication of the geographical representativeness of the data.

*Agricultural systems / modelling tab*

The agricultural systems tab is split into default and custom model tabs, with the aim of enabling the user to model the effect of agricultural systems on biodiversity. The user can click a button to run the default model, which triggers the fitting of a robust linear mixed effects model on all available data using the rlmer function from the robustlmm package (Koller, 2016). This model was initially chosen by Christina Raw due to its ability to handle variation and outliers in data, thus enabling superior fitting compared with traditional linear mixed effects models fitted with the lme4 package (Bates *et al.*, 2015). Additionally, robust models are employed over metafor models (Viechtbauer, 2010) as the meta-analysis studies used by the app insufficiently reported the statistics — such as variance — necessary to implement the metafor package.

The model is designed to compare biodiversity of agricultural systems to the reference conventional agricultural system into terms of log response ratio. It is fitted using the formula: Log response ratio ~ Agricultural system + (1|Paper identification) + (1|Crop), with agricultural system a fixed effect and paper identification and crop random effects to account for the non-independence of the data. Response ratio is a popular effect size in ecology due to its ability to quantify proportionate change between treatments (Hedges *et al.*, 1999) and is more robust to non-independence than the standardised mean difference (Noble *et al.*, 2017). The logarithm is taken to linearise the metric (Hedges *et al.*, 1999; Nakagawa and Santos, 2012).

The results of the model are displayed as a figure in which agricultural systems are plotted against log response ratio. The log response ratio of each agricultural system compares each to the conventional reference level, which has a log response ratio adjusted to zero and is shown with a blue dashed line. Log response ratios for all other agricultural systems are adjusted correspondingly, resulting in a simple system to assess biodiversity by comparing the difference between the log response ratio of a particular agricultural system and the conventional agricultural system. Agricultural systems that have significantly different biodiversity are indicated by blue asterisks and are defined as those which have an absolute t-value greater than two due to p-values not being provided by the robustlmm package (Koller, 2016).

The app is designed so the user can choose which results to graphically investigate. The following options for input are available: checkbox choice of agricultural systems to compare to the conventional reference level, radio buttons for choice of metric to plot (either log response ratio or percentage change), and radio buttons for the choice of whether or not to re-scale the x axis as different agricultural systems are selected. As the user selects and de-selects different options, the dataset is reactively filtered using dplyr (Wickham *et al.*, 2019) and plotted using ggplot2 (Wickham *et al.*, 2019). Log response ratio is converted to percentage change using the formula Percentage change = 100 \* (exp(Log response ratio) - 1) [CITATION].

Alongside the figure, a table is produced displaying selected coefficients extracted from the model and the frequency of instances of each agricultural system that the model is based on. Additionally, the user can click a button to display descriptions of the agricultural systems, as well as download the R model summary, or table of coefficients.

The custom model tab is similar, but here the user has the option to run their own model based on their hypotheses. At present, the user can filter the data to be included in the model based on the biodiversity metric category used by the studies. Once they have made their selections, they press run. This is again fitted using a robust model with the same formula as for the default model. If there is an issue with model fitting, the user is presented with error messages. For example, if the data does not contain the reference conventional agricultural system, or the model does not successfully run, the user is prompted to select additional biodiversity metrics and re-run the model with this updated dataset. An equivalent graph and table as for the default model is produced. Similarly, the user can choose to plot adjusted log response ratio or percentage change, see definitions of the agricultural systems, and download their custom results.

*Uploading data tab*

When results from future meta-analyses are available, the upload data tab is available for this data to be uploaded. The user must input their first and second name (letters only) before uploading their file to the Shiny app. The file is put through some checks to ensure the file is a csv, that it contains columns containing data on log response ratio and agricultural systems, and that it is not a duplicate of a dataset already in the database. Upon passing these checks, the user is presented with a preview of their dataset, and can click a button to upload it to the googlesheets database. Therefore, the next time the app is loaded, the features within the app and the models run will incorporate this new data.

Results

The shiny app currently allows the user to interactively investigate data from 22 studies amounting to 676 data points, 229 of which specify Insecta as the class of organism studied.

*Introduction tab*

Graphical user interface, text, application

Description automatically generatedUpon opening the app using the web address <https://r26dnk-grace-skinner.shinyapps.io/meta_meta_analysis/>, the user is presented with information on the number of agricultural systems studied and total number of data points from each study. The majority of studies investigated two agricultural systems with the number of data points per study ranging from two to 122 (Figure 1). The user decides they want further information on a particular study and do this by selecting, for example, the Fitzherbert.E study. The app generates a table showing this paper studied conventional, disturbed forest, and primary vegetation agricultural systems and their respective numbers of data points. The user also views a world map to gauge the geographical representativeness of the data. The map suggests the data is from Europe and Asia, though the user takes into account that only 58 of the 676 data points have location data allowing them to be plotted.

**Figure 1.** Screenshot from the Shiny app introductory tab giving an overview of the studies utilised within the app.

*Agricultural systems / modelling tab*

Next, the user decides they want to understand how different agricultural systems impact biodiversity, thus they go to the agricultural systems tab. Here, they click “Run default model” to run a robust model on all available data. They are then presented with the results in graphical and tabular form to gain a general overview of the effect of the variable without needing to run their own model. The user concludes that sustainable agricultural systems have the largest positive effect on biodiversity compared to the conventional agricultural system with a log response ratio of 0.57 (t = 18.28). These figures are based on 205 conventional and 10 sustainable data points.

The user decides they only want to view the results for agricultural systems with more than 50 data points and so uses the user input section to de-select traditional, disturbed forest, primary vegetation, and sustainable agricultural systems. They can also decide to plot percentage change instead of adjusted log response ratio, and to re-scale the x axis as different agricultural systems are selected. In response to these selections, the user observes the figure and table update in real-time.

The user realises they do not fully understand what defines the agricultural systems and so they click “Click to see definitions of agricultural systems” to see descriptions. Finally, the user decides they want to store the results and so clicks “Download default model output” and “Download default model coefficients” to locally store the R model output and extracted model coefficients, respectively.

After studying the default model output, the user decides that they wish to run their own custom model based on their specific hypothesis. Hypothetically, the user does not want to include data points that use biomass as a metric for biodiversity because their research suggests this could mask biodiversity trends in species richness. They go to the custom model tab and select all biodiversity metric categories except biomass. They then click “Run custom model” and wait while the model runs. Once the figure and table are produced, the user notices there are substantial differences between the output of this custom and the default model (Figure 2). Conservation agricultural system still has significantly higher biodiversity than conventional in the custom model (t = 4.79), but the percentage change is only 4.08% compared to 36.34% in the default model (t = 21.45), though the user thinks this may be due to it being based on 29 conservation data points compared to 61 in the default model.

Furthermore, traditional agricultural is now not considered significantly different from conventional — biodiversity is actually reduced — whereas in the default model, traditional had significantly more biodiversity than conventional (t = 6.18). In this case, a comparable number of datapoints are used in the default (22) and custom (18) models. This difference owing to biodiversity metrics is important to consider if the researcher decided to conduct further study.

Graphical user interface

Description automatically generated**Graphical user interface

Description automatically generated**

**Figure 2.** Screenshots from the agricultural systems tab displaying the differences between the default model output which includes all available data, and a custom model which excludes data with biomass as their biodiversity metric category.

*Uploading data tab*

Following exploration with the Shiny app, the user decides to conduct their own meta-analysis investigating an interesting finding further. Once they complete their research, they decide they want to upload their data to the Shiny app so future models can be run including this data. To do so, the user goes to the ‘Upload data’ tab and inputs their first and second name. They then click “Browse” to select the file they want to upload. Upon checks being met to ensure the file is a csv, contains required data on log response ratio and agricultural systems, and is not a duplicate of a dataset already in the database, the Shiny app gives the user a preview of their data. The user now clicks “Upload to googlesheets” and observes a message once the data has been successfully added to the remote storage database. If the user wishes to run models including their data, they can refresh the app and run the models again.

Discussion

*Summary and implications*

The Shiny app represents a major contribution towards the improvement of our understanding of insect population trends, which research to date has strived to achieve, but failed to fully understand. We show how the app is designed to use data from a living review of meta-analyses on insect biodiversity, where new studies can be added and the app can update upon new data existing in the database. Using this data within the app, the user can interactively run their own custom models based on their hypotheses and visualise their results.

The app is useful for making decisions specific to the user’s interests. Insect population trends are complex, showing variability geographically, taxonomically, and temporally, which makes it unlikely that literature will exist for the specific combination of variables the user is interested in. However, the Shiny app can partially overcome this by giving the user access to a growing collection of data and the analytical tools needed to gain an indication of how insect populations act in, and are influenced by particular circumstances without the requirement of the user to code in R. This will aid decision-making processes and indicate potential findings that would be interesting to investigate further, perhaps in a new meta-analysis — the results of which could eventually be incorporated into the app.

We demonstrated how the default model results indicate overall differences in biodiversity between agricultural systems and conventional agriculture, typically considered to support low levels of biodiversity (Kremen and Miles, 2012; Tuck *et al.*, 2014). Therefore, the techniques used by systems which support significantly higher levels of biodiversity than conventional agriculture are those we should be considering when attempting to improve the sustainability of agriculture.

As for the custom model run by the hypothetical user, excluding data with biomass as their biodiversity metric substantially changed some of the results. Research has shown choice of biodiversity metric can impact conclusions (Hillebrand *et al.*, 2018), with observed declines in one metric not necessarily corresponding to equivalent declines in another. Declines in biomass and species richness — but not abundance — have been observed in forest arthropods (Seibold *et al.*, 2019) potentially explained by the loss of larger species leading to overall reductions in biomass and species richness, while some smaller species benefit from the reduction in competition to counteract the negative effect on abundance. Meanwhile Homburg *et al.* (2019) only found declines in species richness of carabids implying the loss of smaller, rarer species led to a significant effect on species richness, but not biomass nor abundance. Future studies should study insect in terms of multiple metrics to provide the best overview, though resource-limited studies may have to choose based upon study design — for example, if the research is around pollination services, then abundance of species rather than species richness may be more important for the continuation of this service (Loboda *et al.*, 2018).

*Comparison to existing tools*

Comparing the app presented here to previously created apps, the biggest similarities occur between the Shiny app and a tool called dynamic meta-analysis, created alongside the Metadataset website (Shackelford *et al.*, 2021). Dynamic meta-analysis allows the user to investigate different interventions. After choosing an intervention, the user can perform sub-group analyses in a similar manner to the Shiny app where custom results are based on a filtered subset of data. However, dynamic meta-analysis uses the rma.mv function from the metafor package (Viechtbauer, 2010), taking one or more effect sizes and corresponding variances calculated from each primary study as an input. Meanwhile, the Shiny app runs robust models from the robustlmm package (Koller, 2016) using multiple effect sizes collected from each primary study included in each meta-analysis study. The Shiny app is unable to use metafor due to the meta-analysis studies not reporting the necessary statistics (including variance) needed for metafor.

At this stage, dynamic meta-analysis provides the users with more filters and options on ways to analyse the data than the Shiny app. For example, it provides the option of meta-regression (also called mixed-effects models) where different subsets are analysed whilst accounting for effects of other variables, which is considered more powerful than sub-group analysis due to the model including all of the data.

Nevertheless, dynamic meta-analysis remains a work in progress with the example discussed in Shackelford *et al.* (2021) not replicable using the app in its current state. On the other hand, anyone is able to replicate the example outlined in the results section using the Shiny app. Additionally, the stand-out feature of the Shiny app is the ability of the user to upload their own data directly from within the app. This will allow the app to continue to grow and become increasingly useful in future without the need for someone to be responsible for identifying new data sources and adding them to the database.

*Expanding the functionality*

In its present state, the app has all the necessary framework to prove the value and richness that these kind of tools can provide. Nevertheless, there are a number of things that could be adjusted or added to further increase its usefulness. The app is limited by the quantity and quality of available data, though the issue of quantity will decrease as more studies are added. Deficiencies in the quality — particularly the reporting of statistics necessary to complete meta-analyses with metafor — have been highlighted (Hedges *et al.*, 1999; Stewart, 2010; Gurevitch *et al.*, 2018). However, the robust model approach taken by the Shiny app is less susceptible to this due to it not depending on the reporting of certain statistics that are necessary for metafor.

The custom model that can be run by the user is currently based upon a choice of biodiversity metric category. We plan to expand the range of variables over which a user has choice, which is feasible assuming sufficient data is available. At present, filtering by multiple variables would likely result in limited data quantity, reducing the chance of a model successfully running. Ultimately, including a choice of location of where the data was collected or the taxonomic group studied would be ideal for investigating geographic and taxonomic variation in results, respectively. This proves especially difficult with the current dataset due to the majority of data points not including location or taxonomic data, as well as inconsistent location descriptions; some studies report multiple continents, others individual countries. It also means the map included in the introductory tab undersells the geographic representativeness of the app.

We also intend to expand the app in terms of the different threats that can be investigated. Instead of investigating the effect of agricultural systems on biodiversity, the user will have the choice to investigate the influence of other variables such as land-use or temperature, increasing the usefulness of the app.

In future, the app could provide multiple approaches to analysing data. Firstly, it can continue to analyse the effect sizes from each primary study within each meta-analysis using robust models. Secondly, it could be an option to combine the overall effect sizes calculated for each meta-analysis (one effect size per meta-analysis) using metafor. This would be dependent on sufficient reporting of variance statistics alongside effect sizes, and it would only be feasible for meta-analyses that investigated the same intervention to be analysed together.

*Scaling up*

For maximum potential to be achieved, the app relies upon future meta-analyses following a standardised protocol and data entry sheet. With these in place, the data collected from different studies becomes more comparable and requires less data re-structuring before incorporation into the app. A protocol for the use of the app will also need to be assembled to avoid the issues of cherry picking, where users run multiple models but only report findings which support their hypotheses and ignore those that do not.

Methods will need to be implemented to allow efficient functionality for when multiple users are using the app and as the database expands. Part of this will require a move away from using googlesheets as the database — more accurately defined as a spreadsheet program — and instead use a relational database, which has greater capacity, better security, and faster speed especially when multiple users are accessing the database. As more data is added, robust models will take substantially longer to run, though it also becomes increasingly less necessary to run a robust model. Therefore, the user would benefit if the app was coded to run a standard linear mixed-effects model when the amount of data exceeds a threshold.

Although the app was designed to investigate insect population trends, it has huge potential for applicability in other fields, especially where the data shows high heterogeneity. The design of the app lends itself to be easily adaptable to analyse another database. The Shiny app is a tool which allows researchers to take full advantage of the data we have, as evidenced here with insect population trends, and will aid scientists in disentangling complex patterns and drivers of trends, especially as more data becomes available.

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