Original software publication

Dynameta: A dynamic platform for ecological meta-analyses in R Shiny

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ABSTRACT

Meta-analyses have brought a significant improvement in our understanding of global biodiversity change. However, in ecology the static nature of current approaches, both in terms of the data included and the predictions presented, make meta-analyses difficult for policymakers to fully interrogate and adopt. Here we introduce Dynameta, a living-review (i.e. continually updateable) R Shiny platform for interactive ecological meta-analyses, oriented around testing the effect of anthropogenic threats on biodiversity. This platform is written as an R package and can be applied in the context of any meta-analytic PICO (Population, Intervention, Comparator, and Outcome) question concerning the effect of any threat on any taxonomic group, for any biodiversity metric and with relevance to all geographic regions. Our hope is that, alongside other existing tools, Dynameta can help encourage the broader adoption of dynamic meta-analyses in ecology.

Code metadata

Current code version	*v0.2.0*
Permanent link to code/repository used for this code version	https://github.com/ElsevierSoftwareX/SOFTX-D-23-00129
Permanent link to reproducible capsule	*NA*
Legal code license	*MIT License*
Code versioning system used	*Git*
Software code languages, tools and services used	*R*
Compilation requirements, operating environments and dependencies	*R (>=2.10), bslib, dplyr, DT, leaflet, mapview, metafor, shiny, shinycssloaders, shinydisconnect, shinyjs, shinyWidgets, tidyr (these packages are installed by default upon installing Dynameta). For compiling documentation, and testing: knitr, rmarkdown, shinytest2, testthat (>=3.0.0), tibble.*
If available, link to developer documentation/manual	https://github.com/gls21/Dynameta
Support email for questions	GraSki@ceh.ac.uk

1. Motivation and significance

Ecological meta-analyses have brought a significant improvement in our understanding of global biodiversity change [1,2]. Indeed, meta-analyses carried out within systematic reviews—the wider approach to selecting and synthesising primary studies to investigate a well-defined research question—allow researchers to summarise evidence transparently, while accounting for variation or uncertainty associated with individual evidence sources [3]. These characteristics make meta-analyses highly relevant to policymakers, providing evidence that can be used to inform management decisions, especially compared to alternative approaches which are more subject to author bias and interpretation such as narrative review or vote count synthesis [3–5].

Although meta-analyses in ecology have represented a major step forward, a set of obstacles still hinder their usefulness to evidence synthesists and the environmental decision makers who may be informed by meta-analytical results. First, meta-analyses are typically performed for a given snapshot of the literature at a particular time, i.e. they are static and very infrequently updated.

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After publication, meta-analyses become a fixed representation of that phenomenon at that time and do not change with the publication of contradictory or additional evidence. Second, although the data collected for an ecological meta-analysis typically includes multiple variables (e.g. biodiversity metric, geographic region), the logistics of paper publication (e.g. a limited word count), combined with pragmatic decisions by authors on the paper focus, often mean that only a sub-set of hypotheses are tested. A focus on selected results or hypotheses does not allow users to test how predictions would have changed had the original author made a different set of assumptions. For example, a meta-analysis testing the effect of pesticide application on global insect biodiversity might combine all geographic regions together, not considering how individual geographic regions differ in their response. Such an approach is sufficient to address the hypothesis of that researcher, but it may not be valuable to evidence synthesists advising policymakers who are trying to make informed decisions in their region of interest. Without flexibility evidence synthesists are unable to disaggregate overarching results of meta-analyses.

Concepts of living reviews (the continual updating of synthetic results as new data are collected) [6] and dynamic meta-analyses (user-manipulation of a graphical user interface, for more in-depth exploration of meta-analytic data) [7] both strive towards increasing the usefulness of meta-analyses for policymakers. The medical field demonstrates the potential benefits of living reviews, with a particular focus on the Covid-19 pandemic in recent years [8–10]. In the context of ecology, the authors of Metadataset created a platform that could be updated with new data and used to perform dynamic meta-analysis in real-time [7], however, Metadataset does not yet provide a generalised framework from which others can build their own dynamic meta-analytic platforms. Ideally evidence synthesists need tools that can be easily repurposed and adapted to address a variety of PICO (Problem, Intervention, Comparison, Outcome) questions in ecology. The authors of Metadataset raise this as a priority for the development of future software for research [7].

Here we introduce Dynameta, a living-review platform for dynamic ecological meta-analyses in R Shiny [11]. Dynameta is oriented around testing the effect of anthropogenic threats on biodiversity. Currently, Dynameta is generalised such that it can be applied in the context of any meta-analytic PICO question concerning the effect of any threat (specifically IUCN threats in our case) on any taxonomic group, for any biodiversity metric and geographic region. Researchers can upload meta-analytic data in a standardised format, which can then be run through a metafor model [12] in real-time. This allows rapid and reactive reinterpretation of data. As new meta-analytic data is collected, users can upload this to the platform indefinitely, with figures reactively updating according to these changes (although note that Dynameta does not currently perform model fit checks). We also include sample meta-analytic data testing the effect of pesticide application on dragonfly and damselfly (Odonata) biodiversity, to provide a template for data accepted by the Shiny app and demonstrate the functionality of this application. Moreover, we have built this Shiny app into a single R package, such that researchers can quickly load their own version of the platform locally and adapt it for their own purposes. Adaptability is a core principle that we designed Dynameta around and we actively encourage others to edit or add to the existing codebase to suit specific needs (e.g. by forking the GitHub repository).

Importantly, users of Dynameta should note that it does not dispense of the need to follow established best practice guidelines including rigorous original data collection following a preregistered protocol. Extensive resources are available for conducting and reporting systematic reviews [13–18] to improve their validity, reliability, and repeatability.

2. Software description

2.1. Software architecture

To improve upon static ecological meta-analyses, we have developed Dynameta, an R Shiny platform wrapped up as an R package. Dynameta enables meta-analytic results to be continually updated as new evidence becomes available. Additionally, through user manipulation of the graphical user interface, Dynameta permits investigation of a range of questions based on the interest of the researcher. Dynameta was originally developed for assessing the effect of anthropogenic threats on biodiversity. However, the open-source packaged code is adaptable to suit more specific needs and is currently being used as an underlying analytical framework for the GLiTRS (GLobal Insect Threat-Response Synthesis) project (https://glitrs.ceh.ac.uk/), which is assessing anthropogenic threats to insect biodiversity.

2.2. Software functionalities

The main function in the Dynameta package is *launch_Dynameta()*, which allows researchers to run their own local version of the Shiny platform. *launch_Dynameta()* does not require the specification of any arguments. Upon launching Dynameta, the researcher can choose to analyse the sample data (a pre-collected set of effect sizes for the effect of pesticide application on odonates), or their own meta-analytic data. If the researcher chooses to upload their own data, checks are run to ensure that the data contains required fields such that it will be compatible with the downstream code run by the app. Table S1 in the supplementary material outlines the format of the sample data as an example of data that can be analysed with Dynameta as currently built.

To investigate the effect of anthropogenic threats to biodiversity, the researcher can run meta-analytic models to quantitatively summarise results across studies in a replicable process [3, 19]. Based on their question, the researcher can filter their data by IUCN threat category, geographic region, taxonomic group, and biodiversity metric. This framework allows many possibilities for reanalysis and reinterpretation, while at the same time supporting transparent analysis that can be easily verified or re-queried.

Dynameta calculates effect sizes and corresponding variances from primary measurements using the *escalc()* function in the metafor package [12]. The effect size used to compare biodiversity is the log response ratio (LRR, also known as the log transformed ratio of means [ROM]), a popular effect size in ecological meta-analyses due to its ability to quantify proportionate change between treatments [20] and its robustness to non-independence [21], although alternative effect sizes may preferable in other situations [22].

Dynameta then runs a meta-analytic multilevel model, fitted as follows using the *rma.mv()* function from metafor [12]

```
metafor :: rma.mv(yi, vi, random =∼ 1|Paper_ID/Observation_ID)
```

to estimate an overall effect size and an associated confidence measure. The model accounts for the non-independence of the data by specifying Paper_ID and Observation_ID as nested random effects.

With the outputted model object, the app runs the *forest()* function from metafor [12] to present a forest plot of the results. Also displayed is a summary results sentence including the overall effect size expressed as a percentage change, which can be more intuitively understood. The overall log response ratio is converted into percentage change using the formula [23]

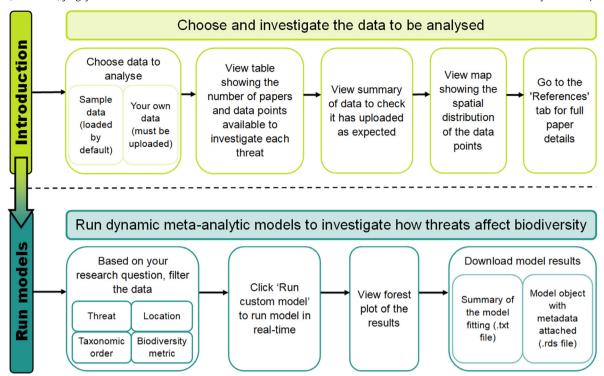$$Percentage\ change = 100 * \left(e^{LRR} - 1\right)$$

Fig. 1. A schematic of a typical workflow in Dynameta. Steps in green refer to any that relate to the Introduction tab, and in blue to performing a dynamic meta-analysis.

where e^{LRR} is the exponent of the log response ratio. Dynameta also presents the user with the I^2 statistic to indicate the percentage of variance due to heterogeneity, and not due to chance, an important aspect of meta-analyses, especially in ecology [24].

Options are available to download the results of a dynamic meta-analysis including a .txt file containing the model summary and a .png file of the forest plot. The researcher can also download an .rds file containing the model object. This has additional attributes (i.e. metadata) which specify the date and time the model was run, the filters that were applied to the data prior to running the model, and the R session information. This .rds file can subsequently be loaded into R, allowing the same analysis to be repeated as more data becomes available.

Dynameta was built using the shiny R package version 1.7.4 [11] in R version 4.2.2 [25].

3. Illustrative examples

Any meta-analysis must be underpinned by a robust evidence gathering framework, which must be completed before proceeding with Dynameta. This includes writing and registering a protocol outlining clearly defined research questions and evidence inclusion criteria [26], carefully considering the suitability of evidence based on these criteria, and determining who will be responsible for updating the meta-analysis with Dynameta, and for how long (as to avoid research waste). Please refer to the reporting standards outlined by PRISMA [14,15] and ROSES [16], in addition to the Collaboration for Environmental Evidence (CEE) [13], Cochrane [17], and Campbell [18] guides for conducting evidence syntheses. Note that ROSES [16] and CEE [13] have been developed specifically for environmental research.

After the evidence gathering stage, Dynameta can be used to facilitate dynamic meta-analyses and living review. If you encounter any issues while using Dynameta, please submit a new issue on the issue tracker on GitHub (https://github.com/gls21/Dynameta/issues) with a detailed description of the problem, including steps to reproduce it.

Installing the Dynameta package requires the devtools package, which can be installed and loaded by running the following code in the R console:

```
install.packages("devtools")
library(devtools)
```

Next, install and load the Dynameta package by running the following code:

```
devtools::install_github("gls21/Dynameta",
build_vignettes = TRUE)
library(Dynameta)
```

All dependencies required by Dynameta will be automatically installed. Please see the README on GitHub for more detailed installation instructions (https://github.com/gls21/Dynameta/tree/main#installing-and-using-the-dynameta-package).

Launch the Dynameta Shiny platform by running the following function:

```
launch_Dynameta()
```

Next, we will run through the process of using the app (Fig. 1) with the sample data provided in the package, which consists of data collected to test the effect of pollution (specifically pesticide application) on dragonfly and damselfly (Odonata) biodiversity. The sample data can be viewed by running:

```
sample_data
```

Once Dynameta has launched, the 'Introduction' tab provides a breakdown of the data to be analysed. By default, this is the sample data until it is updated with new data uploaded by the user. In this sample data, 'Pollution' is the sole threat category considered, for which there are 10 papers contributing a combined 47 data points. The data are also represented on a world map built using the R package Leaflet [27] to visualise the geographic distribution of the data. For instance, for the sample data 24 out of the 47 data points originated in Japan (Fig. 2).

To analyse the sample data, we navigate to the 'Run models' tab where we are provided with options to filter the data (Fig. 3). The sample data consists of data collected for investigating the effect of pollution on Odonata, for records of abundance only. Hence, here we do not have a choice for threat, taxonomic order,

Fig. 2. The spatial distribution of data points across the globe, visualised using the R package Leaflet, which allows interactive viewing of the sample sites. This set of sample data are from a meta-analysis carried out on the effect of pesticide application on Odonata biodiversity. Each circled number in leaflet refers to the number of sites present in that geographic region (greenpoints, 1-10; yellow points, 10-100).

Fig. 3. A screenshot of part of the 'Run models' tab in Dynameta, which allows the user to filter the data before running a meta-analytic model. The user can filter the data based on IUCN threat category, location, taxonomic order, and biodiversity metric used to collect the data.

or biodiversity metric. Nevertheless, we are able filter these data based on location. To run a meta-analytic model on all 47 data points, we 'Select All' locations and click 'Run custom model'. The results indicate that pollution has an overall −65% [−82%, −30%] effect on Odonata abundance for our sampled regions of the globe. Suppose then that we want to investigate the effect of pollution in Japan alone. We could then filter the data by selecting 'Japan' as our location of interest, before re-running the meta-analysis. Now we find an overall −46% [−91%, +210%] effect of pollution on Odonata abundance (Fig. 4).

Although running a meta-analytic model on a subset of data may be informative, we may instead want to perform a full sub-group analysis [28]. To do this, we would need to adapt the current codebase. Please see the Dynameta vignette which includes example code on how to do this (https://gls21.github.io/Dynameta/articles/Dynameta.html#editing-the-codebase).
Sub-group analysis is just one example of extending the capabilities of Dynameta; we encourage others to explore and edit the codebase to meet their requirements.

4. Impact

Interactive meta-analysis and living-reviews have been described as important developments in the field of ecology, and more broadly in research. Here, we introduce Dynameta, a new R Shiny app for performing dynamic meta-analyses in ecology. Dynameta is built around testing the effect of threats on biodiversity, using the existing R package metafor [12]. Our intention was to wrap this app into a package such that it can be used in

the context of any meta-analytic PICO question concerning the effect of any threat on any taxonomic group, biodiversity metric, or geographic region. In doing so, Dynameta provides a workflow that can be easily repurposed in a variety of meta-analytic contexts, helping to achieve greater generality in ecological syntheses [29]. We also believe that the standardised format and user interface could make Dynameta a potentially valuable teaching resource for meta-analyses. Here we describe the potential impact of Dynameta, as well as notable limitations and areas of improvement.

As far as we know, Dynameta is a unique tool in the space of ecological synthesis, though tools with similar aims around living reviews and dynamic meta-analyses exist in other fields such as cancer treatment [30]. Metadataset is the only other interactive platform built in R for the purpose of dynamic meta-analysis in ecology [7]. However, Dynameta differs from Metadataset in a few key ways. First, Dynameta is built with a primary aim of enabling living reviews. Although the authors of Metadataset discuss that their Shiny app links to an online database for the facilitation of living reviews, as far as we know the authors have not yet provided a framework to easily enable this. Second, Dynameta is built into a publicly available R package, such that it can be run locally with little work required of users. Third, Dynameta is more generalised, making it applicable in multiple contexts. Our reasoning again here was to develop something that could be easily repurposed. Dynameta also has some similarity to EviAtlas [31], but differs in that it focusses specifically on dynamic meta-analysis as opposed to systematic mapping.
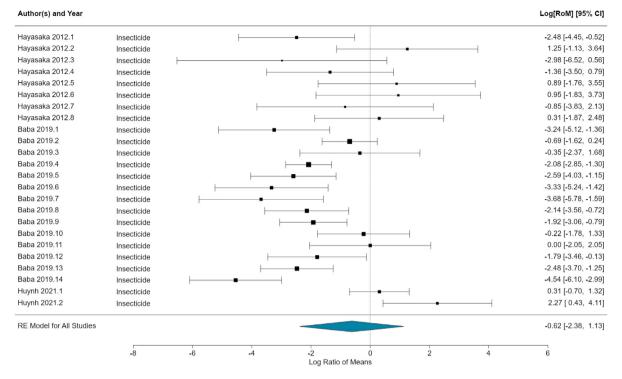
Fig. 4. An example forest plot generated by Dynameta showing the effect of pollution on Odonata in Japan. Effect sizes for each data point are indicated by the black squares, while the diamond indicates the estimated overall effect size—the placement of the centre of the diamond on the *x*-axis represents the point estimate, and the width of the diamond represents a 95% confidence interval. Dynameta dynamically generates a figure legend according to the specific parameters selected by the user.

There are many examples where key policy decisions have been undermined by an absence of up-to-date meta-analyses, which potentially could have been avoided through publication of data to a living review platform built using the Dynameta framework. Potential examples relate to pesticide regulatory decisions on products that are reaching the end of existing regulatory approval, and exceptions on the use of restricted products such as banned neonicotinoid seed treatments in Europe on crops like sugar beet [32]. Without the capacity to reanalyse new research, the evidence base remains opinion driven and lacks a robust meta-analytical framework.

Dynameta also has limitations. There is a risk with tools such as Dynameta that they encourage meta-analyses that do not follow the relevant guidance on how they are conducted [13, 17] and reported [15,16], which is a long-standing issue in this field [33,34]. While Dynameta provides a platform to facilitate dynamic meta-analyses, it does not remove the need for writing and registering a protocol that clearly sets out the original question and inclusion criteria [26] and carefully documenting the search process.

Dynameta also does not remove the need for critical thinking and interpretation of the results for a couple of reasons. First, caution must be taken when using Dynameta due to repeated testing increasing the chance of finding a statistically significant result when there is no real difference (type II error). Thus, p-values should not be relied upon [35]. Second, users should be aware that the combination of high heterogeneity common in ecological studies [24], and reduced sample size resulting from analysis of subsetted data in Dynameta decreases statistical power. It is best practice to carry out power analysis before conducting a meta-analysis to determine an appropriate sample size required to detect an effect when using Dynameta [28,36].

Lastly, in building a dynamic platform there is tension between the extent to which it is generalised, and its usefulness in a given context. In other words, the usefulness of a platform in a given context is inversely proportional to its flexibility. Our compromise with Dynameta has been to build a platform that is as flexible as possible within a broad set of PICO questions. We have also intentionally designed our workflow such that the framework can be easily repurposed (see https://gls21.github.io/Dynameta/articles/Dynameta.html#editing-the-codebase).

5. Conclusions

Here we introduced Dynameta, a generalised R Shiny app for performing living dynamic ecological meta-analyses. This Shiny app has been built into an R package, with an example underlying dataset to act as a reference, for users to load up their own session with little work required. Dynameta will now form the backbone of an interactive platform for the GLiTRS project, with the adapted version hosted at UKCEH (UK Centre for Ecology & Hydrology). This newer version of Dynameta will branch away from the original codebase, which we envisage will be the case for others who adapt for their own specific use case. More broadly, our hope is that Dynameta can facilitate broader adoption of dynamic living review meta-analyses in ecology, alongside other existing and future tools.

CRediT authorship contribution statement

Grace Skinner: Software, Writing – original draft. **Rob Cooke:** Data curation, Software, Writing – review & editing. **Junghyuk Keum:** Data curation, Software. **Andy Purvis:** Conceptualization, Supervision. **Cristina Raw:** Data curation, Software. **Ben A. Woodcock:** Writing – review & editing. **Joseph Millard:** Conceptualization, Supervision, Writing – review & editing.

Declaration of competing interest

The authors declare the following financial interests/personal relationships which may be considered as potential competing

Data availability

The code and data can be found at https://zenodo.org/record/7930601.

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Appendix A. Supplementary data

Supplementary material related to this article can be found online at https://doi.org/10.1016/j.softx.2023.101439.

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