Methods v2 plan

**Building the platform**

* Why Shiny? Why not another tool?
* Introduce Shiny
* Deployed using shinyapps.io (why?). App and code available at…
* Basic structure of the app
  + Different tabs
  + Data from googlesheets - why?

**Models**

* Which model? Why?
* Formula used in model – fixed and random effects
* Why log response ratio?

**Intentions**

1. Transparency of inputs – where data has come from. Tables in intro tab
2. Interactivity
   1. Modelling on the fly.
   2. Uploading data
3. Reactivity
   1. To new data
   2. To choices made by the user. Test by assessing how much results change among selected variables.
4. Efficiency
   1. Test by assessing how long it takes to run models, and upload data

Intro to methods section explaining the structure of your methods to help the reader navigate.

**Developing an interactive platform for insect biodiversity change**

Structure each point as a paragraph, initially setting out that point, why it's important, and then talking about how the way you built your app relates to that point.

1. Interactivity
   1. Introduce Shiny; Why Shiny? Why not another tool? Deployed using shinyapps.io (why?)
   2. Modelling on the fly.
   3. Uploading data
2. Reactivity
   1. To new data -  Googlesheets
   2. To choices made by the user. Test by assessing how much results change among selected variables.
3. Transparency of inputs – where data has come from. Tables in intro tab
4. Efficiency
   1. Test by assessing how long it takes to run models, and upload data

**Leveraged meta-analytic models of insect biodiversity change**

* Which model? Why?
* Formula used in model – fixed and random effects
* Why log response ratio?

Where put? - 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).

Methods – sort out equations

1. Intro paragraph explaining the structure of the methods to help the reader navigate

*Developing an interactive platform for insect biodiversity change*

Interactivity

1. Set out point, why interactivity is important
2. Introduce Shiny in the context of interactivity

* Why Shiny?
* Why not another tool?
* Use Shiny if you already use R for your analytics and you want to make the results more accessible to non-technical teams. statistical computing and data visualization. Creating graphics and data visualizations and Building statistical models. Data wrangling, models used within app all coded in R.

The Shiny R package (Chang *et al.*, 2017) allows the development of interactive web-based applications in R without the use of HTML, CSS, or JavaScript, which are often used for developing 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.

1. Modelling on the fly

Run custom model based on user choice of biodiversity metric(s).

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.

1. Uploading data

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. The next time the app is loaded, the app and the models run within it will incorporate this new data.

Reactivity

1. Set out point, why reactivity is important

Linking closely, if a platform is interactive, then it must also be reactive.

1. Reactivity to new data – googlesheets

The data is remotely stored within googlesheets, from which it is read into the Shiny app using the googlesheets4 package (Bryan, 2021). Why googlesheets?

1. To choices made by the user – the outputs are reactive to what the user has chosen to model, and what they choose to see in the outputs. Test by assessing how much results change among selected variables.

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].

Transparency – of inputs, and outputs

1. Set out point, why transparency is important
2. Inputs - Where data has come from. Tables in intro 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 data points for the set of studies for which we have geographic coordinates. This gives the user an indication of the geographical representativeness of the data.

1. Outputs –

View definitions of systems, and download results – see exact R output.

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.

Warnings: 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.

Efficiency

1. Set out point, why efficiency is important
2. Test by assessing how long it takes to run models, and upload data

*Leveraged meta-analytic models of insect biodiversity change*

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. 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, I do not view this as an issue because once sufficient insect data is available, the app is easily adjustable.

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).

Which model? Why?

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 chosen 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-analytic studies in the data underpinning the app insufficiently reported statistics such as variance, which are necessary for metafor.

Is it also relevant that Christina's data is composed of the overall effects of separate meta-analyses, rather than lots of individual studies within one meta-analysis?

Formula used in model – fixed and random effects

The model is designed to compare biodiversity of agricultural systems to the reference conventional agricultural system in terms of the 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, accounting for the non-independence of the data.

Why log response ratio?

The 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).

Where put? - 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).

Where put? - Deployed using shinyapps.io (why?). 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>.