**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 studies used within the app including the number of agricultural systems studied and total number of instances investigated. 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. 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.