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

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**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.