Introduction

Insects constitute the world’s most species rich 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 chain 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.*, 2021). 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 given their inconspicuous nature and high annual variation (Fox *et al.*, 2019). The imbalance has been somewhat rectified recently with a ten-fold increase in the number of insect decline papers between 2000 and 2010 (Eggleton, 2020), though the disparity between the one million insects described and the 5.5 million thought to exist (Stork, 2018) means studies continue to suffer from a lack of knowledge. 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.

Although more long-term data is needed, current consensus is that insect decline is sufficient to warrant 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, some insect populations are stable or increasing (Boyes *et al.*, 2019; Wagner *et al.*, 2021) such as the 5.5% increase in UK terrestrial insect occupancy (1970-2015) reported by Outhwaite *et al.* (2020). Crossley *et al.* (2020) also found no overall trend in US insect abundance or diversity, though this study has been criticised for using datasets with inconsistent sampling methodologies (Welti *et al.*, 2021).

A variety of reasons contribute to the contrasting results, one being geographical variation, which can be apparent even within countries. Trends in carabids markedly differed across the UK from 50% declines in northern moorlands to 50% increases in southern downlands (Brooks *et al.*, 2012). On a global scale, most research to date has been restricted to human-dominated landscapes in Europe and North America. Recognising this, researchers have begun to search for biodiversity change elsewhere including the tropics (Lister and Garcia, 2018; Wagner *et al.*, 2021) 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. Among taxa, Biesmeijer *et al.* (2006) found that bee richness decreased in 52% of British cells, while no significant changes were observed for hoverflies. Additionally, the choice of biodiversity metric may impact conclusions. It is 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). Likewise, using only biomass or abundance, as done by Van Klink *et al.* (2020), can result in researchers overlooking species richness changes or the replacement of sensitive species with tolerant ones (Jähnig *et al.*, 2021). Overall, this variation indicates that caution must be taken when generalising results especially as temporal, taxonomic, or geographical distance increases.

It is an additional challenge to understand the drivers of insect biodiversity change. The threats 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.*, 2016; Newbold *et al.*, 2018; Seibold *et al.*, 2019; Gillespie *et al.*, 2022). Natural habitats in the vicinity of agricultural land may also experience inflated rates of insect decline due to reduced dispersal ability in a fragmented habitat or increased pesticide exposure (Seibold et al., 2019). Moreover, effects of land-use 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. Among insect orders, Engelhardt *et al.* (2022) observed decreases in butterfly, but not grasshopper nor dragonfly habitat specialists. This is potentially because butterflies possess a higher quantity of specialised taxa, the existence of which are associated with high quality habitats (Poniatowski *et al.*, 2018).

To untangle the trends and drivers, we must synthesise information across the literature to provide scientists, media, and policy-makers with the best available evidence obtained through the aggregation of multiple studies. A necessary step in achieving this is collecting studies, 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 information on study methodology.

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 in which models are built based on collated primary data. Synthetic analyses are common in papers utilising PREDICTS (Hudson *et al.*, 2017), a database designed to explore how biodiversity responds to land-use (Newbold *et al.*, 2014; Gray *et al.*, 2016). Alternatively, meta-analyses can be used to quantitatively summarise results across multiple studies in a replicable process, answering 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 then fed into a statistical model to determine an overall effect size and an associated confidence measure.

Building upon drawing conclusions across studies, the natural advancement is to ensure reviews do not remain static. This is the concept of a living review (Elliott *et al.*, 2017), in which results are updated as new evidence becomes available, allowing decisions to be based upon the current body of evidence. This is done by the Metadataset website and its dynamic meta-analysis R Shiny app, which enables users to browse a living database for relevant data—currently in the fields of invasive species and cover crops—and then perform a meta-analysis on that subset (Shackelford *et al.*, 2021).

As increasing numbers of meta-analyses are completed, we are able to perform meta-meta-analyses, enabling further increases in the accuracy of estimations (due to larger sample size) and increased chance of detecting variables that significantly influence effect size. As I define it here, meta-meta-analyses is the process of analysing multiple meta-analytic studies together by combining effect sizes for each of these.

Here, I present a new interactive platform for running meta-meta-analytic models of insect biodiversity change, built using R Shiny. The app is designed around insect biodiversity meta-analyses, though it would be possible to repurpose it for other means. The Shiny app reads in data from a living review of meta-analyses stored within Google Sheets. Using this data, the user can run a custom model on the fly based on their hypotheses of insect biodiversity change. Estimations of change 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, with the figures then reactively updating to these changes.

The creation of the app is motivated by the need to make best use of existing and future data, helping to improve our understanding of the challenging field of insect biodiversity change. To achieve this, I aimed to build an app that is interactive, reactive, and efficient. The purpose of the app aligns well to and is planned to contribute towards the GLobal Insect Threat-Response Synthesis (GLiTRS) project, which aims to synthesise many lines of evidence of insect biodiversity trends. My hope is that this app can assist scientists in conveying insect biodiversity change to decision makers, as well as the public on how insect declines can be mitigated.