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A Multithreat Meta-Analytic Database for Understanding Insect Biodiversity Change

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ABSTRACT

Aim: Widespread declines in insect biodiversity have been attributed to a diverse set of anthropogenic drivers, but the relative importance of these drivers remains unclear. A key reason for this uncertainty is that their effects depend on many factors, such as taxonomy, geography, sampling method and the biodiversity metric considered. To better understand the relative impact of different drivers on insect biodiversity, effect sizes need to be anchored to major sources of heterogeneity and collected reproducibly through a structured and consistent protocol. This standardised approach will allow a quantitative synthesis of relative threats to insects, enabling more robust predictions of changes in insect biodiversity.

Innovation: Here we publish a global database of effect sizes that quantify the effect of 5 anthropogenic drivers on insect abundance, species richness, biomass and fecundity within the framework of the IUCN threat classification. While we only present results for a subset of major anthropogenic drivers and insect Orders, the database structure allows the addition of new studies for all major IUCN threats and insect Orders. Our current set of effect sizes was collated from 7 meta-analyses, including 6308 effect sizes from 317 studies, focusing on threats ranked highly in an initial expert elicitation process. Data collection followed an overall meta-protocol and a set of individual protocols tailored to each meta-analysis. Our database provides a framework for the first global meta-analytic overview of the response of insects to a range of major anthropogenic drivers.

Main Conclusions: Structured collation of both experimental and quasi-experimental effect sizes, together with metadata that capture the main sources of heterogeneity, is needed to understand the effect of anthropogenic activity on insects. In turn, this understanding opens the way to predicting how we might expect insect biodiversity to have changed in the past and into the future.

1 | Introduction

Many recent studies have tackled the subject of global insect biodiversity loss (Wagner et al. 2021). Most have used time series from Europe (Hallmann et al. 2017) or North America (Wepprich et al. 2019), although insect declines have also been reported from understudied areas such as the tropics (Lister and Garcia 2018) and the Arctic (Gillespie et al. 2020). Many anthropogenic drivers are implicated in insect declines, including land-use change (Seibold et al. 2019), climate change (Outhwaite et al. 2022) and invasive species (IPBES 2019). These often interacting drivers threaten insect abundance, biomass and species richness (including their unique traits), as well as insect communities that underpin services such as pollination, pest control and nutrient cycling (Eggleton 2020; Wagner et al. 2021).

Understanding which drivers are most important is an important step towards effective mitigation (Jaureguiberry et al. 2022). Understanding drivers is difficult, however, because reported effects of anthropogenic drivers on insects vary widely among studies (Wagner et al. 2021), for multiple reasons. Taxonomically, the relative importance of threats will differ among major insect groups. For example, in Germany, anthropogenic land use has caused consistent declines in occupancy of butterflies, but not of grasshoppers or dragonflies (Engelhardt et al. 2022). Geographically, the distribution of anthropogenic threats varies markedly (Bowler et al. 2020), such that even for a single species, abundance trends are likely to vary across space. Variation in threat intensity makes it hard to generalise from trends seen in currently compiled time-series data, given that time-series data overwhelmingly come from North America and Western Europe (van Klink et al. 2020). Both North America and Europe are human-dominated regions with relatively little recent land-use change and relatively strong environmental protections. While there is a clear need for syntheses of insect biodiversity change to be more transparent about the constraints within which their conclusions have been drawn (Spake et al. 2022), accounting for underlying patterns of heterogeneity is also essential, so taxon- or region-specific conclusions can inform policy or conservation measures (Carpenter 2020).

Meta-analyses—the systematic gathering and synthesis of effect sizes that quantify differences between treatment and control groups (Gurevitch et al. 2018)—are an effective approach for estimating how insect biodiversity responds to anthropogenic threats. Meta-analyses fit a statistical model to effect sizes originally gathered from multiple primary studies to estimate an overall effect and an associated confidence measure. While there are limitations to this approach that need to be carefully considered, including how generalisable or transferable individual effect sizes are to specific questions of interest (Spake et al. 2022), meta-analyses are more rigorous than methods such as vote counting, which simply counts positive versus negative effects, ignoring their magnitudes and sample sizes. Importantly, meta-analyses can be used to combine the results of multiple experiments or quasi-experiments (Weisser et al. 2023), enabling a predictive framework that could be used to understand the relative importance of insect biodiversity threats. So far, meta-analyses of insect responses to threats have typically focused on only one or a very few threats, such as land-use change in the context of agriculture (Lichtenberg et al. 2017), and/or focused on a restricted taxonomic group (Méndez-Rojas et al. 2021). Large aggregations of effect sizes from across multiple anthropogenic threats and taxonomic groups that adhere to community-agreed principles for data collection and validation, including highly structured preregistered protocols (e.g., Moher et al. 2009), are notably absent.

Advances in living reviews and dynamic meta-analyses, supported by new software such as Metadataset (Shackelford et al. 2021) and Dynameta (Skinner et al. 2023), enable the aggregation of effect sizes in a controlled manner. In particular, the Dynameta R Shiny platform allows the ingestion of additional data (on the effect of anthropogenic threats on biodiversity) as new evidence emerges, with data structuring, cleaning and validation all integral parts of data collection. These platforms can be made publicly available via R packages, enabling researchers and decision-makers to interact with the data beyond the restrictive nature of static visualisation and publication (Weissgerber et al. 2019).

Here, we introduce a multithreat meta-analytic framework and database for understanding insect biodiversity change. The database stores effect sizes describing how anthropogenic threats locally affect the abundance, richness, biomass and fecundity of different insect taxa, in locations around the world. To ensure consistency between threats and insect groups, each individual collation was conducted from primary literature according to a structured protocol and data extraction spreadsheet, or retrieved from the meta-analysis literature according to a set of criteria guiding the inclusion of previously published meta-analyses. Once effect sizes were collated for a particular meta-analysis, the data were uploaded to a data platform built upon Dynameta (Skinner et al. 2023), which performed a series of validation checks. Our intention is to continue collecting effect sizes to expand coverage of anthropogenic threats (defined according to the IUCN; Salafsky et al. 2008), geographic regions and taxonomic groups. In addition to the database itself, we also provide a web tool for downloading and viewing the database, visualising effect-size spatial distribution, and running meta-analytic models on the fly. We henceforth refer to this web tool as 'GLiTRS Dynameta', which is publicly available as an R package (https://github.com/Joemillard/GlitrsDynametaLocal), is an updated version of Dynameta, an interactive platform for biodiversity meta-analyses (Skinner et al. 2023).

2 | Methods

Here we briefly summarise the process used to develop our database. First, we identified threats to prioritise in our database through an initial expert elicitation exercise that ranked the severity of a comprehensive set of anthropogenic threats to major insect Orders. We defined these threats according to the IUCN threat classification scheme (Salafsky et al. 2008) since these are a well-documented, widely used and comprehensive set of—at least in theory—nonoverlapping threats. Second, for these prioritised threats, we then populated our database with a combination of effect sizes collated within the GLiTRS (GLobal Insect Threat-Response Synthesis) project, and with effect sizes collated from previously published meta-analyses meeting a set of preregistered criteria (Millard 2023). Although we would ideally have raw data for the magnitude of all effects, we reasoned to focus on effect sizes for prior meta-analyses given that raw data is typically not released at publication. Collating effect sizes gives us a common currency between both our GLiTRS meta-analyses and prior meta-analyses. For any GLiTRS meta-analysis, we collated partially disaggregated values (e.g., treatment means), from which effect sizes can be calculated. We henceforth use the term 'collation' to refer to the aggregation of a set of effect sizes.

Our effect size collation is designed to be reconcilable with insect biodiversity change dose–response space-for-time comparisons and an expert elicitation, which are being collected elsewhere on the GLiTRS project. This flexibility should make them amenable to other uses, such as merging with IPBES categories of threats (see Table S4 for a suggested mapping between IUCN and IPBES threats for the current set of threats). Below we first set out the structure of our initial expert elicitation, before describing our meta-analytic approach and the structure of GLiTRS Dynameta. Our full approach is set out in preregistered protocols on the Open Science Framework (OSF) (Millard 2023).

2.1 | Expert Elicitation Process to Rank Threats

The IUCN Threat Classification Scheme recognises 12 major categories of threats to biodiversity, which are divided into 45 discrete second-order threats (Salafsky et al. 2008). To identify which of these second-order threats have the greatest impact on insects, and how this might differ between orders, we ranked them in a series of six expert elicitation workshops. In these six workshops, 30 groups of taxon experts (143 experts in total) developed consensus rankings of 42 second-order IUCN threats (version 3.3; Salafsky et al. 2008) by their importance in driving declines in an insect order globally (henceforth 'threats'). Twelve orders (Coleoptera, Lepidoptera, Hymenoptera, Diptera, Hemiptera, Orthoptera, Odonata, Ephemeroptera, Plecoptera, Trichoptera, Phasmatodea and Dermaptera), representing 96% of insect species, received between one and 10 rankings each. Mean rankings were used to prioritise threats within each order. Threats that topped the resulting rankings were then used to prioritise the extraction of effect sizes, either via new meta-analyses with individual protocols, or from previously published meta-analyses. Given each contributor had their own interests, we only enforced carrying out a particular threat topic where it would have meant duplicating work or covering a threat outside the top 10 threats. Our expert elicitation is distinct from previous insect biodiversity expert elicitations (e.g., Miličić et al. 2021) in that we ranked threats at the resolution of IUCN subthreats.

2.2 | Insect Biodiversity Meta-Analytic Approach

To ensure adherence to a single meta-analytic process, each effect size collation was conducted according to a preregistered protocol on the OSF (Millard 2023), which could guide collation among IUCN threats and taxonomic groups. This preregistration is intended to ensure that all effect sizes are collected in a standardised, systematic, and comparable manner. Any existing meta-analyses found while screening for papers (as well as those known to us from other sources) were flagged and assessed against the set of inclusion criteria in Table S2. If suitable, effect sizes from these previously published meta-analyses were ingested into a set of consistently formatted fields (Table S3; see preregistration for more details), analogous to those used for new collations.

Each effect-size collation followed nine core steps (Figure 1), aiming to ensure in advance that each collation could adequately report against the PRISMA reporting checklist for meta-analysis and systematic review (O'Dea et al. 2021). These core steps are as follows: (1) defining the research question under the PICO (population, intervention, comparator, and outcome) framework in ecology (Foo et al. 2021); (2) developing an initial search string; (3) checking the scope of the literature for that research question; (4) writing a specific protocol for that collation, which was then uploaded to the GLiTRS OSF project page (https://osf.io/mw7xq/); (5) refining the set of search strings; (6) searching for relevant studies; (7) downloading studies and removing duplicates; (8) screening papers for relevance; and (9) extracting effect sizes. Henceforth, we refer to any individual contributing to the production of a GLiTRS effect-size collation or the extraction of data from a previously published meta-analysis as a 'contributor'.

2.3 | The Structure of the Data

During data extraction, all fields were collected in a consistent structure amenable to GLiTRS Dynameta and an analysis carried out using the R package 'metafor' (Viechtbauer 2010) (see Tables S1 and S3 and Millard (2023)).

Each effect size was assigned a unique Observation_ID for that comparison, grouped within Paper_ID if multiple effect sizes originated from the same paper (Table S1). Paper_ID will capture some of the variation in methods between papers, meaning it can be included as a random intercept in models to avoid pseudo-replication among effect sizes. Given that each effect size includes variation across multiple sites, we do not have a site-level nested variable. 'Latitude' and 'Longitude' were coded as the midpoint of all treatment and control sites from which data were collected for that effect size. We also included variables for the quantity of treatment applied ('Treatment_quantity', i.e., pesticide application in kg/ha), for the control where relevant ('Control_Quantity', which could be a lower dose of the treatment or a complete absence of the threat) and the type of experimental evidence for each effect size ('Evidence_type': 'Experimental' or 'Quasi-experimental', e.g., deliberate manipulation of an anthropogenic threat relative to a control measure, or variation in an anthropogenic threat that happens to exist across some gradient).

2.4 | Types of Metric Included

Our eventual aim is to build threat–response models that combine insect biodiversity change predictions from meta-analyses, expert elicitations and the PREDICTS database, and then use this threat–response model to predict time series. Given that aim and time limitation, we opted to prioritise metrics for our meta-analyses that can be a common denominator to all four

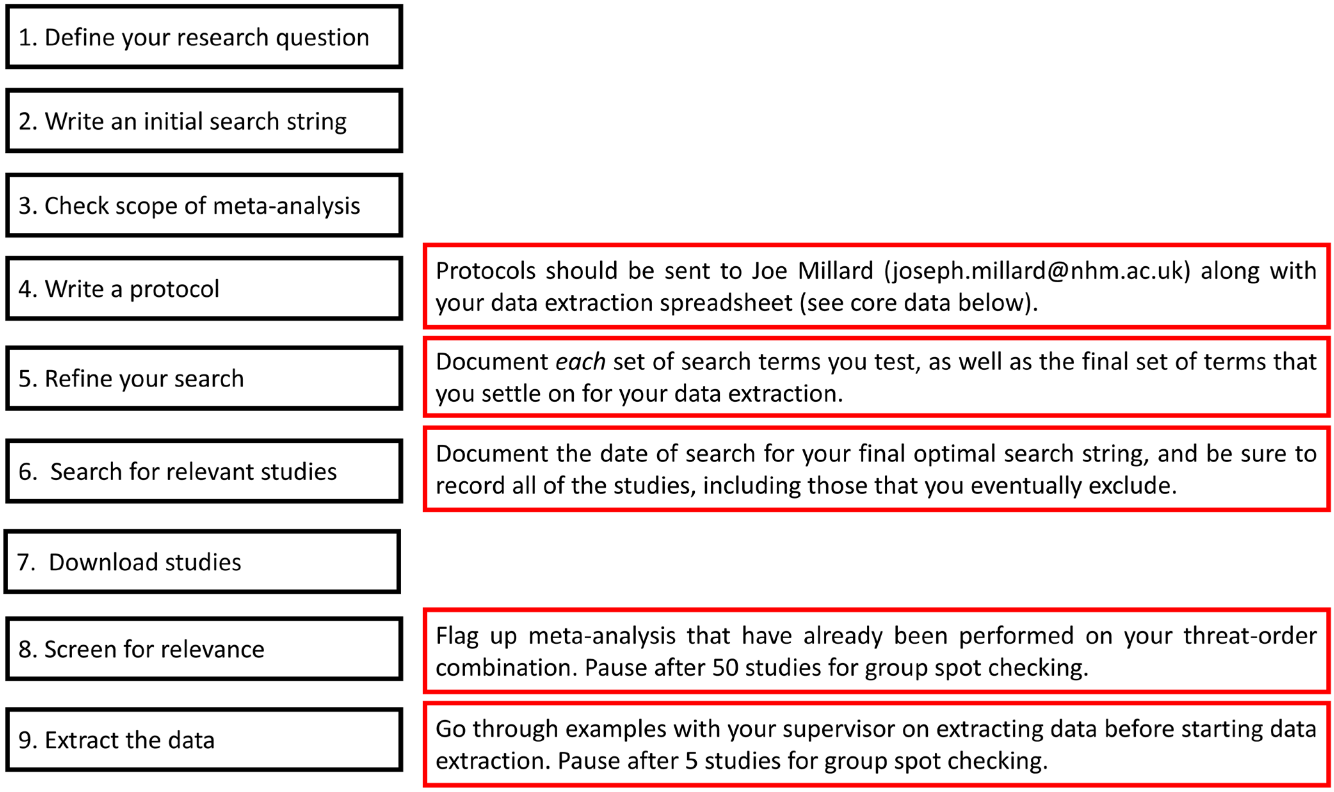

FIGURE 1 | Flow diagram describing the core step (1–9) contributors were instructed to take in collating their meta-analytic data for a GLiTRS project meta-analysis (i.e., not a meta-analysis that had been carried out previously). Black boxes represent individual steps taken, whereas red boxes represent important information to consider at that step.

of these data types. We reasoned that abundance is the most amenable option, followed by richness. We recognise that other measures can be more sensitive to biodiversity change (Santini et al. 2017). If these measures were not available, contributors searched for any metrics that relate to either a measure of biodiversity or some physiological measure from which we might be able to infer biodiversity change (e.g., fecundity). We emphasise that a database of effect sizes for insect abundance and richness can only be indicative of net change in those metrics, rather than overall compositional change.

2.5 | Spot Checking of Contributor Screening and Data Extraction

During the screening and data extraction stages, we checked the data collected to ensure accuracy and reproducibility in three ways. First, after contributors had performed the initial steps of the workflow (Steps 1–7 above) and screened the first 50 papers returned from their search, these 50 papers were sent to another contributor to repeat the screening blind. Disagreements around inclusion or exclusion were discussed to ensure that the inclusion criteria set out in the specific protocol were clear, reproducible and followed correctly. Second, after completing screening (Step 8 above), contributors extracted effect sizes from the first five included papers, and another contributor repeated the effect size extraction blind. Any discrepancies in the extracted data were discussed to ensure accuracy. Third, after contributors had collected all their data, the first 10–15 effect sizes were checked by a supervisor for clear errors (e.g., incorrect conversion of mortality to survival, nonindependence of effect sizes). Contributors were instructed to correct these errors. Where errors were deemed sufficient to have compromised a collation, this collation was fully dropped. We did not check data collated from published peer-reviewed meta-analyses, apart from reconciling any columns in the original data with the GLiTRS Dynameta structure. Any prior effect size is included as the type originally reported in the paper (i.e., we did not do our own conversions between effect size types).

2.6 | Adapting Dynameta to Ingest Insect Biodiversity Effect Sizes

Once a dataset (whether from a GLiTRS collation or a previously published meta-analysis) had been collated, the data were uploaded to GLiTRS Dynameta for validation and storage. GLiTRS Dynameta, which is publicly available as an R package (https://github.com/Joemillard/GlitrsDynametaLocal), is an updated version of Dynameta, an interactive R Shiny (Chang 2024) platform for biodiversity meta-analyses, oriented around the effect of anthropogenic threats on biodiversity (Skinner et al. 2023). Passing each effect size through a data platform allows many kinds of errors to be caught systematically (e.g., latitude or longitude as northings and eastings rather than decimal degrees), and the data to be explored interactively during collection to identify potential issues with validity.

On each set of data uploaded to GLiTRS Dynameta, we carried out a set of validation steps before committing the data. These were as follows: (1) that the file uploaded was a .csv encoded in either UTF-8 or ASCII; (2) that the uploaded file contained all essential columns declared on the OSF (Millard 2023) and no additional columns that would conflict with the data structure expected; (3) that both the 'Latitude' and 'Longitude' fields were numeric, and that values were within the plausible range of latitude and longitude (i.e., $-90 < \text{latitude} < 90$, $-180 < \text{longitude} < 180$); (4) that all the values used to calculate effect size ('Treatment_mean', Treatment_error', 'Control_mean', 'Control_error') were numeric; (5) that the 'Experimental_year_end' was greater than or equal to the 'Experimental_year_start' (i.e., that these start and end sample periods were the correct way around); and (6) that the 'Observation_ID' in each row was unique (Observation_ID refers to a unique effect size within one Paper_ID, meaning it should not be duplicated within a collation). Where any of these validation errors were present in the data, they were flagged to the contributors for checking and correction before writing to Dynameta.

3 | Results and Discussion

Our effect-size framework is unique in the study of insect biodiversity change. Although there are insect time-series aggregations (e.g., 'InsectChange', van Klink et al. (2021); 'ENTOGEM', Grames et al. (2022)), and databases containing land-use associated spatial comparisons (e.g., PREDICTS, Hudson et al. (2017)), as far as we are aware there are no flexible aggregations of experimental or quasi-experimental effect sizes for the impact of a suite of anthropogenic threats on insect biodiversity. Without this, it is impossible to assess which threats are driving changes in insect biodiversity detected by time series. In particular, the framework we introduce differs from previous studies in four key ways. First, our database contains effect sizes for the effect of treatments relative to a control, as opposed to a vote-count synthesis (i.e., counting positive vs. negative effects, ignoring their magnitudes and sample sizes). Second, we preregistered both an initial meta-protocol and individual protocols for each collation of effect sizes, ensuring standardisation in the process of data collection and reducing issues of systematic bias, meaning our meta-analytic process should in principle allow others to contribute effect sizes. This meant a PRISMA-led (Moher et al. 2009) systematic approach within threats (i.e., individual collations of effect sizes for a given threat-order combination), and a systematic approach among collations across the study as a whole. Third, we collated effect sizes for local measures of biodiversity, with the type of biodiversity metric specified. Fourth, for each effect size, we are explicit as to whether the evidence type for that effect is experimental or quasi-experimental.

Thus far, the database contains 6308 effect sizes for 21 taxonomic Orders, four biodiversity metrics (see Table S5 for metric definitions) and five IUCN first-order threats, with the underlying data published from 1970 to 2022 (Figure 2). These effect sizes currently come from seven meta-analyses, three of which were carried out by GLiTRS contributors and four collated from prior literature (Gallego-Zamorano et al. 2023; Liang et al. 2023; Nessel et al. 2023; Wang et al. 2020). Geographic coverage is biased towards North America and Europe, as is typical for most biodiversity datasets (e.g., PREDICTS and BioTIME: Hudson et al. 2017; Dornelas et al. 2018), although there are effect sizes from all continents except Antarctica. Coleoptera provides the largest number of effect sizes (Figure 2). Abundance and species richness are the most frequent biodiversity metrics in our database (Figure 2), owing to our search strategy prioritising these metrics. The IUCN threats included are 'Natural system modifications', 'Pollution', 'Agriculture and Aquaculture', 'Residential and commercial development' and 'Invasive species' (Figure 2). These threats thus far included were ranked highly by experts, meaning we have focussed on these first.

The effect sizes we present are likely reflective of true anthropogenic threat effects, but regardless there are ways in which they can be misused. Primarily, these effect sizes cannot be used to quantify interactions between anthropogenic threats. For example, moderating effects of land-use and climate change, such as those captured by Outhwaite et al. (2022), will not be captured here. To quantify interactions between threats researchers should use data sources such as the PREDICTS database (Hudson et al. 2017), which were built with that purpose in mind. Importantly, wherever researchers use the effect sizes here to predict overall change in insect biodiversity as a function of a set of threats, or to rank the relative importance of threats, researchers must be transparent that these analyses only hold assuming threats do not magnify or buffer one another. A more appropriate use for these effect sizes will be to quantify the relative impact of an individual threat among taxonomic orders, typically for an individual biodiversity metric. For example, within this one database framework, researchers can ask questions such as 'for abundance, which insect orders are most sensitive to invasive species?' or 'for species richness, which insect orders are most sensitive to extreme temperatures?'. The structure of the GLiTRS Dynameta R package is built to encourage users to reason in this manner (Skinner et al. 2023), with only one threat selectable at any given time.

The effect-size database does have a set of limitations. First, linking threats as defined by the IUCN to effect sizes in the literature was a challenge. Although IUCN threat categories are defined such that they are nonoverlapping, in practise retrieving effect sizes that isolate threats was difficult, especially for quasi-experimental effect sizes. With habitat-shifting and alteration resulting from climate change (IUCN threat 11.1), for example, we reasoned that this should be captured in abundance and richness change resulting from the effect of climate itself (e.g., extreme temperature and droughts). We therefore excluded this threat from our priority list for new collations. For agricultural and forestry effluents (IUCN threat 9.3), it was challenging to find threat metrics that were measured consistently among and within studies, or measuring the effect of that threat isolated from the effect of correlated threats such as livestock grazing or land clearance. Our compromise here was to be fully transparent on the nature of any treatment and control measures and emphasise that any effect size should be deemed representative of only the specific nature of that treatment and control, rather than the whole of the IUCN threat category. Second, extracting treatment quantities is complicated to accomplish in a meaningful way for some threats. Our initial aim for each effect size was to collect an associated quantity for the threat, such that it could eventually be used to build a dose–response meta-analysis and predict change in insect biodiversity according to increasing intensities of that threat alone or for multiple threats additively. However,

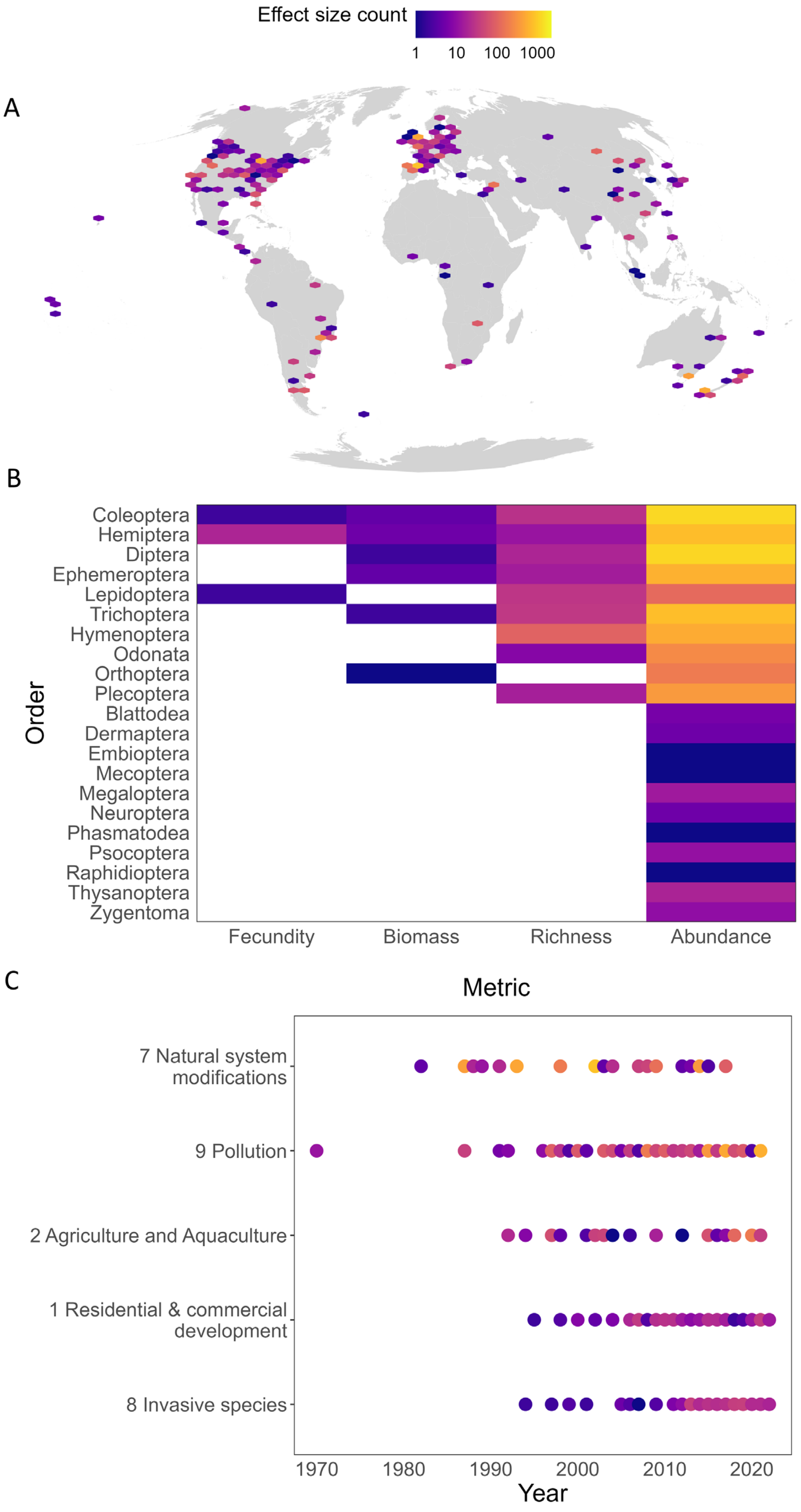

FIGURE 2 | Legend on next page.

FIGURE 2 | Frequency of insect biodiversity effect sizes in our multithreat meta-analytic database according to geography, taxonomy, biodiversity metric, time and anthropogenic threat (i.e., IUCN threat category, here combined to the first-order groupings): (A) The geographic distribution of all effect sizes (max individual value of 831); (B) the taxonomic distribution of all effect sizes broken down by biodiversity metric, sorted by the number of taxonomic orders and biodiversity metrics represented (max individual value of 1230); (C) the temporal distribution of all effect sizes by IUCN anthropogenic threat category, sorted on the y axis by the number of effect sizes for each threat (max individual value of 829). All panel colour scales (see top panel for the legend) are fixed across the same range of values.

reconciling quantities between studies in a meaningful way is challenging. For example, even for one facet of a single threat like fertiliser application for agricultural effluents (IUCN threat 9.3), units and reporting vary, with some studies only reporting whether fertiliser was present/absent, and others reporting dosage of different fertilisers over different timescales or areas. Our compromise here has been to record any treatment and control quantities where we meaningfully can, and otherwise to emphasise that effect sizes are only meaningfully analysed under a modelling framework that accounts for variation predicted by methodology (e.g., a mixed-effects model with Treatment_quantity rescaled within 'Paper_ID'–'Treatment_quantity_unit' combinations). Third, collapsing all effect size collations into a single framework among threats and Orders was challenging to accomplish meaningfully. For many effect sizes, it was apparent that moderator variables (e.g., the focal invading species for IUCN threat 8.1 Invasive non-native/alien species/diseases) were important to provide context for interpretation. Our compromise has been to—as far as possible for quasi-experimental effect sizes—only include effect sizes for which we could be confident that the difference between the treatment and control could be attributed to that treatment. This maintained consistency between meta-analytic effect size collations by contributors and helped to ensure that effect sizes relate to those threats. Fourth, appropriate metrics of biodiversity change differ according to the type of threat investigated, meaning that for some threats we were unable to collect effect sizes for our priority metrics (e.g., abundance and species richness). Given our eventual aim is to understand insect biodiversity change, we opted to ensure a broad acceptance of any metric that relates to insect biodiversity change, reporting the metric for each effect size in that row to ensure internal consistency.

Insect biodiversity is reported to be undergoing rapid change worldwide, driven by a number of anthropogenic threats (Wagner et al. 2021). However, the relative global importance of these threats and how they impact different insect Orders remains unclear. Here, we used a structured, flexible, preregistered meta-analysis protocol to guide the collection of a set of effect sizes describing the impact of a diverse range of threats on insect biodiversity. These effect sizes are associated with consistently formatted metadata, allowing analyses that control for the main sources of heterogeneity. As a critical part of this process, our interactive GLiTRS Dynameta app allows users to interrogate the data to ask unique questions about the preliminary set of effect sizes we provide. Our future intent is to make GLiTRS Dynameta accessible at a public URL, such that users do not have to use R or an R package to launch the platform. As with any data set, the effect sizes should be used with caution and not beyond the set of contexts to which they relate (e.g., taxonomic groups, specific threats, and geographic regions). We intend to continue collecting effect sizes under this framework, aiming to cover a broad spectrum of major threats. Importantly, our database provides a framework for aggregating experimental and quasi-experimental evidence about the major causes of insect biodiversity change (Weisser et al. 2023). We hope that in the long term, our database and associated protocols will encourage others to contribute new studies and meta-analyses to our collation of effect sizes, to build a comprehensive global picture of the impact of anthropogenic threats on insect biodiversity.

Author Contributions

J.M.: conceptualization, methodology, software, formal analysis, data curation, writing – original draft, writing – review and editing, visualization, supervision. G.S.: conceptualization, methodology, software, data curation, writing – original draft, writing – review and editing. A.J.B.: conceptualization, methodology, writing – review and editing, supervision; R.C.: conceptualization, methodology, software, data curation, writing – review and editing, supervision. C.L.O.: conceptualization, methodology, data curation, writing – review and editing, supervision, funding acquisition; J.G.R.: conceptualization, methodology, data curation, writing – review and editing, supervision. L.A.B.: data curation, writing – review and editing, validation. J.E.I.: writing – review and editing, methodology; J.K.: data curation, writing – review and editing, validation. C.R.: writing – review and editing, methodology, software. E.W.-S.: data curation, writing – review and editing, validation. L.V.D.: conceptualization, project administration, funding acquisition, writing – review and editing. C.H.: conceptualization, project administration, funding acquisition, writing – review and editing. J.I.J.: conceptualization, project administration, funding acquisition, writing – review and editing. B.W.: conceptualization, methodology, project administration, funding acquisition, writing – review and editing. N.J.B.I.: conceptualization, supervision, project administration, funding acquisition, writing – review and editing. A.P.: conceptualization, methodology, data curation, supervision, project administration, funding acquisition, writing – review and editing.

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Conflicts of Interest

The authors declare no conflicts of interest.

Data Availability Statement

Data are available on Dryad at this prepublication link (http://datadryad.org/stash/share/tw75J_E8YbZO0CMiPjlbhcc7QWpvf63TFtWfcQfuNvs), and on GitHub for more convenient download from the following URL: https://github.com/Joemillard/GlitrsDynametaLocal.

Peer Review

The peer review history for this article is available at https://www.webofscience.com/api/gateway/wos/peer-review/10.1111/ddi.70025.

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Supporting Information

Additional supporting information can be found online in the Supporting Information section.