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The GLiTRS project (GLobal Insect Threat-Response Synthesis)

Overall Principal Investigator: Nick Isaac (UKCEH)

Presenters: Andy Purvis (NHM), Rob Cooke (UKCEH), Charlie Outhwaite (UCL/ZSL), Joe Millard (Cambridge), Ben Woodcock (UKCEH), John Murphy (QMUL)

UKRI Natural Environment Research Council

UK Centre for Ecology & Hydrology

Natural History Museum

University of Cambridge

UCL

Queen Mary University of London

Stellenbosch University Iyunivesithi Universiteit

Outline

Each section will highlight possibilities for collaboration

- Conceptual framework (Rob Cooke, UKCEH)
- Identifying key threats (Charlie Outhwaite, UCL/ZSL*)
- Three types of evidence on drivers of decline
    - Spatial comparisons (Charlie Outhwaite, UCL/ZSL)
    - Meta-analyses (Joe Millard, Cambridge)
    - Expert elicitation (Charlie Outhwaite, UCL/ZSL*)

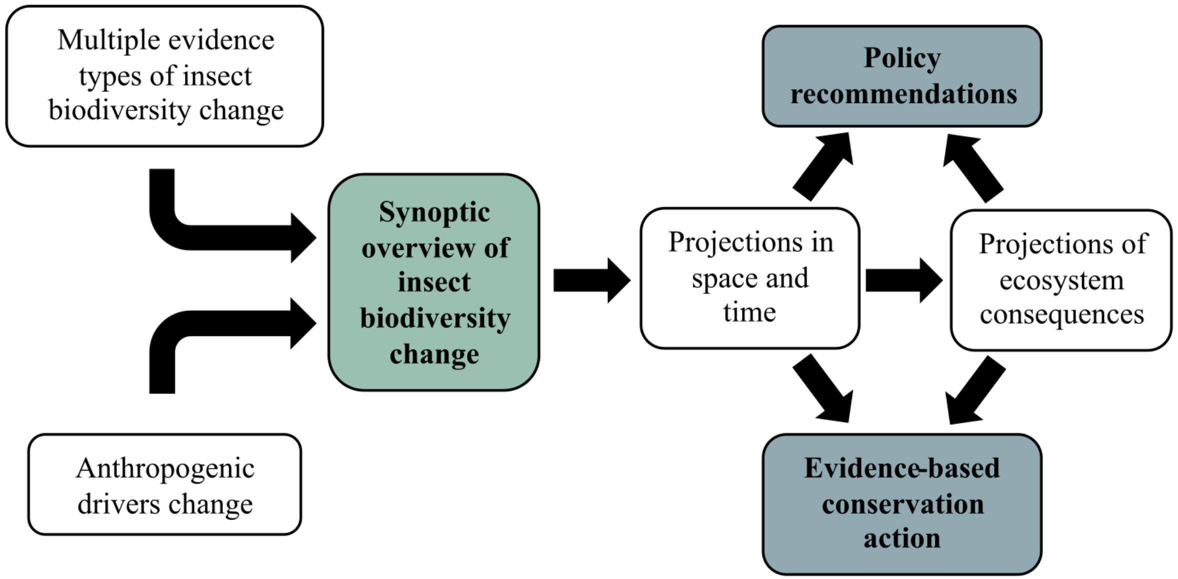
  [Short break for questions]
- Combining evidence types (Andy Purvis, NHM)
- Time-series database (Ben Woodcock, UKCEH**)
- Traits database (John Murphy, QMUL)
- Q&A/Discussion

* Speaking for Andrew Bladon, Reading
** Speaking for Ellie Dyer, UKCEH

The GLiTRS Project

GLobal Insect Threat-Response Synthesis

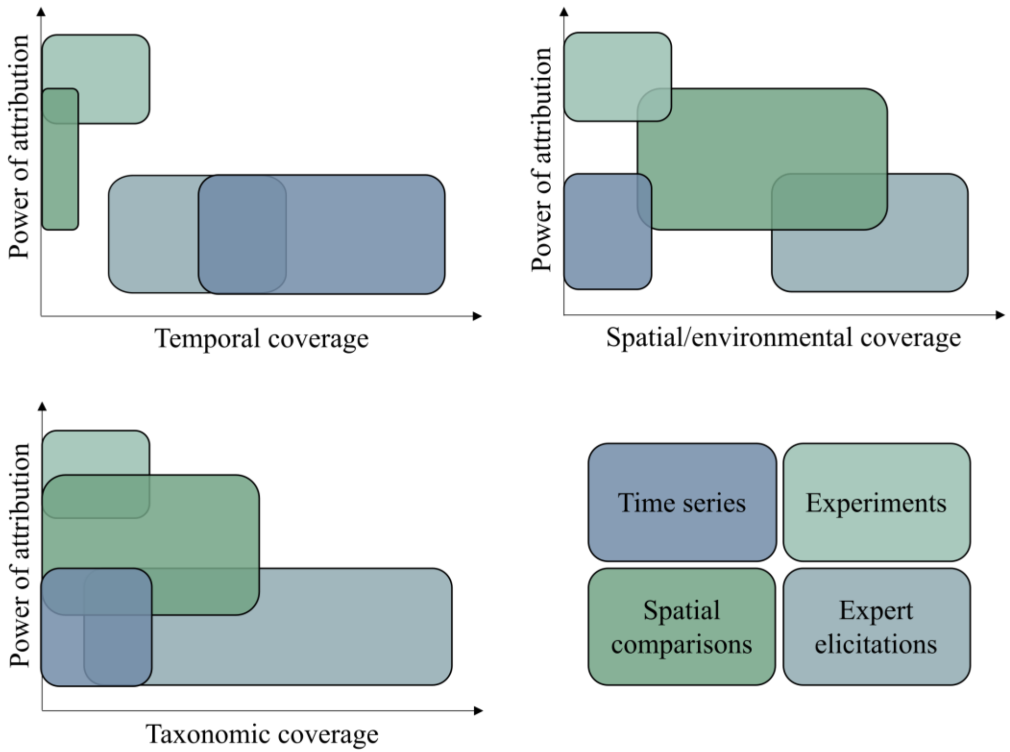
- Insect declines are a problem *now.*
- Cannot wait for more long-term data.
- Need to make the most of currently available data to inform conservation actions.



Cooke, Outhwaite *et al* (in review)

Rob Cooke: roboke@ceh.ac.uk

Strengths of Evidence

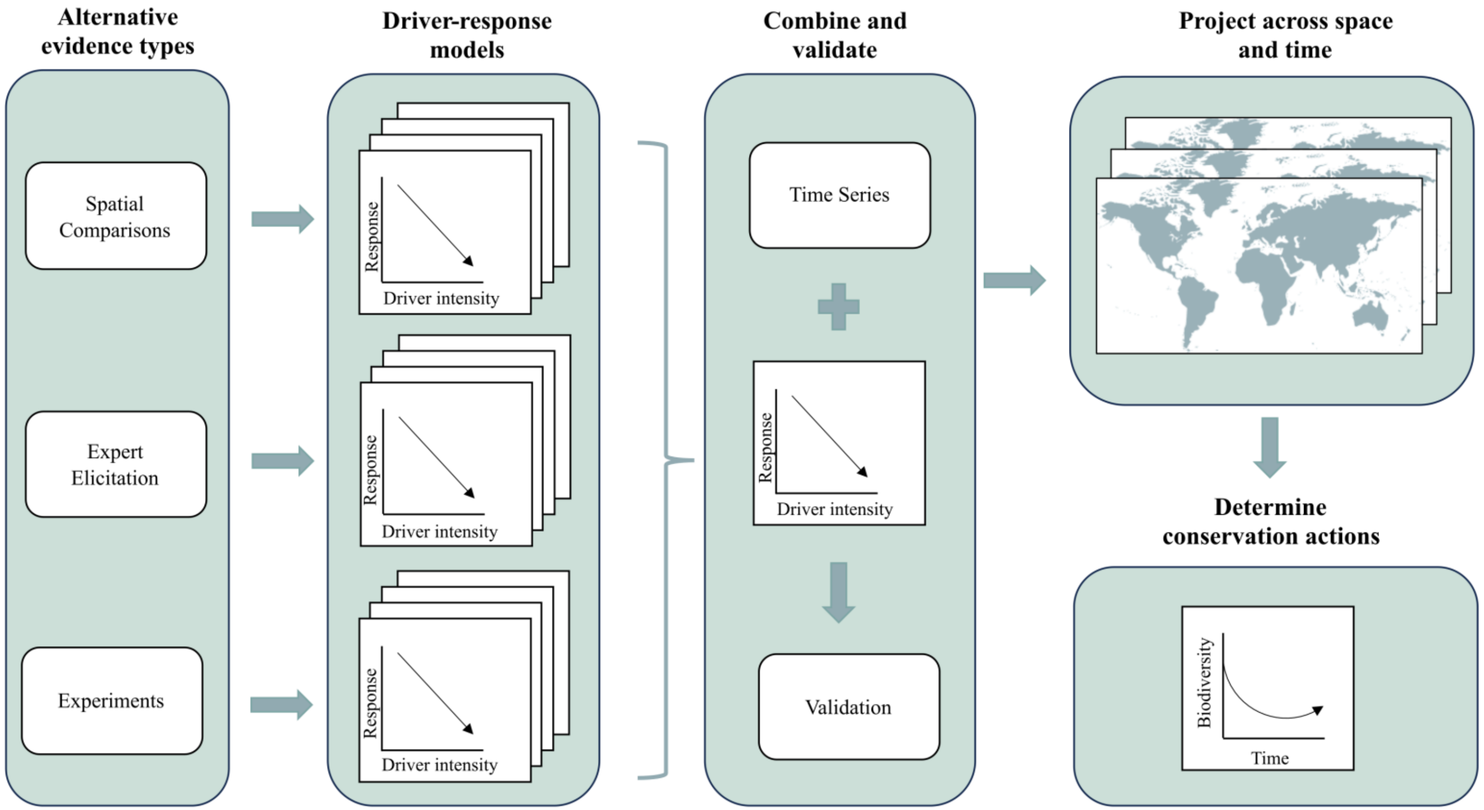


- Different data types have different strengths and weaknesses.
- No one data type is perfect for assessing the effect of threats on insect biodiversity.
- By bringing them together, we can take advantage of the strengths of each.

Cooke, Outhwaite *et al* (in review)

Combining Evidence Types

By combining evidence types, we can be more certain about the impacts of threats on insect biodiversity at the global scale.



Cooke, Outhwaite *et al* (in review)

Rob Cooke: roboke@ceh.ac.uk

Identifying key threats

- IUCN Red List identifies 11 major threats to biodiversity
- Divided into 42 sub-categories, e.g.
  - 2.1 Annual & perennial non-timber crops
  - 2.3 Livestock farming & ranching
  - 9.3 Agricultural & forestry effluents
  - 9.6 Excess energy (e.g. light pollution)
- Used expert workshops to identify ~10 most important threats to each insect Order

1. Residential & commercial development
2. Agriculture & aquaculture
3. Energy production & mining
4. Transportation and service corridors
5. Biological resource use
6. Human intrusions & disturbance
7. Natural system modifications
8. Invasive & other problematic species, genes & diseases
9. Pollution
10. Geological events
11. Climate change & severe weather

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Identifying key threats

- Bespoke workshop run at international conferences
- Experts worked in groups based on taxonomic Order of expertise
- Asked to rank 42 IUCN sub-category threats for importance to that Order based on two questions:
    1. How important is threat X for driving population changes in Order Y?
    2. At a global scale, how do the 42 IUCN threats rank in the strength of their impact on insects?
- Group consultation used to question and check results

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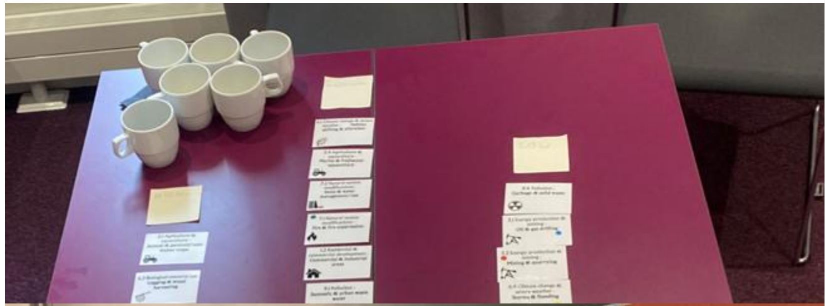
Identifying key threats

- Produced 30 rankings for 12 insect Orders (covering 96% of known species)
- Calculated mean rankings for each Order
- Calculated mean rankings by habitat type (terrestrial and aquatic) to estimate rankings for Orders not covered
- Used to select key threats for rest of project



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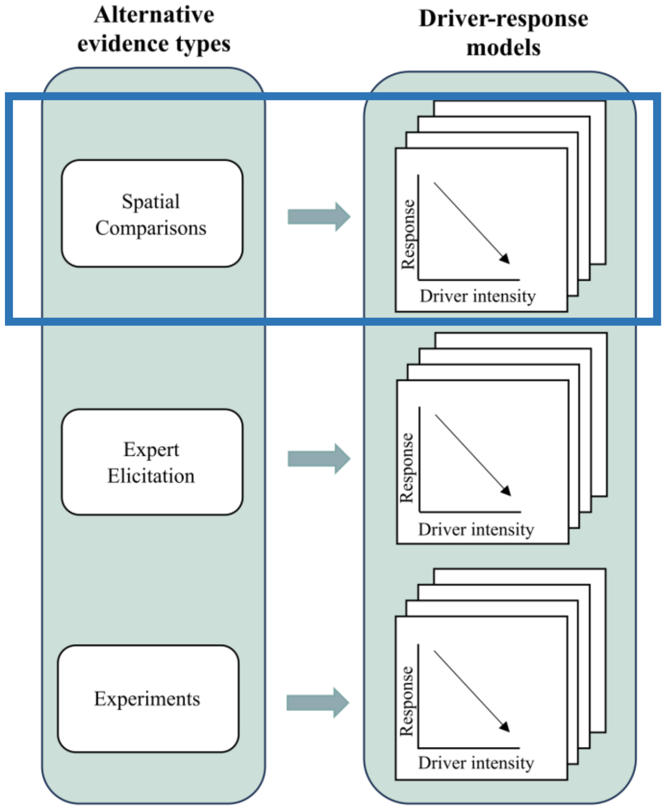
1. Spatial comparisons



Aim: Determine threat-response models for how insect abundance and species richness (across different orders) responds to various threats

Biodiversity data: insect data from PREDICTS database

Strengths: global extent, data for many threats and many species, space-for-time approach

Weakness: poor temporal coverage, correlational relationships

1. Spatial comparisons

Top 10 threats to Hymenopteran biodiversity

1. **Annual and perennial non-timber crops**
2. **Agricultural and forestry effluents**
3. **Livestock farming and ranching**
4. **Extreme temperatures**
5. Habitat shifting and alteration
6. **Droughts**
7. Invasive non-native/alien species/diseases
8. **Logging and wood harvesting**
9. **Housing and urban areas**
10. **Commercial and industrial areas**

- Initially focused on the Hymenoptera only (will expand to more Orders)
- Used the top 10 (of the 42) sub-category threats
- Not all are well suited to the method

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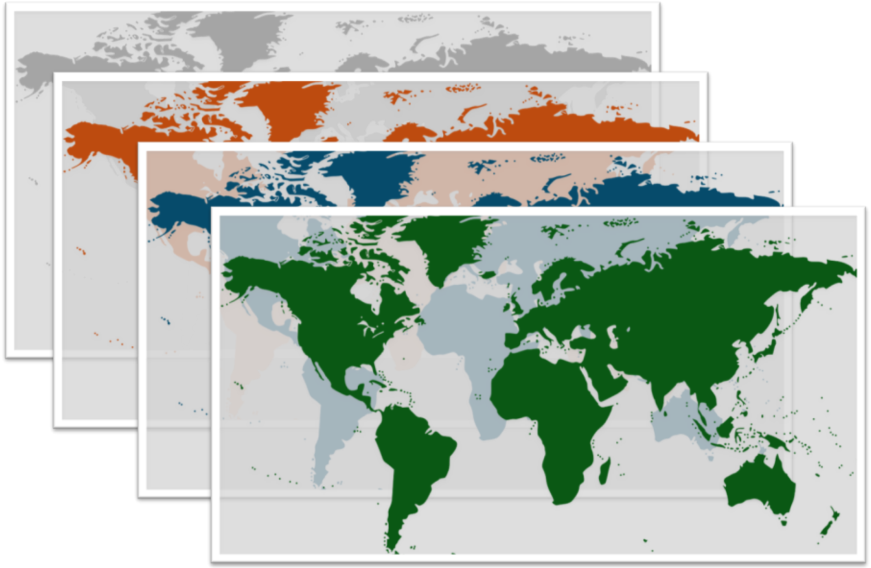
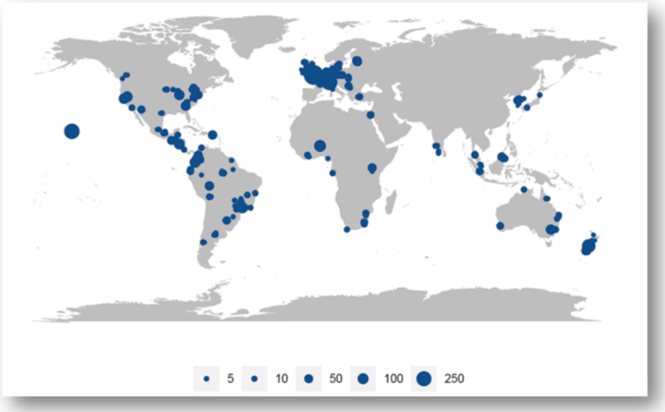
1. Spatial comparisons

- Searched for datasets to represent each of the threats

- *Global extent*
- *As fine resolution as possible*
- *Most representative of the threat (could have multiple maps)*
- *Openly available*

- Extracted information from each of the sites within the PREDICTS data subset





5,943 sites from 229 Studies

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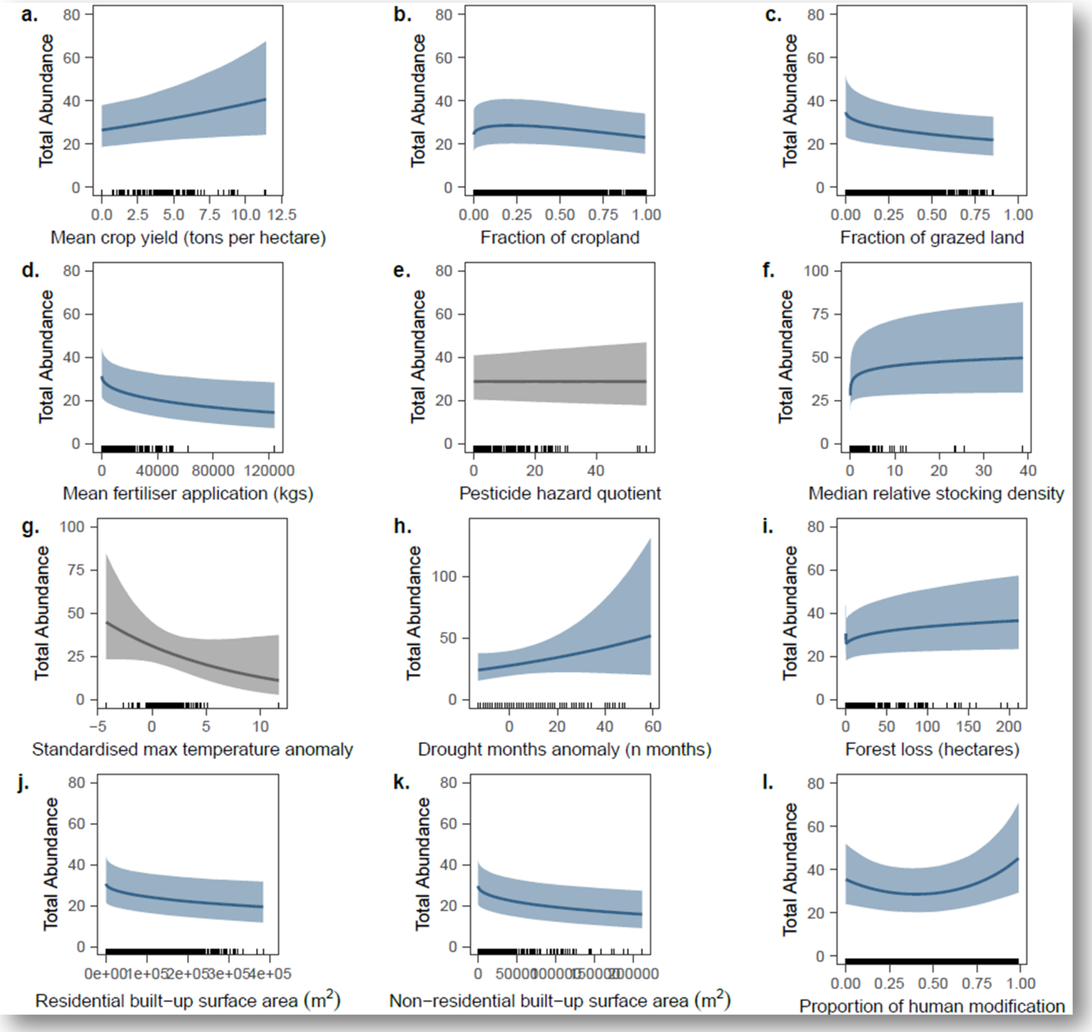
1. Spatial comparisons

- Used a mixed-effects modelling approach in a Bayesian framework
- Response variables included total abundance and species richness
- Assessed linear and non-linear responses



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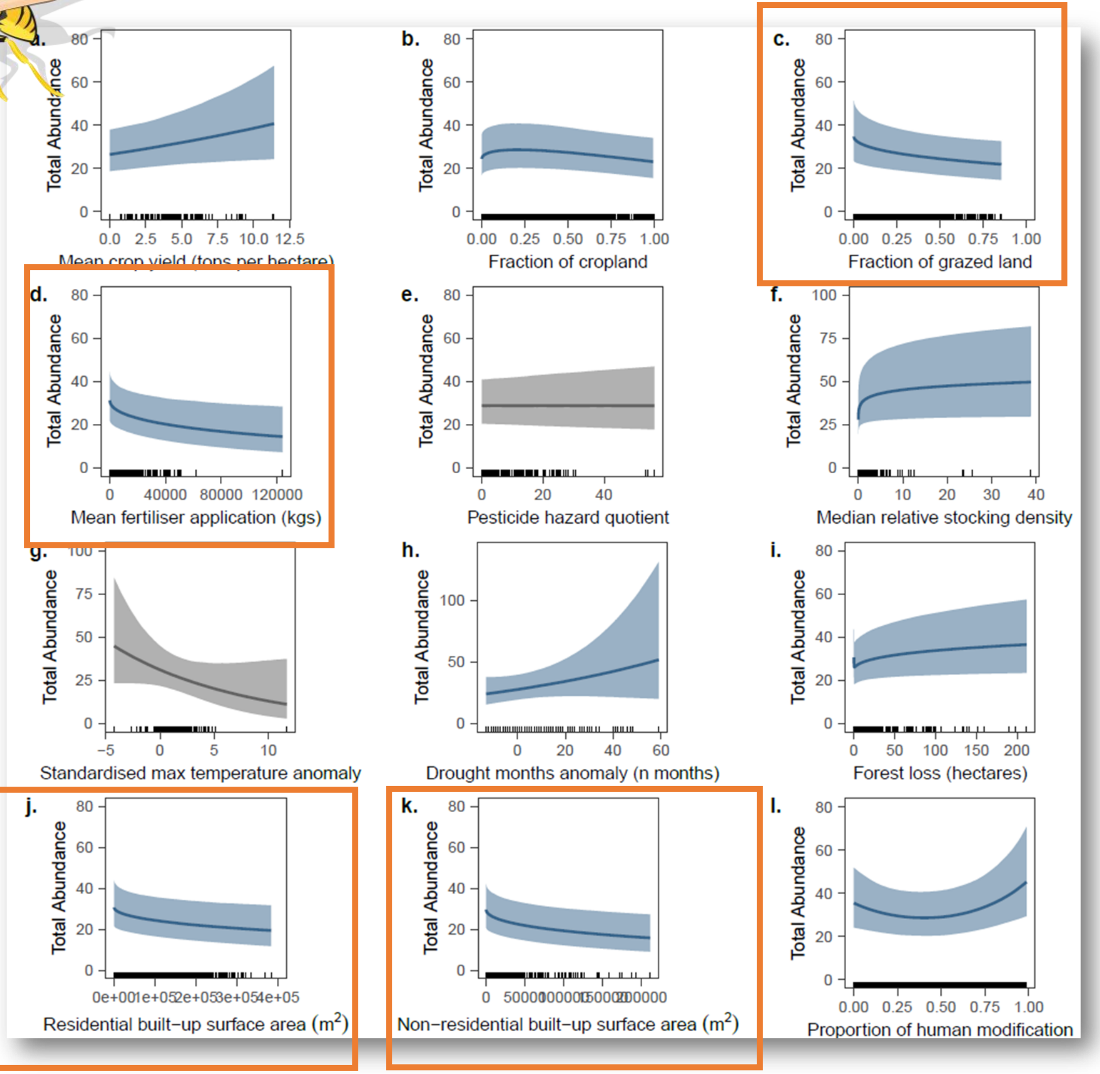
1. Spatial comparisons

The fraction of grazed land, fertiliser application and amount of built-up area showed consistent negative impacts on Hymenopteran biodiversity

Not all threats resulted in negative responses; this may be a result of a mismatch between data resolutions

Next steps: Take a similar approach for more Orders and other threats.



Grey results were non-significant

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Opportunities for improvement and future collaboration

1. Improving threat data resolution

- Better data at smaller scales? i.e. UK? Europe?

2. Consideration of key interactions.

- Additive effect of threats only, some interactions likely important (see our previous paper on land use climate change interactions)

3. What about the effect of positive drivers?

- e.g. interventions etc
- What data is available, could satellite imagery be used?

4. How can we link local scales to global scales?

- All very interesting but change happens at the local scale

Happy to discuss ideas!
charlotte.outhwaite@ioz.ac.uk

2. Meta-analysis (experiments)

		Order
		Hymenoptera
Threat	1.1 Housing and urban areas	
	1.2 Commercial and industrial areas	
	11.1 Habitat shifting and alteration	
	11.2 Droughts	
	11.3 Temperature extremes	
	2.1 Annual and perennial non-timber crops	
	2.2 Wood and pulp plantations	
	2.3 Livestock farming and ranching	
	5.3 Logging and wood harvesting	
	8.1 Invasive non-native/alien species/diseases	
	9.3 Agricultural and forestry effluents	

The sum of all meta-analyses for a given order forms the meta-analytic part of our threat-response model

An inter-threat and inter-order approach to aggregating insect biodiversity effect sizes

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2. Meta-analysis (experiments)

Dynameta: a dynamic platform for ecological meta-analyses

Overview

Table 1. Total number of papers (Paper_ID) and data points available to investigate each threat category. The insect biodiversity meta-analytic database currently contains 2728 effect sizes.

Threat category	Total papers	Total effect sizes
7 Natural system modifications	36	2681
9 Pollution	10	47

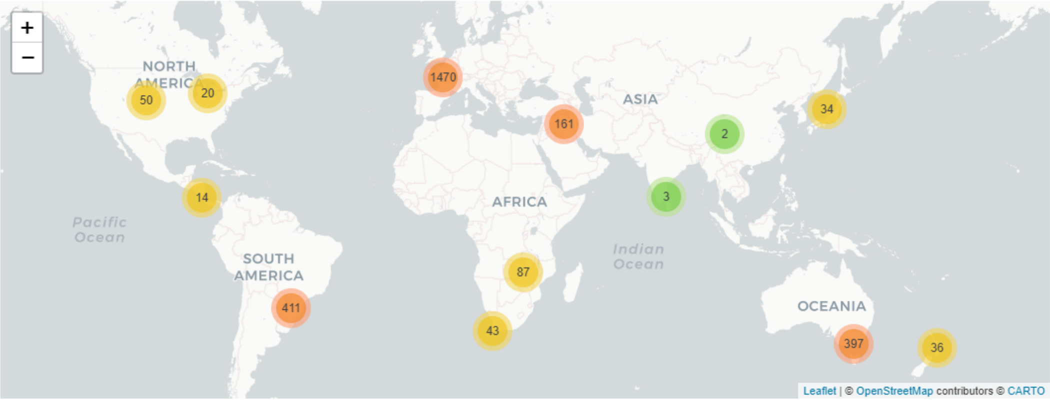

Figure 1. Map showing location of effect sizes, for both current GLiTRS and prior meta-analyses. Currently 2728 out of 2728 data points have associated latitude and longitude coordinates. You can zoom in on, and click on, data clusters to explore the map. Clicking on an individual point provides a link to that paper (if available).

Download map (.png)

View original Dynameta source code.

For any publications using GLiTRS Dynameta, please cite the original software article as follows: Skinner, G., Cooke, R., Junghyuk, K., Purvis, A., Raw, C., Woodcock, B.A., Millard, J. (2023). Dynameta: a dynamic platform for ecological meta-analyses in R Shiny. SoftwareX. https://doi.org/10.1016/j.softx.2023.101439

Grace Skinner

Skinner et al. (2023) SoftwareX

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2. Meta-analysis (experiments)

A metaprotocol to guide across all meta-analyses

1. Define your research question	
2. Write an initial search string	
3. Check scope of meta-analysis	
4. Write a protocol	Protocols should be sent to Joe Millard (joseph.millard@nhm.ac.uk) along with your data extraction spreadsheet (see core data below).
5. Refine your search	Document *each* set of search terms you test, as well as the final set of terms that you settle on for your data extraction.
6. Search for relevant studies	Document the date of search for your final optimal search string, and be sure to record all of the studies, including those that you eventually exclude.
7. Download studies	
8. Screen for relevance	Flag up meta-analysis that have already been performed on your threat-order combination. Pause after 50 studies for group spot checking.
9. Extract the data	Go through examples with your supervisor on extracting data before starting data extraction. Pause after 5 studies for group spot checking.

2. Meta-analysis (experiments)

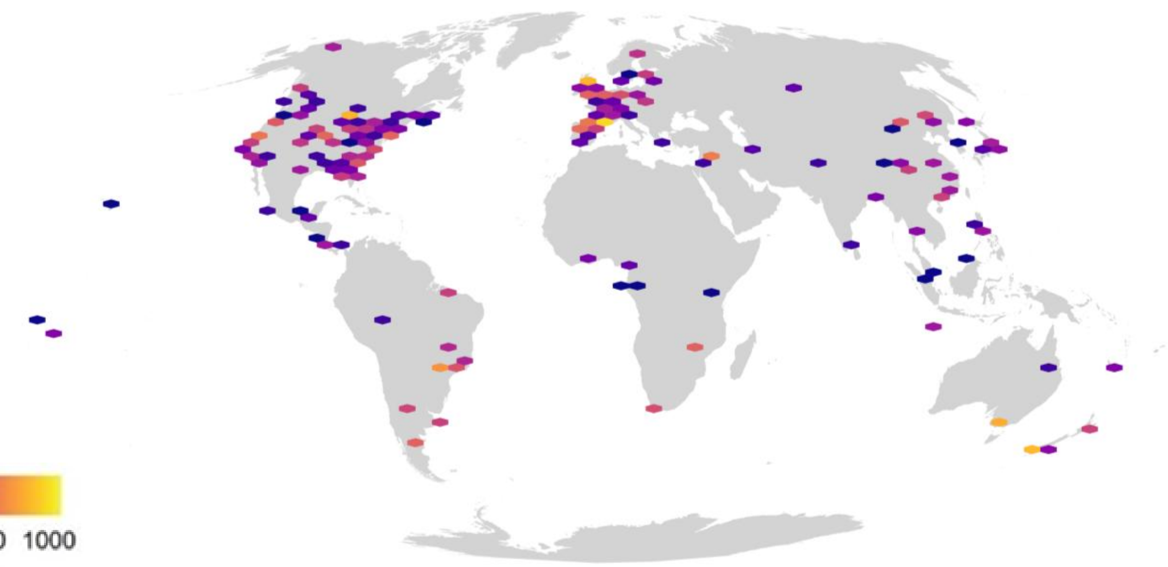
And a set of criteria to guide the inclusion of prior meta-analyses

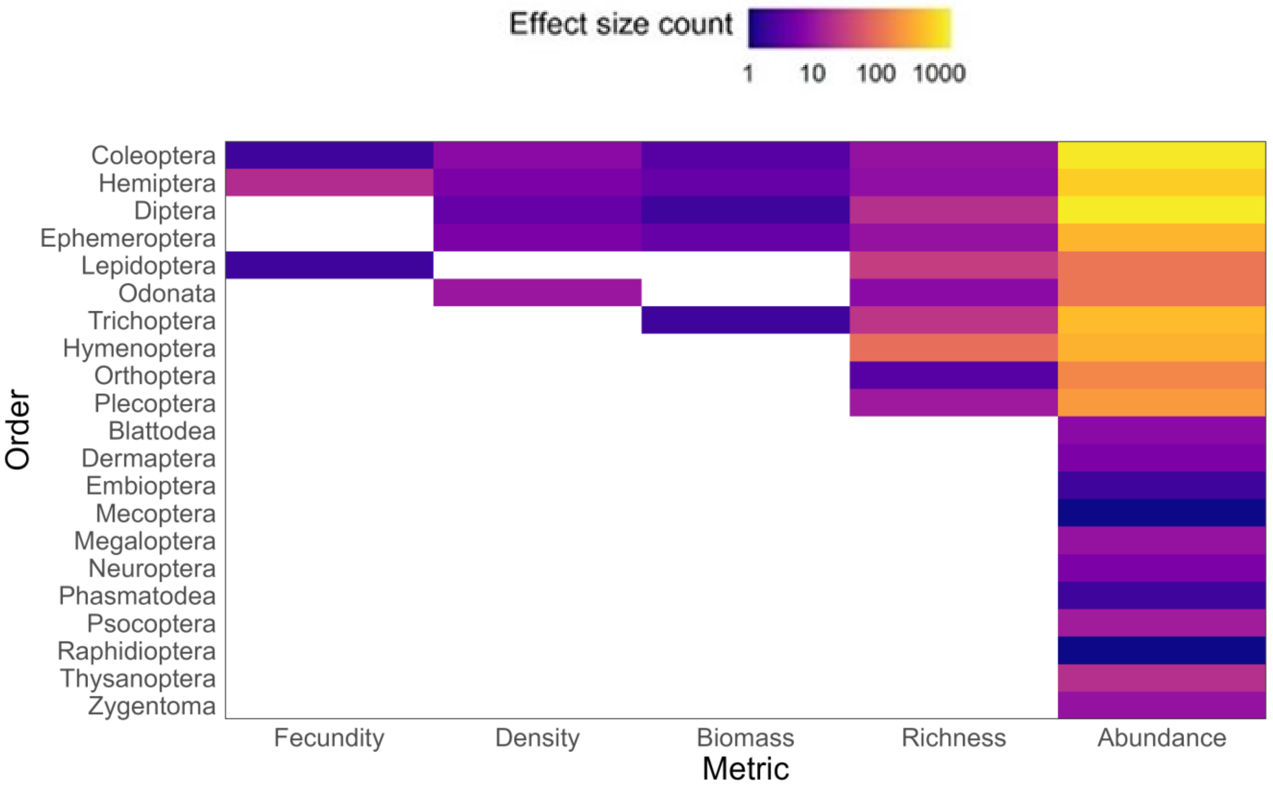
1. Formal meta-analysis for a given taxonomic order and threat
2. Peer reviewed, transparent exclusion criteria, search, terms, PRISMA diagram describing exclusion, and effect sizes transparent on location and metric to which they apply
3. Effect sizes relative to control measure for experimental or quasi-experimental, with a quantitative measure for the threat to which the effect size applies

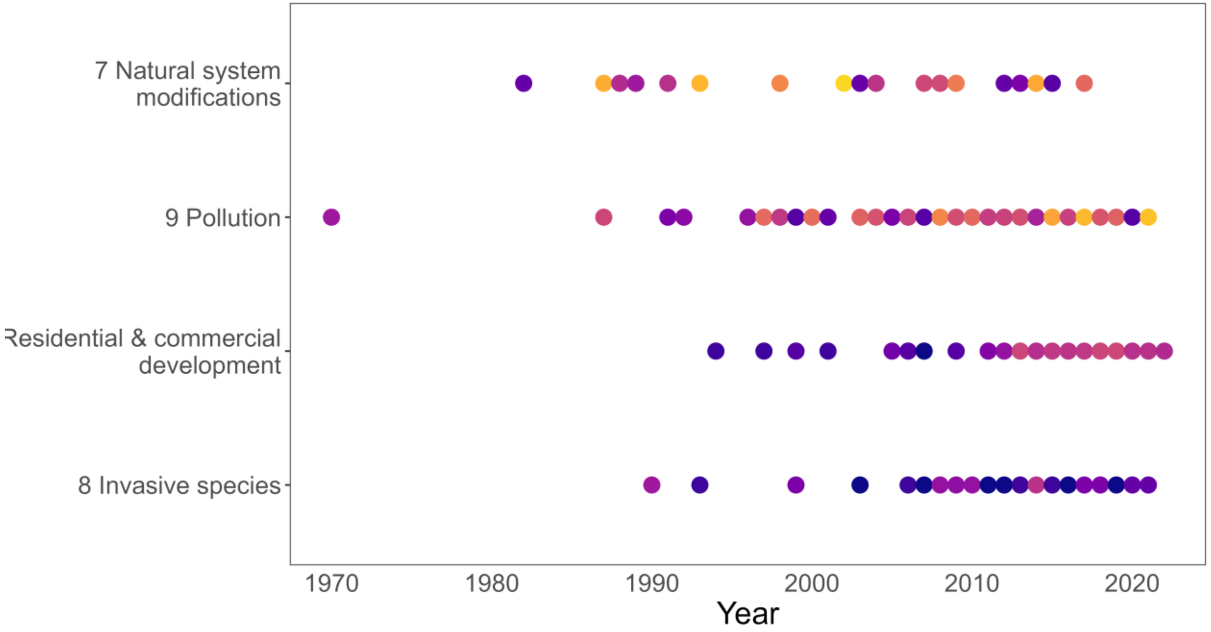
Joe Millard: jwm57@cam.ac.uk

Look out for the database when it's released, and then we'll be looking for help in gap filling meta-analyses

Email: jwm57@cam.ac.uk







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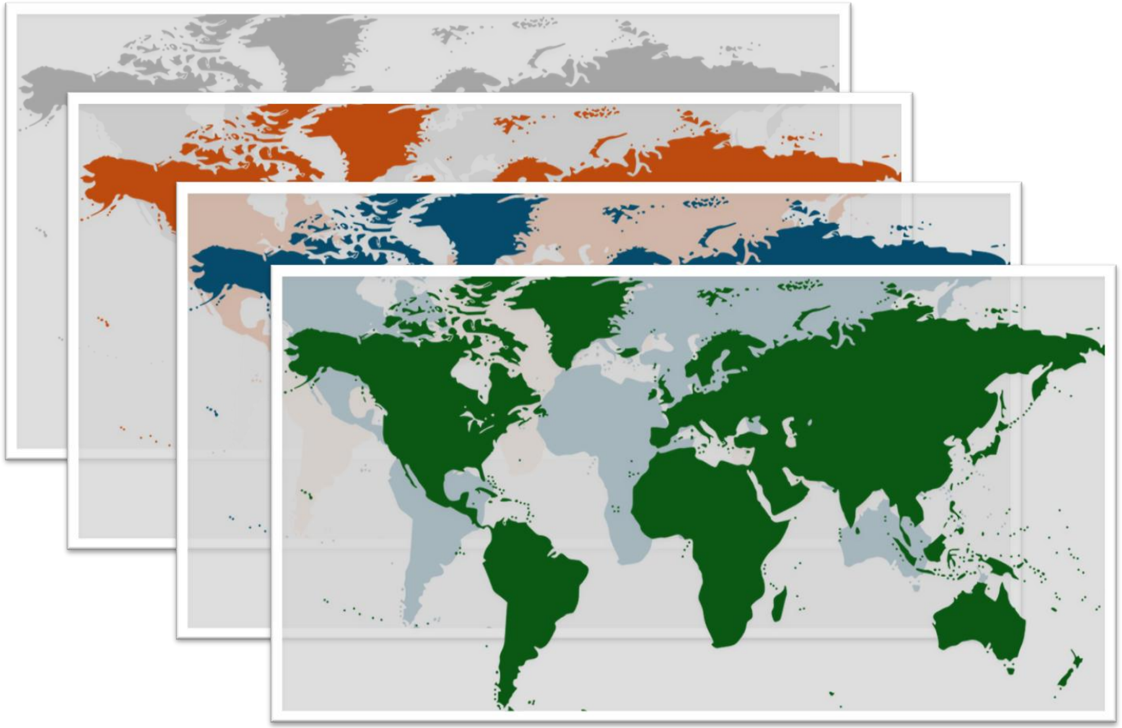
3. Expert Elicitation

- Used global threat layers identified for spatial comparisons to construct axes of threat intensity
- Ranged from zero (threat not present) to maximum intensity of that threat anywhere in the world
- Asked experts about the response of insects to the 10 highest ranked threats for each insect Order



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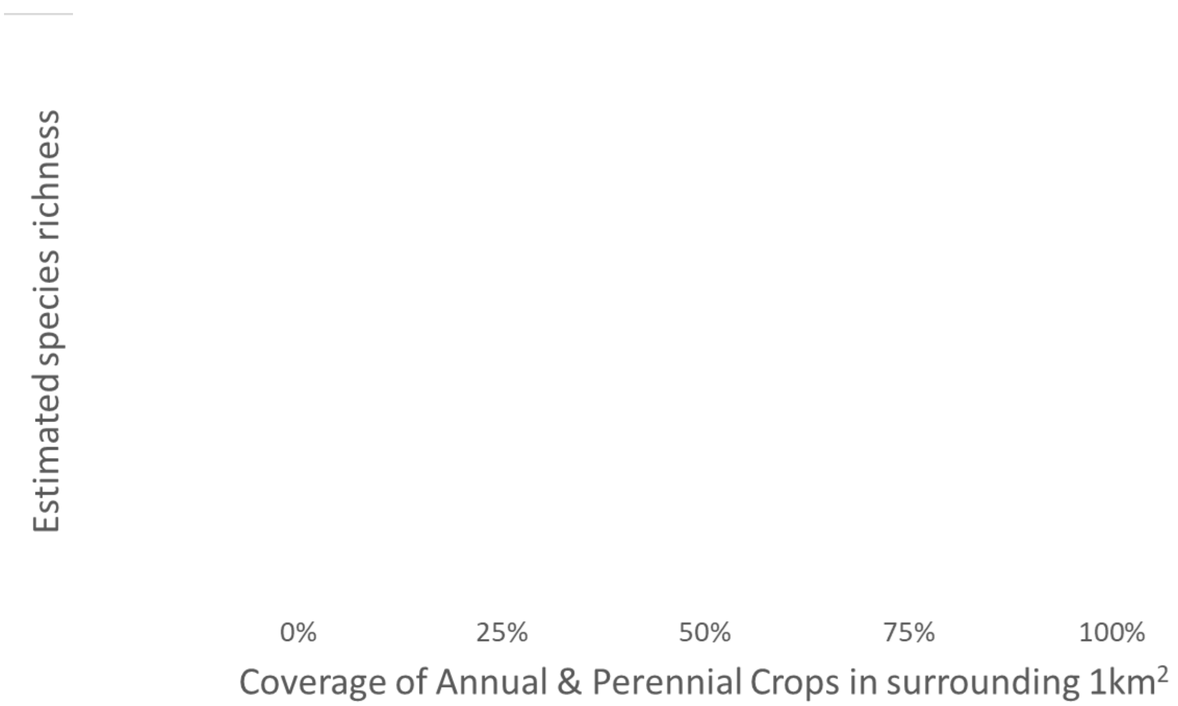
3. Expert Elicitation

- For each insect Order, asked experts to estimate the abundance and species richness they would expect to record:
  - Under known survey conditions
  - In a familiar location and month
  - In areas experiencing different threat intensities across the global range



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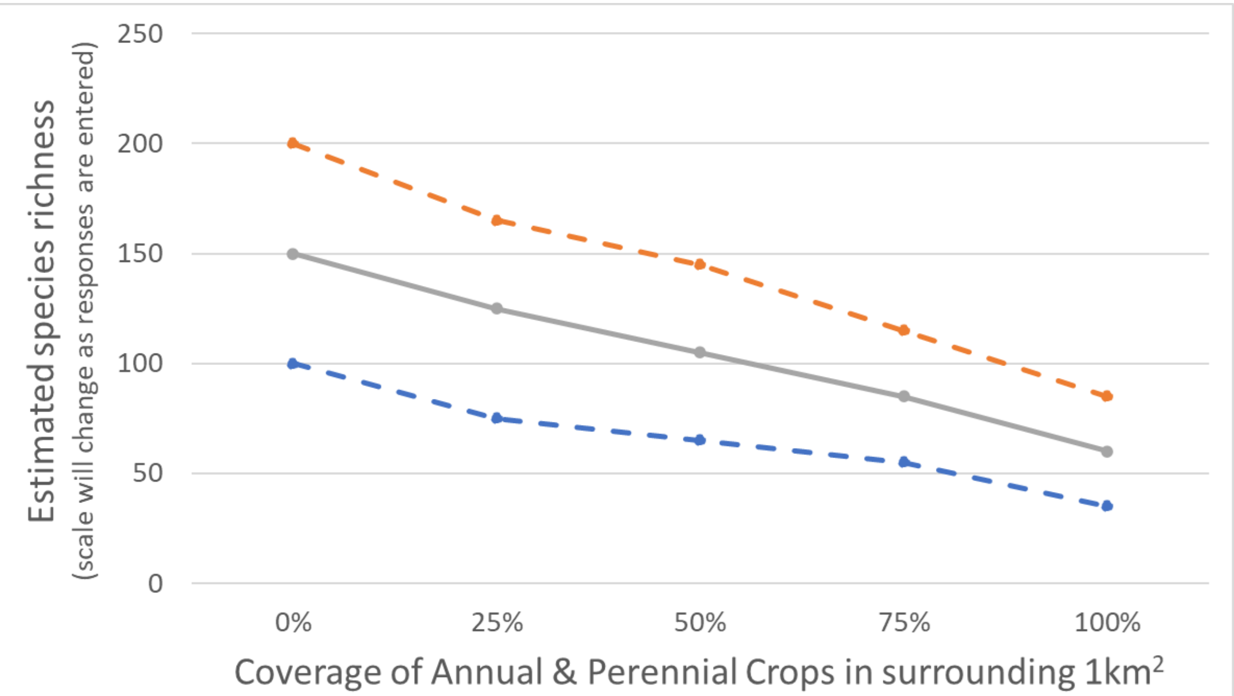

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3. Expert Elicitation

- Asked 414 global entomologists, covering 24 insect Orders
- 105 useable responses, covering 14 insect Orders

Archaeognatha	Hemiptera	Orthoptera
Blattodea	Hymenoptera	Phasmatodea
Coleoptera	Isoptera	Plecoptera
Diptera	Lepidoptera	Trichoptera
Ephemeroptera	Odonata	

- For each Order and threat, modelled response across experts

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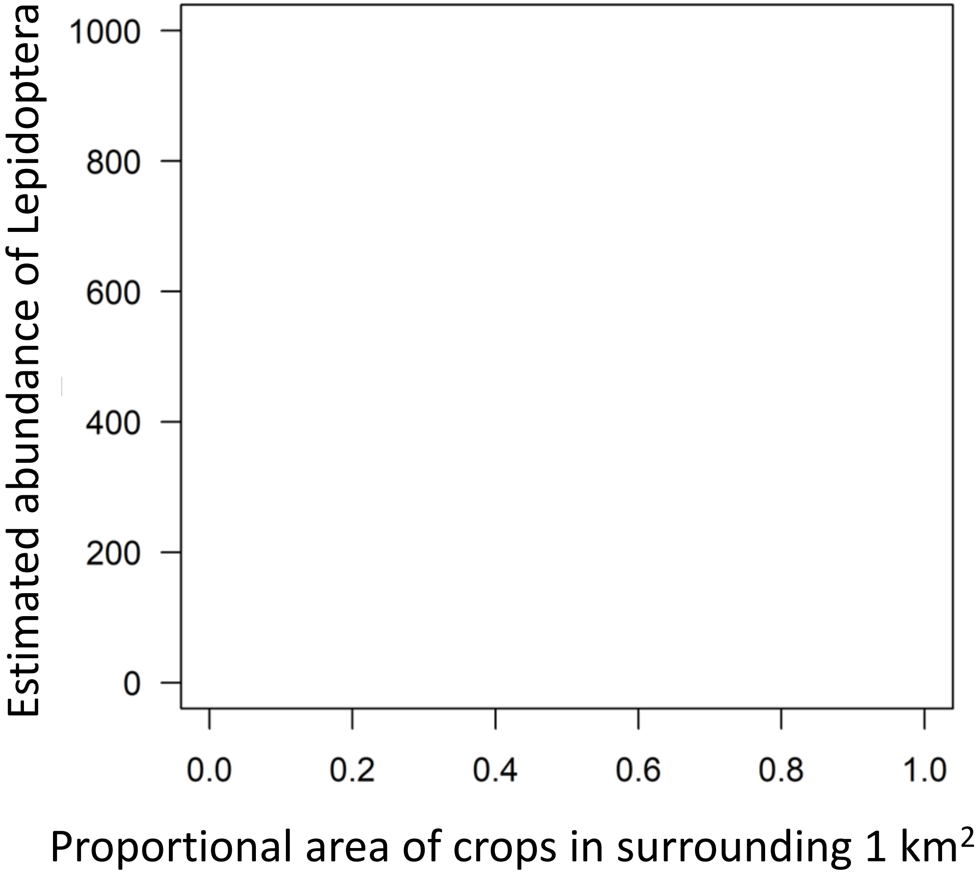
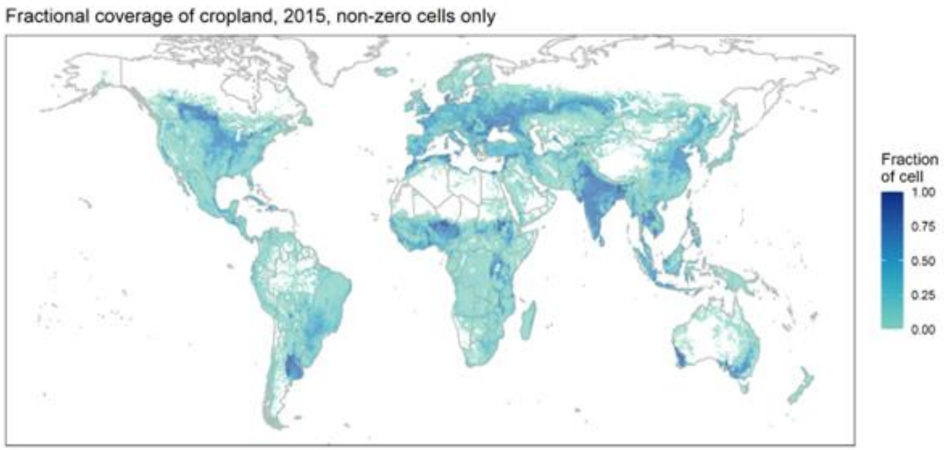
3. Expert Elicitation

Order: Lepidoptera
Threat: Annual & perennial non-timber crops





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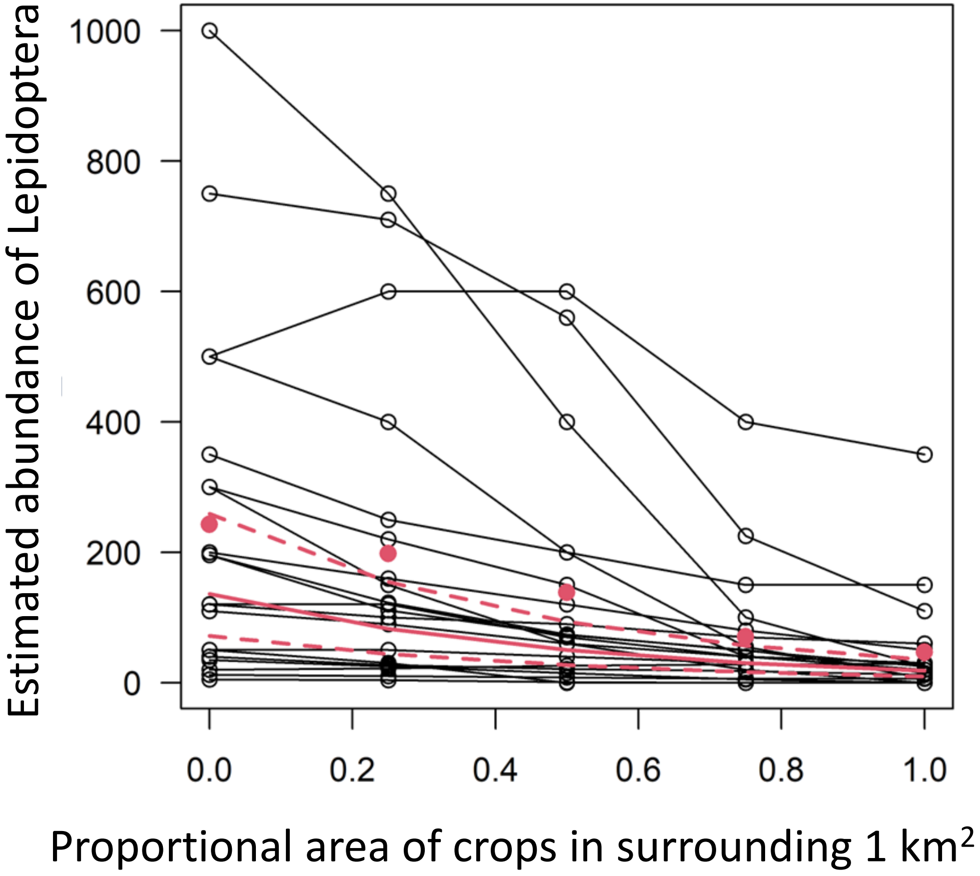
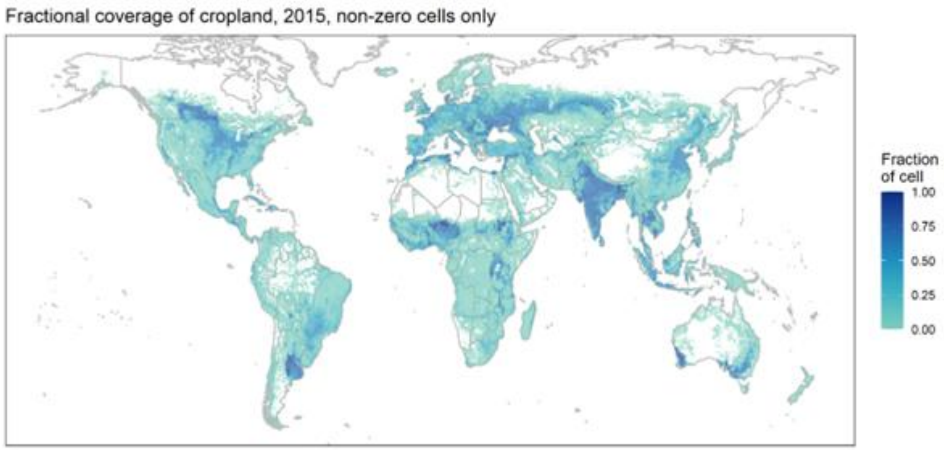
3. Expert Elicitation

Order: Lepidoptera
Threat: Annual & perennial non-timber crops





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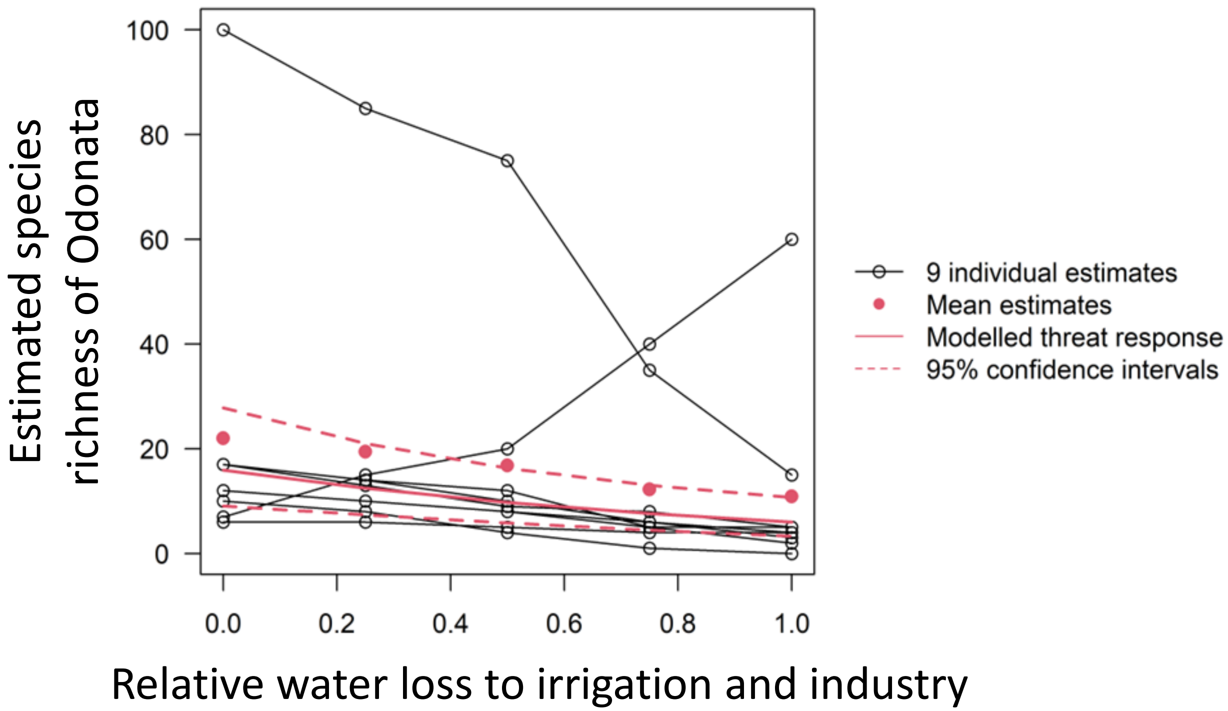
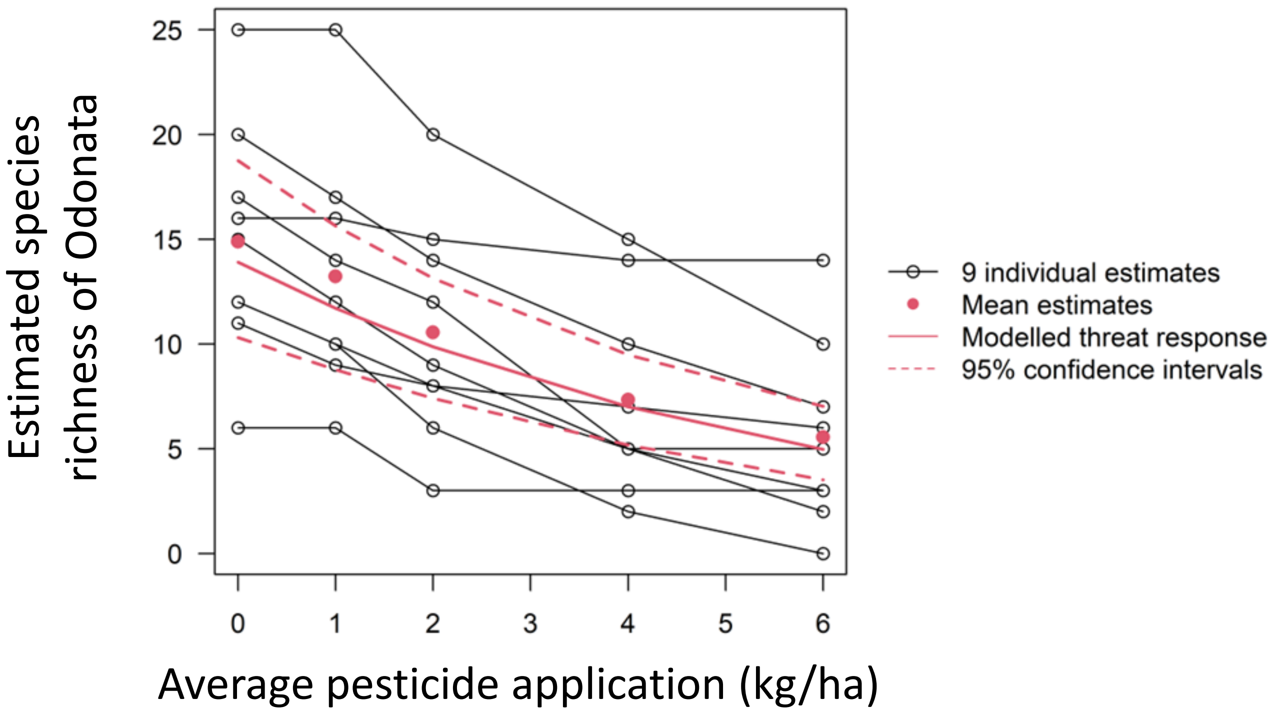
3. Expert Elicitation

Order: Odonata
Threat: Dams and water management



Order: Odonata
Threat: Agricultural and forestry effluents



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3. Expert Elicitation

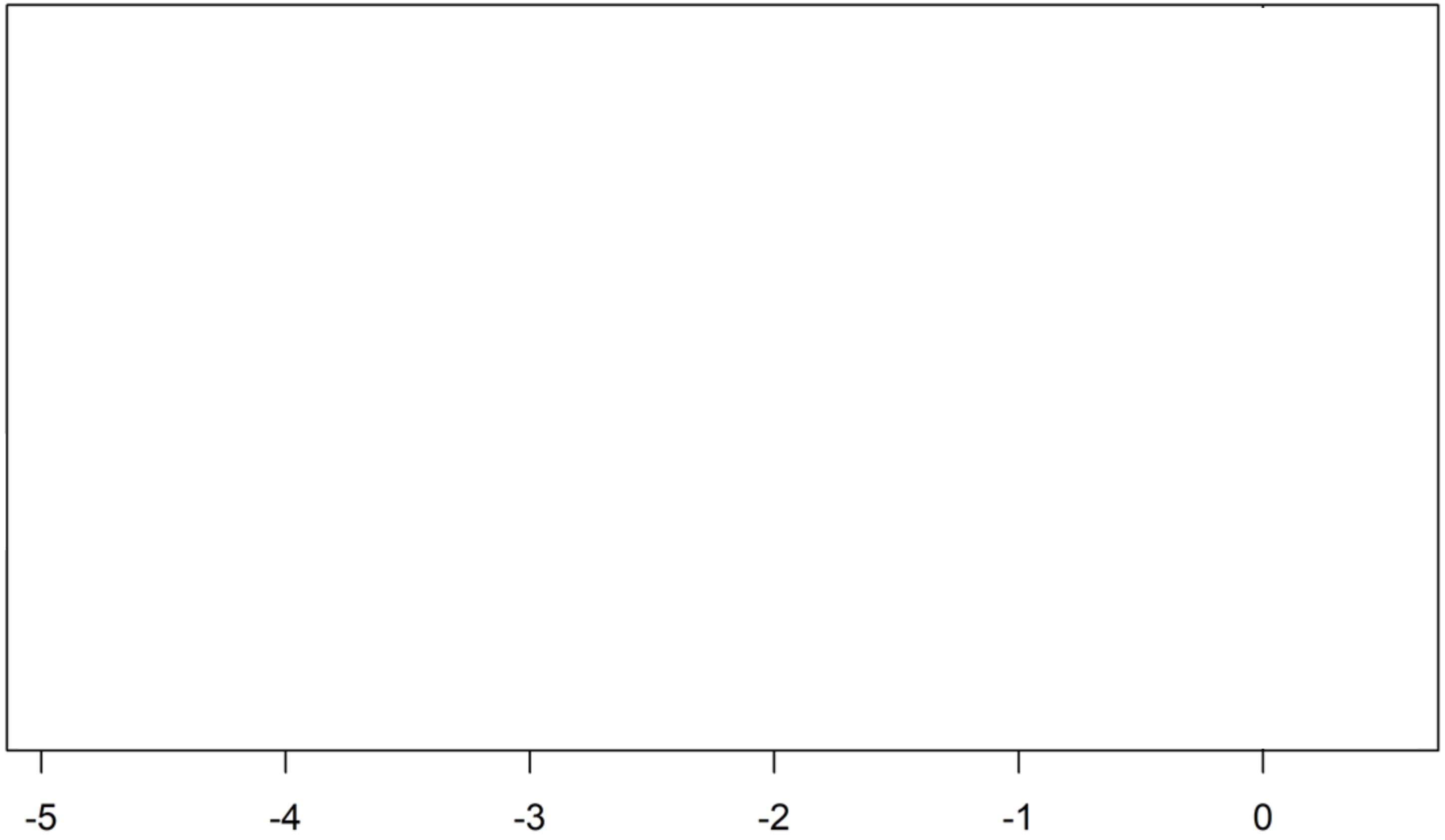
Response: Abundance
Threat: Industrial and military effluents

Coleoptera

Diptera

Ephemeroptera,
Plecoptera, Trichoptera

Odonata



Estimated effect size from model of ‘Abundance ~ Threat intensity’

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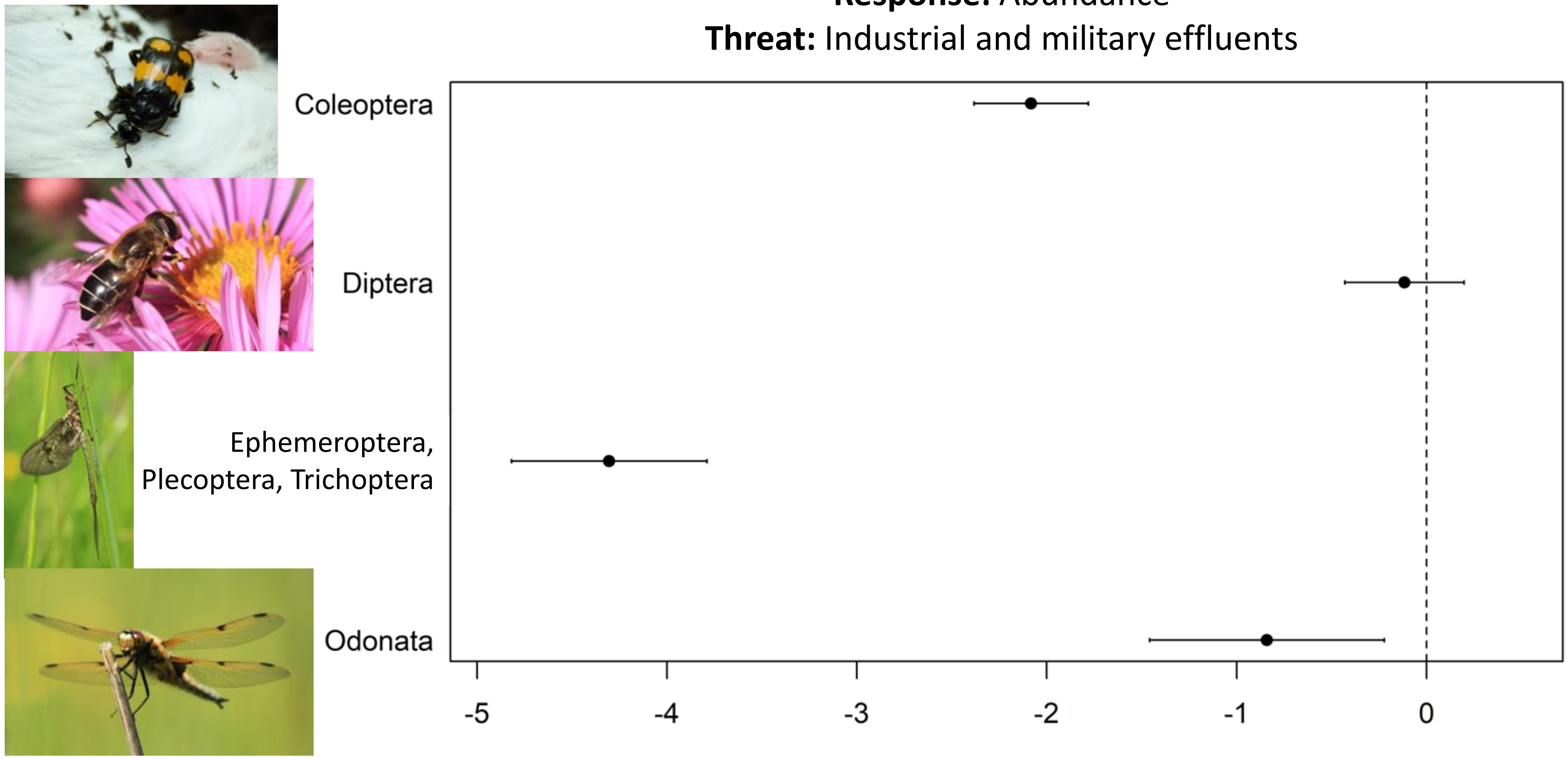
3. Expert Elicitation

Response: Abundance
Threat: Industrial and military effluents



Estimated effect size from model of ‘**Abundance ~ Threat intensity**’

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Questions so far?

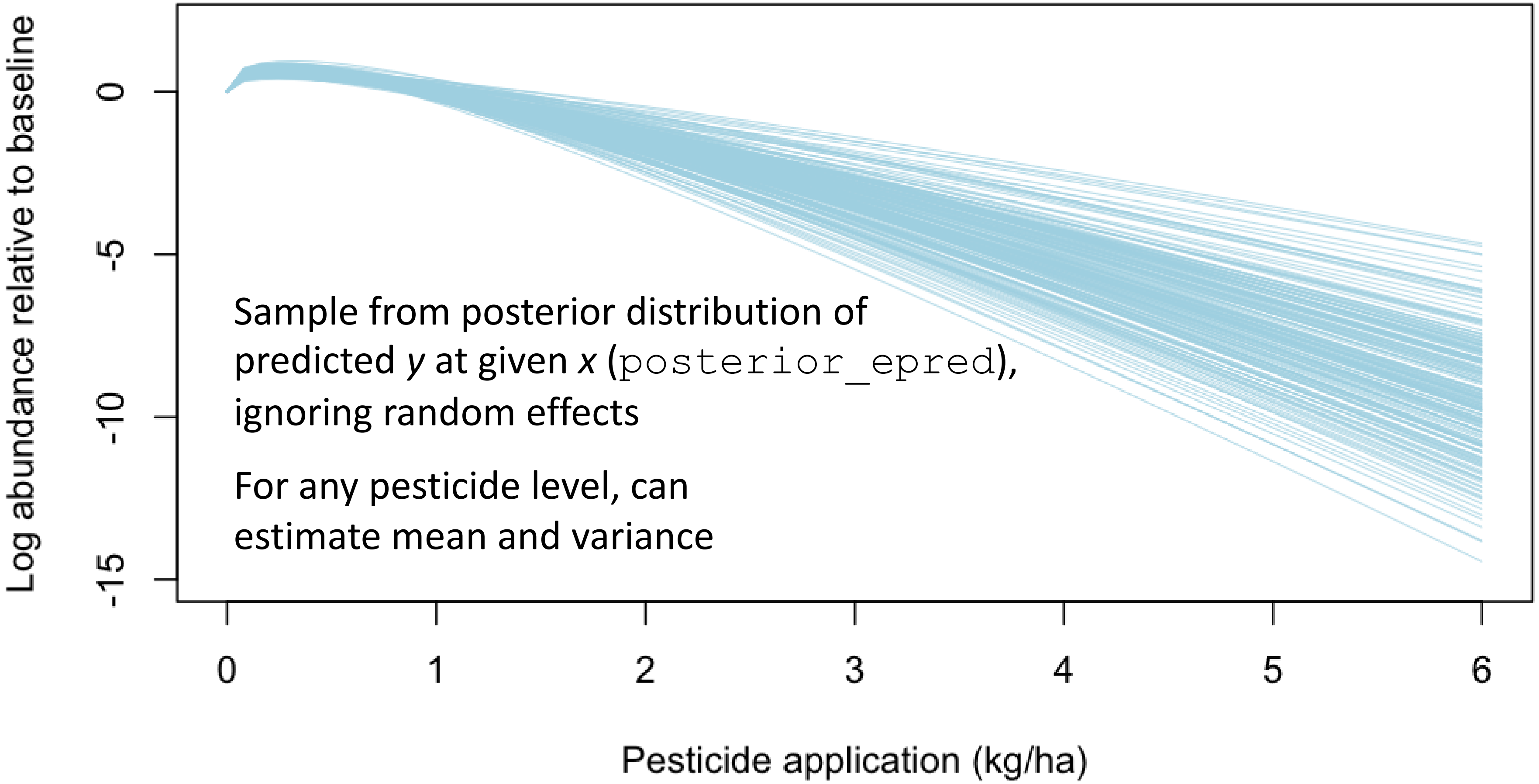
Blending the curve

How should we combine the 3 dose-response relationships?

- The method used to combine relationships needs to:
  - Allow *a priori* weights to differ among evidence types
  - Reflect different precision of parameter estimates among evidence types
- Our approach: Fit Bayesian models using the `brms` package in R
  - Use common scale for threat intensity
  - Sample from posterior predictions of log(abundance) at each intensity
  - Combine these samples to get inverse-variance-weighted mean prediction
- Proof of concept: Combining model of PREDICTS (spatial comparisons) with model based on expert-elicitation estimates

PREDICTS model

```r
predicts_brm <- brms::brm(formula = logAbundance ~ poly(pest_avg_kg_sqrt, 2) +
                            Predominant_habitat + (1|SS) + (1|SSB),
                          data = predicts, chains = 4, iter = iter, cores = 4)
```



Sample from posterior distribution of predicted *y* at given *x* (`posterior_epred`), ignoring random effects

For any pesticide level, can estimate mean and variance

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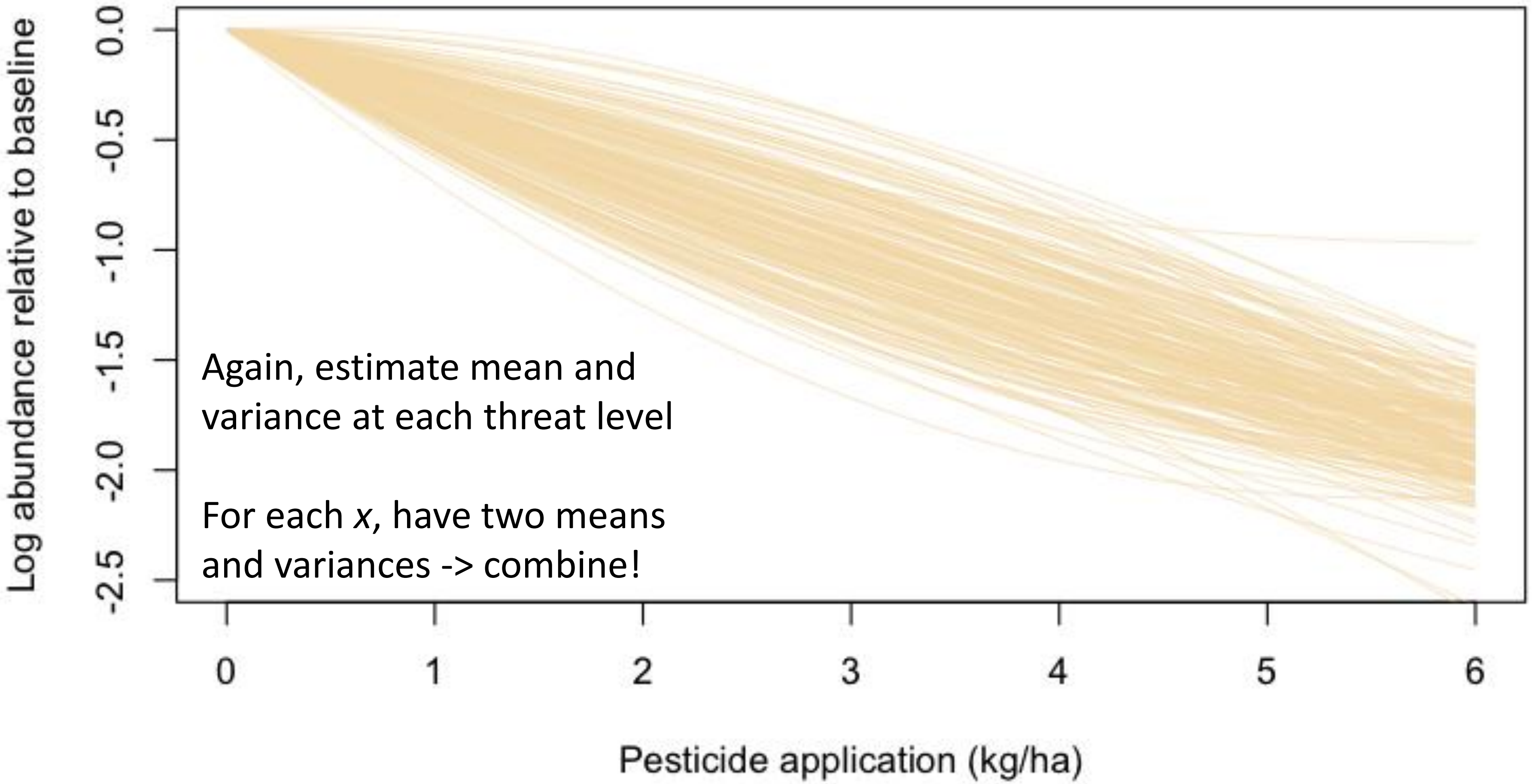
Model of expert estimates

```
expert_brm <- brms::brm(formula = logAbundance ~ poly(Threat_intensity, 2) +
                          (1|Expert),
                        data = expert, chains = 4, iter = iter, cores = 4)
```



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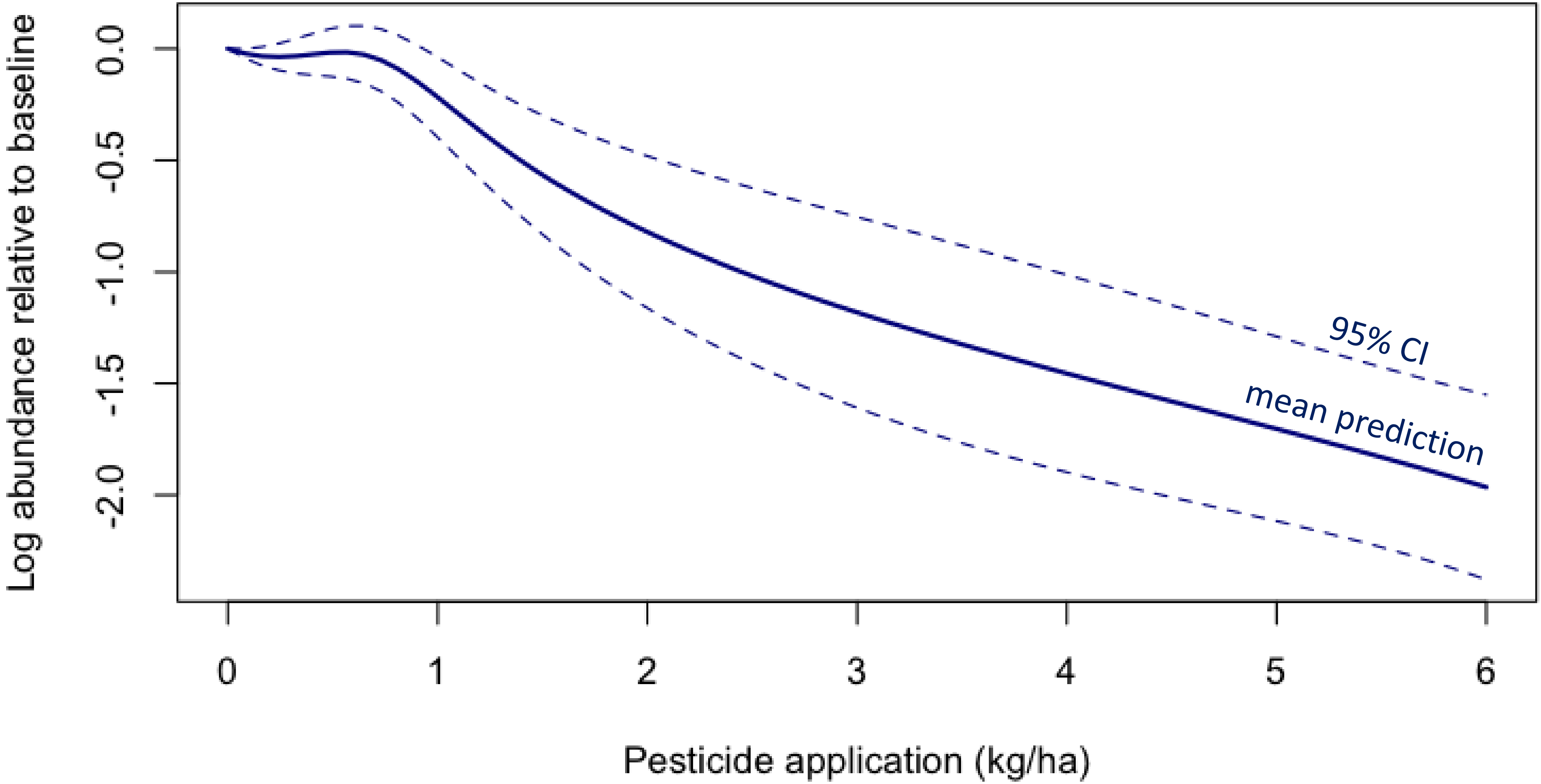
Combined dose-response curve

At each threat value, calculate inverse-variance weighted mean and associated standard error (and hence confidence interval)



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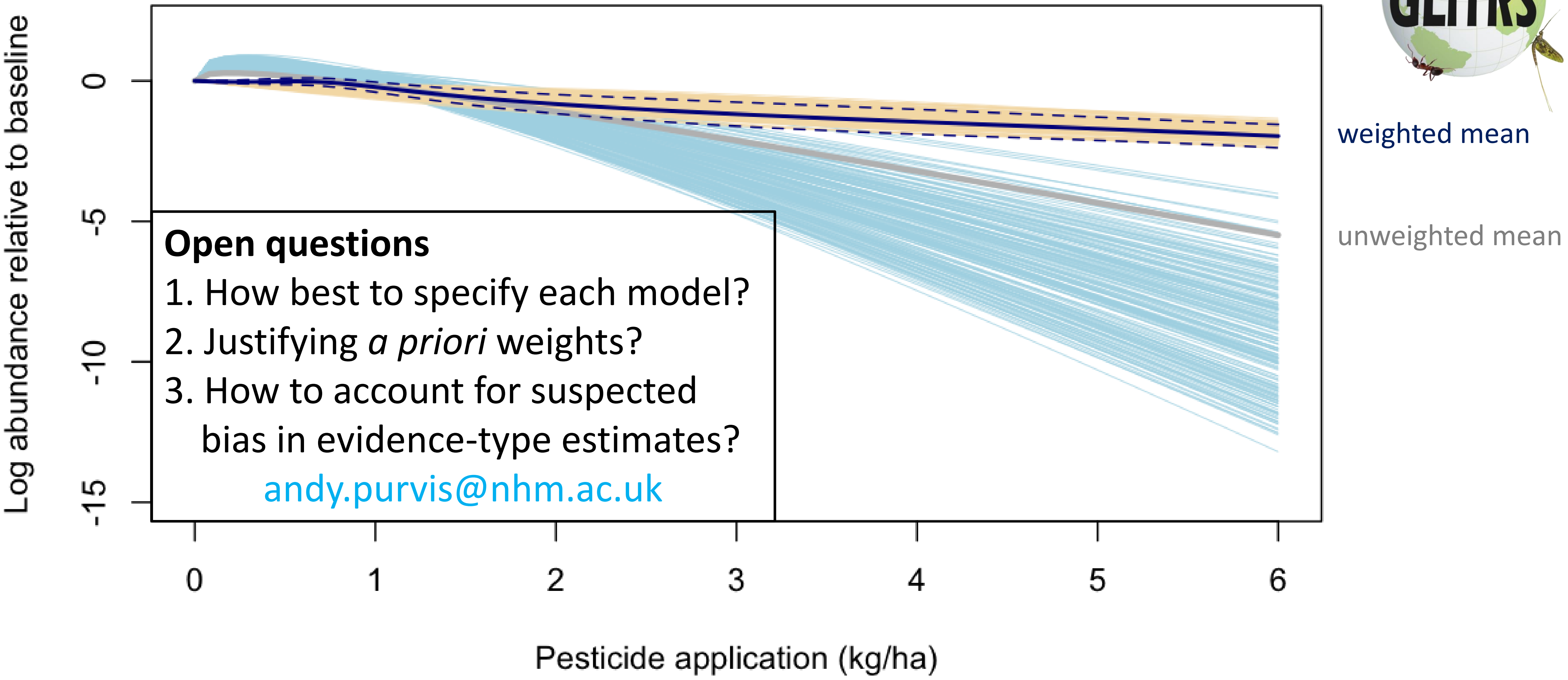
Combined dose-response curve



Open questions

1. How best to specify each model?
2. Justifying *a priori* weights?
3. How to account for suspected bias in evidence-type estimates?

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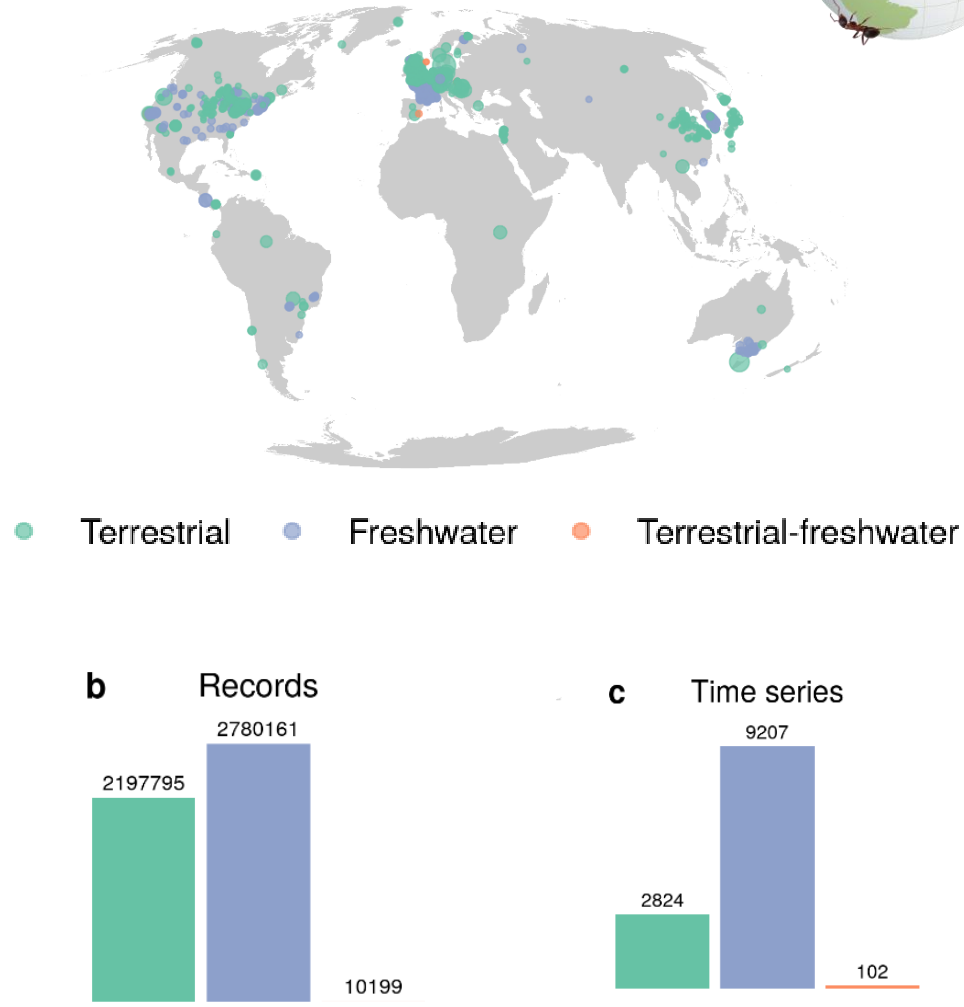
Time Series Database (IN-TIME)

- Time series of insects (>10 years)
- Focus on high taxonomic resolution
- Aquatic and terrestrial - not marine.
- Pre-registered data collection protocol.
- Standardisation of data
    - GBIF taxonomic backbone.
    - Common spatial coordinates.
    - Standardised meta data.
    - Sampling effort measure.
- Open access indicia database (in prog.)



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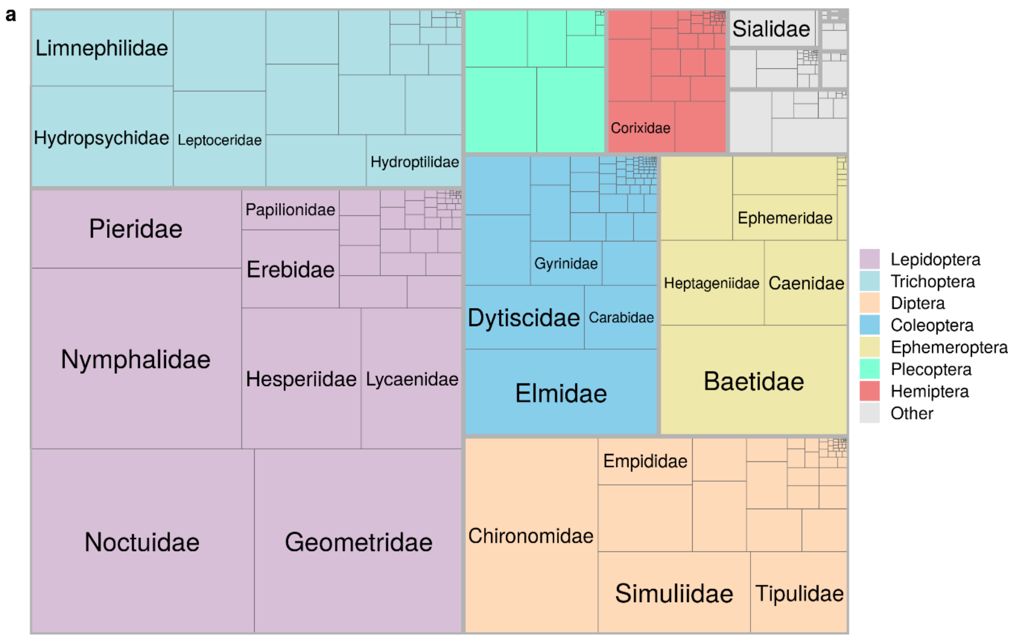
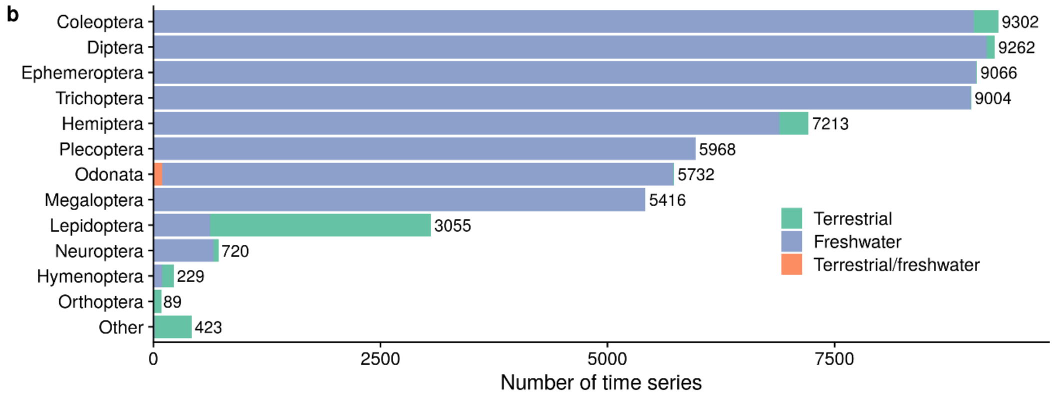
Data coverage

- ~ 5 million insect abundance records.
- 55% (2.7 million) species-level
- 149 studies
- Taxonomic bias - e.g. Lepidoptera
- Regional bias - Palearctic and Nearctic.
- Time series dominated by aquatic monitoring.

Records of insect families



Assemblage time series by order



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Time series

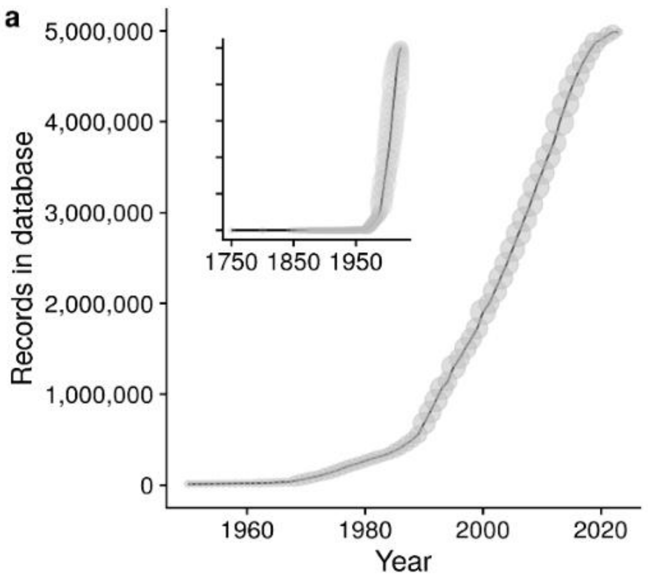
- Median length ~ 20 years (1 – 268 years)

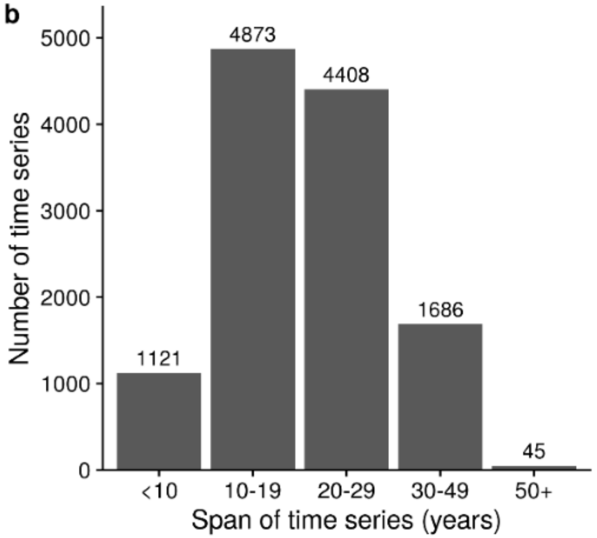
ASSEMBLAGE TIME SERIES: Biodiversity measurements from the same location using the same sampling method at multiple points in time (one to many species).

- 12,133 assemblage time series

POPULATION TIME SERIES: Biodiversity measurements from the same location using the same sampling method at multiple points in time for a single resolved taxon.

- 621,739 population time series
- 49% (305,554) resolved to the species level





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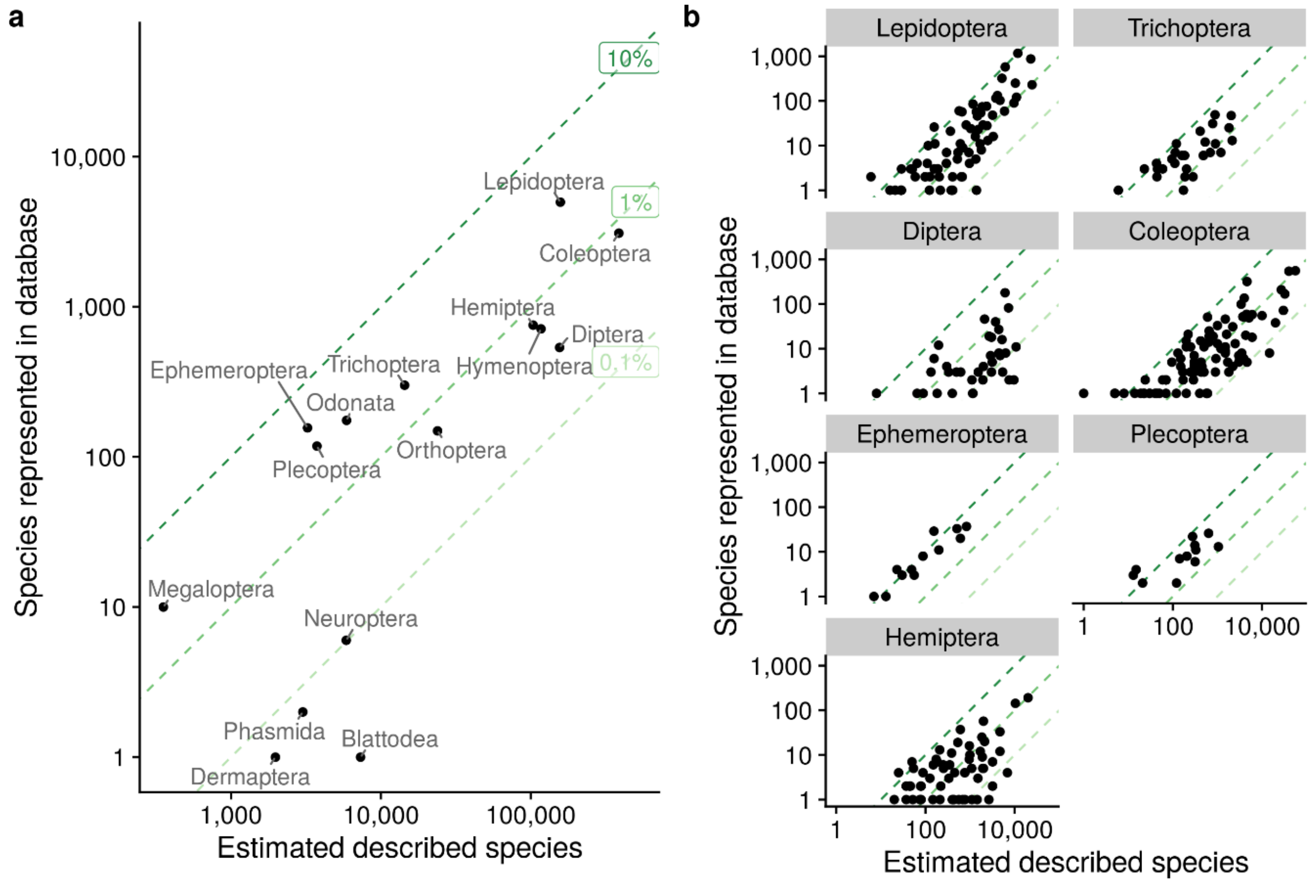
Taxon representation for insect orders

- 15 insect orders
- Taxonomic coverage typically within 0.1 – 10%.
- Reflects 'described' species
- Exceptions, e.g. Phasmida, Dermaptera and Blattodea.
- Unrepresented orders, e.g. ice crawlers (Grylloblattidae).

Database species number vs. the number of described species



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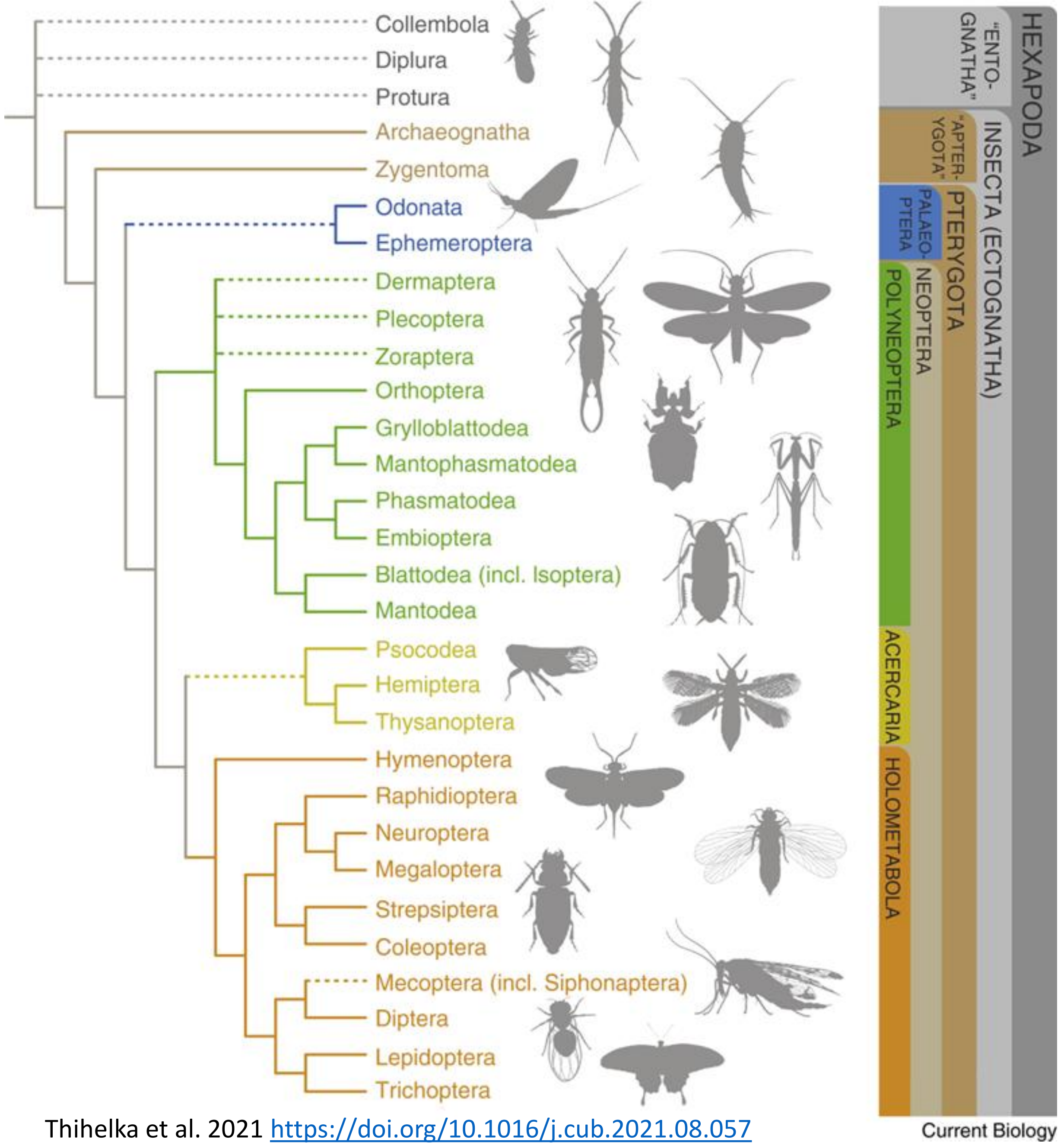
Trait database

GLiTRS will quantify how insect biodiversity changes in response to anthropogenic pressures, how the response varies by functional traits

Create a centralised collation of trait data:

- existing datasets constructed by the team
- open-access databases
- targeted gap-filling



Thihelka et al. 2021 https://doi.org/10.1016/j.cub.2021.08.057

Trait data sources

45+ different databases, compendia of insect trait information considered

SCIENTIFIC DATA

OPEN

SUBJECT CATEGORIES
» Community ecology
» Biodiversity
» Entomology
» Grassland ecology

A summary of eight traits of Coleoptera, Hemiptera, Orthoptera and Araneae, occurring in grasslands in Germany

Martin M. Gossner[1], Nadja K. Simons[1], Roland Achtziger[2], Theo Blick[3,4], Wolfgang H.O. Dorow[4], F

Received: 12 December 2014

GLiTRS

Rainford *et al. BMC Evolutionary Biology* (2016) 16:8
DOI 10.1186/s12862-015-0570-3

BMC Evolutionary Biology

Cook, P.M. *et al*

Traits data for the butterflies and macro-moths of Great Britain and Ireland, 2022

Download data | Supporting docs | View record as | Cite this dataset

https://doi.org/10.5285/33a66d6a-dd9b-4a19-9026-cf1ffb969cdb

DRYAD

Data from: Comparing life groups in multiple dimensi insects?

Bakewell, Adam Thomas [1]; Davis, Katie E. [1] Peter J. [1]

Author affiliations

Published Feb 03, 2020 on Dryad. https://doi.org/1

RESEARCH ARTICLE Open Access

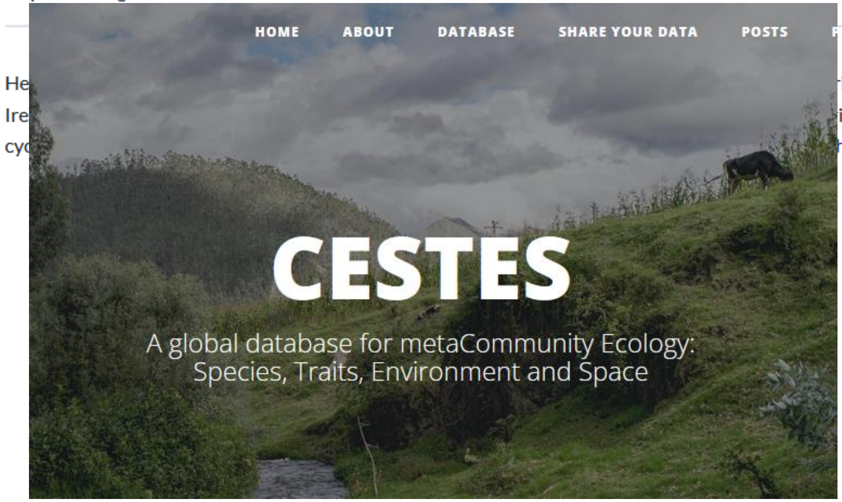
CrossMark

Phylogenetic analyses suggest that diversification and body size evolution are independent in insects

James L. Rainford[1], Michael Hofreiter[2] and Peter J. Mayhew[1*]

Abstract

Background: Skewed l property of a wide ranç



scientific data

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nature › scientific data › data descriptors › article

Data Descriptor | Open access | Published: 03 July 2019

A dataset of egg size and sha insect species

Samuel H. Church, Seth Donoughe, Bruno A. S. de M

Scientific Data 6, Article number: 104 (2019) | Cite this

10k Accesses | 77 Altmetric | Metrics

Data Paper

Biodiversity Data Journal 2: e1041
https://doi.org/10.3897/BDJ.2.e1041 (29 Jan 2014)

Morphological and Geographical Traits of the British Odonata

Gary D Powney, Stephen J Brooks, Louise J Barwell, Phil Bowles, Robert N L Fitt, Alyson Pavitt,

of ecological research, particularly for modeling synthesised information from the literature (mainly museum specimens, providing a comprehensive nt species of Odonata in Britain. Traits included in ts (e.g. body length) to attributes based on the

USGS
science for a changing world

U.S. Geological Survey Data Series

A Database of Lotic Invertebrate Traits for North America

By Nicole K. M. Vieira, N. LeRoy Poff, Daren M. Carlisle, Stephen R. Moulton II, Marci L. Koski, and Boris C. Kondratieff

U.S. Geological Survey Data Series 187

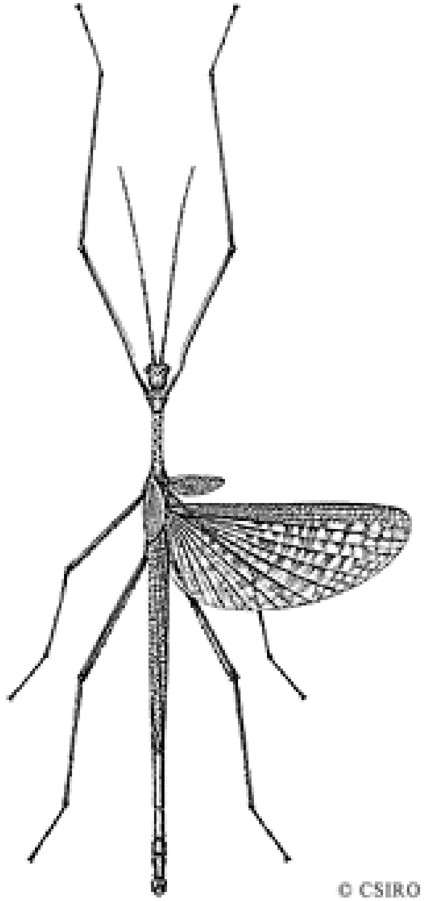
In cooperation with Colorado State University

Trait data compilation

Fuzzy-coded at family-level

Minimum size			Size Categories (mm)											
Order	**Family**	**Richness**	**0.35**	**0.71**	**1.4**	**2.8**	**5.6**	**11**	**22**	**45**	**89**	**178**	**355**	**708**
Phasmatodea	Agathemeridae	8	0	0	0	0	0	0	0	1	0	0	0	0
	Aschiphasmatidae	96	0	0	0	0	0	0	1	0	0	0	0	0
	Bacillidae	54	0	0	0	0	0	0	0	1	0	0	0	0
	Diapheromeridae	1210	0	0	0	0	0	0	1	0	0	0	0	0
	Heteropterygidae	103	0	0	0	0	0	0	1	0	0	0	0	0
	Phasmatidae	991	0	0	0	0	0	0	0	0	1	0	0	0
	Phylliidae	51	0	0	0	0	0	0	0	1	0	0	0	0
	Pseudophasmatoidea	406	0	0	0	0	0	0	1	0	0	0	0	0
	Timematidae	21	0	0	0	0	0	0	1	0	0	0	0	0
		Phasmatodea	**0**	**0**	**0**	**0**	**0**	**0**	**0.62**	**0.04**	**0.34**	**0**	**0**	**0**

Rainford *et al*. 2016 DOI 10.1186/s12862-015-0570-3



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Trait data compilation

Fuzzy-coded at family-level

Larval diet

Order	Family	Richness	Fungivory	Detritivory	Phytophagy	Predation	Parasitoidism	Ecto-parasitism	Non-feeding	Liquid feeding and nectivory
Thysanoptera	Aeolothripidae	201	0	0	0.5	0.5	0	0	0	0
	Heterothripidae	76	0	0	1	0	0	0	0	0
	Phlaeothripidae	3532	0.5	0	0.5	0	0	0	0	0
	Thripidae	2066	0	0	0.5	0.5	0	0	0	0
		Thysanoptera	**0.30**	**0**	**0.51**	**0.19**	**0**	**0**	**0**	**0**

Rainford *et al*. 2016 DOI 10.1186/s12862-015-0570-3

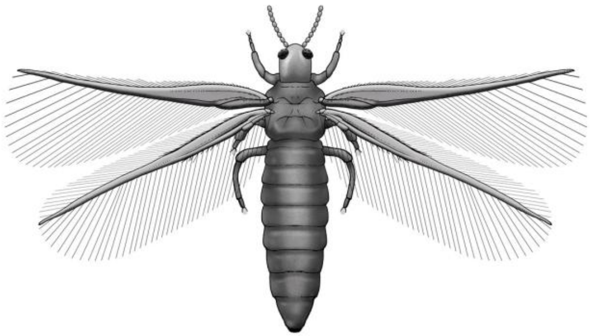

Image: Andrew Howells © Australian Museum

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Order	Family Richness	Minimum size	Maximum size	Larval diet	Adult diet	Voltinism	Lifelong fecundity	Sexual system	Female chromosomes	Male chromosomes	Karyotype	Parental care	Dispersal	Life cycle	Flight	Colony behaviour	Sociality
Entomobryomorpha	5	0.60	0.60	1.00	1.00			0.60	0.80	0.60	0.60						
Neelipona	1	1.00	1.00	1.00	1.00												
Poduromorpha	7	0.57	0.57	1.00	1.00			0.43	0.57	0.29	0.29						
Symphypleona	6	0.17	0.17	0.67	0.67			0.83	0.50	0.50	0.50						
Diplura	10	0.20	0.20	0.40	0.40	0.10	0.10							1	1	1	1
Protura	1	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00			1	1	1	1
Archaeognatha	2	0.50	0.50	0.50	0.50	0.50	0.50			0.50		0.50		1	1	1	1
Zygentoma	3	1.00	1.00	1.00	1.00	0.33	0.33	0.33	0.33	0.33	0.33	0.33		1	1	1	1
Ephemeroptera	43	0.70	0.70	0.72	0.74	0.30	0.28	0.14	0.14	0.14	0.14	0.21		1	1	1	1
Odonata	39	0.67	0.67	0.74	0.74	0.26	0.23	0.41	0.41	0.41	0.41	0.05		1	1	1	1
Orthoptera	43	0.53	0.53	0.63	0.63	0.23	0.19	0.14	0.12	0.12	0.14	0.16	0.09	1	1	1	1
Phasmida	14	0.64	0.64	0.71	0.71	0.07	0.07	0.21	0.14	0.14	0.14	0.14		1	1	1	1
Embioptera	13	0.08	0.08	0.54	0.54	0.08	0.08	0.15	0.15	0.15	0.15	0.31		1	1	1	1
Mantophasmatodea	1	1.00	1.00	1.00	1.00	1.00	1.00							1	1	1	1
Grylloblattodea	1	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00	1.00			1	1	1	1
Plecoptera	17	0.88	0.88	0.71	0.71	0.41	0.41	0.12	0.06	0.12	0.12	0.18		1	1	1	1
Dermaptera	12	0.58	0.58	0.58	0.58	0.08	0.08	0.50	0.50	0.50	0.50	0.50		1	1	1	1
Zoraptera	2	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50	0.50		1	1	1	1
Mantodea	29	0.03	0.03	0.45	0.45	0.03	0.03	0.21	0.21	0.21	0.21	0.14		1	1	1	1
Blattodea	18	0.33	0.33	0.72	0.72	0.11	0.11	0.44	0.44	0.44	0.44	0.22		1	1	1	1
Psocodea	80	0.45	0.45	0.60	0.60	0.03	0.03	0.40	0.36	0.35	0.26	0.10		1	1	1	1
Thysanoptera	9	0.44	0.44	0.44	0.44	0.11	0.11	0.22	0.22	0.22		0.33		1	1	1	1
Hemiptera	168	0.51	0.51	0.54	0.54	0.07	0.07	0.15	0.14	0.01	0.07	0.20	0.13	1	1	1	1
Hymenoptera	95	0.81	0.81	0.76	0.81	0.02	0.01	0.38	0.38	0.38		0.34		1	1	1	1
Strepsiptera	12	0.08	0.08	0.08	0.08	0.08		0.17	0.08	0.08	0.08			1	1	1	1
Coleoptera	185	0.74	0.74	0.61	0.63	0.09	0.08	0.32	0.31	0.31	0.31	0.22	0.23	1	1	1	1
Neuroptera	15	0.93	0.93	0.67	0.73	0.13	0.13	0.40	0.40	0.40	0.40	0.20		1	1	1	1
Megaloptera	2	1.00	1.00	1.00	1.00	0.50	0.50	0.50	0.50	0.50	0.50	1.00		1	1	1	1
Raphidioptera	2	0.50	0.50	1.00	1.00	0.50	0.50	0.50	0.50	0.50	0.50			1	1	1	1
Trichoptera	45	0.84	0.84	0.87	0.87	0.47	0.44	0.16	0.13	0.22	0.13	0.11		1	1	1	1
Lepidoptera	139	0.73	0.73	0.72	0.73	0.05	0.04	0.21	0.11	0.21	0.11	0.16	0.04	1	1	1	1
Diptera	160	0.71	0.71	0.64	0.69	0.14	0.09	0.27	0.29	0.29	0.27	0.21		1	1	1	1
Siphonaptera	20	0.05	0.05	0.75	0.75	0.05	0.05	0.10	0.10	0.10	0.10	0.05		1	1	1	1
Mecoptera	9	0.89	0.89	0.44	0.89	0.11	0.11	0.44	0.56	0.44	0.44	0.33		1	1	1	1

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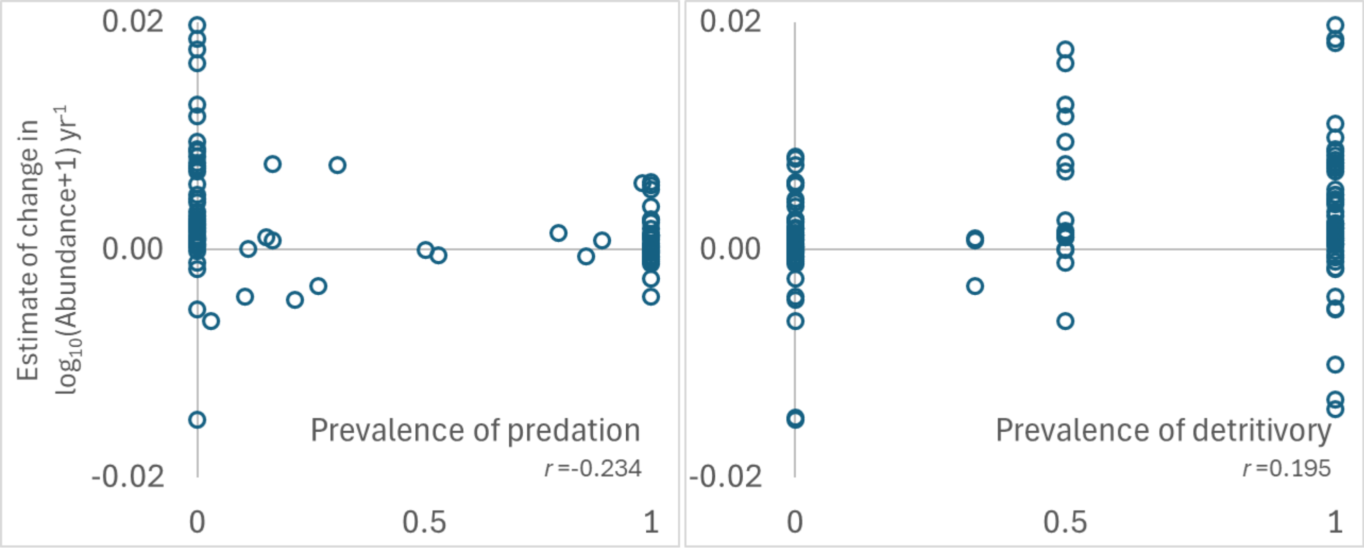
Rate of change in abundance of freshwater insect families varies with prevalence of predation and detritivory within the family



Seeking other insect trait data sources
(ANY SUGGESTIONS WELCOME)
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Some discussion questions

- **Scale:** Insect data mostly local, threat data less so, aims are global
- **Data gaps:** What could be done to fill or mitigate them?
    - What about interactions among threats?
- How might GLiTRS contribute to an RCN overview?
- How could we coordinate and maximise **policy impact** – moving insect diversity up the agenda?

Sharing resources

- Expert elicitation protocol & templates: a.j.bladon@reading.ac.uk
- Meta-analysis open protocol & gaps: jwm57@cam.ac.uk
- Spatial comparisons/PREDICTS data & gaps: andy.purvis@nhm.ac.uk
- Threat maps: charlotte.outhwaite@ioz.ac.uk
- Sources of trait data: j.f.murphy@qmul.ac.uk