

Workshop Report

Building an atlas of knowledge for invasion biology and beyond! 2nd enKORE-INAS Workshop

Maud Bernard-Verdier^{‡,§}, Tina Heger^{‡,|}, Daniel Mietchen^{‡,¶}, Camille L. Musseau[‡], Marc Brinner[#], Alexander Hillig[#], Peter Kraker[□], Sophie Lokatis[§], Ana Luisa Nunes^κ, Nils Scheidweiler[»], Markus Stocker[^], Roxane Vial[§], Lars Vogt^ν, Sven Bacher[!], Eya Baklouti[?], Harsh Bardhan Gupta[§], Jean-Nicolas Beisel^ς, Sandro Bertolino^ϕ, Elizabeta Briski[‡], Gustavo Adolfo Castellanos-Galindo^{‡,§}, Franck Courchamp[‡], Ella Daly^ρ, Wayne Dawson^Α, James Dickey[‡], Thomas Evans[‡], Yuval Itescu^{⊖,‡,§}, Birgitta Koenig-Ries[»], Lohith Kumar[§], Sabrina Kumschick^F, Laura A. Meyerson[‡], Zarah Pattison^{Ν,Κ}, William Pfadenhauer^ϕ, David Renault^ρ, Fiona Rickowski[§], Florian Ruland^{§,?}, Conrad Schittko^W, Tanja Straka^W, Florencia Yannelli[§], Jonathan M Jeschke^{‡,§}

‡ Leibniz Institute of Freshwater Ecology and Inland Fisheries, Berlin, Germany

§ Freie Universität Berlin, Berlin, Germany

| Technische Universität München, Munich, Germany

¶ Ronin Institute for Independent Scholarship, Montclair, United States of America

University of Bielefeld, Bielefeld, Germany

□ Open Knowledge Maps, Graz, Austria

« International Union for Conservation of Nature, Cambridge, United Kingdom

» Friedrich Schiller University Jena, Jena, Germany

^ Leibniz information center for science and technology, Hannover, Germany

ν Rheinische Friedrich-Wilhelms-Universität, Bonn, Germany

! University of Fribourg, Fribourg, Switzerland

? University of Passau, Passau, Germany

ς University of Strasbourg, Strasbourg, France

ϕ University of Turin, Torino, Italy

‡ GEOMAR Helmholtz Centre for Ocean Research Kiel, Kiel, Germany

ρ Université Paris-Saclay, Paris, France

ρ University of Rennes, Rennes, France

Α Durham University, Durham, United Kingdom

⊖ University of Haifa, Haifa, Israel

F Stellenbosch University, Matieland, South Africa

‡ University of Rhode Island, Kingston, United States of America

Ν University of Stirling, Stirling, United Kingdom

Κ Newcastle University, Newcastle upon Tyne, United Kingdom

ϕ University of Massachusetts, Amherst, United States of America

? West Iceland Nature Research Centre, Stykkishólmur, Iceland

W Technische Universität Berlin, Berlin, Germany

Corresponding author: Maud Bernard-Verdier (maud.bernard-verdier@fu-berlin.de)

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Abstract

With the exponential increase in scientific publications, new conceptual and technological tools are needed to help scientists, students, managers and policy-makers to navigate and digest current scientific knowledge. Hi Knowledge is an initiative to synthesise and visualise scientific knowledge, with an initial focus on invasion biology that is currently expanding to include urban ecology, restoration ecology and freshwater ecology. In a workshop on 5-6 June 2023 in Berlin, Germany, we discussed and tested a collection of new open tools related to this initiative in order to publish, curate, explore and synthesise concepts and results in ecology. Three main themes were discussed during in-person breakout group sessions: (1) building and using open tools for knowledge curation, exploration and synthesis; (2) making open knowledge searchable and machine friendly by improving modelling and annotation of scientific knowledge; and (3) extending beyond the field of invasion biology. We report on the discussions of all twelve sessions pertaining to these themes. A main underlying goal of our workshop was to build a community of scientists involved in openly co-designing and using these tools. Overall, the participants were enthusiastic about the usefulness of these tools and discussions gravitated around improving them and finding strategies to scale-up participation by the community. Follow-up user tests and publications are planned for individual tools and topics.

Keywords

conceptual map, data science, ecology, FAIR data, knowledge graphs, knowledge representation, knowledge synthesis, open science, semantic modelling

Date and place

5-6 June 2023 in Berlin, Germany

List of participants

In person:

Sven Bacher, Eya Baklouti, Harsh Bardhan Gupta, Jean-Nicolas Beisel, Maud Bernard-Verdier, Sandro Bertolino, Marc Brinner, Elizabeta Briski, Gustavo Castellanos-Galindo, Franck Courchamp, Ella Daly, Wayne Dawson, James Dickey, Thomas Evans, Tina Heger, Alexander Hillig, Yuval Itescu, Jonathan Jeschke, Birgitta König-Ries, Peter Kraker, Lohith Kumar, Sabrina Kumschick, Sophie Lokatis, Laura A. Meyerson, Daniel Mietchen, Camille Musseau, Ana Nunes, Zarah Pattison, Will Pfadenhauer, David Renault, Fiona Rickowski, Florian Ruland, Nils Scheidweiler, Conrad Schittko, Markus Stocker, Tanja Straka, Roxane Vial, Lars Vogt, Florencia Yannelli

Online:

David Aldridge, Céline Bellard, Vanessa Bremerich, Jane Catford, Katie Costello, Gregory Dietl, Franz Essl, Adrian Garcia-Rodriguez, Ivan Jaric, Anita Kirmer, Andrew Latimer, Bernd Lenzner, Jaco Le Roux, Chunlong Liu, Xuan Liu, Christopher Lortie, Rafael Macedo, Daniela Mahler, Clara Marino, Ana Novoa, Rose O'Dea, Fran Oficialdegui, Anibal Pauchard, Cristian Pérez Granados, Jan Pergl, Pavel Pipek, Petr Pyšek, Núria Roura-Pascual, Laura Saggiomo, Malwina Schafft, Timothy Staples, Dave Strayer, Mark van Kleunen, Giovanni Vimercati, Jean Vitule, Victoria Werenkraut

Introduction

With the exponential increase in scientific publications, it has become difficult to acquire and maintain an overview of expanding fields like invasion biology, urban ecology or restoration ecology. [Hi Knowledge](#) is an initiative to synthesise and visualise scientific knowledge in ecology, which Jonathan Jeschke and Tina Heger started over a decade ago. One aspect of the initiative is an online hub with interactive visualisation tools that uniquely structure data and information to make them better accessible and comprehensible. It is also a community of people — ecologists, philosophers, practitioners — sharing an interest in knowledge synthesis in invasion ecology and beyond. This initiative is constantly in motion and we have currently two ongoing projects: the enKORE project and the INAS project.

The [enKORE project](#) aims to provide tools for the community to navigate scientific knowledge and literature in invasion biology. It combines the power of data science and community engagement to develop an open interactive atlas of knowledge, mainly with a focus on invasion biology, but now also for urban and restoration ecology. Our goal is to foster open knowledge by making the scientific literature machine-readable to help humans and machines navigate it and create new knowledge.

The [INAS project](#) focuses on more fundamental aspects of knowledge science, developing natural language models and ontologies to extract and model research hypotheses from

scientific texts, as well as help guide young scientists build their own research hypotheses. The goal is to enable users to follow ongoing argumentation in a scientific community and to develop their own arguments.

Aims of the workshop

The Hi Knowledge initiative is about building tools to navigate open knowledge with and for our community, which we hope to extend beyond the limits of our own scientific fields (mainly invasion biology, urban, restoration and freshwater ecology) and practice (academic research). Workshops are an integral part of the process, during which we meet the community, build and improve these tools and engage in conversations about how we can make scientific knowledge more open and accessible. Since the beginning of the initiative about ten years ago, Hi Knowledge workshops have tackled topics, such as connecting hypotheses in invasion biology or defining Dark Knowledge (Jeschke et al. 2019).

The first joint INAS-enKORE workshop took place online in May 2022, assembling a group of over 90 international participants from a variety of research fields and academic career stages ([see summary report](#)). That first workshop outlined a path for developing both projects and this second workshop aimed to show the progress made, as well as discuss some new developments and future projects.

In line with the main outcome from the first workshop, this workshop aimed to:

1. Present and test the different tools for curating and exploring knowledge in invasion biology, which we have continued to develop in the last year;
2. Imagine solutions for active community engagement and curation;
3. Discuss current and future efforts and challenges in extending the current map of knowledge beyond invasion biology, to the fields of freshwater biology, urban ecology or restoration ecology, as well as how to connect those fields in conceptual space;
4. Invite new ideas for knowledge synthesis from participants, as has been the custom in all Hi Knowledge workshops.

Programme and process

The workshop took place over two days (5-6 June 2023). Apart from the first morning of presentations, the workshop was entirely dedicated to focused working sessions in small breakout groups. The workshop was held mostly in person, with 39 participants joining us in Berlin from all over Europe, but also America and South Africa (Fig. 1). While our last workshop was entirely online and gathered a large community from around the world, this workshop was designed to be in-person and smaller, to allow for more engaged in-depth discussions in small working groups. As this restricted the number of participants, we held

the first morning of the general presentation as a hybrid session, which was joined by over 30 additional participants from a broader geographical extent (Fig. 2).



Figure 1. [doi](#)

Group photo of the in-person participants on the first day of the workshop.

Detailed programme of the two-day workshop

Morning hybrid session

10:00 Arrival and welcome with a short quiz.

10:30 Overview of Hi Knowledge initiative (Jonathan Jeschke), enKORE and INAS projects (Tina Heger), followed by Q&A.

11:30 Keynote by Rose O'Dea: Limits to synthesising evidence in ecology, followed by Q&A.

12:15 Lunch break.

Afternoon in person

13:15 Group picture.

13:30 Tools fair: Option to explore (like a poster session) the different stations:

- Open Knowledge Maps (Peter Kraker);
- Open Research Knowledge Graphs meets Hi Knowledge (Markus Stocker, Lars Vogt, Maud Bernard-Verdier);
- Causal network graphs (Tina Heger);
- INBIO TST (Marc Brinner, Alexander Hillig, Nils Scheidweiler);
- Wikidata and Scholia (Daniel Mietchen).

14:30 Tool exploration sessions: kicked-off by 1-min pitches; option to switch after 1 hour:

- Open Knowledge Maps scavenger hunt (Peter Kraker);
- Modelling a template for annotating content of publications in ecology (Lars Vogt, Maud Bernard-Verdier);
- Causal network graphs (Tina Heger);
- Wikidata and Scholia (Daniel Mietchen).

16:30 Session groups report back and joint discussion (until ca. 17:30).

19:00 Joint dinner.

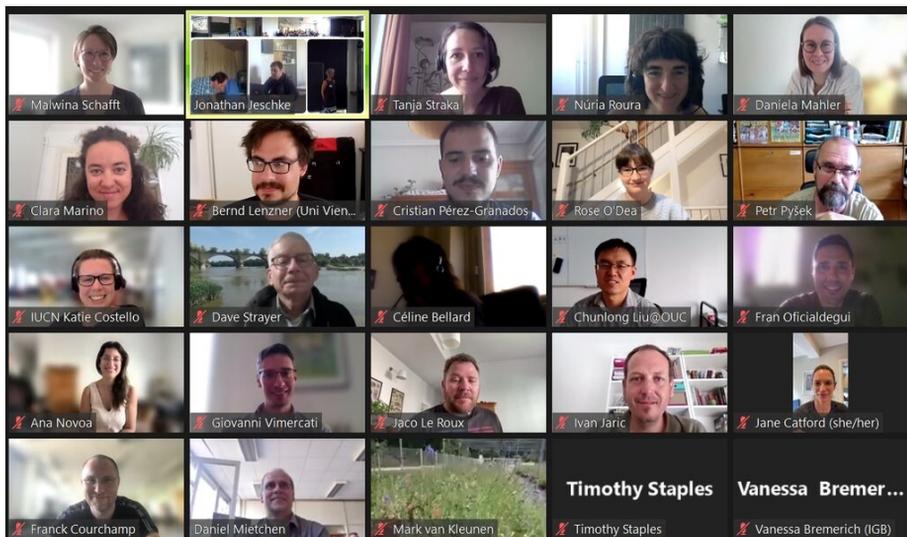


Figure 2. [doi](#)

Group photo of some of the online participants in the hybrid morning session.

Tuesday, June 6

Full day in person

09:00 Overview of day 2.

09:15 Break-out group pitches for the morning:

- Short publications on research hypotheses (Tina Heger);
- Freshwater systems: Practical relevance of invasion hypotheses, connecting researchers and practitioners (Camille Musseau);
- Urban systems: Building a common knowledge base for urban ecology (Sophie Lokatis);
- Towards a general framework/typology of invader impacts (Franck Courchamp).

10:00 Break-out group discussion round 1.

11:00 Coffee break (30 min).

11:30 Break-out group discussion round 2 (opportunity to switch groups).

12:30 Lunch break.

13:30 Break-out groups report back and joint discussion.

14:00 Break-out group pitches for the afternoon.

- Towards a general framework/typology of invader impacts (Franck Courchamp);
- Connecting hypothesis networks across disciplines: the example of urban ecology and invasion science (Roxane Vial, Maud Bernard-Verdier);
- What's the best way to present Hi Knowledge tools? (Tina Heger);
- Connecting Hi Knowledge with IUCN EICAT / GISD, InvaCost and/or IPBES (Jonathan Jeschke, Daniel Mietchen, Ana Nunes).

14:30 Break-out group discussion round 3.

16:30 Break-out groups report back.

17:00 Concluding discussion and next steps.

First morning of presentation

The first morning started as a hybrid session of two hours of presentation and Q&A. Jonathan Jeschke and Tina Heger presented the Hi Knowledge initiative and the current

tools and advances made in the last year within the INAS and enKORE projects (Jeschke and Heger 2023;[link](#)). Rose O’Dea, joining us online from Australia, gave an inspiring [keynote presentation](#) about the limits to synthesising evidence in ecology, focusing on the replication crisis and the challenges of evaluating and improving the quality of scientific research.

Tools fair

Our projects are centred around tools and conceptual frameworks to help knowledge synthesis and exploration. During this one-hour tools fair, different partners of the projects presented the diversity of tools we are working on. Akin to a poster session, participants were free to walk around the room to the different tool stations where presenters gave a quick introduction to their tool and encouraged questions and interactions. By the end of the tools fair, participants were a bit more familiar with the tools and were asked to choose one or two tools to explore in depth during the following two rounds of discussion and test sessions.

Breakout group discussions

Each breakout group on the first and second day was led by one or more moderators working on an aspect of the Hi Knowledge initiative and some topics were repeated twice to give the opportunity for participants to switch groups. In this report, we summarise the main outcome of these discussions by topics classified in three categories: (1) open tools for knowledge curation, exploration and synthesis; (2) new methods for formalising and annotating ecological knowledge to make it more searchable and machine friendly; (3) extending our knowledge map beyond invasion biology and connecting research fields in ecology.

Theme 1 - Open tools for knowledge curation, exploration and synthesis

Open Knowledge Maps

Peter Kraker, chairman and founder of [Open Knowledge Maps](#) (OKMaps), introduced participants to the OKMaps organisation and services and what they are currently implementing in the context of the enKORE project.

OKMaps is an online discovery infrastructure creating visual representations of research topics. Relying on databases, such as PubMed and BASE (Bielefeld Academic Search Engine) as input, the software uses an AI pipeline, based on natural language processing of document metadata, which combines ordination methods (e.g. NMDS, force-directed layout) and summarisation methods (e.g. hierarchical clustering, TF-IDF), to aggregate and display publications according to similarity in topics. The resulting visualisations are interactive, enabling users to obtain a bird’s-eye view of a topic, zoom into related areas

and access relevant documents. For the enKORE project, the OKMaps team is customising the backend, frontend (i.e. interface and visualisation) and integration capabilities for invasion biology.

During the breakout groups, workshop participants had the chance to take part in a [scientific scavenger hunt](#). In groups, the participants explored unknown fields of research using Open Knowledge Maps and found answers to questions along the way. It was a tough competition with only one answer deciding the winner. Congratulations to “Team Two” who came out on top in the end!

Wikidata and Scholia

Daniel Mietchen, biophysicist and data analyst focusing on Wikimedia tools in the enKORE project, presented how [Wikidata](#) and [Scholia](#) are contributing to the Hi Knowledge initiative ([see poster](#)). Wikidata is a massive aggregator of open data, including bibliometric data, providing the basis for community curation of a large corpus of literature, including on invasion biology. This corpus can be openly annotated and organised in various ways, for example, through semi-automated SPARQL queries which the community can design, refine and modify. Scholia is a navigational tool that arranges groups of such queries into scholarly profiles, i.e. to visualise and summarise Wikidata information according to authors, topics, organisations, journals, taxa etc. Wikidata allows the creation of thematic “projects” and an overview of the current enKORE project efforts is provided by [WikiProject Invasion biology](#). This WikiProject currently includes a corpus of over 45,000 publications for invasion biology, a corpus which keeps growing with automatic updates of the published literature. For an overview, see [its Scholia profile](#).

During the breakout group discussions, Scholia profiles of specific taxa, of some workshop participants, as well as of topics related to invasion biology or neighbouring fields like urban ecology, were also shared and curation workflows for creating and annotating the Wikidata entries that underlie Scholia visualisations were demoed. Questions around how specific kinds of data could be represented in Wikidata were addressed too, along with issues of how the data available there can be integrated with other data or how to work with distributed volunteer communities and across disciplines, languages and other kinds of common social barriers to collaboration.

Open Research Knowledge Graphs

Markus Stocker, Head of the Knowledge Infrastructures Research Group at the TIB (Leibniz Information Centre for Science and Technology, Hannover, Germany), presented the [ORKG project](#) (Stocker et al. 2023), which he co-leads. The ORKG project aims to digitalise scientific literature in a way that “unpacks” studies out of their document-based formats and make them machine-friendly to enable searching and meta-analysis of data and results. Machine interpretability and interoperability of ORKG data are made possible by a database structured by graph modelling and semantic annotation (controlled vocabulary from ontologies and Wikidata). This open project relies mainly on manual

curation by users, in particular the contribution of detailed metadata, data and standardised results to describe each publication.

For the enKORE project, an [Invasion Biology Observatory](#) has been set up, which will gather all contributions related to invasion biology. Further on-demand interactive analyses of the results across studies is possible via online tools, such as Jupyter notebooks or R shiny apps. The enKORE project is currently developing an R shiny app ([beta version here](#)) to explore ten major hypotheses in invasion biology which have already been contributed, based on previous work in the Hi Knowledge initiative (Jeschke and Heger 2018). Within the enKORE project, we are now developing a template specifically tailored for ecology and evolution to guide the entering and modelling of manual contribution of publications and results in the field (see Theme 2).

In a further development possibly reflecting the future of scientific publications, Markus demonstrated how the production of ORKG content can be ensured as early as data analysis, with results directly produced and published in machine-readable form. This is achieved by integrating ORKG templates into scripts (currently limited to Python and R languages), which supports the rich and accurate description of results. Minor modifications (one liners) of original code ensures the production of structured information, the submission of such supplementary data together with manuscripts to journals and the DOI-based harvesting by systems such as ORKG. The approach largely bypasses the need for post-publication extraction from articles and manual curation.

INBIO TST, the “invasion biology thesis starter tool”: natural language processing to detect hypotheses in invasion biology

As part of the INAS project, PhD candidate Marc Brinner and four students, amongst them Alexander Hillig and Nils Scheidweiler, developed a tool that helps to identify research hypotheses in a text and, building on this, to formulate their own hypothesis, for example, for a thesis. The tool is under development and available via <https://inbiotst.fmi.uni-jena.de/>; access can be granted on demand.

After entering text (e.g. an abstract from a paper about an invasive species), the tool returns a list of hypotheses with probabilities, allowing one to find out which major invasion hypotheses this abstract is addressing. Further, the tool can highlight which text passages relate to a focal hypothesis. These features are based on a language model which is calibrated to detect 10 major hypotheses in invasion biology, based on the existing dataset of ca. 1000 publications annotated in the book by Jeschke and Heger (2018).

An additional feature of the tool is the option to highlight species names, key invasion biological concepts and habitats. Links to entries in Wikipedia, entries in Ontologies ([INBIO](#) [ENVO](#)) and respective definitions are provided. A student freshly starting in the field of invasion biology can use this to find out more about these concepts he/she might not be familiar with yet.

In a final step, the user receives a graphical representation of a formalised version of the focal hypotheses. In a later version, this will be the starting point for an interface that helps develop a refined, own version of the hypothesis of interest.

What's the best way to present Hi Knowledge tools?

We have developed several complementary tools in the INAS and enKORE projects, but how do we want to present them to the community? Steph Tyszka is a web developer in the enKORE project who will work on a webpage for making the tools more accessible. To do this, he will need input from the community on what this page should look like and how it should work. Since the workshop breakout group was mainly composed of non-ecologists, the discussion revolved around technical questions. Further discussion and feedback will be needed in the future from the ecologist community.

The webpage will present a collection of tools rather than an integrated single tool. While there is programmatic access to many of the tools separately already (separate APIs), bringing these together is tricky and might rather be an aim for future projects. Given the diversity of tools we propose, it would be important to make easy connections to allow navigation across tools. During the 'travel', the user should be provided with links leading to other tools. They should not have to go back to the landing page to do something else. For instance, the hypotheses pointed to in the INBIO TST could link to hypothesis profiles created in Scholia or ready-made knowledge maps on these hypotheses created with OK Maps. We agreed that we should aim to pick the low-hanging fruits here.

We discussed what the landing page should look like. An idea was to display all the tools with short descriptions; however, we should not rely on people reading text; we imagined that most users would want to go ahead and type something and explore before they start reading. Many start pages have a search bar as the main feature, but this does not seem to be enough for our case, since not all the tools focus on search. OK Maps does provide a search bar and the integration of OK Maps functionalities on the [TRIPLE \(Transforming Research through Innovative Practices for Linked Interdisciplinary Exploration\) platform](#) could serve as a template for us. We could think about using the search bar not only as a direct link to the OK Maps search, but instead also use it to offer actions that could be done with our other tools. We agreed it would be good to have a search bar plus buttons leading to other tools, with short descriptions of actions and tools.

We discussed what the search outputs would look like. The search result display could have an upper section providing 'actions'. The lower part of the screen could show the OK Maps search output. For example, if someone types 'enemy release in marine systems', the upper part could show the possible actions 'explore the enemy release hypothesis' (with a link to the ready-made knowledge map and/or the Scholia profile for this hypothesis). We could think about offering different outputs for the search: Knowledge maps, Scholia profile, R shiny app etc. We could also provide ready-made knowledge maps for each of our hypotheses we wanted to integrate (create with OK Maps and update from time to time).

The user group we have in mind for the frontend is invasion biologists of all stages. The backend should already include the option to broaden up to other, related disciplines. For later projects, an aim could be to work on the user experience, for example, by allocating resources for having user experience specialists work on this.

More details concerning presentation and user experience were discussed. We agreed that it would be good to make the page fit also on mobile devices and that it would be great if there would be a common look and feel, no matter which tool the user is applying at the moment. The display language will have to be English only for now. We would rather not require registration or login for now, as most of our tools do not require it, except for INBIO TST, which can be changed and ORKG, whose integration on our website remains unclear at this stage. Finally, we also thought about a shorter domain name.

Theme 2 - Making open knowledge searchable and machine friendly: improving modelling and annotation of scientific knowledge

Beyond keywords: a template for annotating studies in ecology with ORKG

Highlights

- Key characteristics of ecology studies (habitat, taxon, method...) would be easy to annotate, but are currently hidden in the text and not easily searchable;
- Machines are not yet able to do this accurately;
- Authors are the best people to do it accurately and quickly;
- Templates are needed for guidance and structure, to ensure annotations are machine actionable and interoperable;
- We proposed a template via the ORKG platform;
- Participants tested the template on their own papers and provided feedback to improve it;
- We plan to approach publishers to test the template;
- We will be presenting the template and our vision in a joint publication with interested participants.

Ecologists are increasingly committed to open science and FAIR research data management, but we do not generally have a good grasp of the concepts necessary to navigate such open knowledge, such as machine readability, machine interpretability or machine actionability. Lars Vogt, designated Head of the ORKG Curation & Community Building Group at the TIB, introduced us to some of the concepts behind [semantic knowledge graphs](#) and explained how ORKG is one way to fulfil this promise of structured data and knowledge with a human-friendly interface to annotate the content of research studies. ORKG is also the framework we would be using in the session. The first hour was

spent presenting our ideas and discussing applicability and how to engage the community. The second hour was then spent testing and giving feedback on the template in ORKG.

Improving annotation of papers in ecology

While bibliographic metadata about an article (author, journal, year etc.) are currently well annotated by publishers, (mostly) standardised and searchable across search engines, this is not the case for basic ecological information, such as the studied taxonomic groups, habitat, geographical scale or temporal scale of a given study. Our main goal for the session was to test and discuss a new template for annotating studies in Ecology and Evolution and, in particular, in Invasion Biology. Maud Bernard-Verdier presented the rationale behind it: to use the power of semantic structure and graph modelling to radically change and improve the way we describe the content of an ecology paper (Bernard-Verdier 2023; [link to presentation](#)).

The idea is to go “beyond keywords”, which currently attempt to fulfil this function, but have many limitations. They have no semantic context and carry the typical problems of natural language: being only “strings of characters”, with no meaning for a machine like a basic search engine, homonyms will routinely be confused, such as the classic mix-up of “invasive surgery” literature coming up in any literature searches on “invasive species”. Synonyms are not handled in lists of keywords: in any classic systematic literature search, researchers typically attempt to include all possible search terms like alien, exotic, non-native, non-indigenous, invasive and IAS in a hope to hit as many searches as possible. Keywords being usually limited to 10, including synonyms, often means not including other interesting keywords like the habitat, geographical scope, method etc. Finally, the choice of keywords is left mostly at the discretion of the author, with no controlled vocabulary or guidance on what concepts to annotate.

Our solution is a template: a pre-structured form for annotating ecology studies. We wish to provide structure and guidance for authors to fill out the kind of basic key information we ecologists and other users of ecological knowledge care about whenever we search and filter the literature or even prepare a meta-analysis. A template provides an input form for users to add information of a specific type to the database (e.g. a weight measurement). The template automatically translates the information added by the user into a semantic representation in the form of a graph. Consequently, all information added by the same template is semantically interoperable.

For the user, it takes the shape of a quick and pain-free form to fill out, with items that an author would typically be able to list from memory about their most recent paper. We included 13 items that are the “low hanging fruits” of content data about a study in ecology: habitat, study system, type of study, geographical area, temporal extent of the data etc. (Fig. 3). The list of key properties was assembled as a result of discussions during the 2022 first enKORE-INAS workshop ([see report](#)). Behind this template is a graph model (Fig. 4) designed by Lars and Maud which provides machine-actionable and searchable relationships between concepts and maps every property to a broader context using ontologies.

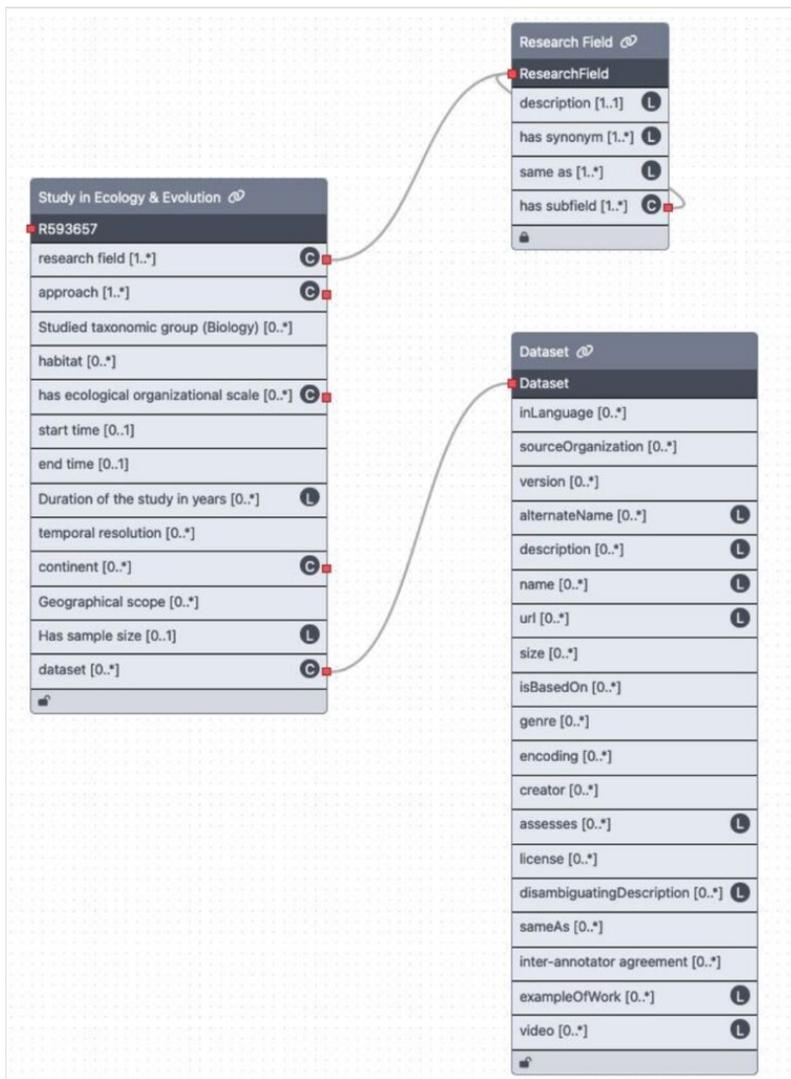


Figure 3. [doi](#)

Tabular representation of the main template for studies in ecology and evolution (left hand box). Some template properties will be themselves described by their own template, such as the research field (top right panel) or the dataset (bottom right panel) (source: orkg.org/template/R593657; screenshot from 2 June 2023).

Interoperability and standardisation

To maximise interoperability, the terms filled out by users are, in some cases, strictly guided (with a type of dropdown list to choose from, although the flexible ORKG system always allows the user to create a new item if needed) and, in other cases, loosely guided by autocomplete suggestions, which link to pre-existing items in the ORKG or Wikidata.

Drawing on the power of Wikidata is a huge advantage, as ORKG benefits from Wikidata's large semantic database and links to other existing ontologies and taxonomies, curated intensively by an active community including in our own project (see above for Daniel Mietchen's automated annotation of invasion biology papers in Wikidata).

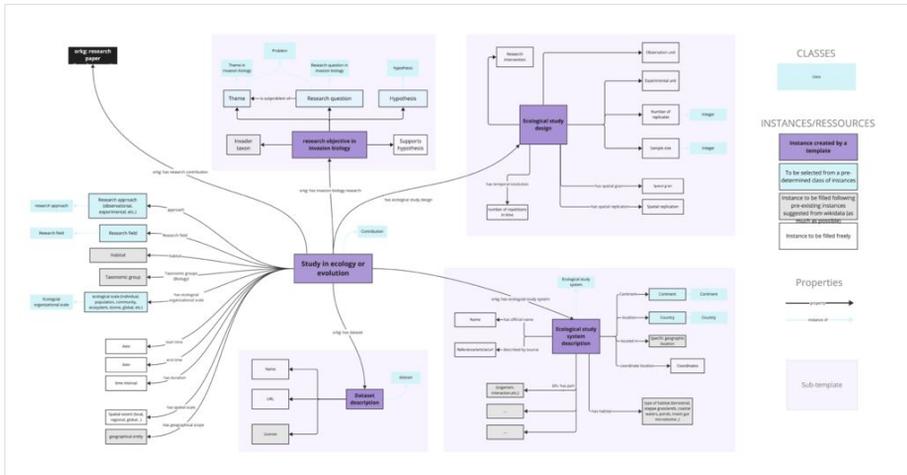


Figure 4. [doi](#)

Graph models underlying templates for a study in ecology and evolution. The main template is the “General scoping” template, while each other box would allow a more detailed description of Dataset, Study system, Study design and research question and hypotheses in Invasion biology (source: [10.5281/zenodo.8334505](https://doi.org/10.5281/zenodo.8334505)).

A major advantage of such semantic modelling is that it promises to erase problems of synonymy and scoping: linking only to the Wikidata entry for the Latin name of an invasive grass we studied, for example, instantly links our paper to all possible species synonyms, common names (including in different languages), higher taxonomic levels and the simple fact that we studied a plant.

How to encourage the community to adopt the template?

A big question remains, how to make this template usable and used by the community? We discussed three parallel strategies:

1. getting publishers to integrate the template at the article submission level;
2. motivating authors to back-annotate their previous publications and
3. encouraging students and researchers starting new meta-analyses to use the template as a guideline.

Such a template has huge potential for annotating publications already at the journal level, during the submission process: if publishers would adopt such a template (and agree on using the same or compatible ones), authors would be asked to fill out the form at the moment of submission (instead of keywords) and all new publications would come out

already fully searchable in terms of ecologically relevant content. We discussed approaching two invasion biology journals about it: [NeoBiota](#), which, as an open journal of the Pensoft ecosystem, is already embedded in a culture and online platform of open science and machine-orientated databases (Pensoft already provides some semantic modelling and controlled vocabulary for Biodiversity data annotation); *Biological Invasions*, as a central journal in our research field, would provide a great platform for a wide community to get to know and use the template.

Even if publishers were to adopt the template today, this does not solve the problem of annotating all the existing literature (45,000 + entries for the topic “Invasion biology” in the curated Wikidata project). One suggestion was to encourage as many authors as possible to add at least a few of their own studies in the ORKG. This would be beneficial for individual researchers immediately: their own work would become more easily findable and more likely to be integrated in a meta-analysis and the template would provide a reusable tool for students preparing a literature review/meta-analysis, which could then be published (with a DOI) as a “comparison” item in ORKG.

Long-term benefits for the community (authors, readers and journals) of more systematic annotation are even more evident. First, such systematic annotation would greatly improve ease and reliability of literature searches, inasmuch as literature search interfaces adapt accordingly. Context scoping provided by semantic enrichment would reduce unwanted search hits (i.e. publications about “invasive” surgery procedures) and allow more flexible specificity of searches, with, for instance, an “intelligent” search understanding different levels of taxonomic groupings (species, genus, kingdom,...). Search results could then directly be filtered by key criteria (habitat, temporal scale, method, taxon...). Second, literature search outputs could come out pre-organised, providing an already filled-out table of study characteristics to facilitate reviewing the literature, but also to quickly identify biases and gaps. Third, this would allow automatic visualisation and synthesis of current research, by creating “ecological dashboards” giving an overview of the field or of some specific sub-fields and keeping track in real time of new studies. An example of what this could look like is the R shiny app ([beta version](#)) we are developing, providing interactive synthesis of literature on ten hypotheses in invasion biology. Scientific journals would also benefit from such a dashboard illustrating the scope and leading topics in their journal.

Testing the template

In a second session, participants tried out the main ORKG template for annotating studies in ecology and evolution. We did not have time to test other, smaller, templates for describing study systems or invasion biology hypotheses. We asked participants (see list below) to choose one of their papers and add it into the ORKG using the template.

Overall, creating accounts and adding paper was done easily by participants. Feedback from participants identified some user experience issues with the ORKG interface and a guideline or a short instruction paragraph would have been useful. Most fields from the template appeared to be no problem and, after a first try, one participant timed that entering a new paper with the main “Study in Ecology and Evolution” template took only 4

mins. No missing information was mentioned by participants, but it might have been due to a lack of time to further test and reflect on the template.

Nevertheless, a few elements in the template form were not obvious and will need to be changed. For instance, participants were confused about the difference between “geographical scope” and “geographical extent”. Participants were also unsure what they should add in the “dataset” input and what to do if the dataset is not shared publicly. They suggested adding a better description of the properties, including examples. Defining the sample size of a study appeared as a major challenge with no obvious solution. We agreed that it is important information, but that it might be too complex and study-specific to model at this point. It is not always clear what sample size refers to and often corresponds to several values in a study with multiple species, a time series etc. We might be able to model it in a separate template describing study design.

We discussed how to go forward to improve the template. First of all, a better description of properties is needed, with a good instruction manual or tutorial specific to the collection of templates for ecology. Second, a set of additional properties and sub-templates might be needed, in particular, to describe datasets and study design. Finally, a broader perspective is to dissociate the templating system from [ORKG](#) and make the templates applicable to other structured databases like Wikidata, which is a project currently discussed at the TIB Hannover.

Short publications on research hypotheses

Another idea developed during the course of the projects is to develop and test a new publication format, which is a ‘Hypothesis paper’. Such a publication format could be used to summarise existing definitions for major hypotheses, suggest revised definitions and suggest formalised versions (see *causal networks* below) of different variants of hypotheses. Directly in the publication, each definition and formalised statement could be linked to a Wikidata item. Single statements could be additionally published as machine-actionable nanopublications with stable URL.

The benefits of such publications would be manifold. Summarising existing definitions and laying open varying meanings with the help of formalised statements could facilitate disambiguation. In addition, it would become possible to directly refer to and cite single versions of definitions and even different variants of a hypothesis. Additionally, AI based tools would get access to these diverse definitions and variants and could, thus, be trained to become helpful for theory development.

During the breakout group session, we first discussed the first version of a hypothesis paper focused on the enemy release hypothesis, published as a preprint (Heger et al. 2023). In a second round, we started filling in the template provided along with the preprint for three other hypotheses.

A first point of debate concerned the list of existing definitions for the hypotheses, as presented in the draft hypothesis paper for the enemy release hypothesis. Participants

recognised that the list is incomplete and ended up agreeing that we should not aim to create complete lists of definitions because this would be quite time-consuming and this new form of publication aims to make knowledge available more quickly. It might be helpful to explain the choice of definitions included in the table somewhere, in the text or the caption of the table.

One solution is to allow versioning, i.e. make such hypothesis papers “living documents”: if somebody feels the need to include more definitions in the table, he/she could publish a new version where these are added. In such living documents, akin to different versions of R-packages, the authors of the first version would stay on the author list, as new contributors are added. The great advantage is that updating an existing text is much less time-consuming than starting over. We agreed on keeping both options open: either update an existing hypothesis paper or publish a completely new paper on the same hypothesis (e.g. in cases where authors completely disagree with the existing hypothesis paper). Workflows for both types of contribution are already in place in the journal [Research Ideas and Outcomes \(RIO\)](#). We could take advantage of this ‘living document’ by inviting authors of original versions on a regular basis to publish updates. Authors of original papers could also have the possibility to state whether they want to be contacted if a new version was submitted. For new versions, the same reviewers could be invited that had reviewed the previous version.

In the preprint on the enemy release hypothesis, different variants of the hypothesis were classified as either causal (e.g. reduced pressure by enemies in the non-native range positively affects invasion success) or comparative (e.g. number of enemies of invasive species has smaller value than number of enemies of native species). We debated whether it is useful to keep comparative formulations: on the one hand, they are a bit redundant, as they seem to convey the same thing as the causal formulations; on the other hand, they seem to be helpful in that they are often more closely linked to what is actually measured. We could think about them as a kind of implementation of the hypothesis. No clear conclusion was reached on this point, but perhaps philosophers could help us figure out how to deal with this.

Participants felt that quality control via peer-review is key also for these hypothesis papers. It was discussed whether it is really useful to put out hypothesis papers even for hypotheses that are not tested yet. The same degree of quality control would be necessary for single hypothesis statements: if these are published as nanopublications, each of them should be carefully checked, to avoid the accumulation of useless or misleading statements ‘swamping’ the field. The good news is that we are now part of the process in which this new form of publication is about to become established, so we can tell the RIO journal that will host this new publication form that we think every part of it has to be peer reviewed. Encouragingly, a workflow for peer reviewing nanopublications is already in place.

A controversial point of discussion was whether these hypothesis papers include information about the current level of evidence for the hypothesis. While this would give a better idea of the usefulness of the different versions of the hypotheses, it would also

duplicate the information that is given elsewhere, for example, in reviews or in the Hi Knowledge hierarchical networks. We concluded that there should be a section that refers to existing review studies and meta-analyses on the hypotheses, without reiterating their results to avoid introducing errors or biased interpretations.

Another point of discussion was whether we should try to indicate related hypotheses in a section of the paper. When some of us tried out the template with further hypotheses, the remark was that it seems to be difficult to decide what counts as 'related' and it could lead to endless lists. We could, instead, provide links to the hypothesis networks built in Hi Knowledge projects, so that people can learn more about similar hypotheses there.

We agreed that, ideally, the authors of the key reference for the hypothesis should be contacted and offered to participate in the hypothesis paper. This could be motivated by the journal, for example, by including a respective statement in the author instructions for this publication type and/or by asking as mandatory information to give at submission 'did you contact the authors of the key reference for this hypothesis?'

Finally, in the second part of this session, three sub-groups formed to try out the template for other hypotheses: the ecological imbalance hypothesis (Fridley and Sax 2014); the anthropogenically induced adaptation to invade (AIAI; Hufbauer et al. (2012)); and Darwin's naturalisation hypothesis (Daehler 2001). The template seemed to work fine so far and the participants found that it was helpful to have the pre-structured form with headers to fill in. Participants estimated it might take only one day to finish a paper for a rather new hypothesis, but rather longer for well-known and highly-cited hypotheses. In general, participants said that they could very well imagine publishing such papers and some of the participants have indicated that they now wish to continue and submit the hypothesis paper they started during the session.

Causal Network Graphs for hypothesis modelling

Tina Heger, one of the PIs of the INAS project, presented the idea of using causal network graphs as tools to model hypotheses in invasion biology in a machine-friendly way. The advantages are that:

- this visualisation of ideas can enhance understanding;
- at some point, we can cooperate with data scientists and experts in formal logics to use their tools for enhancing theory building in invasion biology;
- it will allow us to connect several hypotheses with each other.

This tool was tested and discussed in a dedicated break-group session.

The basic idea is to formulate invasion hypotheses in the form "subject" - "causal relationship [or some other relationship]" - "object". To do this, we have to try to think about the causal mechanisms that are implicit in these hypotheses and build the hypotheses into longer chains revealing underlying assumptions (e.g. "enemy release - positively affects - invasion success" could be expanded to "enemy releases - causes - less tissue damaged -

causes - population growth - contributes to - invasion success"). We built examples of such causal networks using the free collaborative tool 'miro'.

In general, participants were intrigued by this option to visualise hypotheses and their connections. Participants agreed that causal networks could be quite useful for showing existing ideas of how invasions work. Together, we took a closer look at Tina's suggestions and made changes where participants did not agree, although there were no general arguments against the suggested networks. We worked, in particular, on finding better ways to visualise the Island Susceptibility Hypothesis. An interesting idea that emerged from the discussion was to think more about the successive invasion phases and to use causal networks to model and demonstrate the different mechanisms at work during each phase. A suggestion to get started was to use the classification of hypotheses in Daly et al. (2022).

A sub-group tried to build a new causal network from scratch for a new hypothesis, which turned out to be quite difficult. One challenge seems to be to build such a network as a group, because there can be disagreement on many aspects of the modelling. In fact, it is quite likely that we will end up with different versions of networks depending on who built them. It may be easier to build them alone and then open up the discussion. One idea was that whether or not you find it easy to create those graphs depends on 'how your brain works'. We discussed how we could come to some kind of consensus on such networks and whether we can tolerate the existence of different versions.

The aim to create quite complex networks including more and more of the existing ideas is intriguing. There should be the possibility to easily 'zoom in', then to see those parts that are of interest for the respective question. These causal networks could also be combined with study results to highlight the level of evidence for each hypothesised causal relationship in the network and gaps in research. We could even think about providing direct links in the graphs to papers testing the connections (i.e. the hypothesised causal relationships). A very similar idea has already been realised in the ORKG project (Fig. 5).

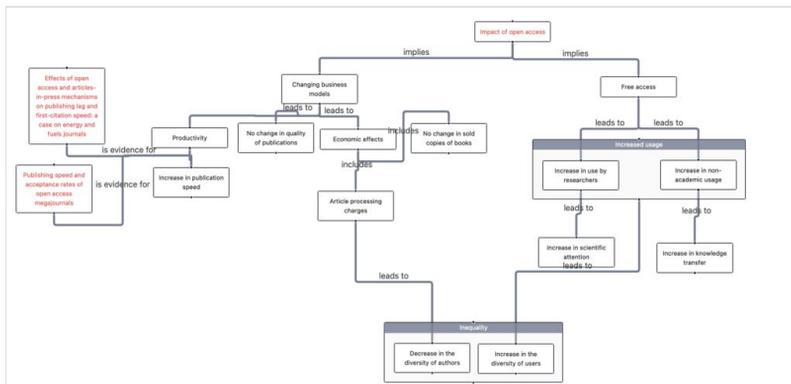


Figure 5. doi Causal relationships and evidence network in the ORKG. The red boxes are papers, linked as supporting evidence for the hypothesised relationship (source: orkg.org/diagram/R218774).

As a take-home, it seems important to better describe how to build such networks and to establish workflows to build them and work on reaching some sort of consensus. Some participants expressed interest to work more on this in the future.

Theme 3 - Extending beyond invasion biology research

Connecting Hi Knowledge with IUCN EICAT

In this group, participants discussed how to integrate the EICAT classification of alien species impacts (Blackburn et al. 2014, IUCN 2020) in Wikipedia. A main concern was how to visually represent it within each species' Wikipedia page. A long discussion about the name of the 'title' to use for the EICAT category box resulted in the decision to name it "Impact as an alien species". To represent each of the EICAT categories, we agreed to use hexagons and the official EICAT colour scheme, arranged in a similar way as the IUCN "species status" icons. This means five impact categories + DD (Data Deficient, which could perhaps be slightly separate from the other categories).

Next steps for the group participants include creating six different vectorial figures (icons) for the EICAT categories in the respective colour (five impact categories and DD). Wikipedia pages for EICAT will be created, based on the example of the Red List page and including some history about the process undertaken. Pages for each EICAT category will also be created, as well as an entry for "impact as an alien species". Some of these decisions will still need to be discussed within the EICAT Authority and, of course, things might also change following scrutiny from the Wiki community. Finally, we discussed the format and process needed to prepare a publication referring to the addition of EICAT categories to Wikipedia species pages, as well as other associated pages.

Connecting hypothesis networks across disciplines: the example of urban ecology and invasion science

Conceptual maps of research fields, or disciplines, have now been built in the form of hypothesis networks for invasion biology (Enders et al. 2018, Enders et al. 2019, Enders et al. 2020) and urban ecology (Lokatis et al. 2023) or are in progress in other fields (e.g. freshwater ecology, restoration ecology). However, these maps remain disconnected within the broader field of ecology. Most ecological research intersects with more than one of those research fields, drawing from theory, hypotheses and concepts across the borders of disciplines; therefore, we need to connect the dots and explore overlaps and theoretical gaps in between.

Connecting hypotheses across disciplines (e.g. uniting them in the same network of hypotheses) aims to:

1. identify similar hypotheses across fields, allowing not only interdisciplinary synthesis, but also a simplification and clarification of theory by reducing redundancy and

2. identifying theoretical gaps and opportunities for cross pollination across fields. Three conceptual issues emerge:
 - What type of links can connect two hypotheses networks?
 - What makes two hypotheses equivalent or similar?
 - How do we define whether hypotheses belong to a given field? Can a hypothesis be common to two fields? Are there different degrees of field membership?

These questions were discussed in our session with the example of two research fields for which we already have conceptual maps: urban ecology and invasion biology.

Preliminary work: assembling a list of hypotheses in both fields

We collated three published lists of hypotheses: two for invasion biology (Enders et al. 2020, Daly et al. 2022) and one for urban ecology (Lokatis et al. 2023). We first compared the three lists to identify exactly identical (i.e. redundant) hypotheses. In total, we obtained a list of 141 unique hypotheses, with only two hypotheses that appeared in identical form in both urban ecology and invasion biology:

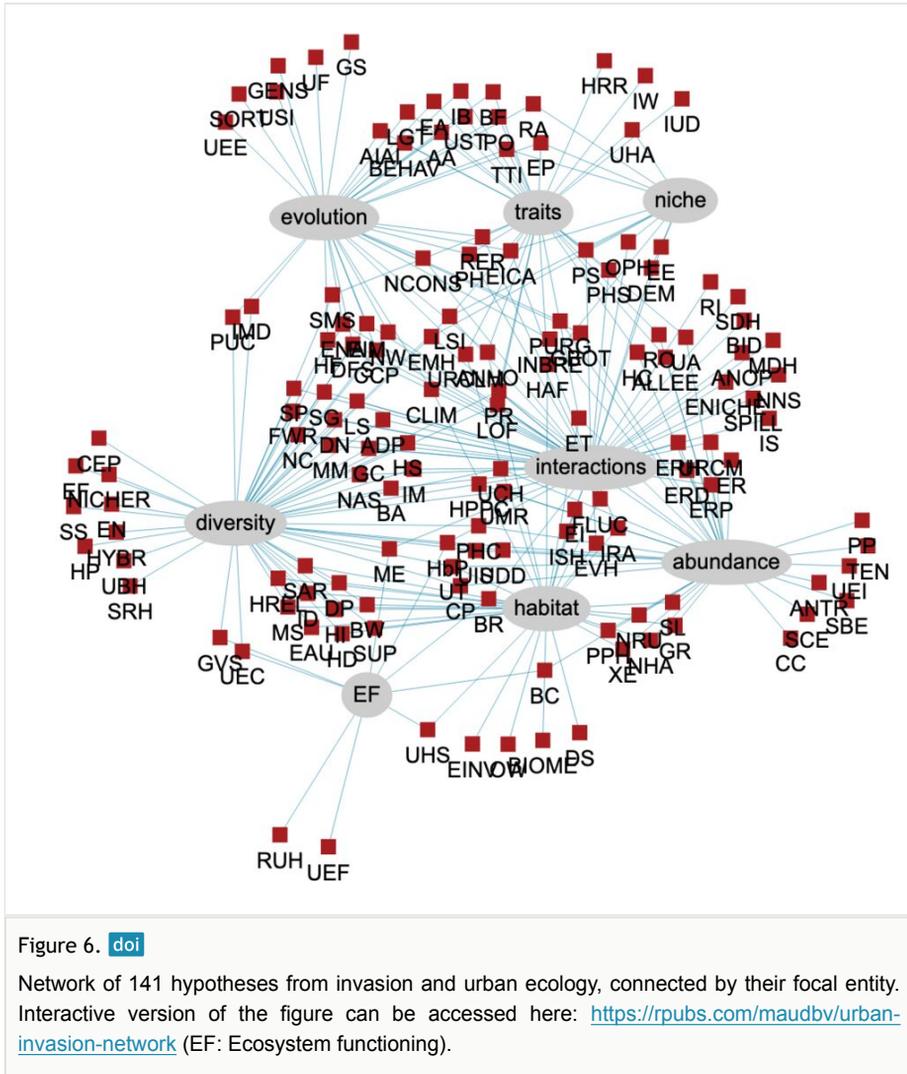
- Enemy release hypothesis: The absence of enemies in the exotic range is a cause of invasion success (Keane and Crawley 2002);
- Human commensality hypothesis: Species that live in close proximity to humans are more successful in invading new areas than other species (Jeschke and Strayer 2006).

Different ways to connect hypotheses across fields

Links in hypothesis networks can be of very different nature, with, for instance, similarity networks (Enders et al. 2020) or trait networks (Enders et al. 2018, Lokatis et al. 2023). To connect across fields, we need to use a method to build links that have the same meaning in both fields. We discussed two main options.

A first method consists in finding common attributes or traits of hypotheses that have meaning in both fields. Hypothesis lists could simply be merged and network clustering could be carried out again as if it were one field (as in Lokatis et al. (2023) for instance). The question then becomes: what type of attributes do we want to use? As an example, we chose to categorise hypotheses by the main focal entity/organisational level at which they operate ([here](#); Fig. 6).

A second method is to identify conceptually equivalent, similar or “analogous” hypotheses. We discussed similarity in terms of underlying process or overarching hypothesis, across fields. Many “analogous” hypotheses, i.e. hypotheses that are somewhat similar, but formulated differently as they are applied to different fields, could be connected at a higher hierarchical level by “overarching” hypotheses or processes or mechanisms (Fig. 7; see also hierarchy-of-hypotheses approach, Heger et al. (2021)). One participant mentioned a similar idea in a study (Latombe et al. 2021) in which they used six underlying ecological processes to characterise “concepts” across invasion biology and community ecology.

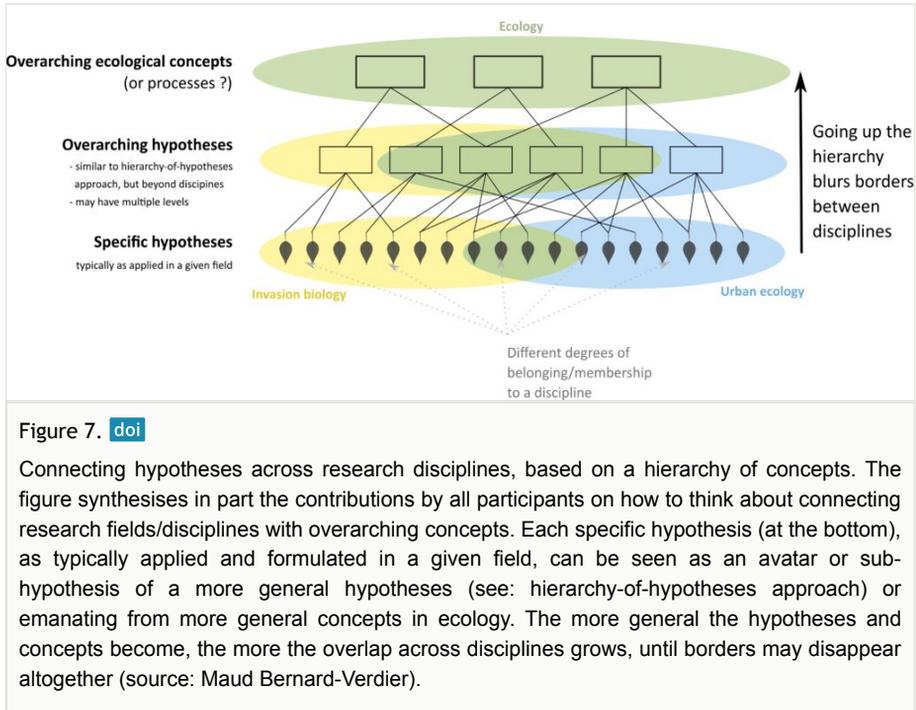


What does it mean for a hypothesis to belong to a field?

While connecting hypotheses is an exercise in which we can ignore borders between research fields, once these networks are created, we are also interested in tracing which hypotheses belong to which field. This would allow us to determine the amount of conceptual overlap across fields and to identify potential research gaps and new opportunities for interdisciplinary work.

Hypotheses do not neatly fall into one field or another: they often originate from one field (though not always), where they are initially conceptualised and formulated and then spread to other fields of ecology. They are either applied and/or adapted to other fields or they might be potentially very relevant in other fields without having been formally “introduced”. The language of biological invasions (‘naturalised’, ‘introduced’, ‘indigenous’)

was often evoked to discuss the conceptual spread of these concepts, reflecting our clear scientific bias with an overwhelming majority of invasion biologists!



We discussed four categories to capture the membership of hypotheses to a given field. The precise name and definition of each category was debated and we note here suggestions from participants:

1. Homegrown/autochthonous/belonging/innate/endemic/indigenous = fully belongs to the field; makes significantly more sense in this field than elsewhere/ OR hypothesis originally theorised/formalised/conceptualised in the field/innate to the field;
2. Applied/borrowed/assimilated/naturalised = hypothesis originating from a different field, but formally applied to the field (with a reference paper to prove it). Proof: an article has formulated or tested or used explicitly the hypothesis in a new context (as a main topic of the article or one of the main conclusions);
3. Relevant/applicable = hypothesis originating from a different field, but which would be particularly relevant/applicable in the field (no burden of proof that this has already been done formally);
4. No obvious overlap/not obviously relevant = not obviously relevant from the definition and our own expert knowledge; the hypothesis does not make significantly more sense in this field than elsewhere.

To explore if this classification makes sense, groups of participants were given a few example hypotheses and asked to describe how these belonged to the field of invasion

biology and/or urban ecology, using the four categories listed above. We chose a few hypotheses from the list of 141 hypotheses, without telling the participants whether it officially belonged to invasion biology (Enders et al. 2020, Daly et al. 2022) or urban ecology (Lokatis et al. 2023).

Overall, the exercise revealed problems with our classification. After much debate about the name of categories, their definition, or even the need to replace them by quantitative scores, we concluded that the confusion stemmed from trying to score two separate concepts at the same time. We can score the origin or historical trajectory of how a hypothesis is created and evolves, but this is conceptually distinct from the level of relevance to a given field.

Moreover, we debated whether any hypothesis is ever completely irrelevant to a field: are there urban ecology hypotheses that are completely irrelevant to invasion biology and vice-versa? We did not come to an agreement on this point. This led us to conclude that, when asking for participation from other scientists, we should only ask researchers to annotate fields they are specialised in, not other fields, as it tends to create confusion and misinterpretations.

One suggestion was to ask participants to score hypotheses in several stages as a sort of decision tree (i.e. first ask whether or not the hypothesis belongs in/comes from the field; if not, ask if the hypothesis is applied in this field; and finally, if not, ask if the hypothesis is relevant in this field). This would allow us to identify relevant hypotheses that have not yet been applied to this field. Finally, some participants suggested asking for a justification when annotating hypotheses as « relevant » to the field, ideally using structured information on components of hypotheses to guide answers.

Conclusion

Our goal was to find a universal typology for annotating hypotheses membership in any research field, beyond our example of urban ecology or invasion biology. Based on the feedback, we will come up with a proposition and send it around to interested participants as a survey and, perhaps, to try it out on a few examples.

Our current idea is a separate annotation of two partially independent concepts:

1. “ **Historical membership** ”: origin and history of a hypothesis (which should in theory be an objective task, based on literature):
 - Indigenous: hypothesis originally developed in the field;
 - Naturalised: hypothesis originating from a related field, but adopted and formally applied/translated to this field;
 - Introduced: concept from another field sometimes used in the field;
 - Undetected/absent: hypotheses not yet used explicitly in the field.
2. “ **Relevance score** ”: ordinal categories (or perhaps rather a scale from 0 to 10):
 - 8-10 - Highly relevant/central to the field;
 - 6-8 - Relevant/important for developing theory in the field;
 - 4-6 - Relevant for interpreting data in the field;

- 2-4 - Applicable;
- 0-2 - No obvious application/not valid for the field.

This work on historical membership will also be combined with the idea of identifying the larger ecological hypotheses/concepts/processes overarching analogous hypotheses across fields, i.e. the different “avatars” of the concepts within each field.

Freshwater systems: Practical relevance of invasion hypotheses, connecting researchers and practitioners

Highlights:

- Revisiting fundamental goals: need to identify the cross-benefits for academics and stakeholders;
- Organising knowledge: a categorisation would enable a more systematic approach and facilitate effective communication;
- Conservation evidence and management orientation: importance of having access to conservation evidence, the proposed tool could be used for management purposes;
- Logistics: exploring a Wiki-based approach would be a good fit for what we want to develop;
- Addressing challenges: engaging stakeholders to drive the project forward successfully.

The participants acknowledged the need to focus on our expectations in this project. This included clarifying goals, understanding the benefits of the proposed approach/platform, defining desired outcomes and identifying the expectations of stakeholders. The exploration of cross-benefits, where researchers and stakeholders can mutually benefit from the collaboration (collaboration is the key), was also highlighted.

It was recognised that it is important to organise knowledge in categories. The categories that could be relevant for stakeholders may differ from the ones used by researchers, including species, pathway, sites and negative impacts. This categorisation would enable a more systematic approach and facilitate effective communication. Additionally, conducting risk assessments is of high importance for stakeholders and we should consider this important aspect for the tool we want to develop.

Stakeholders often express the importance of having access to conservation evidence and the proposed tool could be used for management purposes. The tool was seen as a potential source of evidence-based decision support. To achieve this, it was suggested to make grey literature available, merging existing databases, including specialised scientists/experts lists, management reports and pricing information. Additionally, the meeting emphasised the significance of publishing students' reports on open access platforms like Zenodo to prevent the loss of valuable information.

The idea of using a dedicated management Wiki was proposed as a practical solution for organising and disseminating information. Furthermore, it was suggested to contact stakeholders through a survey, with one participant recommending the use of the IUCN membership list to reach a global audience effectively.

The meeting identified two primary challenges. The first challenge was how to engage stakeholders effectively. It was suggested to start with a survey to understand their expectations and preferences. The second challenge was how to proceed with the project, which led to the consideration of developing a Wiki-related project as a potential solution to overcome these challenges.

Overall, the meeting aimed to emphasise the importance of organising knowledge, aligning researchers' and stakeholders' goals, incorporating conservation evidence, utilising open access platforms, exploring a Wiki-based approach and engaging stakeholders through surveys to drive the project forward successfully.

Urban systems: Building a common knowledge base for urban ecology

The workshop on urban systems was divided into two parts. During the first round, participants took the roles of different stakeholders (e.g. greenspace designer, policy-maker, city gardener, animal activist, conservationist, local inhabitant, urban ecology researcher) and discussed the value of several selected hypotheses from urban ecology (Lokatis et al. 2023). For instance, we discussed possible points of view on hypotheses such as 'Cities as entry points', 'Acoustic adaptation' or 'Green roofs'. The role-playing exercise immediately identified that some hypotheses would be useful tools for certain stakeholders like policy-makers or researchers, but not for others. Hypotheses were not equally clear or applicable and subsets of the 62 hypotheses should be identified that may be more relevant to certain stakeholders. This discussion illustrated the need to reach out beyond our academic circle of urban or invasion ecologists to make our map of urban ecology hypotheses more useful.

The second part of the workshop was dedicated to the recently constructed [Wikidata Project](#) on hypotheses in urban ecology (Fig. 8). The idea behind the Wikidata project is to open up the list of hypotheses from urban ecology (Lokatis et al. 2023) to other urban ecologists with different fields of expertise and backgrounds. The Wikidata project also aims to link the hypotheses listed so far with other resources relating to a specific hypothesis, for example, synthesis papers or relevant original data. Additionally, it is closely linked with knowledge synthesis and visualisation tools like Scholia. This second part of the workshop was led by Daniel Mietchen, a leading member of the Wikidata community, who helped construct and curate the WikiProject. Participants worked on further developing the WikiProject site and coding additional hypotheses in order to make the knowledge gathered there more accessible and findable within the Wikiverse.

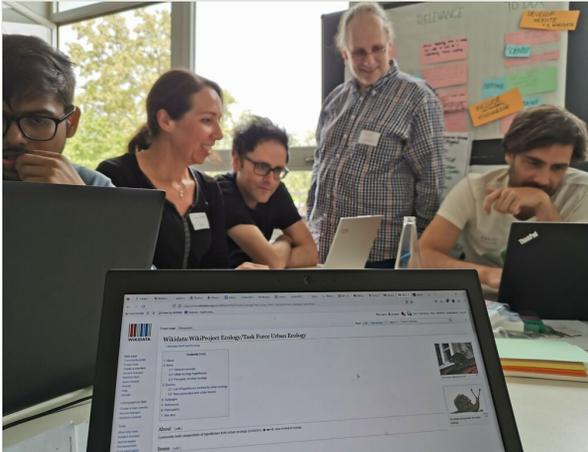


Figure 8. [doi](#)

Breakout group participants working on the WikiProject page for urban ecology.

Conclusion

From the breadth of topics and tools covered in this intense workshop, a few general take-home points emerged:

- Our community of invasion biologists, urban ecologists and freshwater ecologists is interested and ready to use new tools to explore and synthesise knowledge. The general feedback was overwhelmingly positive about the current tools developed.
- Conceptual modelling tools unfamiliar to ecologists, such as semantic modelling and causal networks, appear as a solution to a lot of the existing confusion and inaccessibility of current scientific evidence and should be used to overcome barriers to knowledge synthesis and diffusion.
- The sheer diversity of tools we (and others) currently develop means that we need to guide users and provide clear entry points and instructions to navigate the tools, although, at this point, we have not yet reached a clear consensus on how to organise that.
- These tools should be open source and non-commercial to support FAIR principles.
- Early-career and other researchers are eager to engage with some of the new tools we propose, such as nanopublications or short hypothesis papers.
- We can extend our approach to other fields, but for that, a more flexible conceptual framework may be needed.

A main goal of our workshop was not only to provide information about the tools we are developing in these projects, but to ask participants to engage, criticise and propose new ways to improve these tools. Exploration sessions around the tools provided a wealth of feedback and suggestions which will help project leaders redesign and improve current prototypes. Participants in working groups also agreed, in many cases, to continue

providing feedback on future versions and to disseminate the tools to their network once they are ready. In several cases, the tools and frameworks were actively co-designed by the group, such as, for instance, the plans for integrating the EICAT scores in Wikipedia species pages, the conceptual framework for connecting hypotheses to research fields and the template for annotating publications in ecology, whose prototype already emerged from group discussions in the first workshop.

We also aimed to motivate participants and the rest of the community to actively use these tools and active testing during the workshop provided a first step in that direction. Many participants expressed their willingness to continue testing, improving and using these tools. For instance, the proposed format of short “hypothesis papers”, with accompanying machine-interpretable and citable nanopublications of alternative definitions, had a lot of success and at least two early-career researchers are planning to contribute such publications on two other hypotheses (see Theme 2.2). The benefit of implementing a template for annotating content in ecological publications at the publication level was generally recognised and active collaboration with the journals *Neobiota* and *Biological Invasions* are to be initiated as soon as the template is finalised (see Theme 2.1).

To conclude, the exchange of ideas, joint work and discussions during the workshop were very fruitful and will now be used to improve the introduced tools and work on publications, as well as new project proposals that will allow us to implement more of the collected ideas.

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