MetaBeeAI: an AI pipeline for full-text systematic reviews in biology

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Abstract

The volume and complexity of scientific literature are expanding rapidly, making it increasingly difficult to extract and synthesise information across studies. This challenge is particularly evident in the biological sciences, where data span from molecules to ecosystems and linking across hierarchical levels is inherently challenging. Large Language Model (LLM) pipelines offer a scalable solution, but most lack modularity, transparency, and mechanisms for human oversight. We present MetaBeeAI, an open-source, modular pipeline that uses LLMs to extract structured information from scientific papers for systematic review and meta-analysis. The system includes an intuitive interface that displays model outputs alongside the source text, allowing users to inspect, correct, and iteratively improve performance. MetaBeeAI produces an auditable, machine-readable record of prompts, configuration settings, and expert annotations, supporting reliable replication and continual refinement. We evaluated the pipeline on 924 research papers, extracting information on bee species, pesticides, exposure methodologies, and other environmental factors. Results highlight the value of expert-in-the-loop validation for prompt optimisation and show that MetaBeeAI can handle heterogeneous experimental designs and biological contexts. MetaBeeAI provides a general framework for structured knowledge extraction, enabling scalable, transparent, and reproducible evidence synthesis, and new approaches to accelerate discovery in the life sciences using AI.

Keywords: systematic review, large language models (LLM), knowledge extraction, expert-in-the-loop, interpretable AI/ML

1. Introduction

The volume of bioscience literature has expanded exponentially in the past decade, outpacing researchers' ability to keep abreast of current information. This surge has been accompanied by increasing complexity, fractured data standards, and increasingly specialized nomenclature and practices. As a result, conducting systematic literature reviews, a cornerstone of evidence synthesis and policy development, has become increasingly challenging. This is especially clear for experiments in data-rich fields that report effects and interactions across hierarchical levels, such as in ecology (Cavigelli et al., 2021; Köhler and Triebskorn, 2013).

The explosion of large language models (LLMs) has been proposed as a potential solution to this information bottleneck, yet many AI-based tools fall short (Channing and Ghosh, 2025). While these tools are useful, they often fail to meet the levels

of transparency and adaptability required to be applied to arbitrary subfields in the biosciences. Additionally, it requires great technical expertise to fine-tune existing models to perform bespoke scientific literature review tasks, especially in fields that differ from those standardly available in the training sets. Most pretrained models are biased toward computer science and machine learning corpora, limiting performance in underrepresented domains such as ecology (Dorm et al., 2025).

To address these limitations, we developed MetaBeeAI, a modular LLM-based pipeline for structured data extraction with expert-in-the-loop validation. Users can define a literature corpus, design prompt templates, and iteratively assess model outputs against the source text. The modular architecture keeps MetaBeeAI adaptable as LLM capabilities and tooling evolve, while built-in transparency, testing, and continuous integration support reproducibility, long-term sustainability, and the creation of rich datasets for reinforcement learning from human feedback (Ma et al., 2024; Ziegler et al., 2020).

We demonstrate MetaBeeAI in bee ecology and ecotoxiology. This field, while having great real-world importance for food security and ecosystem functioning (Klein et al., 2006; Potts, 2016; , EFSA), is not well represented in current literature and benchmark datasets used to fine-tune LLMs (Cui et al., 2025). Bees are critical for global food production and biodiversity (Patel et al., 2021; Parreño et al., 2022), yet their populations are threatened by agricultural pesticides and interacting stressors (Goulson et al., 2015). Research on pesticide impacts spans molecular to ecosystem levels, generating an ever-growing and highly heterogenous literature base that is increasingly difficult to synthesise manually. Through a series of workshops, we curated and validated 924 research articles to evaluate MetaBeeAI's performance. Here, we present the outcomes of that validation, assess the pipeline's reliability and generalizability, and provide all associated data and code to facilitate adoption of MetaBeeAI for systematic literature review in other scientific domains.

2. Evaluation of existing methods

The rapid expansion of large language model (LLM)–based tools for scientific text analysis has generated a diverse ecosystem of literature-review pipelines, ranging from domain-specific assistants to general-purpose research agents. However, despite significant progress, most current systems remain limited in scalability, transparency, or adaptability when applied to specialized scientific domains such as biology and ecology. Many popular tools emphasize document summarization or citation tracking rather than full-text data extraction and structured synthesis. For example, current versions of ChatGPT Plus, Edu, and Pro support only 20–40 uploaded files per

project for summarization and synthesis tasks (OpenAI, 2025), whereas our pipeline has been tested on datasets of around 1,000 papers and can scale well beyond that. This technical ceiling fundamentally constrains the feasibility of comprehensive evidence synthesis at the scale required for systematic reviews in data-rich disciplines.

A review of existing LLM-based literature platforms (Table A.3) reveals that, while several tools can perform partial or modular review functions, none offer the combined attributes of full-text ingestion, modular multi-stage processing, expert-in-the-loop validation, and benchmarking that define MetaBeeAI. Systems such as Elicit Elicit (2025), PaperQA2 Lála et al. (2023), AstaAI Allen Institute for AI (2024), and SciSpace Inc. (2025) allow users to query scientific corpora and retrieve summaries but lack structured data output or fine-grained traceability to source text. Others, including Consensus Consensus (2024) and Perplexity (Deep Research) Consensus (2024) emphasize answer generation or conversational exploration rather than standardized, reproducible synthesis workflows.

MetaBeeAI differs fundamentally in that it operates as a multi-pass, modular LLM pipeline capable of parsing, extracting, and benchmarking structured information from full-text PDFs. Unlike single-prompt summarization systems, MetaBeeAI implements explicit stages for chunk-level relevance filtering, iterative prompt refinement, and human expert validation. Each step produces transparent, auditable outputs that can be inspected or replaced without retraining the underlying model. This modular architecture allows continual improvement as newer LLMs and auxiliary tools emerge, providing a long-lived framework for evidence synthesis.

Table A.3 summarizes the capabilities of the principal literature-review and AI-assistance platforms relative to MetaBeeAI. The comparison highlights several key axes of differentiation:

- Full-text processing: whether the tool operates directly on PDFs rather than abstracts or metadata.
- User-specified corpus: ability for users to define and manage their own document sets.
- Web literature search: capacity to automatically retrieve documents from online databases or APIs.
- Domain / question agnostic design: flexibility to address user-defined questions across scientific fields without retraining.
- Modular architecture: presence of discrete, replaceable processing stages.

- Source linking: traceable alignment between extracted information and original text segments.
- Benchmarking: inclusion of automated quality evaluation or expert scoring.
- Open-source: whether all source code is available for adaptation and further development.

Collectively, our landscape analysis demonstrates that MetaBeeAI uniquely integrates end-to-end automation with expert oversight, bridging the gap between proprietary summarization tools and fully manual systematic reviews. Its transparent, benchmarked, and adaptable design directly addresses the limitations of existing literature-review platforms, providing a scalable foundation for reproducible, domain-specific evidence synthesis across the biological sciences.

3. Materials and Methods

3.1. Pipeline overview

MetaBeeAI is a command-line pipeline for performing systematic reviews, designed by and for researchers in the biosciences with the aim of linking the effects of environmental change across levels of biological organization, species, and/or stressor types. Despite these initial design parameters, the pipeline was developed with general applicability in mind. Practitioners in any field can leverage the expert-in-the-loop validation and modular architecture for their domain-specific needs.

The pipeline (Figure 1) utilises established tools from the scientific Python ecosystem alongside solutions for structured data extraction using large language models (LLMs) and graphical user interfaces for annotation and review. The modular design ensures each component: PDF processing and data preparation; text embedding; LLM-based data extraction; and human validation and review; can be independently upgraded as technologies evolve, maintaining long-term sustainability without disrupting existing workflows.

MetaBeeAI is distributed as a Python package on PyPI (`metabeeai`) installable with `pip install metabeeai`, or users can interact directly with the open-source code base, (GitHub: metabeeai/metabeeai). It provides extensive configuration options via both configuration files and command-line arguments, allowing fine-tuning for a user's specific use-case and supporting both novice researchers and advanced developers. This is supported by comprehensive documentation (https://metabeeai.readthedocs.io), that includes API references, step-by-step tutorials, and configuration examples.

3.2. Abstract and title screening

To ensure the inclusion of articles with a relevant scope, users review the titles and abstracts of the papers found during an initial search. We recommend compiling the results from two or more sources to ensure appropriate coverage. Abstract screening is performed in ASReview v1.6.2 (van de Schoot et al. (2021), GitHub: asreview/asreview), which uses active learning to sort abstracts based on relevance. The user establishes relevant papers for inclusion and exclusion with a small subset of examples, following which the model sorts the corpus of abstracts from best to worst. The graphical user interface is easy to navigate, and enhances the speed at which the researcher can evaluate a large number of abstracts.

Once the corpus of relevant papers has been established, reviewers need to download the full text PDFs. This can be done automatically using a free-to-use tool like Unpaywall (unpaywall.org) or similar for open access papers.

3.3. Conversion of PDFs to structured text

Next, Agentic Document Extraction (ADE) from LandingAI v1 (GitHub: `https://github.com/landingai/agentic-doc`) is used to convert full-text documents (Portable Document Format, PDF) to a structured JSON (JavaScript Object Notation) format, a text-based format for data interchange that is human-readable and easy for machines to parse. Prior to document conversion, PDFs are separated into one or two-page PDFs for processing due to LandingAI API restrictions. Pages containing only reference lists can be manually removed at this point to reduce cost. The MetaBeeAI pipeline processes each paper in the database, and automatically stitches together the resulting JSON files with the appropriate page reference for the original PDF. Duplicate text chunks are removed (accounting for the page overlaps). We include only the conversion of the main text and figure captions for subsequent processing (header, marginalia, and figures are automatically removed), as the numerical output from ADE which translates images (e.g., figures) to text descriptions was not sufficiently reliable in this version. We anticipate that the functionality that this tool promises will be highly valuable in future iterations of the model for directly extracting data from figures. The result from this step is a series of structured JSON files that are presented as “text chunks" of approximately one paragraph long, plus bounding box coordinates that relate the text chunk back to the location of the text in the original PDF.

3.4. Multi-pass extraction and prompt chaining

The MetaBeeAI LLM pipeline implements a multi-pass extraction system for querying structured text chunks and extracting domain-specific information from

research papers. The pipeline consists of three main processing stages: chunk relevance filtering, individual chunk querying, and answer synthesis. The system begins by loading question-specific configurations from a YAML file (a human-readable data serialization language that is often used for writing configuration files), which is the main point of interaction of the user with the pipeline (Figure A.1). This file defines the prompt question, in addition to:

- `instructions`: detailed guidance for information extraction.
- `output_format`: structured response template.
- `example_output`: positive examples demonstrating desired responses.
- `bad_example_output`: negative examples showing patterns or content to avoid.
- `no_info_response`: the specific wording to use if the desired information is not present in the text.
- `max_chunks`: the number of top-ranked chunks to select for answer generation.

The system uses a dedicated relevance model (tested with GPT-4o-mini and GPT-4o) to evaluate text chunks against specific questions through a two-stage filtering process. First, rule-based pre-filtering removes obviously irrelevant content (headers, metadata, logos, journal info, DOI, authors, etc.) using keyword matching. Second, LLM-based relevance selection uses a single API (Application Programming Interface) call with a structured prompt containing the question, instructions, output format, good examples, and bad examples from the question configuration. The LLM iterates over all chunks filtered as above and returns an order of relevance over the chunks, selecting the top N most relevant (configurable via `max_chunks` parameter in the YAML configuration). This approach eliminates unnecessary LLM calls by filtering out irrelevant content early while ensuring question-specific relevance through example-driven prompting.

Based on empirical testing and cost-performance analysis in terms of time, we recommend `max_chunks` values of 3-6 chunks: lower values (3-4) for focused questions like “future research directions" that typically appear in specific sections, and higher values (5-6) for comprehensive questions like “experimental methodology" that may span multiple paragraphs. This range balances comprehensive coverage with processing efficiency, as each additional chunk increases both answer generation costs and synthesis complexity, while values below three may miss relevant information and values above six show diminishing returns with increasing costs.

The selected relevant chunks are then processed in parallel batches to optimize API usage and processing speed (tested with GPT-4o-mini and GPT-4o). For each chunk, the system constructs a structured prompt containing the question, instructions, output format, good examples, bad examples, text content (the actual chunk text), and quality guidelines emphasizing conciseness, format compliance, and avoiding speculation. Each chunk query returns a structured response containing the extracted answer and reasoning, formatted to ensure consistent output structure.

The final stage consolidates individual chunk responses into a coherent answer through an LLM powered self-reflection process. The synthesis prompt includes: all relevant chunk texts and their individual answers, as well as the various guidelines from the user prompt (instructions, good and bad examples, output structure), and conflict resolution instructions for handling contradictory information across chunks. The reflection stage can return an `INSUFFICIENT_INFO` flag when available information is inadequate, which is then replaced with question-specific `no_info_response` text. Additionally, if no relevant chunks are found during the initial filtering stage, the system immediately returns the `no_info_response` text without proceeding to answer generation or reflection.

The system implements several performance optimizations, including parallel processing (answer generation occurs in configurable batch sizes), adaptive batch sizing (batch sizes adjust based on available chunks and API rate limits), and asynchronous processing (all LLM interactions use async/await patterns for optimal throughput). The multi-pass architecture ensures high-quality information extraction by combining automated relevance filtering with example-driven prompting and iterative refinement, which can leverage different tiers of models for specific steps to enhance output quality while optimizing API costs.

3.5. Expert-in-the-loop review interface

We have developed software to function as a comprehensive manual validation system for assessing the accuracy and quality of LLM-generated answers against original research papers and the specific portions of the paper used in generating the answers. The system consists of two complementary tools: an automated PDF annotation system and an interactive graphical user interface (GUI) for detailed manual review of the answers with the original full text PDFs.

The annotation system creates visual overlays on original PDF documents to highlight the specific text regions used by the LLM pipeline for answer generation (Figure 2). This enables reviewers to quickly locate and examine the source material underlying each extracted answer. In drawing the bounding boxes, the annotation software leverages the bounding box output by the PDF to text conversion step, the

relevant chunk IDs related to each question, and the original full text PDF.

The PyQt5-based desktop application provides a comprehensive interface for systematic manual review and validation of LLM-generated answers. The user can easily move through different questions and papers, and can select individual text chunks for further investigation. The user can assign a star rating (0 to 10) for each LLM answer, and provide correct answers and reasoning alongside any criticism of the LLM answer or reasoning. The positive answers and reasons provide dual functions for use in pipeline benchmarking (section 3.6) as well as the construction of a domain-specific database of benchmarking questions that could serve for model fine-tuning for those building custom models.

The integrated review system enables systematic human evaluation of LLM performance while maintaining direct visual connection to source materials, supporting both individual answer validation and large-scale quality assessment.

3.6. Benchmarking and prompt refinement

The LLM benchmarking system provides comprehensive evaluation and validation of the LLM-generated answers against human expert assessment using the DeepEval (ConfidentAI) framework. DeepEval employs LLM-as-a-judge evaluation methods (Zheng et al., 2023), where a user-defined LLM evaluates response quality across multiple dimensions. The system implements a multi-layered evaluation approach that combines various metrics to measure answer quality across dimensions (Table 1). The core evaluation pipeline processes LLM outputs through three primary DeepEval metrics (faithfulness, contextual precision, contextual recall), which compare the LLM output versus the text context (full paper and retrieved text chunks), and two G-Eval metrics (completeness, accuracy) that directly compare LLM outputs against human-annotated reference answers ("gold" answers). G-Eval (Liu et al., 2023) is a generalized evaluation framework that uses structured, rubric-based prompts to guide LLMs in scoring outputs along defined criteria, improving consistency and alignment with human judgments across tasks such as summarization and question answering. The benchmarking framework incorporates robust batch processing with flexible user-defined model use, with GPT-4o-mini as the default assessment model. The benchmarking system can be used to compare LLM responses with expert benchmarking responses, as well as comparing between reviewers to demarcate differences in expert responses.

Following benchmarking with the DeepEval metrics, the pipeline automatically identifies edge cases and generates an analysis of poorly performing LLM responses through comprehensive evaluation score analysis and diagnostic reporting. The system identifies edge cases by analyzing evaluation results from DeepEval benchmark-

ing, focusing on responses that received the lowest combined scores across the evaluation metrics. The user can define how many edge cases to include in the final report by changing the relevant setting in the DeepEval framework.

The system then uses these edge cases, their scores on the various metrics, and the automatically generated "reasons" for the scores (generated through the DeepEval framework) to produce a summary report using GPT-4o-mini (or other appropriate model, which can be selected by the user). The output report is a structured, human-readable report that synthesizes edge case findings including the “main issues" that summarize recurring problems for a given question, including specific aspects such as a lack of specificity in responses, inclusion of irrelevant information, omission of key details, and misalignment with expected outputs. The report also includes "recommendations for improving prompt" sections that provide actionable suggestions for prompt modifications (c.f. Section 4.1 for assessment and usage). Each question type analysis includes sample edge cases with specific examples showing the paper, combined scores, input questions, expected output, and problematic LLM responses, enabling researchers to understand failure patterns and develop targeted improvements. Prompts can be updated given these recommendations and the pipeline re-run to quantify improvements. All output, including LLM answers, context (text chunks), benchmarking scores, and reviewer answers, are saved together for further analysis.

3.7. Database standardization and analyses

The final step involves the conversion of the LLM answers into a standardized format allowing for analyses. This includes separating the LLM answers from sentences to structured output. The database can then be queried using a noSQL format via JSON files, and additionally can be flattened to a standard CSV file for rapid analyses using statistical software. Standard names for species, locations, experimental perturbations and endpoints, and other variables can be enforced with the use of a dictionary, and units converted to a standard format across fields.

Several analyses can be performed on specific fields selected by the user, including histograms showing the number of papers per field and the distribution of data within categories. Sankey diagrams show relationships between categorical data and highlight topics that are least represented in the data, and can be used to draw inferences about the interconnectivity of the fields.

3.8. Case study: bee ecotoxicology

The focal use case for testing the pipeline focused on the topic of nicotinic cholinergic pesticides (e.g., neonicotinoids) and bees. Neonicotinoids are used widely in

agriculture, and are often applied prophylactically as seed treatments to crops (Douglas and Tooker, 2015), despite known impacts on beneficial insects like bees (Sgolastra et al., 2020; Hladik et al., 2018). The aim of this literature review was to highlight the current state of scientific knowledge regarding the diversity of study types including bees and nicotinic cholinergic pesticides across "domains" of research from molecule to ecosystem, as well as to highlight studies that include pesticides and additional environmental stressors, like temperature extremes and nutritional stress.

We included all primary research papers that had a nicotinic cholinergic pesticide as at least one treatment effect, and included measured results for any species of bees. We included laboratory, semi-field, and field studies. Residue analyses were omitted. An initial corpus of research articles was constructed using the results from literature searches on Scopus and Web of Knowledge with a search term containing two parts, a bee species term and a pesticides term (wherein * denotes a wildcard term):

```
(bee OR bees OR honey* OR bumble* OR solitary OR stingless OR "wild bees"
 OR pollinator* OR osmia OR apis OR bombus OR xylocop* OR halictid*
 OR colletid* OR peponap* OR megachil* OR nomi* OR andren* OR melip*)
AND
(neonicotinoid* OR sulfoximine* OR butenolide* OR cholinergic
 OR imidacloprid OR clothianidin OR acetamiprid OR thiamethoxam
 OR dinotefuran OR nitenpyram OR thiacloprid OR acetamiprid
 OR sulfoxaflor OR spinosyn OR spinosad OR "seed treatment")
```

We refined the initial set of papers using ASReview (developers, 2024) removing those that did not fit our inclusion requirements (N = 2 reviewers). We additionally assigned "domains" to each paper, describing the level(s) of biological organization studied in the paper (N = 10 reviewers, with 2 or 3 reviewers per domain). The domains included: molecular (receptor binding, gene expression, metabolism), sub-individual (cellular or tissue-level effects), individual (behaviour, fecundity), population (colony-level effects, reproductive rate, survival), and community (field observation of multiple bee species). We included traditional mortality assays (LD50, LC50, etc) as a separate domain, due to the prevalence and traditional importance of these measurements in the field of toxicology (Morris-Schaffer and McCoy, 2021). All abstracts and titles were double-reviewed.

The questions used in the LLM pipeline were:

1. What bee species were experimentally tested in this study?
2. What pesticide(s) were tested in this study? For each, provide the specific dose(s) tested (or field application rates), exposure method(s), and duration of exposure.

3. Were the effects of any additional stressors included in the study (like temperature, parasites or pathogens, other chemicals, or diet and nutrition stress)?

3.9. Statistical methods

Statistical analyses on benchmark metrics were conducted separately for each metric. Reviewer star ratings and inter-reviewer start rating differences were analysed using linear mixed-effects models with question type as a fixed effect and paper ID as a random intercept, with significance assessed via likelihood-ratio tests and Bonferroni-corrected post-hoc contrasts. For the benchmarking performance scores, the random paper-level effect explained negligible variance and produced singular fits, so models were simplified to generalised linear models (GLMs) with system, question type, and their interaction as fixed effects. Metrics were expressed as proportions bounded between 0 and 1 and were analysed using Gaussian GLMs applied to logit-transformed scores. Model significance was assessed using type-II ANOVA, and post-hoc pairwise contrasts were performed using estimated marginal means with Tukey adjustment to test differences among systems and question types.

4. Results

4.1. MetaBeeAI pipeline benchmarking

We selected a subset of 180 papers to test the MetaBeeAI pipeline and obtain domain expert reviews (N = 13 reviewers). Of these, 120 papers were double-reviewed so that we could compare LLM versus reviewer answers, as well as reviewer versus reviewer answers. The star rating provided a rapid demonstration of differences in LLM output across questions, as well as highlighting inter-reviewer differences in assessment (Figure 3). Across all LLM answers, questions on bee species received the highest ratings (mean $\pm$ SE $= 7.00 \pm 0.27$, $n = 142$), followed by pesticide questions (6.23 ± 0.21, $n = 161$) and additional stressors (5.56 ± 0.33, $n = 137$). After Bonferroni correction, ratings for additional-stressors questions remained significantly lower than both bee-species questions ($p < 0.001$) and pesticide questions (difference $= 0.75$, SE $= 0.29$, $p = 0.027$), whereas the difference between bee-species and pesticide questions was not significant ($p = 0.070$). Inter-reviewer agreement, quantified as the absolute difference between two independent ratings, did not differ significantly across question types (likelihood ratio test: $\chi^2(2) = 2.69$, $p = 0.26$). Mean inter-reviewer differences were 1.79 ± 0.30 for bee-species questions ($n = 56$ paired ratings), 2.10 ± 0.33 for additional-stressors questions ($n = 51$), and 2.46 ± 0.27 for pesticide questions ($n = 74$), with no significant fixed effects of question type in the mixed-effects model (all $p \geq 0.10$).

After performing an initial benchmarking ("LLMv1"), we adapted the prompt pipeline to incorporate the suggestions from the edge case analysis. These included: 1) emphasizing specificity with clearer instructions (e.g., species names); 2) clarifying output requirements (e.g., specify response format and instruct what to omit); and 3) providing examples (e.g., show example responses that are in the correct format). With these updates, we re-ran the LLM pipeline to obtain a second set of answers ("LLMv2"). We then compared the output from LLMv1, reviewer vs reviewer, and LLMv2 to assess pipeline improvement. Typically, the improvements involved better formatting, a reduction in extra information, and greater answer specificity (Table 2).

Across metrics and questions, the LLMv1 scores were typically only slightly lower than the reviewer vs reviewer scores, while the LLMv2 answers demonstrate improvement across metrics (Figure 4). The scores for all metrics except for faithfulness were significantly lower for LLMv1 compared with LLMv2. This effect was driven largely by an improvement in answer specificity and answer formatting, and better handling of missing information, and was especially true for the "additional stressors" question, where LLMv1 would output spurious results when there were no additional stressors mentioned in the paper. In LLMv2, we defined output phrases for missing information, which resulted in higher scores for accuracy and completeness.

4.2. Abstract and Title Screening: bees and pesticides literature

The literature searches identified 4,509 papers. This was reduced to 1,053 papers after filtering titles and abstracts using the inclusion criteria. We applied domain labels to each paper, based on the focus of the experiments or observations in each paper (Figure 5). A single paper could have one or multiple domains, and some papers (186) were not given a domain label. There was an average of 83% agreement between reviewers for domain labels. The 186 papers that had not been allocated to a domain were re-reviewed, and 103 of these were removed due to mislabelling at the initial filtering stage. A total of 924 papers were available as full-text, proceeding through the remainder of the pipeline, including PDF to text conversion and the LLM data extraction system.

4.3. Case study: bees and pesticides literature review

Across all the papers in the database, there were 339 unique bee species and 14 unique nicotinic cholinergic pesticides, amounting to 438 unique bee-pesticide combinations. When filtering out studies that included pollinator community surveys, there were 130 unique bee species from 44 genera (Figure 6). *Apis* (honeybees) were studied in 672 papers, followed by *Bombus* (bumblebees) in 223 papers, *Osmia*

(mason bees) in 83 papers, *Melipona* (stingless bees) in 33 papers, and *Megachile* (leafcutter bees) in 26 papers.

We explored the relationships between bee species, pesticides, and additional stressors (Figure 7). Here, "study" refers to the set of experiments within a paper for a given bee and pesticide combination, so a single paper can have multiple studies (i.e., multiple species and/or pesticides, or the same species included in more than one experiment). Unsurprisingly, *Apis mellifera* (honeybee) represented by far the largest number of studies across the main neonicotinoid pesticides (total: 813 studies; imidacloprid: 266 studies; thiamethoxam: 155 studies; clothianidin: 138 studies), followed by *Bombus terrestris* (bumblebee, total: 176 studies; imidacloprid: 55 studies; thiamethoxam: 38 studies). When considering all pesticide studies, *Apis cerana* was the third most studied (75 studies) followed by *Bombus impatiens* (71 studies), *Osmia bicornis* (67 studies), *Megachile rotundata* (31 studies), *Melipona quadrifasciata* (24 studies), *Osmia lignaria* (24 studies), *Apis florea* (18 studies), and *Scaptotrigona postica* (13 studies).

Secondary stressors were included in 182 studies across 106 papers, comprised of 6 broad stressor groups: parasites (55 studies), temperature (45 studies), pathogens (32 studies), chemical stressors (31 studies), 14 "other" stressors (e.g., UV-light), and 5 papers that included nutritional stress.

5. Discussion

5.1. Generalizability and broader applications

MetaBeeAI demonstrates that a modular, expert-in-the-loop AI pipeline can overcome many of the practical barriers to systematic evidence synthesis. While we applied it here to bee ecotoxicology, the framework is broadly applicable to any scientific domain, or potentially across any area of evidence-based reasoning. Its design is not tied to any single field: the hierarchical prompting system, expert-in-the-loop verification, and benchmarking framework provide a generalizable structure that can be adapted to new questions with only minimal changes to prompt files and dictionaries. In this sense, MetaBeeAI fills a critical gap between generic AI literature tools and the highly specialised needs of domain scientists. The framework additionally creates reusable, high-quality benchmark datasets through expert validation, supporting reinforcement learning and fine-tuning for domain-specific tasks. Importantly, MetaBeeAI provides a transparent bridge between human expertise and automated synthesis, offering traceable, auditable outputs that can improve reproducibility and trust in AI-assisted review. Such a framework could underpin scalable, domain-adaptable systems for knowledge extraction, evidence mapping, and model evaluation across scientific and policy domains.

5.2. Performance in case study in bee ecotoxicology

In applying MetaBeeAI to bee ecotoxicology, we benchmarked the pipeline using 924 studies on the impacts of nicotinic cholinergic (neonicotinoid and related) pesticides across biological and ecological scales. This case study provided a stringent test of the system's adaptability to heterogeneous literature, including molecular toxicology, behaviour, and colony- and field-level endpoints. The benchmarking exercise revealed strong alignment on factual extraction tasks (e.g., compound type, species), but highlighted common challenges in areas requiring contextual reasoning. For instance, the model occasionally failed to map commercial formulations to their corresponding active ingredients, or to distinguish between generic and specific pesticide classes when the information was implicit in the text. It also struggled to consistently return structured information such as a single, well-defined species name rather than multiple synonymous terms (e.g., *Apis mellifera*, honeybee, bee). Workshop discussions with domain experts led to refinements in the prompt dictionaries and ontology files, including standardized chemical mappings and structured representations of exposure types. These updates substantially improved recall and consistency across categories, underscoring the importance of domain-specific prompt engineering and expert oversight. The lessons learned from this exercise illustrate how iterative validation, grounded in expert input, can transform a general-purpose LLM pipeline into a reliable tool for specialised evidence synthesis.

5.3. Comparison with other LLM pipelines

MetaBeeAI occupies a distinct position among current LLM-based literature-review systems by integrating the interpretability of traditional systematic reviews with the scalability of modern AI pipelines. Several existing tools are effective for exploratory querying and summarization but are not designed for structured data extraction, benchmark generation, or reproducible synthesis workflows. Their outputs are often non-traceable summaries that cannot be directly integrated into quantitative meta-analyses or regulatory assessments.

In contrast, MetaBeeAI delivers an end-to-end, auditable workflow optimized for full-text extraction, expert validation, and benchmarking. Its architecture allows users to isolate, inspect, and improve individual components, such as document parsing, relevance filtering, or schema definitions, without modifying the entire system. This modularity ensures that advances in LLMs, retrieval methods, or domain ontologies can be incorporated immediately, preserving long-term utility as the underlying AI landscape evolves. MetaBeeAI's explicit alignment of extracted data with original text segments enhances reproducibility and accountability, two features often lacking in commercial or closed-source systems. The pipeline's transparency also makes

it well suited for collaborative benchmarking and community-driven extension, in contrast to opaque proprietary models where provenance and decision pathways are hidden.

Ultimately, MetaBeeAI complements rather than competes with existing literature-assistant platforms. While general-purpose systems enable rapid exploration of scientific corpora, MetaBeeAI provides the structured, verifiable backbone needed for quantitative synthesis, database construction, and model training. It thus fills a critical methodological gap between interactive AI assistants and the rigorous standards of formal systematic review, providing a sustainable framework for transparent, domain-adaptable knowledge extraction at scale.

5.4. Strengths, limitations, and future directions

The main strengths of MetaBeeAI lie in its expert-in-the-loop validation system and pipeline modularity, transparency, and adaptability. Every component of the pipeline, from PDF parsing to prompt design and expert review, can be independently updated, ensuring robustness as technologies evolve. The expert-in-the-loop interface provides transparency and reliability, enabling users to link extracted answers directly to source text, a critical safeguard against LLM hallucinations (Bang et al., 2023). Benchmarking against domain experts showed that even modest prompt refinements substantially improved accuracy and completeness, highlighting the value of the iterative design.

Nevertheless, several limitations remain. The accuracy of extractions depends on the quality of the initial PDF conversion, which may introduce artifacts. Numerical extractions from tables and figures are still unreliable and were excluded from downstream analyses. Although chunk-based prompting and expert validation reduce hallucination risk, they do not eliminate it. Harmonisation of synonyms, units, and taxonomies currently requires manual curation, which limits scalability. A further challenge common to all LLM-based systems is reproducibility: model outputs can vary across runs due to stochastic inference and ongoing model updates (He, 2025). MetaBeeAI mitigates these issues by ensuring full traceability between each extracted statement and its source text, keeping human oversight central to validation even as underlying models evolve.

An additional and more subtle limitation concerns the potential for psychological bias during expert review. Presenting model-generated answers before human evaluation may induce anchoring effects (Tversky and Kahneman, 1974), in which the LLM output unintentionally shapes the human judgement that becomes the "gold standard". Because such biases operate subconsciously, they cannot be ruled out without dedicated controls. Future work should compare expert assessments col-

lected under blinded and non-blinded conditions, or require reviewers to give an initial independent answer before seeing the LLM output. Developing such protocols will help ensure that expert-in-the-loop systems remain reliable and unbiased.

Future developments in both this tool and others could address these issues by integrating domain ontologies and automated synonym mapping, improving numerical extraction through specialised table-parsing models, and building community-curated benchmarking datasets for model refinement. As multimodal models improve, integration of figure and image extraction will likely become feasible, further expanding the scope of data types that can be synthesised.

5.5. Conclusion

MetaBeeAI provides a flexible and transparent solution for structured knowledge extraction from full-text scientific literature. By combining modular AI tools with human expertise, it enables systematic reviews that are more scalable, reproducible, and adaptable than current manual workflows. While demonstrated here in bee ecotoxicology, the pipeline is readily transferable across biological disciplines, from ecology to biomedicine. More broadly, the modular and customizable nature of the pipeline allows for easy application to any field that relies on evidence based reasoning. It has particular promise for those fields where literature is systematically organized and regularly updated, such as those with an archive system like computer science and biology. As the volume and complexity of scientific literature continues to expand, frameworks like MetaBeeAI are essential for bridging the gap between rapidly growing evidence bases and the synthesis required for scientific progress. We envision MetaBeeAI not as a static tool, but as a foundation for community-driven development and collaboration at the interface of AI and life sciences.

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7. Author contributions

R. H. Parkinson led the conceptualization, methodology design, software development, validation, formal analysis, investigation, resources, data curation, visualization, supervision, project administration, writing, and funding acquisition. H. Cerbone contributed to methodology, software development, validation, formal analysis, investigation, resources, data curation, writing, supervision, and project administration. S. Cao contributed to conceptualization, methodology, software development, resources, writing, and funding acquisition. M. Mieskolainen contributed to the conceptualization and software development and validation. A. D. Wilson contributed to software development and validation. S. Roberts contributed to conceptualization, supervision, writing, and funding acquisition.

S. Albacete, E. B. Armstrong, A. Brown, C. Botías, A. K. Jones, H. Siviter, F. Sgolastra, D. A. Stanley, E. A. Straw, A. J. Hayward, L. Herbertsson, N. Nagloo, E. Rigosi, E. Nicholls, R. Tadei, and K. Walter contributed to methodology, investigation and manuscript review. L. Herbertsson also contributed to visualization. C. Bass contributed to investigation, writing, and supervision. L. Straub contributed to manuscript review. R. K. Daniels and H. F. Stevance contributed to methodology, validation, and manuscript review. B. Lambert contributed to writing and funding acquisition.

All authors reviewed and approved the final version of the manuscript.

8. Declaration of generative AI use

During the preparation of this work, the authors used OpenAI's GPT-4.0-mini, GPT-4.0, and GPT-5 models to assist in refining text and summarising aspects of the pipeline methodology. All content generated with these tools was reviewed, verified, and edited by the authors, who take full responsibility for the final text and its scientific accuracy.

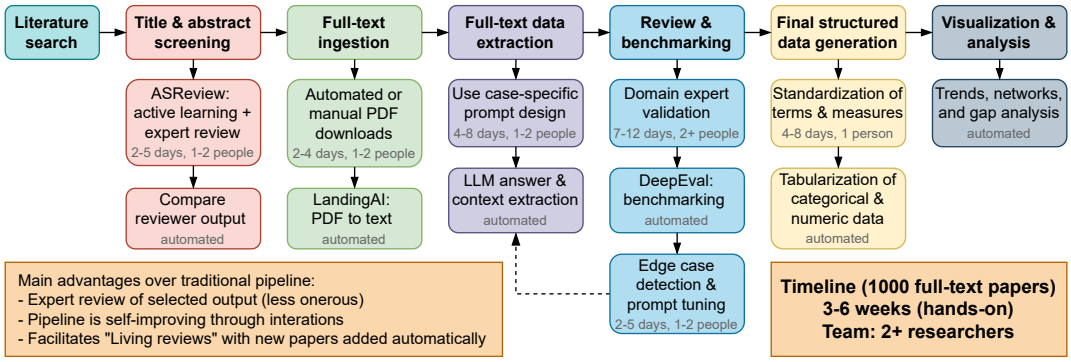

Figure 1: The MetaBeeAI pipeline is an AI-in-the-loop system for enhancing researcher efficiency in the systematic review process. The pipeline begins with a typical search for titles and abstracts of research articles that fit the users' objectives. Once these have been acquired, the user is guided through each stage of the review, with transparent output at each stage that links any information back to the original paragraph(s) from each article. The ultimate output of the pipeline is a database that can be queried for analyses and synthesis. The suggested timeline is representative of a moderate systematic review including 1000 full-text papers for evidence synthesis.

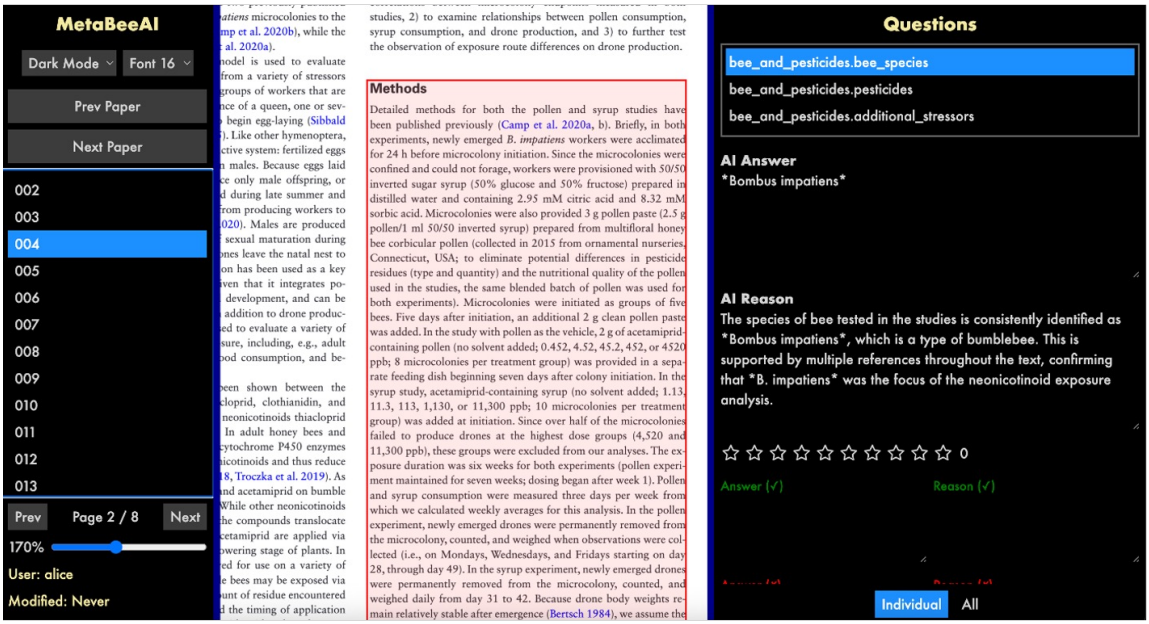

Figure 2: Example screenshot from the review software. The specific paper ID can be selected in the left column, which displays the full text PDF in the centre window. When the user selects a specific question from the right panel, the AI answer and AI reason is printed, and the user can select all or individual relevant text chunks for that question. The user provides a star rating, as well as correct answers and optional LLM answer feedback. Data are automatically stored locally.

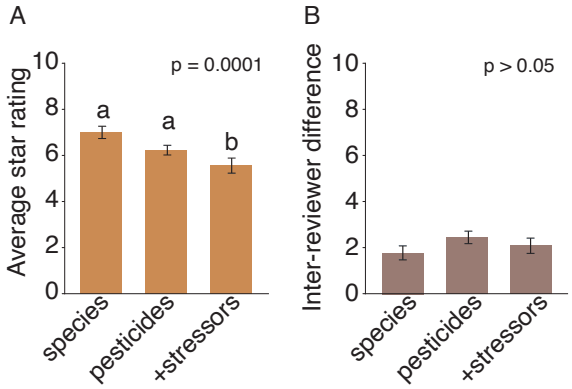

Figure 3: Average reviewer star ratings differed by question type (likelihood ratio test: $\chi^2(2) = 19.74$, $p = 0.0001$) (A), while inter-reviewer agreement, quantified as the absolute difference between two independent reviewer ratings for the same LLM answer, did not differ significantly across question types (likelihood ratio test: $\chi^2(2) = 2.69$, $p = 0.26$) (B).

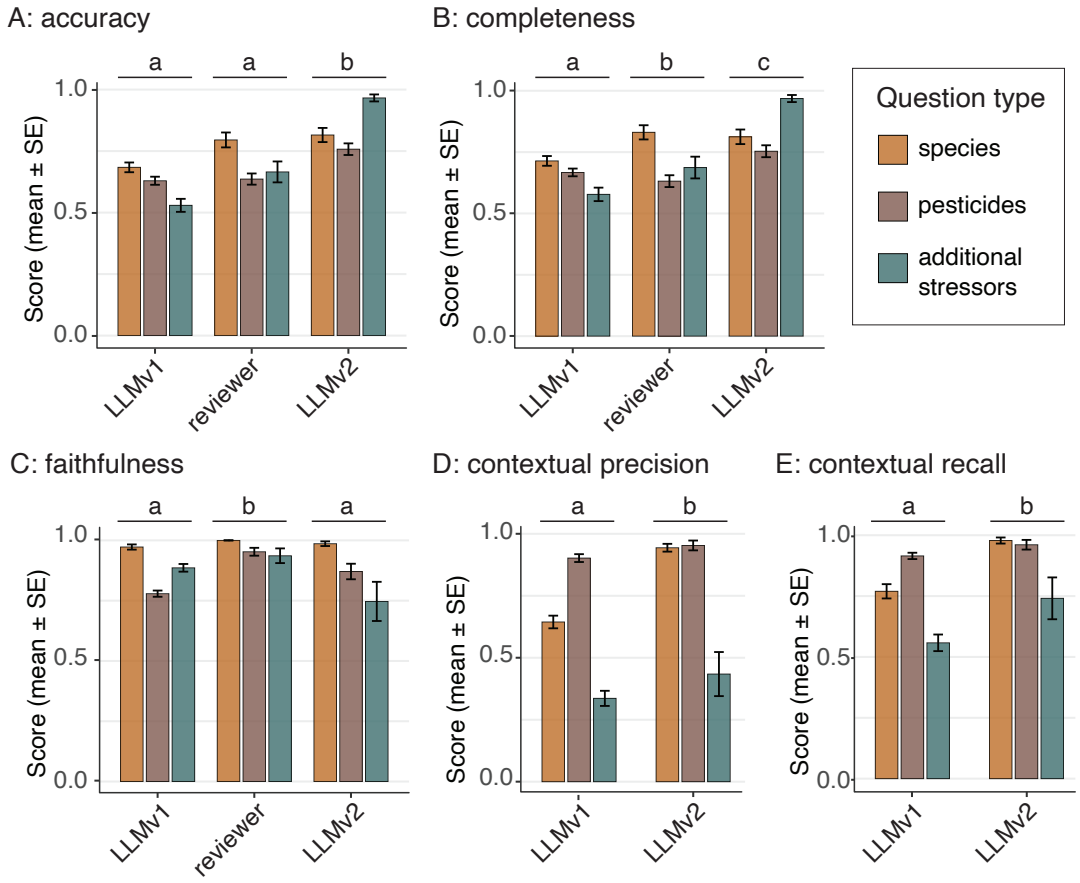

Figure 4: Benchmarks comparing LLMv1 vs reviewer, reviewer vs reviewer, and LLMv2 vs reviewer across accuracy (A, GLM, type: F = 102.3, p < 0.0001; question: F = 12.8, p < 0.0001; type*question: F = 17.9, p < 0.0001), completeness (B, GLM, type: F = 42.2, p < 0.0001; question: F = 5.0, p = 0.0067; type*question: F = 14.3, p < 0.0001), faithfulness (C, GLM, type: F = 26.2, p < 0.0001; question: F = 100.9, p < 0.0001; type*question: F = 12.4, p < 0.0001), contextual precision (D, GLM, type: F = 66.7, p < 0.0001; question: F = 196.3, p < 0.0001; type*question: F = 12.4, p < 0.0001) and contextual Recall (E, GLM, type: F =34.4, p < 0.0001; question: F = 57.0, p < 0.0001; type*question: F = 3.4, p = 0.035) metrics. Letters denote significance between sources (LLMv1, reviewer vs reviewer, LLMv2). Description of metrics can be found in Table 1.

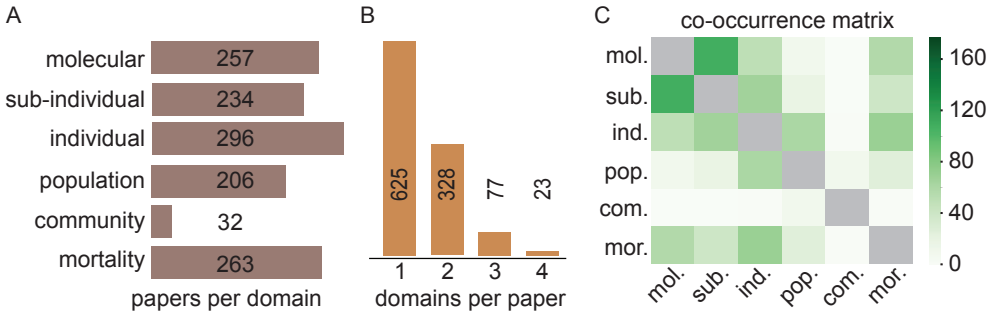

Figure 5: Paper topic distribution across levels of biological organization and domain (A), the number of domains addressed within each paper (B), and the co-occurrence of domains within papers (C).

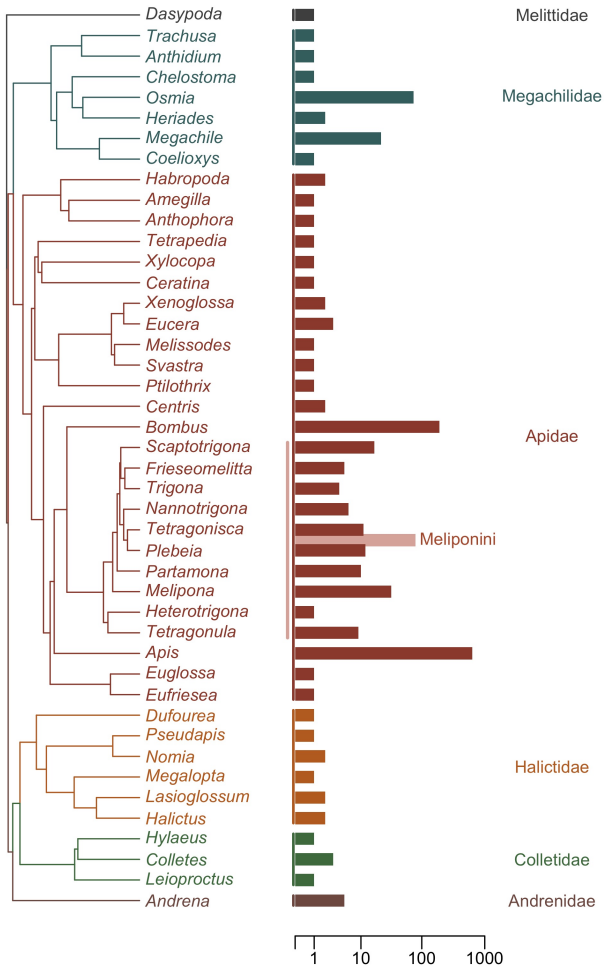

Figure 6: Phylogenetic tree adapted from Henríquez-Piskulich et al. (2024) showing the genera included in the database of papers testing the effects of nicotinic cholinergic pesticides on bees (left), and the number of papers per genus (right). Community survey studies were removed and genera only represented by such studies have been excluded. Vertical colored lines at x = 0 denote families, with family names displayed on the right of the bars. Genera belonging to the tribe Meliponini (stingless bees) are in addition marked with a pink vertical line and the corresponding papers (n = 79) are summarized by a pink bar. To improve readability, the x-axis has been compressed. Honeybees (*Apis*, n = 637) and bumblebees (*Bombus*, n = 192) represent the two most studied genera. In total, 842 of the papers (excluding community surveys) include at least one species from the monophyletic clade consisting of these three eusocial groups (Meliponini, *Apis* and *Bombus*), whereas 57 papers do not.

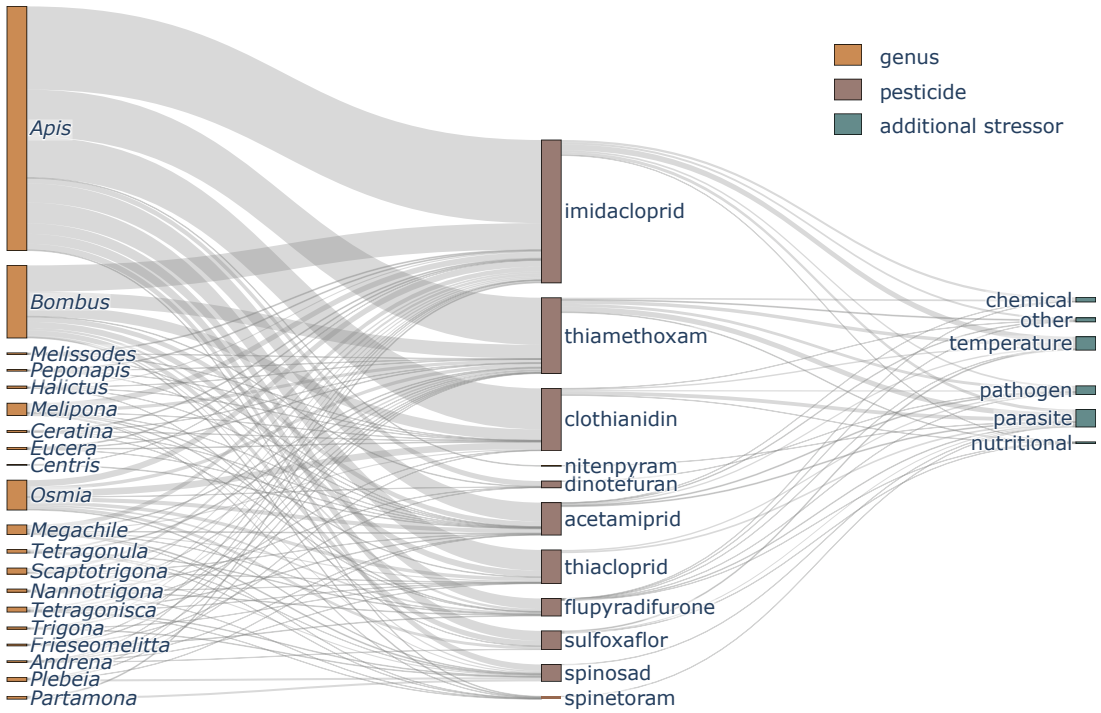

Figure 7: Sankey diagram showing the co-occurrence of bee genera with pesticide types (filtered with min. 3 studies per relationship) and pesticides with additional stressor categories. Thicker lines represent a larger number of studies.

Table 1: Description of benchmarking metrics and the required input data, including LLM answer (output answers from pipeline), gold answer (reviewer-verified benchmarks), retrieval context (relevant text chunks) and context (full paper text).

Metric	**What it measures**	**Required data**
faithfulness	How well the actual output aligns with both the expected output and the paper context. Detects hallucinations and context violations.	- LLM answer - gold answer - context
contextual precision	Evaluates whether the retrieved context contains the specific details needed to answer the question from the gold answer.	- gold answer - retrieval context
contextual recall	Completeness of context coverage. Ensures all necessary information was retrieved from the paper.	- gold answer - retrieval context
GEval completeness	Coverage of all key points mentioned in the expected output. Assesses if the actual output addresses all important aspects.	- LLM answer - gold answer
GEval accuracy	Semantic alignment and information quality. Evaluates if the actual output contains accurate information that aligns with the expected output.	- LLM answer - gold answer

Table 2: Example answers from LLMv1, reviewers, and LLMv2.

Question	LLMv1 answer	Reviewer answer	LLMv2 answer
bee species	The species of bees tested were honeybees, specifically *Apis mellifera* and its subspecies *A. m. carnica*.	*Apis mellifera carnica*	1. *Apis mellifera carnica*
bee species	The species of bees tested were bumblebees and honey bees.	*Bombus terrestris* and *Apis mellifera*	1. *Bombus terrestris* 2. *Apis mellifera*
pesticides	The pesticides used were thiamethoxam and imidacloprid. Exposure was chronic via syrup and pollen at 0, 1.5, 5, 10, and 25 ppb for 18 days.	Bees received only imidacloprid, chronically for 18 days via treated pollen and nectar at 1, 5, 10, and 25 ppb.	1. Imidacloprid (0, 1, 5, 10, or 25 ppb); oral exposure; 18 days
pesticides	The pesticides included linalool, hexyl acetate, Z-3-hexenol, (E)-ocimene, terpineol, clothianidin, imidacloprid, and thiacloprid; exposure methods varied; durations not fully available.	Bees were exposed to either thiacloprid or imidacloprid, chronically in sugar solution for 6 weeks (imidacloprid 50 ppb; thiacloprid 4,500 ppb).	1. Imidacloprid (50 ppb, oral, 6 weeks); 2. Thiacloprid (4,500 ppb, oral via sugar syrup, 6 weeks)
additional stressors	Yes: DWV infection (1,000 genome copies), nicotine (50 ppm), and 32°C; DWV and nicotine via diet; temperature via thermostatic cabinet; DWV/nicotine until death after emergence; temperature continuous.	DWV infection (1,000 genome copies) and 32°C; DWV via diet; nicotine 50 ppm fed; thermostatic cabinet; DWV/nicotine until death after emergence; temperature continuous.	1. DWV infection (1,000 genome copies per bee, via diet before pupation, duration n/s); 2. Nicotine (50 ppm in sugar solution at adult stage, duration n/s); 3. Temperature (32°C, duration n/s)

Appendix A. Example YAML Schema for Pesticide Extraction Task

```
pesticides:
   question: "What pesticide(s) were tested in this study? For each, provide the
specific dose(s) tested (or field application rates), exposure method(s) and
duration of exposure."
   instructions:
     - "Report pesticides that bees were exposed to in the study (including field
studies, controlled experiments, etc.)."
     - "Use the chemical name (not trade name or formulation) unless no other name is
given."
     - "Include doses/concentrations if explicitly reported, or field application
rates if explicitly reported."
     - "Include exposure method if explicitly reported (oral, contact, topical, field
exposure, etc.)."
     - "Include exposure duration if explicitly reported."
     - "List each pesticide separately."
     - "Do not add any interpretation, context, or description of results."
     - "Do not infer missing information-only report what is explicitly stated."
     - "If only the pesticide name is available, report just the name."
   output_format: "List of pesticides with: chemical name, and any available details
(dose, exposure method, duration)"
   example_output:
     - "1. Imidacloprid: 10 and 100 ppb, oral exposure, 7 days; 2. Thiamethoxam: 5 and
25 ppb, contact exposure, acute"
     - "1. Clothianidin: field exposure via treated oilseed rape at 10 g per kg of
seed; 2. Beta-cyfluthrin: field exposure via treated seeds"
     - "1. Clothianidin; 2. Indoxacarb"
   bad_example_output:
     - "In the study, the researchers tested imidacloprid (Admire) and sufoxaflor
(Closer) by feeding bees the pesticides over 10 days."
     - "The study tested several pesticides including neonicotinoids which are harmful
to bees. They used different doses and exposed the bees for some time. The
pesticides were applied in various ways to see how they affected the bees."
   no_info_response: "No pesticides were tested in this study"
   max_chunks: 5
```

Table A.3: Comparison of literature-review / LLM pipelines and capabilities. All metrics are based on information available on the listed tool's homepage (Lála et al., 2023; Paper Digest, 2025; Elicit, 2025; Marshall et al., 2017; Inc., 2025; Consensus, 2024; LLC, 2025; DistillerSR Inc., 2025; Veritas Health Innovation, 2025; Inc, 2025; ReadCube, 2025; Tilda Technologies Inc., 2025; Paper Digest, 2025; Documind, 2025; Anara Labs Inc, 2025; Elsevier, 2025; Allen Institute for AI, 2024).

Pipeline	**Full-text processing**	**User-specified corpus**	**Web literature search**	**Domain & question agnostic**	**Modular architecture**	**Source linking**	**Benchmarking**	**Open-source**
MetaBeeAI	yes	yes	no	yes	yes	yes	yes	yes
PaperQA2	yes	yes	yes	yes	yes	yes	yes	yes
Elicit	yes	partial	yes	yes	no	yes	yes	no
RobotReviewer	yes	yes	no	no	yes	yes	yes	yes
SciSpace	yes	partial	yes	yes	no	yes	yes	no
Consensus	yes	no	yes	yes	no	yes	no	no
Scite.ai	yes	yes	yes	yes	no	yes	no	no
DistillerSR	yes	yes	yes	yes	yes	yes	no	no
Covidence	yes	yes	yes	yes	yes	yes	no	no
Perplexity (Deep Research)	partial	no	yes	yes	no	yes	yes	no
ReadCube / Papers AI	yes	yes	yes	yes	no	yes	no	no
Humata	yes	yes	no	no	no	yes	no	no
PaperDigest	yes	yes	yes	yes	no	yes	no	no
Documind	yes	no	no	yes	yes	yes	no	no
Anara	yes	yes	yes	yes	no	yes	no	no
Scopus AI	yes	no	partial	yes	no	yes	no	no
Asta	yes	partial	yes	yes	no	yes	no	no

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