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Toward a global repository of insect traits (GRIT)

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Abstract

1. The pace of biodiversity loss outstrips our ability to conserve Earth's most diverse group of named species—the insects (Arthropoda: Insecta). We increasingly rely on trait-based metrics to understand how insects respond to and affect their environment. Traits provide insights that aid conservation assessment and planning. Yet, we lack a centralised trait database for insects, hampering insights that could inform ecological research and conservation management planning.
2. We propose the creation of the Global Repository of Insect Traits (GRIT). GRIT will cover all world regions, realms and insect taxa. It will provide open and FAIR access to comprehensive trait data compiled from both currently available and future datasets. This proposal is an open call for all to join a global network of collaborators in a collective effort to accelerate the compilation of insect trait data and increase the transparency of data sharing and accessibility in the field.
3. We envision the use of state-of-the-art methods in trait acquisition and imputation to build computational tools that can extract and validate trait data from unstructured text, accelerating information availability by orders of magnitude. We anticipate the development of analytical tools that contribute to a governance structure, ensuring the long-term success of the database and extraction tools.
4. Finally, we outline future opportunities and identify several research questions that could be readily answered once data are assembled. Recognising the numerous

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challenges inherent in this project, we invite a robust discussion on strategies to effectively address obstacles.

KEYWORDS
Arthropoda, data sharing, ecosystem services, entomology, functional diversity, functional ecology, functional traits, invertebrates, open data, software development

INTRODUCTION

The fields of ecology and conservation biology have traditionally used taxonomy-oriented approaches to characterise and assess biodiversity, with species as the major focal unit. Today, trait-based approaches are increasingly adopted (Chichorro, Correia, & Cardoso, 2022; Mammola et al., 2021). Trait-based approaches use phenotypic characteristics of an individual or population to synthesise complex data into identifiable, generalisable and mechanistic principles underpinning how organisms interact with abiotic and biotic components of environments via their responses and effects (Wong et al., 2019). The use of traits enables biodiversity studies to extend from local to global spatial scales, and from ecological to evolutionary time scales, by allowing comparison of communities with few or no overlapping taxa (Mammola et al., 2021; Palacio et al., 2022).

While there is no consensus on the definition of "trait" in the literature (Dawson et al., 2021), a trait is often considered to be any observable feature measured at the level of individual organisms, including morphology, habitat, ecological interactions, life history, physiology, biochemistry and behaviour. Traits can be quantitative (continuous, integers) or qualitative/categorical (ordinal, nominal, binary). Species or population-level traits are often recorded as derived values (mean, median, minimum, maximum, trait affinities or even mode for categorical traits). Exceptions include sexual dimorphism, polymorphism, ontogeny or other traits that may radically change over an individual's lifetime, for instance, in the case of holometabolous insects. Traits are often categorised into two types: (1) 'response traits' describe how a species reacts to environmental factors and (2) 'effect traits' describe how a species influences ecosystem properties.

Trait-based approaches can be used to answer questions in community ecology (McGill et al., 2006), biogeography (Violle et al., 2014), conservation biology (Chichorro et al., 2019; Chichorro, Correia, & Cardoso, 2022; Chichorro, Urbano, et al., 2022; Oyarzabal et al., 2024), micro- (Chapin III et al., 1993) and macro-evolution (Guillerme et al., 2023), and applied fields (e.g. agronomy; Martin & Isaac, 2015). Additionally, trait-based approaches can offer insights into drivers of behavioural ecology (Dingemanse & Réale, 2005) and invasion biology; these types of investigations seek to identify traits of non-native species that predict their impact and manage invasions (Jarošík et al., 2015; Matzek, 2012). Beyond individual traits, ecological communities can be characterised by the diversity of traits within them, which represents the range of traits of the individuals and species within a community. When traits are functional such that they impact an organism's fitness or higher-level ecological processes and patterns (Wong et al., 2019), quantifying this type of multidimensional diversity is a key facet of biodiversity that links species composition to ecosystem functioning. Traits are an important currency to identify and quantify species' contributions to the provision of ecosystem functions, including ecosystem services. Ecosystem services are essential for human well-being and survival, and increasingly form the basis to justify conservation initiatives (Naidoo et al., 2008).

With ecology, conservation and evolutionary studies encompassing taxa groups, larger geographical areas and longer temporal periods, there is an increasing need for more comprehensive trait databases. Traditionally, trait-based research has relied on the laborious and time-consuming collection of traits from the literature, field and laboratory work, curated museum specimens, and other archival sources. These data are rarely made public. Other data are deprecated, having previously been more accessible and now available only in outdated and variable archival formats. Re-collecting trait data can delay the development of novel studies, particularly those at large spatial, temporal or taxonomic scales. It can also lead to duplicate efforts in data acquisition, wasting time and resources. Vast amounts of trait data are still hidden in historical literature, different languages, grey literature, unpublished records or student projects and theses. More recently, collected data may be stored in digital forms within different online repositories (e.g. Pekár et al., 2021; Tobias et al., 2022) but remain disparate.

While trait data are being compiled at unprecedented rates and span a wide taxonomic breadth, data are often isolated and difficult to access, compile and standardise, especially when sources use different formats and applications and report metadata differently. Recently, the FAIR guiding principles for scientific data management (i.e. findability, accessibility, interoperability and reusability; Wilkinson et al., 2016) have been broadly adopted by researchers to maximise the applicability and use of biodiversity databases. Open trait-based databases not only boost research capacity but also inspire exploratory analyses to detect knowledge gaps or taxonomic and geographical biases that can be remedied in future work.

The existence of global biodiversity data repositories has been widely adopted for geographical (e.g. Global Biodiversity Information Facility – GBIF), genetic (e.g. Genbank [Benson et al., 2012], The Barcode of Life Data Systems – BOLD [Ratnasingham & Hebert, 2007]) and other types of data (e.g. https://pherobase.com/ for pheromones). Databases already exist for traits of several taxonomic groups, such as mammals (Jones et al., 2009), birds (Sayol et al., 2024; Tobias et al., 2022), reptiles (Grimm et al., 2014), spiders (Pekár et al., 2021), corals (Madin et al., 2016), copepods (Brun et al., 2017), different marine taxa (WoRMS Editorial Board, 2025), fungi (Põlme et al., 2020) and plants (Kattge et al., 2011). Yet the most speciose taxonomic group, insects, still lacks a centralised database, except for individual efforts dedicated to a few taxa such as butterflies (Cook et al., 2022; Middleton-Welling et al., 2020; Shirey et al., 2022), ants (Parr et al., 2017), odonates (Waller et al., 2019) and ground beetles (Homburg et al., 2014) (Table 1).

The vast diversity of insects and their extraordinarily diverse life histories compared to any other taxonomic group are likely the primary reasons for the slow development of global insect trait databases. Insect experts often focus on individual taxa, which has resulted in taxon-specific databases, rather than a common insect trait database. Moreover, existing trait databases are disparate in their structure, from simple tables with minimal structure, metadata or inclusion requirements to more rigorous frameworks, but with remaining limitations in scope or accessibility. These disparities are further complicated by the lack of standardisation of how insect trait data are defined, measured, reported and used in global insect research (Maasri, 2019). Databases also differ in how they deal with differences in data acquisition (e.g. different methods used to measure some traits; Moretti et al., 2017) or how uncertainty is treated. These differences often make even simple uses of data laborious, particularly when data are gleaned from different sources. Finally, databases differ in how users are expected to interact with them. Data may be accessed through web-based portals, simple downloads from repositories or through application programming interfaces (API) and specific software packages. Such differences in accessibility and usability can create additional barriers to effective data integration, slowing progress in trait-based research.

Here, we propose the establishment of the Global Repository of Insect Traits (GRIT) (Figure 1). We delineate a roadmap for the development of a series of tools to facilitate trait acquisition, imputation and analysis. We extend an invitation for scientists and practitioners to join our efforts to build a database that covers all regions, biomes and insect taxa. Our initiative will compile and provide open access to unlimited amounts of insect trait data for the benefit of biodiversity research and conservation efforts. GRIT will include a strict governance system that assures its temporal continuity, as well as a variety of methods and tools to facilitate data extraction and curation, maximising the use of trait contributions by researchers, amateur entomologists and the public. GRIT is a collective effort that intends to increase transparency in data sharing and accessibility and accelerate the compilation of insect trait data. Our main goal is to improve research capacity through streamlining trait-based research in entomology and making insect trait data more findable, accessible, interoperable, reusable and impactful for ecology, evolution and conservation.

THE GLOBAL REPOSITORY OF INSECT TRAITS (GRIT)

Given the variabilities and challenges in defining traits, we propose a broad definition of traits that encompasses all observable or quantifiable characteristics at the individual, population or taxa level, regardless of assumed functional roles (Noriega & Schowalter, 2024). These characteristics include functional—or response-and-effect—traits,

TABLE 1 Examples of existing insect trait repositories.

Name	Taxonomic scope	Geographical scope	Traits	References
Amazonian Odonata Trait Bank	Odonata	Brazilian Amazon	A wide range of traits	Ferreira et al. (2023)
Carabid Trait Database	Carabidae	Western Palearctic	Size and dispersal traits	Homburg et al. (2014)
Cook et al. (2022)	Lepidoptera	Great Britain and Ireland	A wide range of traits	Cook et al. (2022)
EOL TraitBank	All taxa including insects	Global	A wide range of traits	Parr et al. (2014)
EuPPollNet	Lepidoptera, Apoidea, Syrphidae	Europe	Pollinator interactions	Lanuza et al. (2025)
Freshwaterecology.Info	Freshwater invertebrates	Europe	A wide range of traits	Schmidt-Kloiber and Hering (2015)
Global Biotic Interactions (GloBI)	Insects and other taxa	Global	Species interactions	Poelen et al. (2014)
GlobalAnts	Formicidae	Global	Morphology and life history traits	Parr et al. (2017)
HOSTS	Lepidoptera	Global	Host plants and type of damage left by larvae	Robinson et al. (2023)
LepTraits	Lepidoptera	Global	A wide range of traits	Shirey et al. (2022)
Logghe et al. (2024)	Multiple orders	NW Europe	Life histories, habitat and thermal niche	Logghe et al. (2024)
Middleton-Welling et al. (2020)	Lepidoptera	Europe and North Africa	A wide range of traits	Middleton-Welling et al. (2020)
Waller et al. (2019)	Odonata	Global	A wide range of traits	Waller et al. (2019)

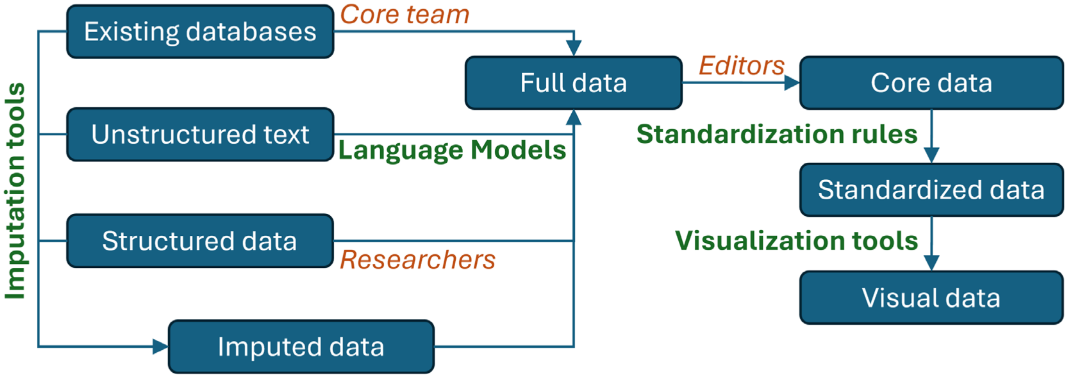

FIGURE 1 Scheme for data (boxes, blue), automated tools (bold, green) and actors (italics, orange) within GRIT. Besides the benefits of access to FAIR data, researchers will be able to use language models for automated trait data extraction and imputation tools for specific project needs.

which can be heritable (Wong et al., 2019) or driven by phenotypic plasticity (McGill et al., 2006; Schneider et al., 2019). For now, we propose to integrate the approaches of Moretti et al. (2017) and Gonçalves-Souza et al. (2023), by classifying traits into six categories, namely: (1) morphology (e.g. body size, wing length), (2) habitat (e.g. habitat range, microhabitat preference), (3) interactions (e.g. guild, parasitism, predation, symbioses, herbivory, pollination), (4) life history (e.g. ontogeny, generation length, phenology, colony size), (5) physiology/biochemistry (e.g. metabolic rate, temperature tolerance) and (6) behaviour (e.g. sociality, dispersal, circadian activity). Additional categories may be incorporated as the database expands. The repository will include several mandatory fields for new entries that allow a minimum set of metadata for analysis and tracing of the data sources (Table 2). GRIT will not contain molecular data or faunistic records, but will link to established repositories such as, for example, GenBank (http://www.ncbi.nlm.nih.gov/genbank/), BOLD (https://v4.boldsystems.org/) and GBIF (https://www.gbif.org/).

We will follow the FAIR Data Principles (Wilkinson et al., 2016) and guidelines from the Open Traits Network (https://opentraits.org/) across all stages of the database assembly and construction. This includes openly sharing data, code, protocols and methods, giving credit to authors, and standardising data acquisition methods. We will create guidelines for future data acquisition so that teams around the world can contribute their data while maintaining high-quality standards that make the data more usable and effective. All information will be checked for quality control, including: (1) unintended duplicate data entries; (2) variable names matching controlled vocabulary values; (3) data values matching expected data types; (4) data values matching allowable values to validate entries; (5) values matching historical minima/maxima and expected scale or sensitivity (range check); and (6) spatial coordinates mapped to identify outliers for further data interrogation and to detect errors (e.g. terrestrial records in marine environments). Data quality flags will be associated with each record where possible.

At a later stage and depending on funding, we plan to leverage available semantic technologies for GRIT's architecture and for logical models to store trait data (Balhoff et al., 2013; Montanaro et al., 2024). Traits will be represented as semantic graphs in RDF format (Montanaro et al., 2024), where nodes represent ontology individuals—such as anatomical structures (e.g. head, leg) or their qualities (e.g. red, punctate, 8 mm)—and edges denote relationships between them (e.g. has_part, has_characteristic). Ontologies are used not only to simplify data acquisition and storage, but also to depict relationships among different traits. Although the designations given at the source will always be kept, the use of ontologies can make the acquired traits understandable and queryable by automated systems. These properties make data accessible and interoperable (Deans et al., 2012, 2015), facilitate analysis and treat trait data as machine-readable and interpretable.

HETEROGENEITY OF DATA

Common problems in synthetic trait databases include traits measured at different taxonomic resolutions, trait measurement variability and nomenclatural changes. Traits are often reported at taxonomic levels other than species, from subspecies to entire families or orders. This information is often useful and would be lost if only species and subspecies traits were used. GRIT will accommodate all taxonomic levels, allowing users to select the desired taxonomic resolution depending on their needs and purposes. Besides sorting and pulling data existing at higher taxonomic levels, we will create tools to aggregate data at lower levels. The database will accommodate different types of derived data, including inter- and intraspecific trait data. For species, reported values in publications are often averages or ranges, and whenever feasible, we will seek to obtain original raw data. For individuals, a single value is often reported, but sometimes numerous quantifications of a trait are made even at the individual level (e.g. the range of movement over multiple days).

Data can be recorded in a large number of different formats. Body size, for example, might be represented as a number (e.g. 4 mm), a range (e.g. 3–6 mm) or a category (e.g. large). Diet breadth can be represented as a proportion (e.g. 10% animal, 90% plant), a category (e.g. stenophagous), a number (e.g. 5 prey species) or as a string of

TABLE 2 Database records to include information from the following fields, using DarwinCore terms whenever applicable for interoperability. Further fields may be added to these core terms if they are found to be useful.

Field	Description	Eligible values or examples	DarwinCore link (if available)
occurrenceID	Global unique identifier	A00000001; Z12345678	http://rs.tdwg.org/dwc/terms/occurrenceID
datasetName	Name of original dataset	BALA; ALAS; "Borges et al. (2023)"	http://rs.tdwg.org/dwc/terms/datasetName
licence	A legal document giving official permission to do something with the resource	CC-BY; CC0	http://rs.tdwg.org/dwc/terms/license
informationWithheld	Embargo date	YYYY-MM-DD	http://rs.tdwg.org/dwc/terms/informationWithheld
basisOfRecord	The specific nature of the data record	PreservedSpecimen; LivingSpecimen	http://rs.tdwg.org/dwc/terms/basisOfRecord
scientificNameID	GBIF backbone taxon ID	gbif.org/species/2879737	http://rs.tdwg.org/dwc/terms/scientificNameID
scientificName	The full scientific name, with authority and date of publication, if known	Acrididae; *Cephalotes atratus* (Linnaeus, 1758)	http://rs.tdwg.org/dwc/terms/scientificName
taxonRank	The taxonomic rank of *scientificName*	Species; genus; family	http://rs.tdwg.org/dwc/terms/taxonRank
verbatimIdentification	Taxon name as reported in the original source where the trait was made available	Acridid; *Cephalotes atratus*	http://rs.tdwg.org/dwc/terms/verbatimIdentification
measurementType	Trait as mentioned in the original source	Body size; wing length; weight; respiration rate; 3D morphometry	http://rs.tdwg.org/dwc/terms/measurementType
measurementMethod	Definition of the trait according to the source	"Measured from tip of rostrum to tip of tail"; "specialist was defined as species that nest on a single plant"	http://rs.tdwg.org/dwc/terms/measurementMethod
measurementValue	Measured value of a trait	110; large; forest	http://rs.tdwg.org/dwc/terms/measurementValue
measurementUnit	The unit used for the value	mm; g; years	http://rs.tdwg.org/dwc/terms/measurementUnit
measurementStatistic	Type of *measurementUnit*	Single observation; mean; median; min; max	NA
measurementRemarks	Any note related to information provided	"cerci missing"	http://rs.tdwg.org/dwc/terms/measurementRemarks
sex	Sex	Female; male; both; unknown	http://rs.tdwg.org/dwc/terms/sex
lifeStage	Ontogenetic stage as used in the original source	Egg; larva; nymph; caterpillar; instar I; pupa; adult; all	http://rs.tdwg.org/dwc/terms/lifeStage
caste	Categorisation of individuals for eusocial species	Queen; male alate; minor worker; soldier	http://rs.tdwg.org/dwc/terms/caste
sampleSizeValue	A numeric value for a measurement of the size	45; >50; 50%	http://rs.tdwg.org/dwc/terms/sampleSizeValue
sampleSizeUnit	The unit of measurement of the size	Metre; day	http://rs.tdwg.org/dwc/terms/sampleSizeUnit
sampleTreatment	Treatment and conditions at which it was measured	5 mg active ingredient; 5°C; no management	NA
samplingProtocol	Sampling method employed	SLAM; pitfall; Pollard walks	http://rs.tdwg.org/dwc/terms/samplingProtocol
verbatimLocality	The original textual description of the place	Lisbon; "25 km East of Tamale, Ghana"	http://rs.tdwg.org/dwc/terms/verbatimLocality
verbatimCoordinates	The original spatial coordinates	"N41.76 W34.78"; "21 T 63 48"	http://rs.tdwg.org/dwc/terms/verbatimCoordinates
VerbatimEventDate	The verbatim original representation of the date and time information	21.08.1976; 2012; "March 2001"	http://rs.tdwg.org/dwc/terms/verbatimEventDate

(Continues)

TABLE 2 (Continued)

Field	Description	Eligible values or examples	DarwinCore link (if available)
associatedOccurrences	Unique identifier marking related data (same individuals)	a1, B	http://rs.tdwg.org/dwc/terms/associatedOccurrences
associatedReferences	Full reference of the published or unpublished data, including DOI if available. For consistency, follow APA style	"Oyarzabal et al. (2024)"	http://rs.tdwg.org/dwc/terms/associatedReferences
externalLink	Link to external database related to this entry (e.g. specimen in museum, cox1 in iBOL)	http://id.luomus.fi/GZ.54935; https://portal.boldsystems.org/record/ABWYT10515-24	NA

descriptive text (e.g. feeding on many prey). Our database will accommodate these different data types, as long as the meaning of each value is provided as metadata (in *measurementMethod*, see Table 2) or is unambiguous (Jones et al., 2006). By providing metadata, users can filter data to comparable units. We should note, however, that controlled vocabularies will be used for multiple fields where appropriate, following the DarwinCore guidelines and facilitating the use of data from different studies. We will further include standardisation tools to facilitate data extraction and transformation for common analyses, even if such transformations are not straightforward in many cases and might require extensive work by data analysts.

Nomenclatural changes, junior synonyms, *nomina dubia* or *nuda* and multiple other taxonomic issues arising from improved systematic studies mean that valid species names and higher taxonomic rank names are constantly changing, particularly for taxa with unstable taxonomy. Keeping track of the latest taxonomic classifications and nomenclature can be challenging, with the scientific names in databases quickly becoming outdated. To automate the process as much as possible, we propose using the Catalogue of Life and GBIF backbones and accepted name usage ID, which currently matches species names for over two billion occurrences of almost two million species using multiple taxonomic lists and biodiversity databases. We will follow the recommendations of Grenié et al. (2023) for name harmonisation, namely the three steps for preprocessing names, matching databases and resolving unmatched names with fuzzy matching. For new taxa not yet present in the Catalogue of Life or GBIF, we will use a Zoobank identifier. This will match most taxa to current names (Sandall et al., 2023). The name stated in the source (*verbatimIdentification*; Table 2) will always be kept for reference, allowing it to be rematched as better backbones and tools for name matching become available.

WORKFLOW AND RESOURCES

GRIT will include data spread across numerous databases, peer-reviewed publications and other formats. GRIT will be hosted and maintained by a team in the Faculty of Sciences at the University of Lisbon (Research Centers CE3C and LASIGE). Yet, GRIT will be an open and ever-evolving repository, subject to change as needs and resources change, and welcoming contributions by experts on any insect taxon and from every region of the world. In this sense, this paper serves as an open call for all interested parties willing to share data under the FAIR principles, though large contributions are preferred given the need to optimise the use of human resources by the core team. The database will be able to accommodate all kinds of traits and data types, with trait coverage only depending on contributions by the global community (Figure 2). We will, however, actively seek to cover taxonomic and geographical gaps identified throughout the process (less studied orders and regions) and from previous work by team members, to limit biases impeding future research. We will build on both global (e.g. Shirey et al., 2022) and regional (e.g. Logghe et al., 2024) initiatives, explicitly avoiding global biases whenever possible by teaming with partners in the Global South (e.g. Ferreira et al., 2023).

To upload data, contributors will be asked to use a template that supports the corresponding metadata. The template will be made available on the online platform that will also host the database. In the meantime, we invite researchers to contact the corresponding author to join the team and contribute to this first stage. Once ready to launch, a corresponding manuscript detailing the database will be prepared. Contributors will be invited to join the list of authors if a minimum number of records, to be determined by the core group, is met. Any future major changes to the structure or contents of the database, to the core team or any significant landmarks, will be accompanied by new publications. It is our goal that all data will be provided under a CC-BY or CC-BY-NC 4.0 licence. Following the FAIR guiding principles (Wilkinson et al., 2016), contributors must cite the original data sources, which will also be referenced in the repository. There is disagreement about whether original sources must be cited in a publication that uses data from databases that compile data from different sources; thus, we will encourage users to cite the original sources when they constitute a fundamental part of any study, but this decision will ultimately be left to the users (Gallagher et al., 2020).

It is envisaged that a globally distributed team of curators for each taxon, region and trait type will provide expertise to validate each dataset and strengthen the future of the database. Tools to facilitate accurate data curation will be developed to overcome limitations of manual curation, a task that is inherently error-prone. Inconsistencies will be checked using automated methods through format

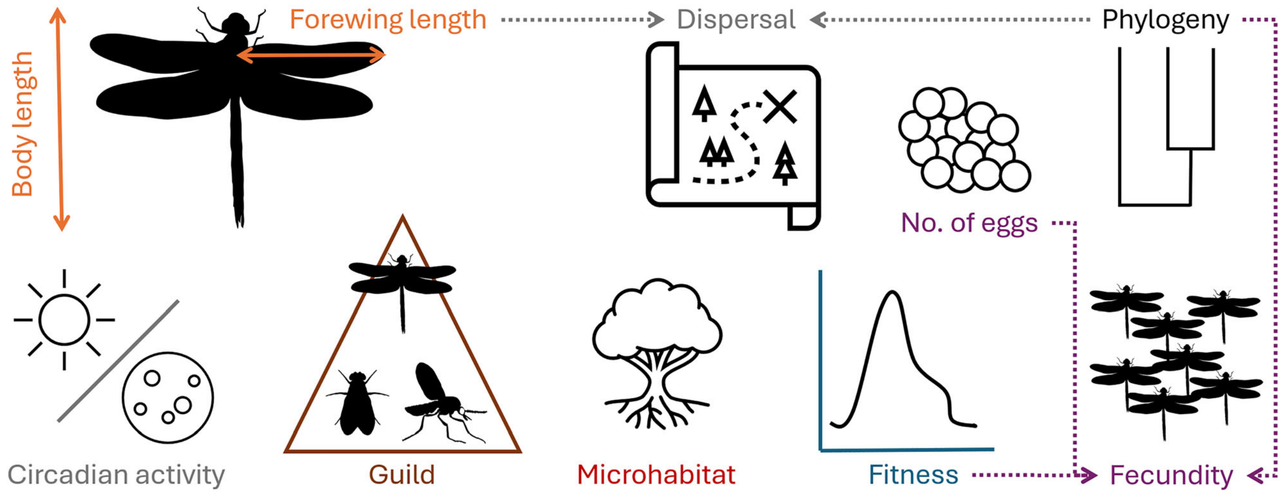

FIGURE 2 Examples of traits to include in GRIT, including morphology (body length, forewing length, orange), behaviour (circadian activity, grey), interactions (guild, brown), habitat (microhabitat, red), physiology/biochemistry (fitness, blue) and life history (number of eggs, purple). Based on existing traits and phylogenies, additional traits can be imputed with variable confidence (represented by dashed lines), e.g. dispersal can be imputed from forewing length and fecundity can be imputed from number of eggs and fitness.

matching and automated detection of outliers. As examples, a body size that is represented by a string of letters would be flagged due to a potentially incorrect format (although it could be, e.g. the category "large"), and "500" or similarly unusual numbers should flag a possible incorrect entry, maybe due to a missing decimal point. These features were established when developing the World Spider Trait database (Pekár et al., 2021) and will be emulated in GRIT.

DEVELOPMENT OF TOOLS FOR DATA ACQUISITION AND IMPUTATION

As manual labour is resource-intensive, especially when considering an incredibly diverse group such as insects and the many thousands of documented sources containing trait data, it becomes crucial to develop a computational workflow capable of automatically extracting trait data from unstructured text. This will significantly increase the speed at which data becomes available. Large Language Models (LLMs) and related approaches within the field of Natural Language Processing (NLP) are transforming how information is parsed and structured, offering unprecedented opportunities for biodiversity research (Castro et al., 2024; Domazetoski et al., 2023; Folk et al., 2024; Keck et al., 2025; Rafiq et al., 2025; Tamaddoni-Nezhad et al., 2013). LLMs have been applied to extract domain-specific models for trait data in plants (Bamba & Sato, 2025; Marcos et al., 2025) and animals (Scheepens et al., 2024) and are emerging at a rapid pace, matching the release of new general-purpose LLMs. Leveraging LLMs for data extraction occurs through two main approaches. The simplest involves prompt engineering: designing specific prompts or sequences of prompts to guide general-purpose models. While this method is effective for simple tasks, our preliminary attempts with trait data revealed limitations due to the contextual dependencies of trait descriptions and increased complexity in both the variability of data formats and the evaluation of results. Consequently, we are prioritising fine-tuning LLMs specifically for insect trait data (Dorm et al., 2025) and using them to populate GRIT. Importantly, it is well known that LLMs using massive computing power are resource-intensive (de Vries, 2023) and this is increasingly a concern in the use of automated systems in biodiversity research (Cardoso et al., 2025). The LLMs we will develop will be locally hosted to limit their environmental impact.

To maintain high data quality, trait data extracted via LLMs will undergo automated consistency checks. However, given the importance of human validation, LLM-generated records will be flagged initially as "unvalidated" within GRIT, making them available to the public while undergoing curator review. The manual verification process will, in turn, contribute to the iterative improvement of our models, forming a continuous feedback loop for training and validation. With the rapid development of LLMs, we anticipate that their capabilities in trait data extraction will continue to improve. Advances in model architecture, domain-specific training and integration with structured biodiversity databases aim to enable more accurate and scalable extraction workflows. By staying at the forefront of these developments, we seek to refine and expand our approach to accelerate the availability of high-quality trait data for research.

Additionally, we will seek funding to assess computer vision models to extract morphological traits from images, particularly museum images calibrated in both size and colour. Calibration requires some sense of scale (either a scale bar or ruler) and a colour target card so that photographs can be colour-corrected for comparison (Shirey et al., 2024). We will test convolutional neural networks (CNNs) to detect scales and save the conversion factor from pixels to centimetres for each image. A second CNN will be used to segment body parts and extract sizes. To obtain colour information, we will use α-shapes based on RGB (Red-Green-Blue) 3D spaces (Gruson, 2020), with the possibility to expand toward other light frequencies.

Finally, we will develop an R package to facilitate the download and basic manipulation of trait data in GRIT, following the example of the R package for spider traits, *arakno* (Cardoso & Pekár, 2022). The R package will include several basic functions to check taxonomic name validity, retrieve geographic coordinates from GRIT, GBIF and other sources, summarise trait values, impute missing values using both extant trait data and phylogenies, and map the results within the widely used R statistical environment.

Even if the full suite of conceptualised trait extraction tools were employed, most described species would still lack information for most traits. This can lead to biased analyses (e.g. if existing traits are limited to a non-random subset of species). Multiple methods for trait imputation have been developed using information from other species, phylogenies and more or less complex algorithms. The simplest metric is to use the average or median values for the relevant genus or family. However, methods using phylogenetic information generally perform better (e.g. Debastiani et al., 2021; Johnson et al., 2021; Penone et al., 2014). Multiple R packages such as *Rphylopars* (Goolsby et al., 2017) and *missForest* (Stekhoven & Buhlmann, 2012) provide excellent tools for trait imputation. Some methods such as Bayesian hierarchical probabilistic matrix factorisation (Schrodt et al., 2015) do not use phylogenies, but allow users to provide the taxonomic hierarchy structure, which is often desirable (e.g. Joswig et al., 2023). We will create a workflow and incorporate tools within both GRIT and the above-mentioned R package to be newly developed by us. These tools, which take advantage of multiple imputation methods, will allow users to easily fill in gaps for traits that have enough information for imputation. However, no imputation method is perfect, and they all suffer from some degree of bias (Gorné et al., 2025). This can be addressed upstream by calculating a confidence value (e.g. informed by the percentage of missing values in a dataset). Regardless, imputed values should be checked by experts to ensure congruence and applicability to the specific question. In some cases, imputation methods may not perform well. In these situations, users may need to restrict their analyses to taxa with more complete data (Johnson et al., 2021). Overall, trait imputation should be done carefully, validating the method, always referring to the original sources, and flagging imputed data to avoid their spurious use on further imputations and inappropriate analyses, thus reducing biases that might lead to incorrect conclusions (Gorné et al., 2025) and their proliferation in subsequent literature.

FUTURE RESEARCH FACILITATED BY GRIT

We anticipate that a global insect trait database and its supporting tools will exponentially accelerate the speed at which many questions in insect science can be addressed and facilitate faster and more effective environmental decision-making. Here, we provide examples of how trait data have been used in the past to demonstrate how GRIT will enable rapid understanding of the evolution, diversity, conservation and ecosystem functioning of insects across the world.

Understanding trait evolution and insect diversification

Identifying patterns of trait distributions across the tree of life can provide insight into evolution and its history. Exploring the morphospace of traits—by quantifying trait space across communities to assess trait or functional diversity—offers a powerful framework to investigate changes in niche dynamics across phylogenies (McGill et al., 2006, 2019; Violle et al., 2007). Additionally, traits, when studied in a phylogenetic context, allow us to identify and understand which key innovations may have accelerated diversification rates of evolutionary lineages. For example, in Western European arthropods, phylogenetic signals were found to be highly variable and strongly influenced by both the specific trait and arthropod order, with body size and development having strong phylogenetic conservatism, thermal niche largely independent of shared ancestry, and dispersal and fecundity strongly conserved in some orders but minimally predicted by phylogenies in others (Logghe et al., 2025). In a separate large-scale study across insect orders, a positive correlation was found between herbivory and diversification (Wiens et al., 2015), while other traits considered to be key to insect success, such as the development of flight or complete metamorphosis, were not associated with immediate changes in diversification (Condamine et al., 2016). In a more restricted study on selected Coleoptera families, a transition to phytophagy positively affected species richness (Zhang, 2013). Understanding the distributions of traits across phylogenies helps to disentangle broad biological patterns from those more attributable to shared ancestry (Felsenstein, 1985).

Studying large-scale spatial patterns of biodiversity

Insect traits can provide a powerful framework for understanding large-scale spatial patterns of diversity (McGill et al., 2019). By characterising species based on measurable traits rather than solely on taxonomic identity, researchers can explore how environmental gradients or environmental change shape community composition and ecosystem functioning on a global or regional scale (e.g. Alahuhta et al., 2019; Suding et al., 2008; Wong et al., 2019; Yazdanian et al., 2023). For example, a recent study demonstrated how the wing length of female geometrid moths has evolved in montane environments, often becoming shorter with increasing elevation, thereby promoting diversification through reduced dispersal capabilities and increased isolation of populations (Lee et al., 2024).

Traits have also been instrumental in linking the characteristics of individuals or taxa to large-scale ecological patterns. For instance, by measuring traits such as body length and converting these into body mass and metabolic rates using established scaling relationships, researchers can derive key state variables that underpin macroecological models, like the maximum entropy theory of ecology (Brush et al., 2022). This trait-based approach allowed Brush et al. (2022) to analyse species abundance distributions, metabolic rate distributions and species–area relationships across different habitats and reveal how shifts in trait composition—particularly between indigenous and introduced species—explain deviations in macroecological patterns under varying levels of anthropogenic disturbance.

Moreover, trait-based approaches coupled with long-term ecological monitoring at larger scales can provide the temporal depth and replication needed to understand not just which species occur where, but how their functional roles change through time. Dornelas et al. (2014) showed that although local species richness often remained stable, functional trait space could expand or contract significantly over 30–50-year time series in marine and terrestrial assemblages of many taxonomic groups.

Examining species interactions

Species interaction research seeks to understand the structure of mutualistic networks, the diversity of food webs and parasite–host interactions (Montoya et al., 2012; Traveset et al., 2018). Under environmental change, modifications in species composition may have severe cascading effects through the network, with putative consequences for network stability and functioning (Schmitz, 2008). Reconstructing such networks can be facilitated by trait integration, starting with traits related to trophic position and body size (Brose et al., 2013). Trophic interactions among plant-associated arthropods are, for instance, well predicted from body size ratios and are considerably improved when traits related to hunting strategy and anti-predator defences are included (Van de Walle et al., 2023). A trait perspective on mutualist arthropods inhabiting ant nests (Parmentier et al., 2020) conversely explains the increased stability of these symbiont communities with succession (Parmentier et al., 2024).

Linking traits and ecosystem functioning

Trait-based approaches in functional ecology are increasingly used to link animal traits to ecosystem services (e.g. Elizalde et al., 2020; Wong et al., 2019). Functional traits influence (1) species' contributions to ecosystem services and (2) species' adaptations to ecosystem change through their fitness. For example, in agroecology, Wood et al. (2015) argue that trait-based approaches could help (1) predict how agricultural practices shape biodiversity and ecosystem services and (2) develop generalisable agricultural and land use management strategies. To advance these objectives, they emphasise the need to "establish a universally accessible agricultural trait database for all species in agroecosystems". Traits such as body size, proboscis length and foraging behaviour influence the efficiency of pollinators. Predatory insects such as ladybird beetles, parasitic wasps and lacewings possess traits that make them effective at controlling agricultural pests without the need for pesticides. Body size can influence ant species' contributions to decomposition rate (Nooten et al., 2022). Host-plant range of herbivorous insects, prey suite of predators and host range of parasitoids have been linked to their status as pest or beneficial species in agriculture (Schellhorn et al., 2010; Wood et al., 2010).

Quantifying environmental impacts on biodiversity

Traits provide mechanistic insights into how and why ecosystems are changing (Green et al., 2022) that extend beyond documenting fluctuations in species abundances. Multiple ecological studies of dung beetles find that trait diversity is an excellent indicator of the degree of anthropogenic disturbance and its effect on functional processes (Buse & Entling, 2019; de Castro-Arrazola et al., 2020; Noriega et al., 2023). A similar example comes from staphylinid beetles (Clough et al., 2007), where functional groups based on feeding guilds were found to be important predictors of responses to agroecosystem management intensity. Functional diversity can clarify the effect of increasing livestock grazing on ecosystem functioning, with functional group structure varying with livestock grazing intensity (Ford et al., 2013), and depending on the taxonomic groups (Chillo et al., 2017; Torma et al., 2019) and the regional scales studied (Guerra Alonso et al., 2022). Trait-based analyses have also elucidated mechanisms underlying shifts in tropical stingless bee communities under forest loss (Campbell et al., 2022; Lichtenberg et al., 2017) and variation in functional strategies of freshwater insects along the longitudinal carbon gradients of temperate rivers from their source to their mouth (Vannote et al., 1980; Verberk et al., 2013).

Physiological traits have emerged as valuable predictors for how species will respond to climate change (Kellermann & van Heerwaarden, 2019). Among these, critical thermal limits (CT_{min} and CT_{max}) are particularly informative, as they vary geographically (Diamond, Sorger, et al., 2012) and closely track insect responses to experimental warming (Diamond, Nichols, et al., 2012). Beyond thermal tolerance, other physiological traits such as those related to development rate, phenology and desiccation resistance further enhance our ability to forecast species responses to rising temperatures (Botsch et al., 2024; Kazenel et al., 2024; Penick et al., 2017).

Traits underlying life history variation can show complex covariation and are integrated into so-called syndromes (Reich et al., 2003; Wright et al., 2004). Understanding the organisation of trait syndromes not only allows us to estimate missing trait data in understudied taxa but also allows more accurate forecasting of species distributions under environmental change. Gámez-Virués et al. (2015) found that species with short activity periods, small body sizes and specialised habits were selected against in simplified landscapes and intensively managed fields. However, increasing landscape heterogeneity could mitigate intensive in-field management by enhancing biodiversity. In a recent study using life history traits of >4000 terrestrial arthropods, and after correcting for evolutionary constraints, "fast" life histories were shown to be associated with higher dispersal capacities and broader thermal niches compared to species with "slower" life histories. Since these traits enhance range-shifting potential, they show that a specific group of arthropods will be equipped to mitigate the effects of future climate change (Logghe et al., 2025).

Predicting species extinction risk

Traits have been extensively used to predict the extinction risk of species across the tree of life (Chichorro et al., 2019). Many of the extinction risk assessments in the IUCN Red List are based on the relationships among species traits and their influence on population trends. Strict preference for declining habitats may justify inferred population declines, and low dispersal ability may infer fragmentation of subpopulations (sensu IUCN). Additionally, recent work by Chichorro, Correia, and Cardoso (2022) found that habitat range and speed of life history traits (e.g. generation length, fecundity or offspring size) are potential universal predictors of extinction risk for all terrestrial taxa, from vertebrates to invertebrates and plants.

Two key impediments to implementing legal protection of threatened species by regulatory bodies are requirements that (1) species must be named and valid, and (2) sufficient data exist on its population size, population trends, and/or geographic range to facilitate a threat classification. Undescribed species cannot be protected in many jurisdictions, and many insect species are considered “Data Deficient” following the IUCN guidelines due to a lack of information on their population dynamics or biogeography, precluding them from protection. Regulatory authorities increasingly take relevant trait data into account, such as poor dispersal capabilities and specific environmental requirements (i.e. Harvey, 2002). Trait data of high integrity thus have the capacity to inform conservation decisions leading to regulatory outcomes.

CHALLENGES AND WAYS FORWARD

Insects exhibit extremely diverse life histories and represent about half of the species described on Earth, with total diversity possibly as high as 21 million species (Li & Wiens, 2023). Their sheer diversity poses a significant challenge to the implementation of a global insect trait database. This diversity is reflected in the ways that traits are defined, collected and represented across different taxonomic groups (e.g. families, orders). GRIT will allow the inclusion of multiple types of data, even if unstandardised, as long as they are validated by an expert curatorial team. The inclusion of heterogeneous data transfers the responsibility to assess and standardise trait data across taxa, regions and sources to the end user, with trait harmonisation expected to vary with research needs. GRIT will provide methods to facilitate standardisation for certain widely available traits, always maintaining the original coding of the traits for reference and transparency, and allowing specification of the uses that might require different data standardisation procedures.

A further challenge is the enormous number of undescribed insect species. GRIT will prioritise traits for described species while allowing the inclusion of data for higher taxonomic levels and undescribed species. Trait data should be gathered with the appropriate and traceable metadata, allowing them to be easily incorporated if the trait is assigned to a broader suite of taxa in the future. This would be the case for species in BOLD whose BINs are identifiable entities. Strict guidelines will be developed for undescribed species in the future to allow easy traceability and updates.

Another challenge, common to all long-term projects, is to secure sustained funding mechanisms for continued database support, maintenance and development. Databases may disappear or be archived due to a lack of personnel, while additional challenges connected to maintenance need to be addressed to guarantee future accessibility (e.g. Robinson et al., 2023). Our goal is to guarantee GRIT's future principally by automating many processes, from data extraction to validation. We will assemble a voluntary team of curators distributed across taxa, regions and trait types that will oversee data validation. Such non-profit community efforts have proven successful in cases such as BugGuide, Observation.org and iNaturalist. Long-term data storage and efficient retrieval will be guaranteed by basic funding and multiple projects operating at the host institution (University of Lisbon).

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CONFLICT OF INTEREST STATEMENT

All authors declare that there are no conflicts of interest related to this work.

DATA AVAILABILITY STATEMENT

Data sharing not applicable to this article as no datasets were generated or analysed during the current study.

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