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Special issue series: Advancing wild bee research and conservation through standardized methods

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We are living in a time of unprecedented global change and biodiversity loss. To "monitor" is, at its essence, to pay attention to and track the status of something. All wild creatures are deserving of respect, attention, and conservation intervention when needed. Monitoring is the practice that helps us know when action needs to be taken to help support the continuation of wild populations during these problematic times.

This special issue series of the *Journal of Melittology* is a product of the U.S. National Native Bee Monitoring Research and Coordination Network (https://www.nativebeemonitoring.org/). This network was funded by the Pollinator Health Program of the National Institute of Food and Agriculture within the United States Department of Agriculture. The network has worked from 2020 onward to connect and support the bee research, monitoring, and conservation communities; establish standardized protocols and practices in wild bee data collection; and identify strategic next steps for implementation of a unified national monitoring program. Network members (>800) come from local, state, and federal governments, academia, non-profits, and other groups. Network members are primarily based at US institutions, as the research coordination network focuses on US bee monitoring. Members are diverse in terms of their career stage, gender, and geography within the US. The articles in this special issue series were authored by a subset of network members. These authors were given information from the broader bee research and conservation communities that was captured through a series of workshops held from 2021–2023. The authors then transformed this information into the articles presented here.

This special issue series focuses on advancing standardized, reproducible methods for the study of wild bees. In Levenson *et al*. (2025a) and Cariveau *et al*. (2025), we outline methods for two of the most popular types of wild bee data collection: assessing

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wild bee communities and analyzing plant-pollinator interactions. In Otto *et al*. (2025), we provide methods for generating occupancy data, which is an emerging type of data collection for wild bees that is already used extensively in vertebrate monitoring programs. We also provide methods for collecting wild bee samples for parasite and pathogen analyses in Strange *et al*. (2025), and samples intended for genetic/genomic and other molecular analyses in López-Uribe *et al*. (2025). In Du Clos *et al*. (2025), we outline a framework for wild bee data management, *The Wild Bee Data Standard*, for how data can be recorded, managed, and reported, regardless of whether data collection efforts follow the aforementioned protocols. The methods in these articles can be embedded within monitoring schemes or can also be used for stand-alone data collection efforts. We see a community need for establishing standardized methods that are scalable in this way, as we outline in Levenson *et al*. (2025b). The standards presented here can, for example, help reduce the barrier to entry for new data collectors, ensure that data meet quality thresholds, and support interoperability across projects.

We recognize that data collected using other methods are, and will continue to be, of enormous value. We also acknowledge the value of related, previously-published protocols; many of the authors of these previous protocols have also co-authored the articles in this special issue. Our intention here is to build on previous methods and provide additional guidance that we ourselves would have appreciated having earlier in our work. We place a heavier emphasis on data standards than previous efforts, integrating insights from the broader biodiversity data standards community. We also developed the protocols and practices in these articles through a more open process than has been previously used, receiving guidance from the broader bee research, conservation, and monitoring community on many of the design aspects of these protocols.

We fully intend to update these protocols as our fields continue to evolve and as new methods are developed. Our protocols heavily emphasize lethal collection, given that many bees cannot be readily identified to species. We have, however, included non-lethal methods whenever possible and we look forward to a future where emerging non-lethal methods are field-deployable at the scale of lethal methods. Although these protocols are based on the experience of North American researchers, we expect they can be modified or adapted to other regions of the world. We also envision many exciting opportunities to collaborate with wild bee researchers around the world to develop global standards for wild bee data collection.

We are honored to publish these articles in the *Journal of Melittology*, a journal founded by the late Charles Michener at the University of Kansas, along with his colleagues, and now managed under the revitalizing leadership of Victor H. Gonzalez. We extend our sincere thanks to Victor H. Gonzalez for his leadership and support, Claus Rasmussen for his editorial guidance, and to the reviewers for their timely and valuable comments and suggestions. We are also grateful to Marianne A. Reed, Digital Publishing and Repository Manager at the University of Kansas Libraries, and Eric Bader, Publishing Specialist and Layout Editor of the journal, for their invaluable support in ensuring the success of this project. The *Journal of Melittology* has a cherished history amongst wild bee researchers, and we are grateful for the opportunity to share our work in this venue and contribute to its legacy.

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A call for standardization in wild bee data collection and curation

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Abstract. Standardizing data collection methods is essential for advancing research, monitoring, and conservation efforts on bees. Greater consistency in data practices will enable the production of higher-quality, interoperable datasets, fostering a deeper understanding of bee populations and trends over time. This special issue series of *Journal of Melittology* presents six articles outlining standardized protocols and data standards to support wild bee data collection efforts, together with this article, which makes a general argument for greater standardization. These protocols are applicable to a wide range of research efforts to maximize the quality and use of wild bee occurrence data and can also be integrated into formal monitoring programs. Here, we first outline the need for, and an overview of, a series of standardized protocols and data standards developed in association with the U.S. National Native Bee Monitoring Research Coordination Network. We provide guidance on how to decide among the protocols to achieve different objectives. We then summarize key features of the protocols, including (i) how they are designed to focus on collecting only essential information, while also providing additional recommendations; (ii) that they are intended to be embedded within whatever broader sampling schemes have been designed to meet individual project or program objectives; and (iii) their emphasis on data standards. Lastly, we argue for the collection of additional ecological information that can be used to contextualize wild bee occurrence data. This information supports hypothesis testing to better understand the causal drivers underlying the status and trends of wild bees.

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INTRODUCTION

Wild bee research and conservation efforts worldwide have increased in number and geographic coverage in recent years. In some parts of the world, this has resulted in collaborative initiatives to better understand and protect populations of bees and other pollinators, such as the European Union Pollinators Initiative (https://environment.ec.europa.eu/topics/nature-and-biodiversity/pollinators_en) and the International Union for the Conservation of Nature's Wild Bee Specialist Group (https://wildbees.org/). There have also been increased calls for greater standardization in insect monitoring methods and data management (Montgomery *et al.*, 2021) along with formal pollinator population monitoring schemes. Outcomes of these calls include the UK Pollinator Monitoring Scheme (https://ukpoms.org.uk/) and the Distributed System of Scientific Collections (Nelson & Paul, 2019).

In the U.S., wild bee data collection has grown steadily over the last two decades (Rousseau *et al.*, 2024) owing to an expanding body of knowledge on pollinator population statuses and an interest in investigating threats and trends (Kremen *et al.*, 2002; Potts *et al.*, 2010; The White House 2014; Woodard *et al.*, 2020). This expansion includes an increasing number of taxonomically or regionally restricted, organized bee data collection schemes in the U.S. These include projects such as the Xerces Society for Invertebrate Conservation's Bumble Bee Atlas projects (MacPhail *et al.*, 2024) and state-level wild bee atlases (*e.g.*, Vermont Wild Bee Study; Hardy *et al.*, 2022, 2023; the Empire State Native Pollinator Survey, Schlesinger *et al.*, 2023). Additionally, specimen collections and associated data management at two major federal laboratories (The USGS Bee Lab at the Eastern Ecological Science Center and the USDA-ARS Pollinating Insect-Biology, Management, Systematics Research unit) have also expanded (Ikerd, 2019; Droege & Maffei, 2023; Carril *et al.*, 2023). To date, collecting wild bee occurrence data has involved varied and project-specific methodologies for collection, management, and sharing. This stems from projects having diverse and uncoordinated objectives. Thus, using data from these studies to estimate widespread or long-term changes in bee populations or communities is challenging, because datasets are not always widely available and can be difficult to compare.

All properly managed wild bee occurrence data, regardless of whether they are collected as part of a formal program or not, are valuable. Standardized methodologies provide additional benefits, assuming they are compatible with program designs and capacity. First, standardization increases the ability to aggregate and collectively analyze bee data from multiple studies, particularly when they meet FAIR (findable, accessible, interoperable, reproducible) data principles (Wilkinson *et al.*, 2016). Data compiled from multiple studies are fundamental for quantifying patterns of bee communities, species distributions, and their dynamics across space and time (Chesshire *et al.*, 2023; Dorey *et al.*, 2023). Data that are not interoperable (meaning, formatted in ways that allow for aggregation), also hinder conservation-related efforts. For example, as of 2021, only < 0.05% of publicly available wild bee occurrence records report accurate and specific location information, sampling protocol, and sampling effort; yet this information is essential for assessing bee population status and trends (Rousseau *et al.*, 2024). Second, data gaps limit the capacity for answering original research questions that may not have been considered during original data collection (Orr *et al.*, 2021; Chesshire *et al.*, 2023). Third, differences in sampling design can

significantly impact the resulting data and inferences drawn from them (Levenson *et al*., 2024). Descriptions of specific protocols, with sampling effort clearly described, help to ensure that subsequent data users know how data were collected, allowing for adjustment of abundance and richness data to standard sampling effort, and improving reproducibility of published work. Fourth, expert-derived standardized protocols can help guide less-experienced data collectors when initiating new projects. The international honey bee research community has developed a series of standardized protocols that have been widely adopted and cited by honey bee researchers to support their community and make their research more aligned, and thus comparable across studies (Dietemann *et al*., 2013a,b, 2019). We need similar efforts in wild bee research. Fifth, bee data collectors may be able to more readily find funding for their studies, or gain approval for carrying out work, if they have formal plans to follow community-developed standardized methods, such as what we present here.

Within this special issue, we provide standardized protocols for collecting wild bee occurrence data to support the goals of estimating occupancy of focal bee species (Otto *et al*., 2025); collecting community-level bee data (Levenson *et al*., 2025); collecting plant-pollinator interaction data (Cariveau *et al*., 2025); and collecting bee samples for generating genetic, genomic, and other molecular data (López-Uribe *et al*., 2025) or parasite and pathogen data (Strange *et al*., 2025). We also provide *The Wild Bee Data Standard*, a set of guidelines for wild bee occurrence data management (Du Clos *et al*., 2025) as well as examples of proper data entry (Du Clos *et al*., 2024). Within this article, we more fully outline the methods we used to arrive at these protocols. We also provide guidance for deciding among the options and how to use them, and we argue for the importance of collecting additional information that can support hypothesis-testing about the factors that influence bee status and trends, including decline.

METHODOLOGY FOR ARRIVING AT PROTOCOLS

This set of protocols was developed by a subset of members of the U.S. National Native Bee Monitoring Research Coordination Network (hereafter referred to as the Bee Monitoring RCN). This project, funded by the United States Department of Agriculture's National Institute of Food and Agriculture, was established in 2020 to connect members of the wild bee research, monitoring, and conservation communities across the United States (and beyond) to develop a more systematic approach to monitoring wild bee populations in the country. To date, the Bee Monitoring RCN includes more than 800 members from diverse institutions including local, state, and federal government agencies, universities, and non-profit organizations. Since 2021, the Bee Monitoring RCN has hosted multiple open workshops, symposia, and meetings with members to discuss key issues relevant to wild bee monitoring and solutions for monitoring these bees at a national scale. One priority of the project was to provide an opportunity for a large group of experts to co-develop standardized protocols that were guided by the work of the Bee Monitoring RCN. A group of dozens of experts from across the U.S. created the set of standardized protocols presented in this special issue series of *Journal of Melittology* by drawing from their own experience and the relevant literature, synthesizing the key information needed for collecting different types of bee data, and working with authors of *The Wild Bee Data Standard* (see Du Clos *et al*., 2025) on protocol-specific data standards. This expert group was selected because they are among the members of the bee research and monitoring community who have published extensively on wild bee sampling methods, including development of

standardized methodologies (LeBuhn *et al*., 2003, 2012, 2013; Droege *et al*., 2016; López-Uribe *et al*., 2017; Woodard *et al*., 2020). We recognize that the group that developed these protocols is a subset of the larger RCN and there are many additional experts in our field who did not participate in the development of these protocols. Wherever possible, however, the protocols directly incorporate general input from the broader member group of the Bee Monitoring RCN, provided during workshops held from 2021–2023. These protocols can be embedded within formal bee monitoring schemes but also used as-needed by any data collection effort. The resulting protocols support collection of occurrence data or specimens for occupancy modeling, community-level bee data, plant-pollinator interaction data, bee samples intended for genetic and other molecular analysis, and bee samples intended for parasite and pathogen analyses. These specific foci were selected because they address many of the primary objectives of federal and state agencies involved in pollinator protection, land managers, and policy-makers, and support the broader wild bee research and monitoring communities.

GUIDANCE FOR DECIDING AMONG THE PROTOCOLS

Before wild bee occurrence data are collected as part of an organized scheme, project goals must be defined. Clearly articulated goals inform which protocols are best-suited to a planned project. Figure 1 provides a decision tree to aid in selecting the most appropriate protocol(s). The protocols can be combined for projects that have multiple goals, or they can be added to in ways that will provide supplemental information. Whether using a single protocol or combining protocols within a single project, the data generated will be interoperable because they all follow *The Wild Bee Data Standard* (Du Clos *et al*., 2025). For example, someone interested in documenting the number of species occurring in two locations and their associated host plants will follow protocols for community-level data (Levenson *et al*., 2025) and plant-pollinator interaction data (Cariveau *et al*., 2025).

GUIDANCE FOR USING THE PROTOCOLS

The protocols and data standards provided in this issue are designed to maximize reproducibility, interoperability, and the utility of wild bee data for hypothesis testing and conservation decision-making. Each protocol provides an overview, a set of expert-guided requirements, and best practices to support effective data collection. The protocols focus on levels of data collection and reporting that are described as *core*, or absolutely essential for achieving one's objectives (Table 1); these are methods that need to be used, or data fields that need to be recorded and reported, in light of the purpose of each protocol and current best practices in biodiversity data management. Importantly, information can be beneficial to collect but not meet our definition of *core*. We also provide *recommended* practices, which are extremely beneficial to the specific objective(s) of the protocol, albeit not essential (Table 1). *Recommended* data fields should be provided, if collected, because they greatly increase the quality and potential uses of data, specifically in relation to its originally intended purposes. Lastly, we provide practices we describe as *optional* (Table 1). These practices would also increase the quality of collected data, but in ways that are less closely related to the specific objectives of a protocol. *Optional* data fields can be provided if collected, and project managers may decide that they are worth the additional effort required to acquire them, depending on their specific objectives. The roles of *core*, *recommended*,

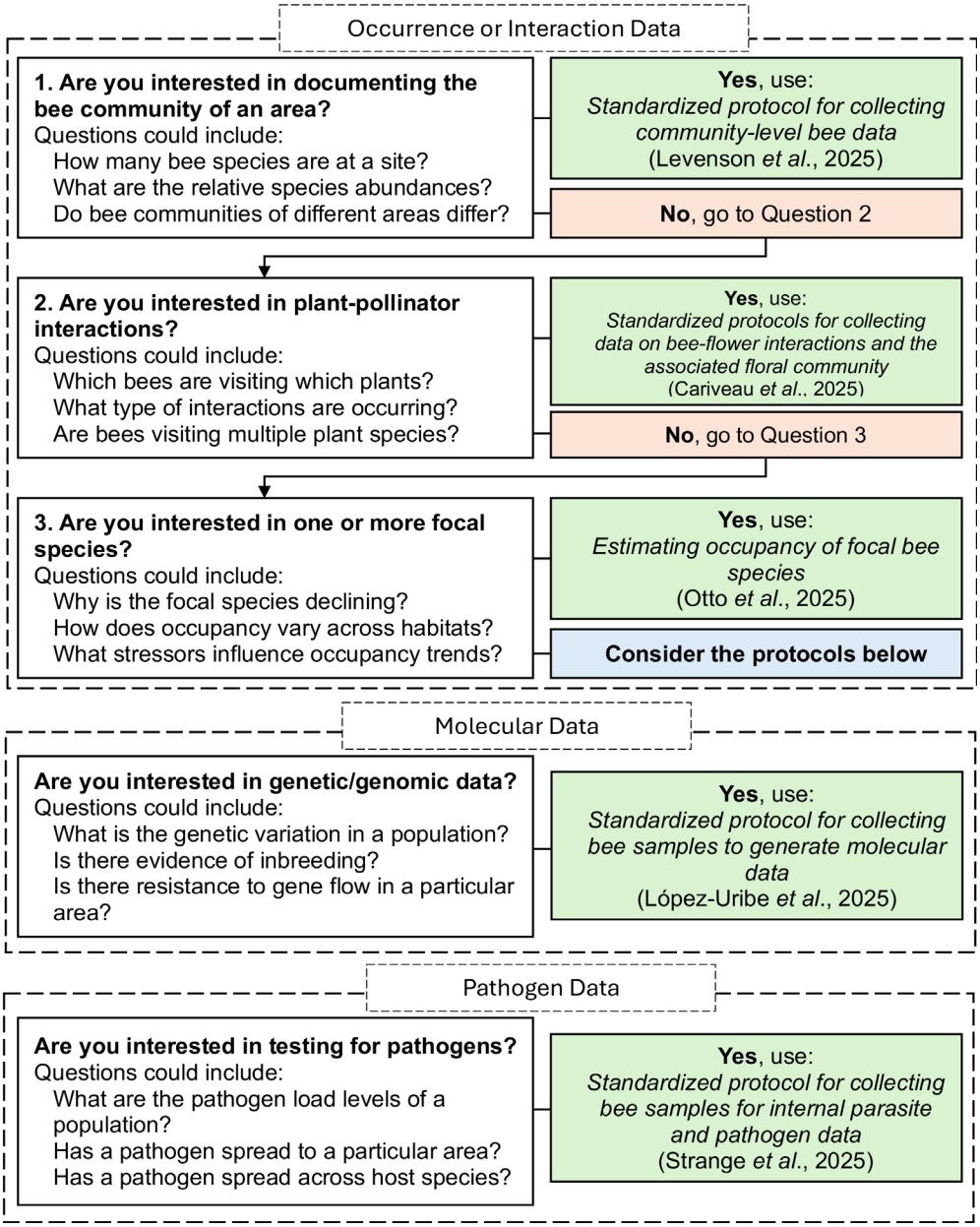

Figure 1. Decision tree for selecting the appropriate protocol based on overarching research questions (in bold) framing the data collection. Standardized protocols must be paired with statistically rigorous sampling frameworks for meaningful results. Specific example research questions are provided below the overarching questions, but protocols can be adapted or expanded to address other questions as needed. Moreover, multiple protocols can be combined within a single project to collect multiple kinds of data.

and *optional* information when collecting and reporting wild bee occurrence data are expanded on in *The Wild Bee Data Standard* (Du Clos *et al*., 2025) As an example of the distinction between these terms, our community sampling protocol (Levenson *et al*., 2025) does not include collection of plant association data as a *core* or *recommended* practice. Yet, this is inarguably valuable information for studying relationships between bee and plant communities and it can optionally be added using our plant-pollinator protocol (Cariveau *et al*., 2025). Similarly, the protocol for collecting specimens for pathogen analyses provides the recommendation to collect honey bee specimens to better understand pathogen spillover between bee species at collection sites. Such data might be especially important given the increasing evidence supporting pathogen spread from honey bees to wild bee species (Tehel *et al*., 2016; Mallinger *et al*., 2017). In a few instances, the protocols contain specific practices that were subjectively decided on by the protocol authors. Examples of this include the site size categories in Cariveau *et al*. (2025) and the minimum number of passive traps deployed in an array in Levenson *et al*. (2025). Protocols state when decisions were made subjectively and provide justification for them. All protocols require users to report the sampling protocol, describing the method(s) used for sampling, and sampling effort, including amount of time spent sampling and area sampled. These two last pieces of information are extremely valuable (Montgomery *et al*., 2021) but are rarely reported in data shared with public data repositories (Rousseau *et al*., 2024).

We recognize that data collection is generally expensive, time-intensive, and it is carried out by collectors with a wide range of experience levels who need to know which aspects of protocols are absolutely necessary for their primary objectives. The protocols can be expanded and made more complex, but if their *core* components are carried out as-is, they will generate the data required to address the specific objective (for example, characterize the bee community in an area) that the protocol is designed to help achieve. We highly recommend seeking out additional resources generated by the bee monitoring community, including *The Very Handy Bee Manual* (A Collective, 2024), which provide more specific bee sampling methods and techniques. These resources provide detailed information, including recommended materials and purchasing sources, that supplement our standardized protocols.

Table 1. Summary of the protocol structure. Examples are provided based on the protocol for community-level data (Levenson *et al*., 2025).

Protocol Data Level	Definition	Example
Core	Practices that are essential for achieving one's objective(s) and need to be used to meet the purpose of the protocol.	Record and report length and width of transect used.
Recommended	Practices that are extremely beneficial, but not essential, to the specific objective(s) of the protocol.	Sample within 1 meter to either side of the transect.
Optional	Practices that can be followed and may be worth the additional effort required, depending on one's objective(s).	Record and report plant association information.

IMPORTANCE OF COLLECTING ADDITIONAL INFORMATION

We re-emphasize the value of collecting *optional* data fields that provide ancillary information to better understand bee natural history, ecology, and drivers of changes in status and trends. Hereafter, we refer to this simply as "additional ecological information", but we are specifically referring to what might be divided into *natural history information* and *stressors*. The first is *natural history information* that is more centered on a species' needs, such as the soil type for ground-nesting bee nests. *Stressors* refer to environmental conditions that might cause stress or harm to bees, such as pesticide use, habitat quality (*i.e.*, quality of resources used for nesting, foraging, overwintering, *etc*.), habitat connectivity, air quality, pathogens, competitive interactions, predation, evidence of parasitism, extreme weather events, and information about collection, harvest, and commercialization. This additional ecological information helps to contextualize wild bee data and will support analyses to understand factors that influence the status and trends of wild bees.

Ecological information can also be integrated into sampling frameworks to improve their design. For example, to develop an effective occupancy-based monitoring program, some basic aspects of a species' biology must be known, such as where they might occur, when they are generally active (time of day and seasonality), and their host plants. With time, the program will also generate additional information about these variables that might shape data collection strategies and can be integrated into analyses to understand drivers of occupancy. Ecological information can be used to inform conservation status assessments, including species status assessments (or SSAs), carried out by the U.S. Fish and Wildlife Service to assess species viability and inform Endangered Species Act listing decisions. This information can also be used to develop or refine conservation and management plans.

UNIQUE FEATURES OF PROTOCOLS

The Bee Monitoring RCN protocols are flexible and adaptable into any number of sampling frameworks. Protocols generally omit details describing some crucial components of bee sampling frameworks, as they are heavily dependent on the broader goals of a data collection project or initiative. For example, the protocols do not provide information about the number of sites that should be visited for deploying them because that choice is dependent on the project question(s), the total study area, and the number of habitat types and how they are defined. When applicable, the protocols offer guidance on key considerations for designing effective sampling frameworks, supplemented with references to exemplary studies. We strongly encourage users to consider analyses to be performed during the project design phase to develop sampling frameworks that are statistically rigorous and will ultimately allow users to test hypotheses with their data.

The protocols heavily emphasize FAIR data principles (Wilkinson *et al*., 2016) and align with the Darwin Core standard (Wieczorek *et al*., 2012), two leading data management frameworks in biodiversity informatics. Data standards have not yet been incorporated into standardized bee protocols, but their importance is increasingly recognized by the bee biodiversity and broader data science communities (Montgomery *et al*., 2021; Rousseau *et al*., 2024). We provide additional information

about standardizing wild bee occurrence data in *The Wild Bee Data Standard* (Du Clos *et al.*, 2025). Here too, *The Wild Bee Data Standard* aims to provide guidance for how to treat bee data in the most efficient and effective ways to align with best practices, while avoiding unnecessary complexity. *The Wild Bee Data Standard* is also aligned with existing federal government efforts to increase data transparency and standardization, such as the Biotic Observation Minimum Specification for Fish Wildlife Service Refuges Inventory and Monitoring Surveys (BOMS; US Fish and Wildlife Service, 2023), and initiatives within the U.S. Department of Agriculture and U.S. Department of the Interior, such as the Bureau of Land Management's Strategic Plan for Pollinator Conservation (Bureau of Land Management, 2022). All Bee Monitoring RCN protocols adhere to *The Wild Bee Data Standard*. Importantly, these standards can also apply to bee data that are not collected using these protocols or associated with any standardized sampling scheme.

INVENTORIES, SURVEYS, AND MONITORING

The protocols were designed with an eye towards collecting data needed to detect changes in bee statuses and trends over time. This goal is best supported by repeatedly applying the standardized protocol over time either within a project or among subsequent projects that duplicate at least *core* practices of the protocol. Sampling schemes also need to be statistically rigorous and have the power to detect meaningful patterns through hypothesis-testing. Where applicable, the protocols outline how to collect data for *inventories*, *surveys*, and *monitoring* efforts. We define, here, *inventories* as an attempt to build a species list for an area, not standardized for space or time; *surveys* as an attempt to record data of an area, standardized over space and/or time; and *monitoring* as an attempt to record changes in community measures over time, employing a consistent and repeated protocol, standardized over space and time. When possible, the protocols provide methods for both lethal and non-lethal data collection, however, currently there is a much stronger emphasis on lethal collection methods. Those collecting wild bee occurrence data hold mixed opinions about lethal collection. Potential risks include unintentionally harming study populations through over-collection (Gibbs *et al.*, 2017, but see Gezon *et al.*, 2015), whereas benefits are being able to confirm species identity, increase statistical rigor, and the ability to store specimens in perpetuity (LeBuhn *et al.*, 2013; Turney *et al.*, 2015). Presently, to achieve most of the specific goals outlined by the protocols while also having high confidence in species identity, some lethal sampling is still necessary. As methods for non-lethal collecting, such as automated image recognition of unique bee species and eDNA surveillance, become more developed, these protocols can–and should–be revisited and updated to minimize lethal collection as much as possible (Montero-Castaño *et al.*, 2022).

We include recommendations in the protocols that can help to minimize over-collection and improve data quality, such as avoiding the use of blue vane traps that bias collections and increase the risk of over-collecting of particular bee groups (Acharya *et al.*, 2022).

CONCLUDING REMARKS

Here, we outline the need for, and provide an overview of, a series of standardized protocols and data standards developed in association with the U.S. National Native

Bee Monitoring RCN. The protocols and best practices provided will be updated and refined through time, for example, as new technologies and approaches are developed. This will be especially true for all protocols as methods for non-lethal data collection continue to improve. We expect this will be most frequent for the protocols for collecting samples for genetic and other molecular data (López-Uribe *et al*., 2025), and parasite and pathogen samples (Strange *et al*., 2025), as these are rapidly changing research areas. We anticipate publishing updated protocols in the future and the articles will be linked so that specific editions can be referenced. Moreover, as new approaches are developed, such as eDNA or AI camera-based data collection, entirely new protocols may be developed. There are additional data collection goals–such as estimating wild bee abundance, nesting resources, and data collection for threatened species–that are not addressed by the current protocols. These will be developed into standardized protocols in the future and connected to this collection of protocols to guide wild bee monitoring.

Another frontier, from the perspective of the U.S. National Native Bee Monitoring RCN, is to work collaboratively with the wild bee research, monitoring, and conservation communities to implement these protocols and integrate them into sampling schemes that best meet their data collection needs. We recognize that field-testing of these protocols and their scalability (Carvell *et al*., 2016), and assessments of their costs and benefits (Breeze *et al*., 2021), are additional next steps that are important for helping our community make decisions about their implementation. The process of integrating these protocols into formal sampling schemes need not be linear; as data are generated and used for hypothesis-testing, this can continually inform actions (such as conservation interventions) and lead to improvements or modifications in sampling design.

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Improving the standardization of wild bee occurrence data: Towards a formal wild bee data standard

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Abstract. Conservation and management of wild bees is hindered by the variety of ways wild bee occurrence data are recorded, managed, and shared. Here, we present solutions to address this issue and introduce *The Wild Bee Data Standard*, a standardized means of recording and reporting data associated with wild bee occurrences, including physical specimens and photo observations. This standard aligns with contemporary data management practices widely adopted by the broader biodiversity data community. We propose a set of terms for the standard that describe various features of bee occurrences, including collection method and location, taxonomic verification, and final record storage. We emphasize the importance of providing sampling protocol and effort information with wild bee occurrence data and offer guidance to make this a more common practice. We describe how to translate data not currently aligned with the standard to meet its conditions, and how to upload those data to an accessible online repository. We provide case studies, data entry templates, a glossary of terms, and additional resources to guide new users to implementing the standard. We also present a forum, established as a GitHub repository, to support continued development of the standard. Recognizing the significant change this represents for current data practices, we outline the benefits for the bee research and conservation community that will result from improved data standards. We advocate for making all historical, current, and future bee occurrence data openly available to facilitate more rigorous and comprehensive research, conservation, and management of wild bees. This contribution is part of a series developed in association with the U.S. National Native Bee Monitoring Network to standardize bee monitoring practices.

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INTRODUCTION

Wild bee occurrence data are generated when bees are collected or observed in the field, and include the date collected or observed, collector or observer identity, geographic location, and other information. Occurrence data generated from specimens housed in collections are foundational to biological research (Meineke *et al*., 2018; Nachman *et al*., 2023). Occurrence data are increasingly being generated by field observations of live organisms, which can supplement collections-based data (Briggs *et al*., 2022; Boone *et al*., 2023; MacPhail *et al*., 2024) but are currently suitable only for a subset of bee species (Turley *et al*., 2024). Occurrence data are most useful when digitized (Cobb *et al*., 2019), annotated (Rousseau *et al*., 2024), georeferenced (Seltmann *et al*., 2018), and made openly available (Nelson & Ellis 2018), yet these conditions are often unmet, which limits reproducibility (Turney *et al*., 2015; Packer *et al*., 2018). Openly available occurrence data can be viewed and downloaded online from a number of biodiversity data portals, including the Global Biodiversity Information Facility (GBIF; https://www.gbif.org/), Integrated Digitized Biocollections (iDigBio; https://www.idigbio.org/portal/search), iNaturalist (https://www.inaturalist.org/), the Symbiota Collection of Arthropods Network (SCAN; https://scan-bugs.org/portal/), Ecdysis (https://ecdysis.org), and the Bee Library (https://library.big-bee.net). These data portals typically provide data following FAIR principles (Findable, Accessible, Interoperable, and Reusable; Wilkinson *et al*., 2016).

Adhering to FAIR principles can be accomplished in part by following data standards, or agreed-upon terms that describe data points or datasets. The Darwin Core data standard (DwC; https://dwc.tdwg.org/) includes a set of standardized terms that can be applied to any biodiversity dataset as column headings in spreadsheets or delimited files. The terms are linked to definitions about the data, providing a consistent way of sharing biodiversity data (Wieczorek *et al*., 2012). Darwin Core is managed by Biodiversity Information Standards (TDWG), previously known as the Taxonomic Databases Working Group, and is used by leading biodiversity data providers, including GBIF, iDigBio, and iNaturalist. The Biotic Observation Minimum Specification (BOMS) is a data standard in development at the U.S. Fish and Wildlife Service for use in inventory and monitoring work on National Wildlife Refuges that is aligned with Darwin Core (U.S. Fish and Wildlife Service, 2023). Here, we used Darwin Core terms, and drew influence from BOMS, to create *The Wild Bee Data Standard* v.1.0.0 (Appendix 1). When working with DwC terms, whether by creating new datasets or translating existing data, not all terms need to be used; therefore, *The Wild Bee Data Standard* only includes DwC terms that are most relevant to wild bee occurrence-based analyses. Many of these terms describe information that is familiar to those working with wild bee occurrence data, including date, time, location, and species collected, but we also emphasize reporting information on sampling methods and study design (Montgomery *et al*., 2021; Rousseau *et al*., 2024; Levenson *et al*., 2025b). Some DwC terms recommend using controlled vocabularies, which are lists of allowable entries that constrain data entries for particular types of information. Controlled vocabulary lists for DwC terms are provided as needed in *The Wild Bee Data Standard*.

Also important for FAIR data is the creation and inclusion of detailed metadata, or information that describes the data, which can also be provided following a set of standards (Bloom *et al*., 2021). Ecological Metadata Language (EML) is typically used in biodiversity data management, with standard methods for reporting the source information for occurrence datasets, including the project name, data creator(s), and

data provider(s), along with the type of data being provided, how it should be cited, and other descriptive information (Jones *et al.*, 2019).

In this contribution, we aim to clarify how to create, find, access, format, share, and use openly available wild bee occurrence data and metadata to promote FAIR principles and advance wild bee species conservation and management. We propose implementing *The Wild Bee Data Standard* and provide a framework for doing so. We provide a glossary of terms (Appendix 2) and a list of additional resources (Appendix 3) to supplement this manuscript. This standard was developed as part of the U.S. National Native Bee Monitoring Research Coordination Network, hereafter referred to as the Bee Monitoring RCN. Although *The Wild Bee Data Standard* was developed to support standardized protocols for wild bee monitoring written by the Bee Monitoring RCN (Cariveau *et al.*, 2025; Levenson *et al.*, 2025a; López-Uribe *et al.*, 2025; Otto *et al.*, 2025; Strange *et al.*, 2025), any project that collects information on wild bee occurrence, particularly with physical specimens or photo observations, can use the standard to plan data collection, digitize data, and ultimately, make data openly available. Those who generate wild bee occurrence data often gather similar variables (*i.e.*, species name, sex, date, location, collector), but may be naming and managing those variables differently. Adhering to the *The Wild Bee Data Standard* and the data management practices outlined here ensures that wild bee occurrence data collected for any project can be synthesized and used by various entities for more thorough and rigorous analyses. For example, analyses relying on the knowledge of wild bee species' ranges and population statuses, which are a cornerstone of conservation, are currently severely limited by the availability and suitability of openly available wild bee data (Graves *et al.*, 2020; Chesshire *et al.*, 2023; Rousseau *et al.*, 2024; 2025). We thus advocate for making all historical, current, and future wild bee occurrence data openly available following FAIR principles and *The Wild Bee Data Standard*, which will ultimately lead to more effective management and conservation actions for wild bees. Although this goal is clear, we anticipate the following obstacles to this request and provide solutions for each:

First, some historical data may not have associated information on sampling effort and protocol to report. We emphasize these two pieces of information in *The Wild Bee Data Standard*, as they allow more rigorous conservation status assessments and other quantitative analyses of wild bee occurrence (Bloom *et al.*, 2021; Rousseau *et al.*, 2024). Even if sampling effort and protocol information are not available, occurrence data should still be made openly available, as it is valuable for other purposes, such as determining potential ranges of wild bee species and population shifts over time (Burkle *et al.*, 2013; Mathiasson & Rehan, 2019; Graham *et al.*, 2021). Future collecting efforts should improve documentation on sampling effort and protocols.

Second, most digitized datasets will not follow *The Wild Bee Data Standard* in their current form. Conversion to Darwin Core terms (a process known as mapping) to conform to *The Wild Bee Data Standard* can be done by using one of the accompanying templates (Du Clos *et al.*, 2025) or a GBIF template, by updating existing in-house templates, or as part of the publication process to a platform that exports datasets in the Darwin Core Archive format that is usable by GBIF. There are multiple platforms that have built in mapping tools to help with this conversion, including the GBIF Integrated Publishing Toolkit (IPT; Robertson *et al.*, 2014) and Collections Management Systems (CMS, which we elaborate on below). Additionally, photo observation data can be uploaded to iNaturalist, which provides research-grade occurrence data to GBIF following Darwin Core standards, effectively mapping the data for uploaders.

Third, we recognize that some data cannot be made openly available or must be masked due to privacy, security, conservation-related, or other concerns. We advise that data providers use the Darwin Core term **dwc:informationWithheld** to indicate that the precise location, full taxonomic name, or other information has not been shared owing to these concerns. This allows for transparency of occurrence information, alignment with *The Wild Bee Data Standard*, and a path towards contacting data providers for special uses of data, while protecting threatened or endangered species. We recommend reviewing current data masking policies and engaging partners in discussions about data transparency in an effort to bring more data online.

METHODS FOR SHARING AND STANDARDIZING WILD BEE OCCURRENCE DATA

STANDARDIZING CURATION OF WILD BEE DATA AND PHYSICAL SPECIMENS. Curating wild bee occurrence data involves the preparation, handling, and storage of digital records and physical specimens. Following *The Wild Bee Data Standard*, we advise digitizing field-collected data with selected Darwin Core terms as column headings. This promotes interoperability, or the ability to exchange information across platforms, and improved data understanding between users. We provide templates aligned with *The Wild Bee Data Standard* to simplify digitization and mapping of currently existing datasets (Du Clos *et al*., 2025).

Occurrence data can be extended beyond a specimen or an observation to include additional data about the occurrence (*e.g.*, image data of the specimen or its habitat, genetic data, interaction or floral use data; Lendemer *et al*., 2020). Sharing occurrence data and any related information is crucial, as these extended resources are critical for confirming specimen identifications, understanding bee functional traits, and enhancing our comprehension of environmental influences on bee abundance and diversity. Tools for the generation, management, and sharing of image and functional trait data are being developed by the Big-Bee project (https://big-bee.net; see also Ostwald *et al*., 2024). We provide standards for both image data and floral use data in *The Wild Bee Data Standard*. We also provide standards for bee occurrence data to be used in molecular (López-Uribe *et al*., 2025) and pathogen analyses (Strange *et al*., 2025).

Improving the curation of wild bee physical specimens for identification, long-term storage, and extraction of new and derived data (*e.g.*, molecular work, physical measurement, pollen collection) is essential for wild bee occurrence data to more accurately inform our understanding of bee distribution, population trends, conservation status, and other relevant metrics. Specimens, particularly those collected in a bowl or cup trap, should be cleaned following guidance from *The Very Handy Bee Manual* (A Collective 2024). Specimens caught with a net may not need to be cleaned, as they may have pollen or pathogens that could be collected for identification or further study. Specimens should be pinned neatly so that all external anatomy can be seen, and internal anatomy can be accessed if necessary and labeled with the date, coordinates, and name(s) of the collector(s) (Burrows *et al*., 2021; A Collective 2024).

Once prepared for curation, and either before or after identifications have been verified, specimens are best placed in a public natural history collection (*i.e.*, accessioned), allowing access to the specimens for taxonomic study and research purposes in perpetuity. Collections would ideally be located within museums or other established collection facilities; however, it is often difficult to accomplish museum

accession owing to the limited space and infrastructure to support current collections (Cobb *et al*., 2019). To improve the management and curation of wild bee physical specimen collections in the US, we need more collection facilities to store specimens and more collection management personnel to support these specimens. Collection management personnel have a vast suite of responsibilities including, but not limited to, proper specimen care and storage, digitizing specimens for in-house and openly accessible databases, managing specimen databases, managing specimen status (*i.e*., accessions, acquisitions, loans, de-accessions), coordinating with visiting scientists for access to those specimens, and conducting public outreach related to the collections. Natural history collections of wild bee specimens are foundational to pollination biology, ecology, and conservation; their importance cannot be overstated and increased and sustained support is critical for their continuity (Bartomeus *et al*., 2019).

Standardizing data access. Making occurrence data openly available has multiple benefits to wild bee research, conservation, and policy (Rousseau *et al*., 2024). To be openly available, data must be downloadable by users without explicit permission from the provider (*i.e*., users do not need to email the provider to obtain a dataset), and the conditions for using the data are made clear by the provider. Conditions for reuse are typically determined by adding a use license, such as a Creative Commons license, to the data when published online. In order for data to be openly available, they first need to be digitized, or converted into a digital format using an electronic device with internet connection capabilities (*e.g*., computer, tablet, phone, etc.) (Nelson & Ellis, 2018). Given the rich history of insect specimen collection, there are an estimated 4.7 million undigitized bee specimens across the US that could contribute valuable information on long-term wild bee population trends (Chesshire *et al*., 2023). Digitizing these would more than double the number of bee records available for the US, as 2.9 million digitized bee records were acquired after an extensive search across multiple platforms by Chesshire *et al*. (2023). A primary funding source for collections digitization efforts, Advancing the Digitization of Biological Collections (ADBC), was recently archived by the National Science Foundation (NSF), and collections funding was moved to a more general infrastructure program, called the Capacity Program. One of the last ADBC-funded projects focused on digitizing wild bee specimens was Big-Bee (DBI#2102006; https://big-bee.net), whereas another wild bee digitization project, iDigBees (DBI#2216927; https://idigbees.org), was funded through the Capacity Program. We strongly support these projects and advocate for continued funding support for bee specimen digitization.

Digitizing field-collected data into one of the templates accompanying *The Wild Bee Data Standard* (Du Clos *et al*., 2025) facilitates uploading to a data aggregator, CMS, or other web-based data platforms that adhere to the Darwin Core data standard. One barrier to making occurrence data openly available is selecting a platform for data sharing. Here, we highlight three platforms (Fig. 1) and provide guidance for uploading data to each, while recognizing that other valid options could also be pursued. We are not advocating for all data providers to follow the same data sharing pathway or to use the same platform; if you are a data provider with established data sharing practices following Darwin Core standards, we encourage you to continue those practices. Our guidance here is intended for those who do not have these practices in place and are looking for a starting point to begin sharing their data. Our goal is for all historical, current, and future wild bee occurrence data to be openly available following FAIR

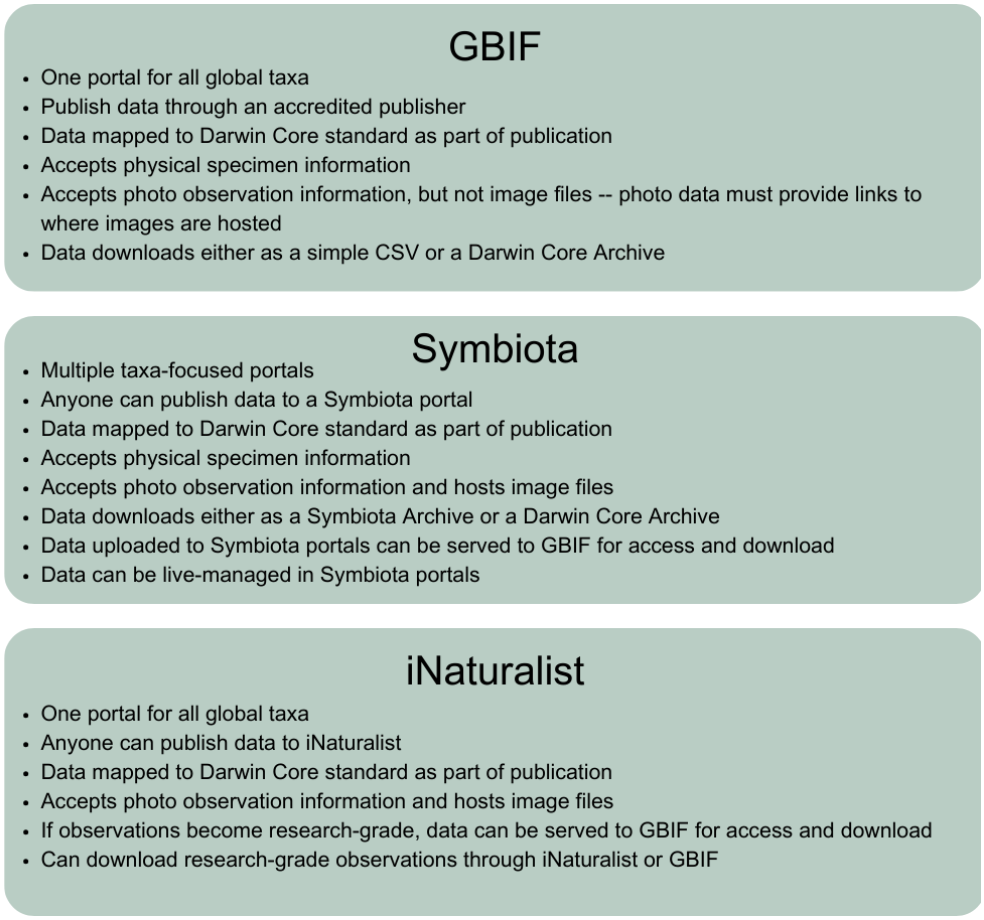

Figure 1. Details of three platforms that provide openly available wild bee occurrence data following FAIR data principles. Occurrence data can be downloaded from all three platforms; however, Symbiota and iNaturalist also send data to GBIF, meaning that data from all three platforms can be accessed in one place. This also means that providers unable to publish data directly to GBIF can use either Symbiota or iNaturalist to get data there.

principles and *The Wild Bee Data Standard*, which will ultimately lead to more effective management and conservation actions for wild bees.

The first option is GBIF, a data aggregator that publishes physical specimen and photo observation occurrence data through its IPT and makes them openly available for download. The GBIF IPT implements FAIR principles by mapping occurrence data to Darwin Core terms as part of the publishing process and producing an accompanying metadata document following Ecological Metadata Language (EML, Robertson *et al*., 2014; Jones *et al*., 2019). It is worth noting that familiarity with GBIF can vary by employment sector, with government employees often using other platforms to share and download occurrence data (Martín-Mora *et al*., 2020). Additionally, data can only be published to GBIF through accredited publishers. This can present a barrier to data providers looking to make their occurrence data openly available, if they are not already connected with a publisher. However, with dedicated digitization efforts and effective communication involving new or existing accredited publishers, the

awareness and use of GBIF for sharing data could grow, allowing data from multiple agencies and sectors to be published online.

The second option for data publishing is Symbiota (https://symbiota.org; Gries *et al.*, 2014), an open-source CMS supporting taxon-focused data portals that manage and share occurrence data, including physical specimens, photo observations, and published datasets. As Symbiota portals host multiple datasets and make them openly accessible for download, these portals also function as data aggregators. Any data provider can publish occurrence data directly to a Symbiota portal. Within the portals, data providers have the option to edit and publish updated datasets through a web-accessible databasing infrastructure; these datasets are called "live data" See https://ecdysis.org/collections/misc/collprofiles.php?collid=120 for an example of live wild bee occurrence data on a Symbiota portal. Data providers can also choose to publish data managed elsewhere to a Symbiota portal; these datasets are called "snapshots". See https://library.big-bee.net/portal/collections/misc/collprofiles.php?collid=34 for an example of a snapshot dataset on a Symbiota portal. Symbiota portals that manage and share insect data include Bee Library, SCAN, and Ecdysis. These portals support digitization and data sharing efforts, in part by providing data management and quality control tools, but also through a robust community of users, providers, and developers. Importantly, Symbiota portals can publish data directly to GBIF (https://docs.symbiota.org/Collection_Manager_Guide/Data_Publishing/publishing_gbif/; see https://www.gbif.org/dataset/a42d07b3-e34d-4a65-b7e3-6aafa9f8f27b for an example of live data from a Symbiota portal published to GBIF). Other CMS that manage occurrence data include Arctos (https://arctosdb.org/; Cicero *et al.*, 2024) and Specify (https://www.specifysoftware.org/). Like Symbiota, these platforms support the management of physical specimen and photo observation data through web-accessible databasing infrastructure, have engaged user communities and accessible developers, and can publish or format these data for publication to GBIF. Arctos is also a data aggregator (https://arctos.database.museum/), but Specify does not currently aggregate data. Thus, if you are currently using other CMS to manage and share data, then we advise continuing to do so.

The third option is iNaturalist. For current and future projects involving photo observations only, iNaturalist can be used to share occurrence data following FAIR principles if verifiable observations that provide a date, latitude and longitude coordinates, and a photo of an organism that is not captive or cultivated become research-grade. An observation becomes research-grade if more than ⅔ of identifiers agree on a species-level taxonomic identification (Campbell *et al.*, 2023). Providing a suggested identification when uploading observations can increase the visibility of records, making it more likely that community identifiers provide the verifications to achieve research-grade status. Data can be downloaded directly from iNaturalist, and a subset (depending on the license applied to the observation) of research-grade observations are pushed to GBIF following Darwin Core standards. We advise only using research-grade records if using iNaturalist data for statistical analyses.

Promoting data accuracy. Data shared in online repositories can have taxonomic or geographic inaccuracies (Orr *et al.* 2021; Chesshire *et al.*, 2023; Dorey *et al.*, 2023). When conducting analyses with wild bee occurrence data downloaded from online biodiversity data platforms, cleaning the data (*i.e.*, removing erroneous data and updating data fields as appropriate) to improve their accuracy is of critical importance.

The statistical software R (R Core Team 2024) has an add-on package called BeeBDC (Dorey *et al*., 2023) that cleans occurrence data to provide more accurate taxonomic and geographic information. We strongly advise either cleaning downloaded data using BeeBDC before any analysis or using the cleaned wild bee occurrence dataset provided in Dorey *et al*. (2023) to conduct analyses relying on bee species locations and validated identifications. BeeBDC can also be used to clean data before uploading, as can GBIF and some other CMS in a more limited fashion, further reducing the propagation of erroneous data for future users. Following these methods helps prevent spurious conclusions that can arise from inaccurate data.

CREDITING DATA SOURCES. It is important to acknowledge and credit everyone who contributed to a shared dataset, whether they collected, prepared, or managed the occurrence data, or collaborated on the project for which the occurrence data were collected (Duke & Porter, 2013). There are multiple ways to accomplish this. Here, we outline practices that are simple to adopt and standardize across shared datasets, in order of preference. When using shared data, give appropriate credit to those involved in generating and managing the data by:

Following proper citation procedures for data downloaded from portals. GBIF provides clear citation guidelines (https://www.gbif.org/citation-guidelines), the most important of which is to *cite the Digital Object Identifier (DOI) of any data downloads in work involving those data*. We cannot emphasize the importance of citing DOIs enough; it is a critical practice that must be adopted by all users of occurrence datasets downloaded online. GBIF creates DOIs for every data download; sharing the DOI allows end users to access the same dataset(s) used in published works. DOIs can be provided for individual datasets or groups of datasets, which are called derived datasets by GBIF. For example, https://doi.org/10.15468/6autvb is the DOI for Droege & Maffei (2025), and https://doi.org/10.15468/dl.6cxfsw is the DOI for most of the data used in Chesshire *et al.* (2023); see Chesshire (2023). Always cite DOIs for derived datasets generated from search filters; for individual datasets, see below. Symbiota provides general citation guidelines (https://docs.symbiota.org/Collection_Manager_Guide/data_citations); each Symbiota portal can customize these guidelines to suit their needs. At a minimum, the portal itself should be cited. Further, each dataset downloaded can be listed in the citation. This is feasible for a small number of citations; for large lists of datasets, use a supplementary file (see below).

Including names of personnel and institutions in data fields. It is important to avoid ambiguity when naming personnel and institutions in occurrence data, especially if there are similar names. To credit bee collectors, use the term **dwc:recordedBy** and list their full name(s) (when known) for each occurrence in the dataset. For additional detail, if possible, list an ORCID iD (https://orcid.org/; Haak *et al*., 2012) for the collector under the term **dwc:recordedByID**. To credit bee identifiers, use the term **dwc:identifiedBy** and list their full name(s) (when known) for each occurrence in the dataset. For additional details, if possible, list an ORCID iD for the identifier under the term **dwc:identifiedByID**. This allows users of the published data to clearly determine the personnel involved in generating occurrence records; further, this information can then be integrated into the online database Bionomia (see below). The term **dwc:georeferencedBy** can be used to cite personnel who handled spatial location of the data. Indicating where the data are housed using the terms **dwc:institutionCode** and/or **dwc:collectionCode** acknowledges the role of the hosting institutions and promotes

access to specimens for further study. If possible, provide a unique identifier using the terms **dwc:institutionID** and **dwc:collectionID**; these identifiers may be found in the Global Registry of Scientific Collections (GrSciColl; https://scientific-collections.gbif.org).

Promoting the use of Bionomia (https://bionomia.net; Shorthouse, 2020) to aggregate digitized identified specimens to identifier(s) and collector(s). Bionomia is an online database that connects specimen occurrence records from GBIF to identifier(s) and collector(s) using unique identifiers, allowing for those personnel to develop an online profile of specimens they identified or collected. Bionomia downloads these records from GBIF every two weeks, and any records with content in the **dwc:identifiedBy,dwc:identifiedByID, dwc:recordedBy,** or **dwc:recordedByID** columns are reviewed, resolved, and published to the website. Identifiers or collectors can claim Bionomia profiles with their ORCID iDs (*e.g.*, https://bionomia.net/0000-0002-8822-2315) and create a DOI for the dataset displayed in their profile that becomes citable and trackable; see Seltmann (2022) for an example of a dataset generated by Bionomia. Note, however, that Bionomia does not collect information on photo observations.

Citing datasets and acknowledging data curators by name in published work. When using data from a platform such as GBIF or a Symbiota portal, a list of all datasets used must be provided. When downloading from GBIF, this list is provided for you (see GBIF, 2021). If there are datasets that comprise more than 5% of a download, providers of those datasets must be specifically named and cited in published work. An example of this can be found in the Acknowledgements section of Rousseau *et al*. (2024): "*A big thank you to all data owners and providers, and especially to the following, who provided at least 5% of the records used in the dataset: American Museum of Natural History, iNaturalist, University of Kansas Biodiversity Institute, U.S. Department of Agriculture, and U.S. Geological Survey; we also cite the providers associated with these collections in our references*." Alternatively, personnel associated with the datasets can be named. This idea is adopted from the USGS Bird Banding Laboratory Data Release Policy and can be adopted through wild bee research as well. In addition to naming and citing large dataset providers, citations for all downloaded datasets must be listed in either a table in the main body text (see Levenson *et al*., 2024) or a supplementary file. If using a supplementary file to list these dataset citations, that file must then be referenced in the main body text of any published work.

The Contributor Role Taxonomy (CRediT) includes a role for Data Curation, defined as "management activities to annotate (produce metadata), scrub data and maintain research data (including software code, where it is necessary for interpreting the data itself) for initial use and later re-use" (Brand *et al*., 2015). Co-authors who curate data used in analyses can be acknowledged in a CRediT statement included in any published work. We recognize, however, that curatorial activities are vast and CRediT may be too broad for sufficient acknowledgement. We advocate for continued development of standardized acknowledgement methods for those who contribute to and curate shared occurrence datasets (Thessen *et al*., 2019). More broadly, we advise crediting or acknowledging the stewards, managers, or owners of the land where wild bees are observed or collected for research purposes. This can be done in the Acknowledgements section of publications relying on such data.

Formalizing data sharing policies and preparing for future data policy shifts. Beyond concern for proper credit, scientists may hesitate to share data because they are concerned about how their data may be used. We advise adopting language from one

or multiple existing documents on data ethics, data integrity, data sovereignty, data agreements, and other guidance to create a Code of Conduct or Norms for Data Use for using data following *The Wild Bee Data Standard*. Examples include the USGS Bird Banding Laboratory Data Release Policy, the CARE Principles for Indigenous Data Governance (Carroll *et al*., 2020), the US Federal Data Strategy Data Ethics Framework, the Canadensys Norms for Data Use, and the VertNet Norms for Data Use. Links to all of these examples are provided in Appendix 3. These documents typically describe a series of behaviors that data users should understand before downloading and using any data, including proper use cases, crediting practices, and caveats related to data accuracy.

Further, to ensure data used in publications can be located online, we advise the use of data availability statements in published manuscripts, which are now required to accompany peer-reviewed publications in many scientific journals. A data availability statement is a short, straightforward statement that describes where the data supporting a peer-reviewed publication can be found. An example that would represent data shared following *The Wild Bee Data Standard* is: "Data and metadata are aligned with *The Wild Bee Data Standard* (citation) and are available in [repository of choice, such as GBIF or a Symbiota portal] at [insert dataset DOI]."

IMPLEMENTING *THE WILD BEE DATA STANDARD.* Implementing a data standard requires adequate resources and infrastructure to ensure its credibility and longevity. Here, we have provided guidance on publishing data to GBIF, any insect-focused Symbiota portal, and iNaturalist (Fig. 1). Maintaining these portals demands dedicated personnel and funding to support ongoing user assistance, including data mapping, quality assessments, digitization efforts, and helping users access shared data. Additionally, using these portals requires adopting Darwin Core terminology to describe wild bee occurrence data. *The Wild Bee Data Standard*, which we introduce in the remainder of this manuscript, facilitates this transition by removing barriers for scientists who are unsure how to map or translate their data to align with Darwin Core. *The Wild Bee Data Standard* can be found on GitHub (https://github.com/Big-Bee-Network/wild-bee-data-standard), where comments and updates can be submitted and incorporated. Full implementation of *The Wild Bee Data Standard* will require creating a formal working group to develop a code of conduct for using data following the standard, monitor the GitHub repository, and update the standard over time to ensure it remains in active development and evolves alongside changes in wild bee monitoring practices (see https://www.tdwg.org/community/dwc/).

As more federal and funding agencies begin to require openly accessible data from supported projects (*e.g.*, USDA, NSF; Nelson, 2022), implementing *The Wild Bee Data Standard* and following our proposed digitization pipeline provides a pathway to meeting these requirements. Given the importance of openly accessible data to pollinator conservation (Chesshire *et al*., 2023; Rousseau *et al*., 2024), we hope to see these practices widely adopted and supported in perpetuity.

THE WILD BEE DATA STANDARD, VERSION 1.0.0: GUIDANCE FOR USE

The Wild Bee Data Standard consists of metadata guidelines and a list of 75 Darwin Core terms, or data fields, that describe wild bee occurrence data (Appendix 1). All 75 terms do not need to be used; the term list is divided into 26 *core* terms, 22 *recommended*

Table 1. Organizational structure of *The Wild Bee Data Standard*. *The Wild Bee Data Standard* contains 75 Darwin Core terms within three tiers of data collection and reporting (Levenson *et al*., 2025b). Within these tiers, the terms are presented in Darwin Core categorical order. For more information on these categories and the complete list of Darwin Core terms, please visit https://dwc.tdwg.org/terms/

Tiers of data collection and reporting		
Core	Recommended	Optional
These 26 terms must be collected and provided.	These 22 terms should be provided if the information was collected.	These 27 terms can be provided if the information was collected, depending on one's objective(s).
Categories of Darwin Core terms presented in The Wild Bee Data Standard		
Record-level	Generic data that might apply to any type of record in a dataset.	
Occurrence	Data that describe the existence of an organism at a particular place at a particular time.	
MaterialEntity	Data that describe an entity that can be identified, exists for some period of time, and consists in whole or in part of physical matter while it exists.	
Event	Data that describe an action that occurs at some location during some time.	
Location	Data that describe a spatial region or named place.	
Identification	Data that describe a taxonomic determination.	
Taxon	Data that describe a group of organisms.	

terms, and 27 *optional* terms (Table 1). *Core* terms are those that we argue must be collected and provided with all current and future wild bee occurrence data to ensure data quality; these are listed first, followed by *recommended* terms that should be provided if collected and *optional* terms that can be provided if collected (Levenson *et al*., 2025b). The standard is intended to guide field collection and specimen processing procedures (including taxonomic verification), streamline digitization, and support FAIR data principles. We advise establishing field collection and specimen processing procedures with metadata guidelines and *core* terms in mind, then consider the *recommended* and *optional* terms and choose to record those relevant to experimental goals. Field-collected data can then be digitized using one of the provided templates (Du Clos *et al*., 2025). These digitized data are then ready for taxonomic verification and ultimately to be made openly available by uploading to GBIF, a Symbiota portal, or another web-based data aggregator, portal or repository. Data downloaded from these sources will then be fully interoperable with each other.

Creating metadata. When uploading occurrence data to GBIF, Symbiota, or another web-based data aggregator, portal, or repository, descriptive information about the dataset, called metadata, must also be provided. Metadata offers important source information for occurrence datasets, promoting interpretation and reusability by data users. To meet GBIF's minimum metadata requirements, please provide the required metadata fields listed in Table 2 when publishing wild bee occurrence data. Required metadata fields contain basic information about an occurrence dataset, including the title, description, and contact information. Recommended metadata fields include data collection methods and the proper citation for use when working with a dataset downloaded from GBIF. Providing highly descriptive metadata improves data quality and contributes to more rigorous analyses (Bloom *et al.*, 2021). When a new dataset is published to GBIF, the IPT translates the provided metadata into an EML-compliant

Table 2. Metadata fields required or recommended by GBIF for any published dataset.

Field name	Definition	Required or recommended
Title	The title of your dataset. Aim to provide a detailed title that will distinguish your dataset from others.	Required
Description	A brief description of the dataset that may include where, when, and why the data were collected, who collected it, and what research conclusions the data has provided.	Required
Publishing organization	The organization publishing the dataset to GBIF. Organizations that have published wild bee occurrence data on GBIF include the USGS Bee Lab at the Eastern Ecological Science Center (previously the Bee Inventory and Monitoring Laboratory, Droege & Maffei, 2025) and the USDA-ARS Pollinating Insects Research Unit (Ikerd, 2019; Carril *et al*., 2023).	Required
Type	Choose from Occurrence, Taxon, or Event. Most data uploaded following The Wild Bee Data Standard will be of the Occurrence type.	Required
License	Choose a Creative Commons License (https://creativecommons.org/share-your-work/cclicenses/) to apply to your dataset. GBIF encourages publishers to adopt the least restrictive license possible from among three provided options: CC0 1.0, CC-BY 4.0, or CC-BY-NC 4.0.	Required
Contact(s)	Name and contact information for those with knowledge of the dataset.	Required
Creator(s)	Name and contact information for those who created the dataset, in priority order.	Required
Metadata provider(s)	Name and contact information for those who created the metadata for the dataset, in priority order.	Required
Sampling methodology	Providing information about the study extent in space and time and a description of sampling protocol and effort promotes transparency and reproducibility. More details are provided in the Metadata section of the IPT User Manual: https://ipt.gbif.org/manual/en/ipt/latest/manage-resources#sampling-methods	Recommended
Citation	Please provide a citation to use when citing the dataset. This citation can link to the dataset page on GBIF or it can link to any scientific publication that uses the provided data. More details are provided in the Metadata section of the IPT User Manual: https://ipt.gbif.org/manual/en/ipt/latest/manage-resources#citations	Recommended

metadata document, similar to how it maps Darwin Core terms (Robertson *et al*., 2014; Jones *et al*., 2019). For more information, please see the Metadata section of the IPT User Manual: https://ipt.gbif.org/manual/en/ipt/latest/manage-resources#metadata. We provide a GBIF-compliant metadata template with our worksheet and workbook data standard templates (Du Clos *et al*., 2025), which contains the terms listed in Table 2. See Droege & Maffei (2025) for an example of highly descriptive metadata for a wild bee occurrence dataset on GBIF.

Publishing metadata to a Symbiota portal is similar, though the upload to Symbiota will ask for slightly different metadata fields (https://docs.symbiota.org/Collection_Manager_Guide/editing_collection_metadata/#collections-metadata). Importantly, if your dataset is published to GBIF through a Symbiota portal, the relevant metadata provided to Symbiota will also be shared to GBIF, meeting their minimum metadata requirements. If using another CMS to publish to GBIF or publishing to another data

aggregator, portal, or repository, please determine their metadata requirements and prepare accordingly before publication.

Generating unique identifiers. Unique identifiers simplify and standardize data management and sharing practices. In *The Wild Bee Data Standard*, we describe two types of unique identifiers. Machine-readable identifiers are typically computer-generated, long, complex, and ideally globally unique. They are intended for use by software when sharing, managing, or analyzing data. An example of a machine-readable identifier is: 1edef0b2-df7e-4e0b-ab8a-6c367e622206. Human-usable identifiers are created and used by individuals and organizations managing data but are not expected to be unique outside of a given dataset or organization. Examples include specimen label numbers, site numbers, or combinations of site, date, and location information created to distinguish sampling events. Darwin Core provides fields to accommodate both machine-readable and human-usable identifiers.

There is one machine-readable identifier in *The Wild Bee Data Standard*: **dwc:occurrenceID**. In order to upload data to GBIF, **dwc:occurrenceID**s must be provided for each record in a dataset. While **dwc:occurrenceID**s can be created automatically through the use of a CMS to manage and share wild bee occurrence data, which we elaborate on below, they will sometimes need to be created by data providers. Creating unique **dwc:occurrenceID**s for each record is a critically important task. We recognize that this can present a barrier to preparing occurrence data for upload to GBIF and provide the following guidance. While it is acceptable for **dwc:occurrenceID**s to be unique within a dataset, we advise making them globally unique identifiers. Creating **dwc:occurrenceID**s has often been done by combining various cells, including event, location, and taxon identifiers, into an identifier unique within the dataset, but an issue with this approach is that even these resulting identifiers may not be globally unique. As such, we advise creating universally unique identifiers (UUIDs) to serve as **dwc:occurrenceID**s. UUIDs are 128-bit labels and can be created via R functions, Excel macros, or website applications, examples of which are provided in Appendix 3. Importantly, most CMS will create UUID-based **dwc:occurrenceID**s for each record created or uploaded, eliminating the need for data providers to create these identifiers on their own. For example, datasets uploaded to a Symbiota portal will have UUID-based **dwc:occurrenceID**s created for each record automatically. Using Symbiota or another CMS to manage occurrence data and share it to GBIF presents an approachable solution to generating UUIDs to serve as **dwc:occurrenceID**s for each record in an occurrence dataset. We reiterate that unique **dwc:occurrenceID**s for each record in an occurrence dataset are required for publication to GBIF.

Remember that **dwc:occurrenceID**s are long and complex for machine readability, not human usability. GBIF and other data management and analysis systems use **dwc:occurrenceID**s to keep track of each record in an occurrence dataset. When a dataset is modified and reuploaded, the **dwc:occurrenceID**s can be matched to update the modified records. GBIF has practices in place to monitor changes in **dwc:occurrenceID**s and notifies publishers if it detects new **dwc:occurrenceID**s for existing datasets (https://data-blog.gbif.org/post/improve-identifier-stability/). Managing data through Symbiota or other CMS makes modification of **dwc:occurrenceID**s extremely difficult, generally avoiding the same record ending up with multiple **dwc:occurrenceID**s. To prepare downloaded data for analyses, **dwc:occurrenceID**s can be used to filter out duplicates in cases where data may have been downloaded from multiple sources, such as GBIF or a Symbiota portal.

Human-usable identifiers are important in identifying a specimen or field site within a dataset, as in the terms **dwc:catalogNumber** and **dwc:fieldNumber**, which identify a specimen in a collection and a field site where occurrence data were collected. We describe the use of other human-usable identifiers in *The Wild Bee Data Standard* to help organize occurrence data internally within spreadsheet workbooks or relational databases. These identifiers include **dwc:eventID** to identify a unique sampling event, **dwc:locationID** to identify a unique sampling site location, and **dwc:taxonID** to identify a unique taxon name. The workbook template provided with *The Wild Bee Data Standard* uses these identifiers to separate sampling event information, site location information, and species identification information from the occurrence information of the wild bee specimen or observation (Du Clos *et al*., 2025). Providing the human-usable identifiers in the Darwin Core archive when uploading could aid data users in interpretation of the dataset and provide another way to remove duplicate records when preparing downloaded data for analyses.

Other unique identifiers mentioned in *The Wild Bee Data Standard* are connected to the places or people associated with the occurrence data. The IDs used in the terms **dwc:institutionID** and **dwc:collectionID** are generated by people working at the institution housing the data or the specimen collection. These can be cataloged in the Global Registry of Scientific Collections (https://www.gbif.org/grscicoll), though they can be other identifiers. The IDs used in the terms **dwc:recordedByID** and **dwc:identifiedByID** are created by the people doing the data collection and identification. Typically, these will be ORCID iDs, though they can be other unique identifiers. We recommend these terms to connect and properly credit relevant places and personnel with hosted or handled occurrence data.

USING CONTROLLED VOCABULARIES. Some of the terms included in *The Wild Bee Data Standard* have controlled vocabularies, or an allowable list of entries. Controlled vocabularies help standardize large amounts of data derived from different sources by allowing all users to glean the same information across multiple datasets. This makes the data more interoperable. Terms in *The Wild Bee Data Standard* with controlled vocabularies include: **dwc:basisOfRecord**, **dwc:occurrenceStatus**, **dwc:samplingProtocol**, **dwc:sampleSizeUnit**, **dwc:stateProvince**, **dwc:disposition**, **dwc:identificationQualifier**, **dwc:sex**, **dwc:caste**, **dwc:lifeStage**, **dwc:vitality**, **dwc:behavior**, **dwc:habitat**, **dwc:organismQuantityType**, **dwc:associatedTaxa**, and **dwc:dynamicProperties**. Further, **dwc:samplingProtocol**, **dwc:associatedTaxa**, **dwc:associatedOccurrences**, **dwc:georeferenceRemarks,** **dwc:dynamicProperties**, and **dwc:habitat** are or can be reported using key:value pairs to format the complex information within. In a key:value pair, the key is the type of information being provided, and the value is the actual information. Multiple key:value pairs can be reported in a single term. All terms with controlled vocabularies include a controlled vocabulary list of all allowable entries, and when applicable, the use of key:value pairs is thoroughly described for relevant terms.

FOLLOWING STANDARD TEMPLATES. To aid in the adoption and publication of data following *The Wild Bee Data Standard*, we provide two templates for entering compliant data into a computer (10.5281/zenodo.14187861; Du Clos *et al*., 2025). Both templates contain descriptive information and instructions for use in a README tab, a metadata tab that can be used to populate metadata when publishing online, and a full-term list

with definitions and links to their Darwin Core webpage. Data following the Darwin Core standard are presented in a single worksheet with each DwC term listed as a column heading. Therefore, we provide a single worksheet template that demonstrates the use of all terms in *The Wild Bee Data Standard*, with *core* terms in bold. At minimum, all *core* terms must be provided. The template can be modified as needed to provide additional data.

We also provide a workbook template as an option for those who use multiple spreadsheets in a workbook or a relational database to manage their data. We urge caution with the workbook template and only advise using it if your data management scheme follows its format. The workbook template represents one of multiple possible architectures for a database of wild bee occurrence data, a many-to-one database with occurrence information as the primary table. The workbook template contains an occurrence worksheet, an event worksheet, a location worksheet, and a taxon worksheet. All relevant terms are provided within their respective worksheets, with *core* terms in bold. At minimum, all *core* terms must be provided. The workbook template uses three human-readable unique identifiers to connect the worksheets together: **dwc:eventID**, **dwc:locationID**, and **dwc:taxonID**. Since uploading to web portals does not support multiple tables, the workbook template then concatenates all sheets to generate a large single worksheet suitable for uploading to GBIF, Symbiota, or another web-based data aggregator, portal, or repository.

We provide example data entries in both templates that describe how data are recorded for the case studies presented in the protocols developed by the Bee Monitoring RCN (Cariveau *et al*., 2025; Levenson *et al*., 2025a; López-Uribe *et al*., 2025; Otto *et al*., 2025; Strange *et al*., 2025), and provide scenarios here.

EXAMPLES OF IMPLEMENTING *THE WILD BEE DATA STANDARD*

Collecting community-level bee data examples. To demonstrate how the standard can be used to collect community level bee data, three case studies are presented in Levenson *et al*. (2025a). Our worksheet and workbook template examples (Du Clos *et al*., 2025) report data collected in the following scenarios, with full details for each provided in Levenson *et al*. (2025a). The following case studies describe several different bee data collection scenarios and the associated Darwin Core terms that would be used to record each piece of data:

Case Study I. An Inventory

Two entries are provided here, one for a bee caught in a bowl trap and one for a bee caught with a hand net. The first entry describes a bee collected by Field Scientist (**dwc:recordedBy**) in a bowl trap (**dwc:samplingProtocol**) at site 12 (**dwc:fieldNumber**, **dwc:locationID**) on July 12, 2009 (**dwc:eventDate**, **dwc:year**, **dwc:month**, **dwc:day**) at 4:00 pm (**dwc:eventTime**). The bee is later identified as *Agapostemon texanus* Cresson, 1872 (**dwc:scientificName**, **dwc:genus**, **dwc:specificEpithet**, **dwc:scientificNameAuthorship**) by Bee Taxonomist (**dwc:identifiedBy**). Further, Bee Taxonomist provided citations for the literature used to make this identification (**dwc:namePublishedIn**, **dwc:identificationReferences**). The second entry describes a bee collected by Field Scientist (**dwc:recordedBy**) in a net (**dwc:samplingProtocol**) while foraging on *Rubus parviflorus* (**dwc:associatedTaxa**) at site 6 (**dwc:fieldNumber**, **dwc:locationID**) on August 23, 2009 (**dwc:eventDate**, **dwc:year**, **dwc:month**,

dwc:day) at 1:20 pm (**dwc:eventTime**). This bee is later identified as *Bombus nevadensis* Cresson, 1874 (**dwc:scientificName**, **dwc:genus**, **dwc:specificEpithet**, **dwc:scientificNameAuthorship**) by Bee Taxonomist (**dwc:identifiedBy**). Further, Bee Taxonomist provided citations for the literature used to make this identification (**dwc:namePublishedIn**, **dwc:identificationReferences**). For both entries, site coordinates are taken from Google Maps (**dwc:decimalLatitude**, **dwc:decimalLongitude**, **dwc:georeferenceRemarks**) and reported to six decimal places (**dwc:coordinateUncertaintyInMeters**, **dwc:coordinatePrecision**). The researchers share their data under public domain (**dwc:license**, **dwc:rightsHolder**).

Case Study II. A Survey

Two entries are provided here, one for a bee caught in a bowl trap and one for a bee caught with a hand net. The first entry describes a bee collected by Field Scientist (**dwc:recordedBy**) in a bowl trap (**dwc:samplingProtocol**) at site 8A (**dwc:fieldNumber**, **dwc:locationID**) on May 6, 2017 (**dwc:eventDate**, **dwc:year**, **dwc:month**, **dwc:day**) after a 24-hour deployment (**dwc:eventDate**). The bee is later identified as *Lasioglossum* cf. *versatum* (**dwc:scientificName**, **dwc:genus**, **dwc:specificEpithet**, **dwc:verbatimIdentification**, **dwc:identificationQualifier**, **dwc:taxonRank**) by Bee Taxonomist (**dwc:identifiedBy**). Further, Bee Taxonomist provided a citation for the nomenclatural revision used to make this identification (**dwc:nameAccordingTo**). The second entry describes a bee collected by Field Scientist (**dwc:recordedBy**) in a net (**dwc:samplingProtocol**) while foraging on *Monarda fistulosa* (**dwc:associatedTaxa**) at site 8A (**dwc:fieldNumber**, **dwc:locationID**) on May 6, 2017 (**dwc:eventDate**, **dwc:year**, **dwc:month**, **dwc:day**) between 10:40 and 10:50 am (**dwc:eventTime**). This bee is later identified as *Osmia lignaria* subsp. *lignaria* (**dwc:scientificName**, **dwc:genus**, **dwc:specificEpithet**, **dwc:infraspecificEpithet**) by Bee Taxonomist (**dwc:identifiedBy**). For both entries, site coordinates are taken from Google Maps (**dwc:decimalLatitude**, **dwc:decimalLongitude**, **dwc:georeferenceRemarks**) and reported to six decimal places (**dwc:coordinateUncertaintyInMeters**, **dwc:coordinatePrecision**). The researchers share their data under a CC-BY license (**dwc:license**, **dwc:rightsHolder**).

Case Study III. A Monitoring Program

Three entries are provided here for three specimens of the same species collected by Field Scientist (**dwc:recordedBy**) in a bowl trap (**dwc:samplingProtocol**) at site 4 (**dwc:fieldNumber**, **dwc:locationID**) on September 13, 2021 (**dwc:eventDate**, **dwc:year**, **dwc:month**, **dwc:day**) after a 24-hour deployment (**dwc:eventDate**). These bees are all later identified as *Megachile relativa* (**dwc:scientificName**, **dwc:genus**, **dwc:specificEpithet**) by Bee Taxonomist (**dwc:identifiedBy**). For all entries, site coordinates are taken from a GPS unit and reported to four decimal places (**dwc:decimalLatitude**, **dwc:decimalLongitude**, **dwc:coordinateUncertaintyInMeters**, **dwc:coordinatePrecision**). The researchers share their data under public domain (**dwc:license**, **dwc:rightsHolder**).

OCCUPANCY OF FOCAL BEE SPECIES EXAMPLE. To demonstrate how the standard can be used in monitoring for occupancy of focal species, we provide an example aligned with the *Bombus affinis* monitoring framework described in Otto *et al*. (2025). Steps 3–5 of this framework are directly applicable to the use of *The Wild Bee Data Standard*. Our

worksheet and workbook template examples (Du Clos *et al*., 2025) report details of the sampling scheme created in Step 3 of the framework, including sampling unit size (**dwc:samplingEffort**), date sampled (**dwc:eventDate**, **dwc:year**, **dwc:month**, **dwc:day**), time of day sampled (**dwc:eventTime**), amount of time sampled (**dwc:samplingEffort**), observer experience (**dwc:eventRemarks**), land cover type sampled (**dwc:habitat**), caste (**dwc:caste**), and photo voucher metadata (**dwc:associatedMedia**). The template examples also report details associated with the field sampling methods described in Step 4 of the framework, including detections and non-detections (**dwc:occurrenceStatus**) and weather conditions (**dwc:dynamicProperties**). The template examples report data collected in the following scenario, which represents one collection event:

Three sites (**dwc:fieldNumber**, **dwc:locationID**) in the St. Paul, Minnesota area are sampled in early August 2023 (**dwc:eventDate**, **dwc:year**, **dwc:month**, **dwc:day**). The exact coordinates for these sites are masked, as *B. affinis* is an endangered species (**dwc:decimalLatitude**, **dwc:decimalLongitude**, **dwc:informationWithheld**). As determined by remotely sensed data, two sites are in urban areas, and one is in grassland (**dwc:habitat**). Visual sampling (**dwc:samplingProtocol**) is conducted in the daytime for 30 minutes by a single observer, reported in person-hours (**dwc:eventTime**, **dwc:samplingEffort**). Weather conditions are reported before each sampling event (**dwc:dynamicProperties**). Data are recorded for each sampling event even if *B. affinis* was not detected (**dwc:eventID**, **dwc:occurrenceID**). *B. affinis* is detected at one site and is not detected at two sites (**dwc:occurrenceStatus**, **dwc:scientificName**, **dwc:genus**, **dwc:specificEpithet**). At the sites where *B. affinis* was not detected, **dwc:individualCount** is reported as zero. At the site where *B. affinis* was detected, three workers (**dwc:individualCount**, **dwc:caste**) were observed foraging on *Spiraea alba* (**dwc:associatedTaxa**) and one drone (**dwc:individualCount**, **dwc:caste**) was observed foraging on *Eutrochium purpureum* (**dwc:associatedTaxa**). Two photo vouchers are captured; one of a worker foraging on *S. alba* and one of the drone foraging on *E. purpureum*. URLs for both vouchers are shared on iNaturalist (**dwc:associatedMedia**). The researchers share their observation data in the public domain (**dwc:license**).

To comply with the framework, these surveys must be repeated at regular intervals throughout a defined sampling season. Data collection and recording began for this season on June 15, and will continue until September 15. The goal is to complete six 30-minute surveys at each sampling unit over the sampling season. Ideally, surveys take place during multiple sampling unit visits, spaced roughly two weeks apart. A single sampling visit may include one or multiple observers and each observer should be treated as an independent survey. When multiple observers are used, survey information for each observer should be recorded separately. All preceding and subsequent surveys will be recorded and reported as demonstrated here.

Collecting data on bee-flower interaction examples. To demonstrate how the standard can be used to collect bee-flower interaction data, two case studies are presented in Cariveau *et al*. (2025). Our worksheet and workbook template examples (Du Clos *et al*., 2025) report data collected in the following scenarios, with full details for each provided in Cariveau *et al*. (2025):

Case Study I. An Inventory for a Government Agency

Four entries are provided here, two for non-bumble bees that were lethally collected and two for bumble bees that were captured, cooled, photographed, and released.

The bees were sampled at Site 6 (**dwc:fieldNumber**), a dry prairie (**dwc:habitat**), on July 27, 2023 (**dwc:eventDate**), during the morning sampling period of the inventory (**dwc:eventID**). There is a single collector, Agency Technician, (**dwc:recordedBy**, **dwc:sampleSizeValue**, **dwc:SampleSizeUnit**) walking the 400 x 2 m meandering transect (**dwc:samplingEffort**) for a 1-hour sampling duration (**dwc:samplingEffort**). For each bee collected, the plant species it was caught on and the nature of the interaction is recorded (**dwc:associatedTaxa**). The timer is stopped when handling bees, therefore the total event time is reported as 1 hour and 50 minutes (**dwc:EventTime**). One non-bumble bee was collected on a plant that was later photographed as the representative voucher for that plant species (**dwc:associatedOccurrences**). The time the bumble bees spent in the cooler before being photographed was recorded (**dwc:preparations**). Site coordinates were obtained with a handheld GPS (**dwc:decimalLatitude**, **dwc:decimalLongitude**, **dwc:georeferenceRemarks**) and reported to four decimal places, for an accuracy of 5 m (**dwc:coordinateUncertaintyInMeters**). The non-bumble bees were later identified as *Lasioglossum subviridatum* and *Melissodes bimaculatus* (**dwc:scientificName**, **dwc:genus**, **dwc:specificEpithet**) by Bee Taxonomist (**dwc:identifiedBy**). The specimens were then accessioned at Local Museum (**dwc:collectionCode**). Specimen data were reported under a CC-BY license (**dwc:license**). The bumble bee photo vouchers were posted to iNaturalist (**dwc:associatedMedia**). They were identified in the field by Agency Technician (**dwc:identifiedBy**) as *Bombus ternarius* and *Bombus bimaculatus* (**dwc:scientificName**, **dwc:genus**, **dwc:specificEpithet**). The bee photo vouchers were shared under public domain (**dwc:license**).

Case Study II. Monitoring to Determine Effects of Prescribed Fire

Three entries are provided here, two from a burned site and one from an unburned site. These two sites (**dwc:fieldNumber**) were sampled on the same day (May 21, 2019; **dwc:eventDate**) during the afternoon sampling period (**dwc:eventTime**), but by different teams of two technicians (**dwc:sampleSizeValue**, **dwc:sampleSizeUnit**, **dwc:recordedBy**). At each site, the technicians walked along a 200 m meandering transect, collecting bees on 1 m of either side of the center of the transect (**dwc:samplingEffort**), for a sampling duration of 10 minutes, reported in decimals of person-hours (**dwc:samplingEffort**). The timer is stopped when handling bees, so **dwc:eventTime** is longer than 30 minutes. For each bee collected, the plant species it was caught on and the nature of the interaction was recorded (**dwc:associatedTaxa**). One bee was collected on a plant that was later photographed as the representative voucher for that plant species (**dwc:associatedOccurrences**). Site coordinates were confirmed in Google Maps (**dwc:decimalLatitude**, **dwc:decimalLongitude**, **dwc:georeferenceRemarks**) and reported to six decimal places, for an accuracy of 0.1 m (**dwc:coordinateUncertaintyInMeters**). The bees at the burned site were later identified as *Lasioglossum abanci* and *Andrena imitatrix* (**dwc:scientificName**, **dwc:genus**, **dwc:specificEpithet**) by Bee Taxonomist (**dwc:identifiedBy**). The bee collected at the burned site was identified in the field by Student Technician (**dwc:identifiedBy**) as *Bombus impatiens* (**dwc:scientificName**, **dwc:genus**, **dwc:specificEpithet**). The specimens were accessioned into the host university's invertebrate zoology collection (**dwc:collectionCode**). The data were shared under public domain (**dwc:license**). This scenario was developed using locations, habitats, and species found in Ulyshen *et al*. (2022).

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APPENDIX 1
The Wild Bee Data Standard, version 1.0.0: List of Terms

This appendix presents the complete term list for *The Wild Bee Data Standard*, designed to ensure consistent collection and sharing of wild bee occurrence data. The standard includes 75 Darwin Core terms, organized into 26 core, 22 recommended, and 27 optional fields (see Table 1). Each entry provides a definition, rationale, usage instructions, and examples, with controlled vocabularies where appropriate. Links to the Darwin Core reference guide and alignment with Bee Monitoring RCN protocols are also provided. An example of the term entry format is as follows:

Term name: Term name in bold.
Definition: What information the term describes.
Rationale: Reason for using the term to describe wild bee occurrences.
Requirement: One of the following three categories (Table 1):
Core: These terms must be collected and provided.
Recommended: These terms should be provided if the information was collected.
Optional: These terms can be provided if the information was collected.
How to use: Instructions for using the term to align with *The Wild Bee Data Standard.*
Controlled vocabulary list: The list of allowable entries for terms with a controlled vocabulary.
Example(s): Practical example(s) of text that would be entered into a field for that term.
Relevant protocols: Most terms are relevant to all Bee Monitoring RCN protocols: Cariveau *et al*. (2025), Levenson *et al.* (2025a), López-Uribe *et al.*, (2025), Otto *et al.* (2025), and Strange *et al*. (2025).
For more detail: Link to the term entry in the Darwin Core quick reference guide (https://dwc.tdwg.org/terms/).

Term List Index

Core (26 terms)

Record-level: institutionCode, basisOfRecord, informationWithheld
Occurrence: occurrenceID, catalogNumber, recordedBy, individualCount, occurrenceStatus
Event: eventDate, eventTime, year, month, day, samplingProtocol, sampleSizeValue, sampleSizeUnit, samplingEffort
Location: country, stateProvince, decimalLatitude, decimalLongitude, coordinateUncertaintyInMeters
Identification: identifiedBy
Taxon: scientificName, genus, specificEpithet

Recommended (22 terms)

RECORD-LEVEL: license, institutionID, collectionID, collectionCode,
OCCURRENCE: recordedByID, sex, associatedTaxa
MATERIALENTITY: disposition
EVENT: eventID, eventRemarks
LOCATION: locationID, geodeticDatum
IDENTIFICATION: verbatimIdentification, identificationQualifier, identifiedByID, dateIdentified, identificationReferences
TAXON: taxonID, nameAccordingTo, family, infraspecificEpithet, scientificNameAuthorship

Optional (27 terms)

RECORD-LEVEL: rightsHolder, dynamicProperties
OCCURRENCE: lifeStage, caste, behavior, vitality, associatedMedia, associatedOccurrences, occurrenceRemarks
MATERIALENTITY: preparations, associatedSequences, materialEntityRemarks
EVENT: fieldNumber, habitat
LOCATION: county, locality, verbatimElevation, coordinatePrecision, georeferencedBy, georeferenceRemarks
IDENTIFICATION: typeStatus, identificationRemarks
TAXON: namePublishedIn, tribe, subgenus, taxonRank, vernacularName

Core Terms

Record-level

TERM NAME: **institutionCode**
DEFINITION: The name (or acronym) in use by the institution or organization having custody of the object(s) or information referred to in the record.
RATIONALE: Indicates the institution that holds or curates the specimen or observation record, which may lead to a point of contact for more information about an occurrence.
REQUIREMENT: Core.
HOW TO USE: Provide a name or acronym for the institution or organization that houses the specimen or coordinated the observation. If the institution or organization is registered in the Global Registry of Scientific Collections (https://scientific-collections.gbif.org/), please use the code listed there. For lab collections managed in-house, please provide the name of the lab.
EXAMPLES: USDA-ARS, UNHC, iNaturalist, AMNH, Woodard Lab
RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:institutionCode

TERM NAME: **basisOfRecord**

Definition: The specific nature of the data record.
Rationale: This term is *required for publication to GBIF.* This term describes the type of occurrence record to indicate whether it includes a specimen, an observation, tissue material, or is gathered from the literature. This is essential context for interpretation.
Requirement: Core.
How to use: This term uses a controlled vocabulary. *The Wild Bee Data Standard* follows the GBIF vocabulary for the basis of record.

- Controlled vocabulary list for **dwc:basisOfRecord**:
  - PreservedSpecimen, to describe labeled wild bee specimens preserved on pins or in vials.
  - HumanObservation, to describe wild bees observed in the field and captured in photographs taken in person when using non-lethal sampling methods.
  - MachineObservation, to describe wild bees captured in photographs taken via camera trap when using non-lethal sampling methods.
  - MaterialEntity, taken from the Darwin Core vocabulary for **dwc:basisOfRecord** to describe genetic or pathogen material.
  - MachineCitation, to describe occurrences gathered from published literature.

Examples: PreservedSpecimen, HumanObservation
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:basisOfRecord
https://docs.gbif.org/course-data-use/en/basis-of-record.html

Term name: **informationWithheld**
Definition: Additional information that exists, but that has not been shared in the given record.
Rationale: If any core information is not shared, the type of information and the rationale for not sharing it must be provided. In particular, if the exact location of the record is masked, this cell must indicate what information has been omitted or changed, and describe why masking occurred.
Requirement: Core, if applicable (see rationale).
How to use: This is a text-based term that allows any word-based entry.
Examples:

- Exact location removed to mask for endangered/threatened/rare bee or host plant species or owing to private land ownership.
- Decimal latitude/longitude rounded to obscure exact location because it is private land.

Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:informationWithheld

Occurrence

Term name: **occurrenceID**
Definition: A unique identifier for the occurrence.
Rationale: This term is *required for publication to GBIF.* Please see the section "Generating unique identifiers."

REQUIREMENT: Core.
HOW TO USE: We advise creating universally unique identifiers, or UUIDs, to serve as **dwc:occurrenceID**s. These can be created using R packages, Excel macros, or website applications, examples of which are provided in Appendix 3. While GBIF will not generate these for you, consider that uploading to a CMS automatically creates **dwc:occurrenceIDs** for each record. Please see the section "Generating unique identifiers" for more details.
EXAMPLE: 8d13f958-10fa-490a-8c32-5938be9d2037
RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:occurrenceID
https://www.gbif.org/data-quality-requirements-occurrences#dcOccurrenceID

TERM NAME: **catalogNumber**
DEFINITION: A unique identifier within a dataset or collection.
RATIONALE: Physical specimens accessioned into a collection will have a unique ID assigned to them; that number gets reported through **dwc:catalogNumber** to reference back to the original dataset.
REQUIREMENT: Core, if applicable (see rationale).
HOW TO USE: Use **dwc:catalogNumber** to share the unique ID of a record or specimen in an original dataset or collection. To improve uniqueness, human-readability, and machine interpretation in large, multi-institution datasets, please include a sufficient amount of both letters and numbers when creating these IDs.
EXAMPLES: BBSL319283, AMNH PBI 82341, UNH-150861
RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/list/#dwc_catalogNumber

TERM NAME: **recordedBy**
DEFINITION: A list of names of people, groups, or organizations responsible for recording the original occurrence. This is a synonym of "Collector."
RATIONALE: Providing the names of the collector or observer creates a potential point of contact for more information regarding an occurrence.
REQUIREMENT: Core.
HOW TO USE: Use full names (First [Middle Initial, if provided] Last) whenever possible. When multiple collectors are working simultaneously, list the specimens collected by each collector individually. If that is not possible, the primary collector or observer should be listed first. Separate the values in a list with space vertical bar space (|); this separator is used throughout the Darwin Core standard to concatenate multiple entries in a cell. Please be sure to record the number of collectors in **dwc:samplingEffort**.
EXAMPLES:

- For one collector:
  - Frank D. Parker
- For more than one collector:
  - Olivia J. Messinger | Terry L. Griswold

RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:recordedBy

Term name: **individualCount**
Definition: The number of individual organisms present at the time of the occurrence.
Rationale: Most records of wild bee occurrences represent one bee. This indicates a detection of a bee, but it is important in many cases to also indicate non-detections of focal bee species, represented as zeros.
Requirement: Core.
How to use: Report the number of individual organisms counted in the occurrence. Only whole numbers are permitted. When sampling for occupancy of focal species (Otto *et al.*, 2025), if they are not found at a sampling site, use this term to report non-detections.

- A 0 entry for **dwc:individualCount** represents a non-detection.
- Most records will have an entry of 1 for **dwc:individualCount**, as most records correspond to an observation or collection (a detection) of a single organism.
- Entries larger than 1 are possible in some cases; for example:
  - If a large number of the same species is collected, but only a subset of specimens of that species are preserved.
  - If multiple bees of the same species are in a photo observation on a plant.
  - If multiple bees of the same species are observed at the same site, but a photo voucher is created for only one of those bees.

Examples: 0, 1, 2, etc.
Relevant protocols: All, but particularly important for the occupancy of focal species protocol (Otto *et al.*, 2025).
For more detail: https://dwc.tdwg.org/terms/#dwc:individualCount
https://www.gbif.org/data-quality-requirements-occurrences#dcCount

Term name: **occurrenceStatus**
Definition: A statement about the presence or absence of a taxon at a location.
Rationale: This term indicates if a species was detected or not detected during a sampling event and is particularly important to report when conducting occupancy surveys. Providing both detections and non-detections are crucial for occupancy modeling.
Requirement: Core.
How to use: This term uses a controlled vocabulary. Although the Darwin Core standard recommends the use of "present" and "absent" to designate occurrence status, we suggest observers instead use "detected" and "notDetected" when recording results from sampling events. Absence is seldom known with certainty and we recommend avoiding the use of this term during data collection.

- Controlled vocabulary list:
  - detected
  - notDetected

Examples: detected, notDetected
Relevant protocols: All, but particularly important for the occupancy of focal species protocol (Otto *et al.*, 2025).
For more detail: https://dwc.tdwg.org/terms/#dwc:occurrenceStatus

Event

TERM NAME: **eventDate**
DEFINITION: The date-time or interval during which a sampling event occurred.
RATIONALE: This term is *required for publication to GBIF*. Providing a collection or observation date provides essential context for interpreting an occurrence.
REQUIREMENT: Core.
HOW TO USE: Recommended best practice is to use a date that conforms to ISO 8601-1:2019. Provide the date or dates sampling occurred in YYYY-MM-DD format. If reporting an interval of dates, separate the dates with a slash (/). Please be sure to provide accompanying sampling protocol and effort information in the terms **dwc:samplingProtocol**, **dwc:sampleSizeValue**, **dwc:sampleSizeUnit**, and **dwc:samplingEffort**.
EXAMPLES:
- 2015-08-14
  - For single day sampling.
- 2015-08-14T16:00:00/2015-08-15T16:00:00
  - For sampling over a maximum 24-hour period that spans two dates. This is interpreted as: collections started on August 14, 2015 at 4pm local time and ended August 15, 2015 at 4pm local time. Note that in this case, **dwc:eventTime** does not need to be provided, but can be, as it is included in **dwc:eventDate**.

RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:eventDate
https://www.gbif.org/data-quality-requirements-occurrences#dcEventDate

TERM NAME: **eventTime**
DEFINITION: The time or interval during which a sampling event occurred.
RATIONALE: This term is used in conjunction with **dwc:eventDate** to clarify the sampling time interval and is best used when sampling occurs on a single day.
REQUIREMENT: Core.
HOW TO USE: Recommended best practice is to use a time that conforms to ISO 8601-1:2019. Report in local time. Report the total sampling time interval, covering the start and end time of either passive trap deployment or active sampling. The correct format is start time/end time. Use **dwc:samplingEffort** to report the duration of sampling time in hours, person-hours, or decimals of hours or person-hours. Please be sure to provide accompanying sampling protocol and effort information in the terms **dwc:samplingProtocol**, **dwc:sampleSizeValue**, **dwc:sampleSizeUnit**, and **dwc:samplingEffort**.
EXAMPLES:
- 09:00/15:00, 09:30/09:40, 11:50/12:00, 14:15/14:25
  - For a 24-hour interval, please use **dwc:eventDate** instead.
- 08:30/08:30
  - If choosing to report a 24-hour interval.

FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:eventTime

Term name: **year**
Definition: The four-digit year in which the sampling event occurred, according to the Common Era Calendar.
Rationale: Separating the full **dwc:eventDate** into year, month, and day simplifies data entry and sorting for analysis.
Requirement: Core.
How to use: This is a numeric field. Enter the four-digit year the sampling event occurred.
Examples: 1965, 2013
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:year

Term name: **month**
Definition: The integer month in which the sampling event occurred.
Rationale: Separating the full **dwc:eventDate** into year, month, and day simplifies data entry and sorting for analysis. Bee communities vary widely by month.
Requirement: Core.
How to use: This is a numeric field. Enter the one or two-digit month when the sampling event occurred.
Examples: 1, 10
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:month

Term name: **day**
Definition: The integer day of the month on which the sampling event occurred.
Rationale: Separating the full **dwc:eventDate** into year, month, and day simplifies data entry and sorting for analysis.
Requirement: Core, unless sampling occurred over multiple days.
How to use: This is a numeric field. Enter the one or two-digit day of the month when the sampling event occurred. If sampling occurred over multiple days, *i.e.*, passive traps were used, do not use this term, as it only records one day. The terms **dwc:year** and **dwc:month** should still be used if sampling occurred over multiple days.
Examples: 8, 23
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:day

Term name: **samplingProtocol**
Definition: The names of, references to, or descriptions of the methods or protocols used during a sampling event.
Rationale: Describing the sampling method(s) used is a requirement for some types of species distribution models. It also improves replicability of study methods and provides insights into life-history useful for recollection.
Requirement: Core.
How to use: This term uses two controlled vocabularies; one for active sampling methods and one for passive sampling methods. Additionally, some of the active sampling entries are provided using key:value pairs. Select the sampling method

used from the list of allowable entries.

- Controlled vocabulary lists for **dwc:samplingProtocol**:
  - Active sampling: hand net:lethal, hand net:released, sweep net:lethal, sweep net:released, vial:lethal, vial:released, photograph, visual observation
  - Passive sampling: bowl traps, glycol cups, malaise traps, vane traps

In addition to providing the sampling method(s) following the controlled vocabulary list, cite the source of your protocol following a vertical bar space character (|)

Cariveau, D.P., K.-L.J. Hung, N.M. Williams, D.W. Inouye, C.T. Burns, I.G. Lane, R.E. Irwin, H.K. Levenson, B. Du Clos, & S.H. Woodard. 2025. Standardized protocols for collecting data on bee-flower interactions and the associated floral community. Journal of Melittology 123(5): 104–138. https://doi.org/10.17161/jom.vi123.23861

Levenson, H.K., O. Messinger Carril, N.E. Turley, C. Maffei, G. LeBuhn, T. Griswold, N.M. Williams, K.-L.J. Hung, R.E. Irwin, B. Du Clos, & S.H. Woodard. 2025. Standardized protocol for collecting community-level bee data. *Journal of Melittology* 123(4): 78–103. https://doi.org/10.17161/jom.vi123.22649

López-Uribe, M.M., J.P. Strange, L. Whiteman, B.N. Danforth, S. Jha, M.G. Branstetter, J.B.U. Koch, H.K. Levenson, B. Du Clos, & S.H. Woodard. 2025. Standardized protocol for collecting bee samples to generate molecular data. *Journal of Melittology* 123(7): 163–181. https://doi.org/10.17161/jom.vi123.22596

Otto, C.R.V., L.L. Bailey, B. Du Clos, T. Smith, E. Evans, I. Pearse, S. Killingsworth, S. Jepsen, & S.H. Woodard. 2025. Estimating occupancy of focal bee species. *Journal of Melittology* 123(6): 139–162. https://doi.org/10.17161/jom.vi123.22555

Strange, J.P., M.M. López-Uribe, L. Whiteman, B.N. Danforth, S. Jha, H.K. Levenson, B. Du Clos, J.B.U. Koch, & S.H. Woodard. 2025. Standardized protocol for collecting bee samples for internal parasite and pathogen data. *Journal of Melittology* 123(8): 182–194. https://doi.org/10.17161/jom.vi123.22598

LeBuhn, G., T. Griswold, R. Minckley, S. Droege, T. Roulston, J. Cane, F. Parker, S. Buchmann, V. Tepedino, N. Williams, C. Kremen, & O. Messinger. 2003. A standardized method for monitoring bee populations—the bee inventory (BI) plot. Available from https://www.nativebeemonitoring.org/s/Bee-Plot-2003.pdf

A Collective and Ongoing Collaborative Effort by Those Who Love to Study Bees in North America. (2024). The Very Handy Bee Manual (2.0). Zenodo. https://doi.org/10.5281/zenodo.12812754

Maffei, C., Lent, S., Lane, I., Jones, P., & K. Dillon. 2025. National Protocol Framework for the Inventory and Monitoring of Bees. Version 3.0. Inventory and Monitoring, National Wildlife Refuge System, U.S. Fish and Wildlife Service, Fort Collins, Colorado. https://iris.fws.gov/APPS/ServCat/Reference/Profile/179113

Packer, L., & G. Darla-West. 2021. Bees: How and Why to Sample Them. In: Santos, J.C., Fernandes, G.W. (eds) Measuring Arthropod Biodiversity. Springer, Cham. https://doi.org/10.1007/978-3-030-53226-0_3

Other protocols used can be cited.

Papers published that describe the protocol used to collect the specimen can be cited.

EXAMPLES:

bowl trap | *The Very Handy Bee Manual* (A Collective 2024) https://doi.org/10.5281/zenodo.12812754

hand net:lethal | Maffei et al., (2025) https://iris.fws.gov/APPS/ServCat/Reference/

Profile/179113
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:samplingProtocol

Term name: **sampleSizeValue**
Definition: A numeric value for a measurement of the size (time duration, length, area, or volume) of a sample in a sampling event.
Rationale: Allows for full reporting of sampling effort, supporting analyses of species distribution. This term is used to describe the number of traps used when passive sampling or the number of personnel conducting active sampling in a sampling event.
Requirement: Core.
How to use: Use of this term varies with active or passive sampling methods, but it must always be used with **dwc:sampleSizeUnit**. Provide a number of sampling units specific to passive samples (number of traps collected) or active samples (number of collectors or observers).
Examples: 1, 25
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:sampleSizeValue

Term name: **sampleSizeUnit**
Definition: A unit of measurement of the size of a sample in a sampling event.
Rationale: Allows for full reporting of sampling effort, supporting analyses of species distribution. This term is used to describe the type of equipment used in passive sampling or the role of personnel conducting active sampling during a sampling event.
Requirement: Core.
How to use: This term uses a controlled vocabulary. Use of this term varies with active or passive sampling methods, but it must always be used with **dwc:sampleSizeValue**. Provide a sampling unit specific to passive samples ([type of] traps collected) or active samples (collectors or observers).
- Controlled vocabulary list for **dwc:sampleSizeUnit**:
  - bowl, cup, Malaise, or vane traps collected
  - collectors
  - observers

Examples: Bowl traps collected, cup traps collected, observers
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:sampleSizeUnit

Term name: **samplingEffort**
Definition: The amount of effort expended during a sampling event.
Rationale: Describing the sampling effort expended to obtain a species observation is a requirement for some types of species distribution models.
Requirement: Core.
How to use: This term is used to report both sampling area (in metric units) and duration of sampling time. Report duration of passive sampling time in hours or decimals of hours. Report duration of active sampling time in person-hours (*i.e.*, the amount of work done by one person in one hour) or decimals

of person-hours. If reporting both sampling area and duration of sampling time, separate them with space vertical bar space (|); this separator is used throughout the Darwin Core standard to concatenate multiple entries in a cell. Use **dwc:eventDate** to report the start and end times of sampling.

EXAMPLES:

- 100 m transect, 1 ha, 100m2
  - For reporting amount of area sampled.
- 6 hours, 24 hours
  - When recording duration of passive sampling.
- 0.6 person-hours
  - Total time spent active sampling in person-hours; in this case, 2 people each spent 20 minutes surveying live bees.
- 0.25 person-hours
  - Total time spent active sampling in person-hours; in this case, 1 person spent 15 minutes netting.
- 0.5 ha plot | 0.5 hours
  - Recording both area sampled and duration of passive sampling time.

RELEVANT PROTOCOLS: All.

FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:samplingEffort

Location

TERM NAME: **country**

DEFINITION: The name of the country or major administrative unit in which the sampling location occurs.

RATIONALE: Providing finer grain location information provides essential context for interpretation and supports data filtering for analysis.

REQUIREMENT: Core.

HOW TO USE: This term uses a controlled vocabulary. See the Getty Thesaurus of Geographic Names (https://www.getty.edu/research/tools/vocabularies/tgn/) for a full controlled vocabulary list.

EXAMPLES: United States, Canada, Mexico

RELEVANT PROTOCOLS: All.

FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:country

TERM NAME: **stateProvince**

DEFINITION: The name of the next smaller administrative region than the country (state, province, etc.) in which the sampling occurs.

RATIONALE: Providing finer-grain location information provides essential context for interpretation and supports data filtering for analysis.

REQUIREMENT: Core.

HOW TO USE: This term uses a controlled vocabulary. See the Getty Thesaurus of Geographic Names (https://www.getty.edu/research/tools/vocabularies/tgn/) for a full controlled vocabulary list.

EXAMPLES: Kansas, Michigan

RELEVANT PROTOCOLS: All.

FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:stateProvince

Term name: **decimalLatitude**
Definition: The geographic latitude (in decimal degrees, using the spatial reference system given in **dwc:geodeticDatum**) of the geographic center of a sampling location.
Rationale: A precise location of a wild bee observation provides essential context for interpretation. Providing a precise location supports species status assessments, distribution models, and other analyses relying on occurrence location.
Requirement: Core.
How to use: Positive values are north of the Equator, negative values are south of it. Legal values lie between–90 and 90, inclusive. If coordinates are obtained from a phone or non-professional grade GPS then the accuracy is likely, at best, around 5 m, which would be best reflected in reporting 5 decimal places. If coordinates are derived from geographic computer software (*i.e.*, Google Maps or GIS programs), they may have as many as six decimal places.
Examples:–41.09837
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:decimalLatitude

Term name: **decimalLongitude**
Definiion: The geographic longitude (in decimal degrees, using the spatial reference system given in **dwc:geodeticDatum**) of the geographic center of a sampling location.
Rationale: A precise location of a wild bee observation provides essential context for interpretation. Providing a precise location supports species status assessments, distribution models, and other analyses relying on occurrence location.
Requirement: Core.
How to use: Positive values are east of the Greenwich Meridian, negative values are west of it. Legal values lie between–180 and 180, inclusive. If coordinates are obtained from a phone or non-professional grade GPS then the accuracy is likely, at best, around 5 m, which would be best reflected in reporting 5 decimal places. If coordinates are derived from geographic computer software (*i.e.*, Google Maps or GIS programs), they may have as many as six decimal places.
Examples:–121.17616
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:decimalLongitude

Term name: **coordinateUncertaintyInMeters**
Definition: The horizontal distance (in meters) from the given **dwc:decimalLatitude** and **dwc:decimalLongitude** describing the smallest circle containing the sampling location.
Rationale: A precise location of a wild bee observation supports species status assessments, distribution models, and other analyses relying on occurrence location. Sometimes the location of an observation must be masked for species or other security; the extent of masking can be provided here.
Requirement: Core.
How to use: Report this value if coordinates are obtained from a GPS device, including a phone or non-professional grade GPS. The coordinate uncertainty for these devices is likely around 5 meters. Leave the value empty if the uncertainty is unknown, cannot be estimated, or is not applicable (because there are no coordinates). Zero is not a valid value for this term. This value, in most cases for

current and future occurrences, should not be greater than 10. Exceptions include if the occurrence location is masked for security reasons or if the most accurate coordinates available are less precise, as is the case for much historically-collected occurrence data.

EXAMPLES:

- 5
  - When precise GPS-derived coordinates with five decimal places are provided (see **dwc:decimalLatitude** and **dwc:decimalLongitude**).
- 0.1
  - When coordinates are derived from geographic computer software (i.e., Google Maps or GIS programs) with six decimal places.
- 100, 1000
  - When occurrence location is masked by 100 meters, if providing GPS-derived coordinates with three decimal places, or 1 km, if providing GPS-derived coordinates with two decimal places. Report any location masking, if applicable, in **dwc:informationWithheld**.

RELEVANT PROTOCOLS: All.

FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:coordinateUncertaintyInMeters https://www.gbif.org/data-quality-requirements-occurrences#dcUncertainty

Identification

TERM NAME: **identifiedBy**

DEFINITION: A list of names of people, groups, or organizations who identified the specimen associated with an occurrence.

RATIONALE: Providing the names of the identifying personnel creates a potential point of contact for more taxonomic information regarding an occurrence.

REQUIREMENT: Core.

HOW TO USE: Use full names (First [Middle Initial, if provided] Last) whenever possible. Separate the values in a list with space vertical bar space (|); this separator is used throughout the Darwin Core standard to concatenate multiple entries in a cell. This term can be used in conjunction with **dwc:identifiedByID** to connect the occurrence to the identifying personnel through platforms such as Bionomia.

EXAMPLES:

- For one identifier:
  - Erika M. Tucker
- For more than one identifier:
  - Theodore Pappenfuss | Robert Macey

RELEVANT PROTOCOLS: All.

FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:identifiedBy

Taxon

TERM NAME: **scientificName**

DEFINITION: The full scientific name, with authorship and date information if known.

RATIONALE: This term is required for publication to GBIF. Further, accurate

identification to the lowest taxonomic rank possible creates the most useful data from a set of occurrences.
Requirement: Core.
How to use: This should be the name in lowest level taxonomic rank that can be determined. This term should not contain identification qualifications, which should instead be supplied in the **dwc:identificationQualifier** term. Authorship of the scientific name, including the date, can also be provided separately in **dwc:scientificNameAuthorship**.
Examples: Hymenoptera, Halictidae, *Sphecodes* sp., *Osmia atriventris* (Cresson, 1864).
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:scientificName
https://www.gbif.org/data-quality-requirements-occurrences#dcSciName

Term name: **genus**
Definition: The full scientific name of the genus in which the occurrence is classified.
Rationale: Separating the full **dwc:scientificName** into genus and specific epithet simplifies data entry and sorting for analysis.
Requirement: Core.
How to use: Provide the genus of the bee with the first letter capitalized.
Examples: *Andrena*, *Coelioxys*
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:genus

Term name: **specificEpithet**
Definition: The name of the first or species epithet of the **dwc:scientificName**.
Rationale: Separating the full **dwc:scientificName** into genus and specific epithet simplifies data entry and sorting for analysis.
Requirement: Core.
How to use: Provide the specific epithet of the bee with the first letter lowercase. If not available, specify sp.
Examples: *mirabilis*, *carlini*, sp.
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:specificEpithet

Recommended Terms

Record-level

Term name: **license**
Definition: A document indicating the preferred terms of data use by the data provider.
Rationale: Assigning a license to a dataset informs users what can be done with that dataset and the appropriate crediting procedure. Some data providers do not want their data used for commercial purposes and may specify that with their license choice.
Requirement: Recommended.
How to use: Choose a Creative Commons license that aligns with the desired potential use cases of the dataset and crediting criteria of the provider. Provide a

link to the full license terms. Licenses to use include: public domain, CC-BY, CC-BY-SA, CC-BY-NC, or CC-BY-NC-SA. You may provide the name of the license holder with the optional term **dwc:rightsHolder**.
EXAMPLES: https://creativecommons.org/publicdomain/zero/1.0/, https://creativecommons.org/licenses/by/4.0/, https://creativecommons.org/licenses/by-sa/4.0/
RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dcterms:license

TERM NAME: **institutionID**
DEFINITION: An identifier for the institution having custody of the object(s) or information referred to in the record.
RATIONALE: Provides a location where occurrence information came from; may be used to find a point of contact for more information about an occurrence.
REQUIREMENT: Recommended.
HOW TO USE: If available, use identifiers from the Global Registry of Scientific Collections (https://scientific-collections.gbif.org/).
EXAMPLES: http://grscicoll.org/institution/american-museum-natural-history
RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:institutionID

TERM NAME: **collectionID**
DEFINITION: An identifier for the collection or dataset from which the record was derived.
RATIONALE: Provides more precise information regarding the location where occurrence information came from; may be used to find a point of contact for more information about an occurrence.
REQUIREMENT: Recommended.
HOW TO USE: If available, use identifiers from the Global Registry of Scientific Collections (https://scientific-collections.gbif.org/).
EXAMPLES: http://grbio.org/cool/je3k-bvrg, http://grscicoll.org/institutional-collection/entomology
RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:collectionID

TERM NAME: **collectionCode**
DEFINITION: The name, acronym, code, or initialism identifying the collection or dataset from which the record was derived.
RATIONALE: Provides more precise information regarding the location where occurrence information came from; may be used to find a point of contact for more information about an occurrence.
REQUIREMENT: Recommended.
HOW TO USE: Provide a name or acronym for the collection within the institution or dataset within a lab that houses the specimen or coordinated the observation. If the collection is registered in the Global Registry of Scientific Collections (https://scientific-collections.gbif.org/), please use the code listed there.
EXAMPLES: BBSL, CUIC
RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:collectionCode

Occurrence

Term name: **recordedByID**
Definition: A list of the globally unique identifier(s) for the person, people, groups, or organizations responsible for recording the original occurrence.
Rationale: A unique identifier for a data collector, such as an ORCID iD, can be used to aggregate contributions to natural history collections on platforms such as Bionomia.
Requirement: Recommended.
How to use: Recommended best practice is to provide a single identifier that disambiguates the details of the identifying agent. If a list is used, separate the values in the list with space vertical bar space (|); this separator is used throughout the Darwin Core standard to concatenate multiple entries in a cell.
Examples:

- For one collector:
  - https://orcid.org/0000-0002-1825-0097
- For more than one collector:
  - https://orcid.org/0000-0002-1825-0097
  - https://orcid.org/0000-0002-1825-0098

Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:recordedByID

Term name: **sex**
Definition: The sex of the biological individual(s) represented in the occurrence.
Rationale: Providing demographic information can improve and inform general knowledge on bee life history habits and species distribution models, particularly for at-risk species.
Requirement: Recommended.
How to use: This term uses a controlled vocabulary. Provide the appropriate category following the controlled vocabulary list.

- Controlled vocabulary list for **dwc:sex**:
  - female
  - male
  - gynandromorph

Examples: Female, male, gynandromorph
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:sex

Term name: **associatedTaxa**
Definition: A list of identifiers or names of taxa and the associations of this occurrence to each of them.
Rationale: Providing the plant a bee was observed on can inform plant-pollinator networks, species conservation plans, and habitat management.
Requirement: Recommended for any active sampling conducted on bees visiting blooming flowers.
How to use: This term uses a controlled vocabulary. Using a key:value pair,

provide the appropriate relationship from the controlled vocabulary list, using a combination of an action and a part of the plant where the bee was found. Provide at least the genus name of the plant, though the full plant scientific name (Genus species) is preferred. We advise reporting the source for the taxonomic name with the authority key:value pair. If using both the plant species and the authority key:value pairs, separate them with a comma. Enclose the entire term with curly brackets ({}, see Examples) :

- Controlled vocabulary list for **dwc:associatedTaxa**:
    - Action vocabulary: "caught on", "observed on", "visits"
    - Plant part vocabulary: "flowers of", "leaves of", "stem of"

EXAMPLES:

- {"visits flowers of":"*Rubus*"}
    - For reporting plant interaction only and identifying plant to genus level.
- {"observed on flowers of":"*Solidago canadensis*", "authority":"example authority"}
    - For reporting plant interaction, full scientific name of the plant, and the source of the taxonomic identification of the plant.
    - The authority should be a full citation of the source used to identify the plant. Examples include:
        - Flora Novae Angliae. 2011. Yale University Press https://plants.usda.gov/home/plantProfile?symbol=SOCA6
        - The Jepson Manual: Vascular Plants of California. Second Edition, 2012. University of California Press
        - For further details on reporting taxonomic authority for species identifications, see **dwc:namePublishedIn**.

RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:associatedTaxa

MaterialEntity

TERM NAME: **disposition**
DEFINITION: The current state of a specimen with respect to the collection identified in **dwc:collectionCode** or **dwc:collectionID**.
RATIONALE: This term can indicate the availability of a specimen for further study.
REQUIREMENT: Recommended.
HOW TO USE: This term uses a controlled vocabulary. Specify the appropriate **dwc:disposition** from the controlled vocabulary list. If using different terms, please define them in **dwc:materialEntityRemarks**.

- Controlled vocabulary list for **dwc:disposition**:
    - inCollection: specimen is preserved in a collection.
    - missing: specimen is missing from the collection.
    - onLoan: specimen is on loan to another institution, organization, or individual.
    - destroyed: specimen has been destroyed.

EXAMPLES:

- inCollection
- destroyed
- Awaiting processing (with details provided in **dwc:materialEntityRemarks**)

- Missing head (with details provided in **dwc:materialEntityRemarks**)

Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:disposition

Event

Term name: **eventID**
Definition: An identifier for the set of information associated with a sampling event. May be a global unique identifier or an identifier specific to the dataset.
Rationale: When digitizing data and connecting sampling events to occurrence records, a **dwc:eventID** can be linked to a separate event table, eliminating redundancy throughout an occurrence table.
Requirement: Recommended.
How to use: Create a unique identifier for a sampling event by combining site, date, and location information associated with that event. See the section "Generating unique identifiers."
Examples:

- 0320190603
    - If you sampled site 3 on June 3, 2019, with 03 coming from site 3 and the remainder of the ID coming from the date formatted for **dwc:eventDate**.

Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:eventID

Term name: **eventRemarks**
Definition: Comments or notes about the sampling event.
Rationale: Provides additional context regarding the sampling event. This can include, but is not limited to, notes on present or historical field conditions, collector experience, or additional information on passive trap deployment.
Requirement: Recommended.
How to use: Provide any additional information about the sampling event. Separate entries with space vertical bar space (|); this separator is used throughout the Darwin Core standard to concatenate multiple entries in a cell. Field condition information can include habitat change such as mowing, fire, harvesting, etc., or pesticide application history. To report collector experience, self-identify as: Novice, Advanced Beginner, Competence, Proficient, or Expert. Additional information on passive trap deployment can include the trap colors used, trap size, height at which traps were deployed, or trap liquid type. Additional information on transects used for active sampling can indicate whether the transect was linear or meandering.
Examples:

- Site planted with seeds on 2022-04-29 | collectorExperience: Advanced Beginner | meandering transect
    - Describes an active sampling event at a site where seeds were planted on April 29, 2022. The collector, who has some experience, walked a meandering transect as they sampled.
- Blue, yellow, and white traps used | 3.25 oz cups | Dawn dish soap | site recently mowed
    - Describes a passive sampling event where all three commonly used trap colors were deployed using soapy water in Solo souffle cups at a site that was recently mowed.

RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:eventRemarks

Location

TERM NAME: **locationID**
DEFINITION: An identifier for the set information about a sampling location. May be a global unique identifier or an identifier specific to the dataset.
RATIONALE: When digitizing data and connecting sampling locations to occurrence records, a **dwc:locationID** can be linked to a separate location table, eliminating redundancy throughout an occurrence table.
REQUIREMENT: Recommended.
HOW TO USE: Create a unique identifier for a sampling location with information associated with that location, including a site number, coordinates, or place name. See the section "Generating unique identifiers."
EXAMPLES:
- Site09, site15, site3A
    - Site numbers can also be provided in **dwc:fieldNumber**.

RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:locationID

TERM NAME: **geodeticDatum**
DEFINITION: The ellipsoid, geodetic datum, or spatial reference system upon which the geographic coordinates given in **dwc:decimalLatitude** and **dwc:decimalLongitude** are based.
RATIONALE: Providing a datum gives context to provided coordinates. GBIF assumes the datum is WGS84. If you don't know what coordinate system you are using it is most likely WGS84, which is the default for publicly available maps like Google Maps and is what is used for Global Positioning Systems (GPS). If coordinates were provided from a different datum, that should be specified. For instance, NAD27 was once a common datum, but coordinates in NAD27 can be up to 200 meters away from those in WGS84.
REQUIREMENT: Recommended.
HOW TO USE: The best practice is to use the EPSG code for the datum or spatial reference system. The EPSG code for WGS84 is EPSG:4326 (https://epsg.io/4326). If an EPSG code is not available, the name of the datum or spatial reference system may be provided.
EXAMPLES: EPSG:4326, EPSG:4269, WGS84, NAD27, NAD83
RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:geodeticDatum
https://www.gbif.org/data-quality-requirements-occurrences#dcGeodeticDatum

Identification

TERM NAME: **verbatimIdentification**
DEFINITION: A string representing the taxonomic identification as it appeared in the original record. This term is meant to be used in addition to **dwc:scientificName**, not instead of it.
RATIONALE: This term can be used to translate original label text on preserved

specimens, to store the original identification if the **dwc:scientificName** changes, or in any other case where the original identification is different from the current identification.
Requirement: Recommended.
How to use: Translate label text verbatim when digitizing.
Examples: *Osmia besseyae* Cockerell TYPE (https://library.big-bee.net/portal/collections/individual/index.php?occid=1667260)
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:verbatimIdentification

Term name: **identificationQualifier**
Definition: A brief phrase or a standard term ("cf.", "aff.") to express the determiner's doubts about the identification.
Rationale: This term can provide more context about a taxonomy of an occurrence.
Requirement: Recommended, if applicable. Must be used with **dwc:taxonRank**.
How to use: This term uses a controlled vocabulary. Provide the appropriate qualifier, if applicable.

- Controlled vocabulary list for **dwc:identificationQualifier** (definitions taken from Sigovini *et al.*, 2016):
  - Affinis (aff.): affinity with a known species; has affinity with
  - Confer (cf.): to compare or be compared with
  - Species incerta (?, sp. inc, or inc.): uncertain species
  - Species proxima (prox.): the nearest species
  - Species near (nr.): near but not identical to a species
  - Stetit (stet.): further identification has not been attempted

Examples:

- cf. *vincta*
  - (for *Nomada* cf. *vincta* with accompanying values *Nomada* in **dwc:genus**, vincta in **dwc:specificEpithet**, and cf. species in **dwc:taxonRank**).
- aff. *modestus*
  - (for *Hylaeus* aff. *modestus* with accompanying values *Hylaeus* in **dwc:genus**, *modestus* in **dwc:specificEpithet**, and aff. species in **dwc:taxonRank**).

Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:identificationQualifier

Term name: **identifiedByID**
Definition: A list of the globally unique identifier(s) for the person, people, groups, or organizations responsible for identifying the specimen associated with an occurrence.
Rationale: A unique identifier for bee identifying personnel, such as an ORCID iD, can be used to aggregate contributions to natural history collections on platforms such as Bionomia.
Requirement: Recommended.
How to use: Recommended best practice is to provide a single identifier that disambiguates the details of the identifying agent. If a list is used, separate the values in a list with space vertical bar space (|); this separator is used throughout the Darwin Core standard to concatenate multiple entries in a cell.

EXAMPLES:
- For one collector:
  - https://orcid.org/0000-0002-1825-0097
- For more than one collector:
  - https://orcid.org/0000-0002-1825-0097 | https://orcid.org/0000-0002-1825-0098

RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:identifiedByID

TERM NAME: **dateIdentified**
DEFINITION: The date a specimen associated with an occurrence was identified.
RATIONALE: Provides context for the taxonomic identification.
REQUIREMENT: Recommended.
HOW TO USE: Provide the date the taxonomic identification was determined, using a date that conforms to ISO 8601-1:2019.
EXAMPLES: 2020-08-09, 1987-04, 1963
RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:dateIdentified

TERM NAME: **identificationReferences**
DEFINITION: A list of references used to identify a specimen.
RATIONALE: Provides context and improves reproducibility for the taxonomic identification.
REQUIREMENT: Recommended.
HOW TO USE: Provide citations for references used to identify specimens, separating the values in a list with space vertical bar space (|); this separator is used throughout the Darwin Core standard to concatenate multiple entries in a cell.
EXAMPLE: Portman, Z.M., M. Arduser, I.G. Lane, & D.P. Cariveau. 2022. A review of the *Augochloropsis* (Hymenoptera, Halictidae) and keys to the shiny green Halictinae of the midwestern United States. *ZooKeys* 1130: 103–152. https://doi.org/10.3897/zookeys.1130.86413 | https://www.discoverlife.org/mp/20q?guide=Bee_genera
RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:identificationReferences

Taxon

TERM NAME: **taxonID**
DEFINITION: An identifier for the information describing the taxonomy of an occurrence. May be a global unique identifier or an identifier specific to the dataset.
RATIONALE: When digitizing data and connecting species identifications to occurrence records in a relational database or an Excel workbook, a **dwc:taxonID** can be linked to a separate taxon table, streamlining an occurrence table.
REQUIREMENT: Recommended.
HOW TO USE: See the section "Generating unique identifiers." There are multiple sources for **dwc:taxonID**s for bees; these include species pages on GBIF or DiscoverLife and ITIS taxonomic serial numbers. Any or all of these identifiers

can be provided in **dwc:taxonID**; separate multiple identifiers in a list with space vertical bar space (|); this separator is used throughout the Darwin Core standard to concatenate multiple entries in a cell.
Example: https://www.gbif.org/species/5042859 | Taxonomic Serial No.: 757559 | https://www.discoverlife.org/20/q?search=Agapostemon+texanus
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:taxonID

Term name: **nameAccordingTo**
Definition: The reference to the source in which the specific taxon concept circumscription is defined or implied, traditionally signified by the Latin "sensu" or "sec." (from secundum, meaning "according to").
Rationale: Providing taxonomic reference information allows occurrence identifications to be verified or examined in further study.
Requirement: Recommended.
How to use: For taxa that result from identifications, a reference to the keys, monographs, experts and other sources should be given.
Example: Ascher, J.S., & J. Pickering. 2024. Discover Life bee species guide and world checklist (Hymenoptera: Apoidea: Anthophila). http://www.discoverlife.org/mp/20q?guide=Apoidea_species
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:nameAccordingTo

Term name: **family**
Definition: The full scientific name of the family in which the occurrence is classified.
Rationale: Provides important taxonomic context and supports data filtering for analysis.
Requirement: Recommended.
How to use: Provide the family name.
Examples: Halictidae, Colletidae
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:family

Term name: **infraspecificEpithet**
Definition: The name of the lowest or terminal infraspecific epithet of the **dwc:scientificName**, excluding any rank designation.
Rationale: Provides important taxonomic context. Accurate identification to the lowest taxonomic rank possible creates the most useful data from a set of occurrences.
Requirement: Recommended.
How to use: Provide the subspecies name.
Examples:

- *virginica*
  - for *Xylocopoides virginica virginica*
- *propinqua*
  - for *Osmia lignaria propinqua*

RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:infraspecificEpithet

TERM NAME: **scientificNameAuthorship**
DEFINITION: The authorship information for the **dwc:scientificName**
RATIONALE: Provides important taxonomic context.
REQUIREMENT: Recommended.
HOW TO USE: Provide the authorship and date of the scientific name.
EXAMPLE: Cockerell, 1906
RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:scientificNameAuthorship

Optional Terms

Record-level

TERM NAME: **rightsHolder**
DEFINITION: A person or organization owning or managing rights over the resource.
RATIONALE: Provides contact information regarding use of shared data and license choice.
REQUIREMENT: Optional.
HOW TO USE: Provide the name(s) of the person, organization, or institution responsible for the rights of a shared dataset. Separate multiple values with space vertical bar space (|); this separator is used throughout the Darwin Core standard to concatenate multiple entries in a cell.
EXAMPLE: The Regents of the University of California
RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dcterms:rightsHolder

TERM NAME: **dynamicProperties**
DEFINITION: A list of additional measurements, facts, characteristics, or assertions about the record. This term is meant to provide a mechanism for structured content.
RATIONALE: Reporting site conditions during sampling events can inform occupancy models. Darwin Core does not currently have terms for these conditions; therefore, *The Wild Bee Data Standard* uses **dwc:dynamicProperties** to report them.
REQUIREMENT: Optional.
HOW TO USE: This term uses a controlled vocabulary. Report any or all of the following site conditions using key:value pairs. Note that numeric values do not need quotation marks. If providing multiple key:value pairs, separate them with commas. Enclose the entire term in curly brackets ({}, see Example).

- Controlled vocabulary list for **dwc:dynamicProperties**:
  - airTemperature: report degrees Celsius
  - relHumidity: report relative humidity percent value
  - windSpeed: report wind speed and unit measure
  - cloudCover: report one of the following: clear, partly cloudy, mostly

cloudy, light overcast, dark overcast
    - precip: report one of the following: none, light rain
        - Note light rain is only allowed for long term passive traps, such as cup or vane traps. Nearly all wild bee sampling should be conducted with no precipitation.
    - AQI: air quality index as reported for the sampling area

Example: {"relHumidity":28, "airTemperature":22, "windSpeed":"3 kph", "cloudCover":"light overcast", "precip":"none", "AQI":34}
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:dynamicProperties

Occurrence

Term name: **lifeStage**
Definition: The age class or life stage of the organism(s) at the time the occurrence was recorded.
Rationale: Providing demographic information can improve and inform general knowledge on bee life history habits and species distribution models, particularly for at-risk species.
Requirement: Optional, but required if the specimen is not an adult.
How to use: This term uses a controlled vocabulary. Provide the appropriate category following the controlled vocabulary list.

- Controlled vocabulary list for **dwc:lifeStage**:
    - egg
    - larva
    - pupa
    - adult

Examples: Larva, adult
Relevant protocols: All, particularly the occupancy of focal species protocol (Otto *et al.*, 2025).
For more detail: https://dwc.tdwg.org/terms/#dwc:lifeStage

Term name: **caste**
Definition: Categorization of individuals for eusocial species.
Rationale: Providing demographic information can improve and inform general knowledge on bee life history habits and species distribution models, particularly for at-risk species.
Requirement: Optional.
How to use: This term uses a controlled vocabulary. Provide the appropriate category following the controlled vocabulary list.

- Controlled vocabulary list for **dwc:caste**:
    - queen
    - worker
    - drone

Examples: Queen, worker
Relevant protocols: All, particularly the occupancy of focal species protocol (Otto *et al.*, 2025).

FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:caste

TERM NAME: **behavior**
DEFINITION: The behavior shown by the subject at the time the occurrence was recorded.
RATIONALE: Providing demographic information can improve and inform general knowledge on bee life history habits and species distribution models, particularly for at-risk species.
REQUIREMENT: Optional.
HOW TO USE: This term uses a controlled vocabulary. Provide the appropriate category following the controlled vocabulary list.
- Controlled vocabulary list for **dwc:behavior**:
  - foraging
  - collecting pollen
  - collecting nectar
  - nesting

EXAMPLES: Collecting pollen, nesting
RELEVANT PROTOCOLS: All, particularly the occupancy of focal species protocol (Otto *et al.*, 2025).
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:behavior

TERM NAME: **vitality**
DEFINITION: An indication of whether an organism was alive or dead at the time of collection or observation.
RATIONALE: Providing demographic information can improve and inform general knowledge on bee life history habits and species distribution models, particularly for at-risk species.
REQUIREMENT: Optional.
HOW TO USE: This term uses a controlled vocabulary. Provide the appropriate category following the controlled vocabulary list.
- Controlled vocabulary list for **dwc:vitality**:
  - alive
  - dead
  - moribund

EXAMPLES: Alive, dead
RELEVANT PROTOCOLS: All, particularly the occupancy of focal species protocol (Otto *et al.*, 2025).
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:vitality

TERM NAME: **associatedMedia**
DEFINITION: A list of identifiers of media associated with the occurrence.
RATIONALE: Provides links to accompanying photos related to the occurrence, including but not limited to site photos, plant photos, trap photos, specimen photos. May instead provide a host institution housing non-public image data or other media.
REQUIREMENT: Optional.
HOW TO USE: Media shared publicly via **dwc:associatedMedia** must have an associated identifier, whether that is a website, a publication, or a UUID. Please

provide any relevant identifiers, separated by a vertical bar if necessary. For non-publicly held media, please provide the name of the institution that manages the media data.

Examples: https://www.flickr.com/photos/usgsbiml/52264266775/, University of Minnesota

Relevant protocols: All.

For more detail: https://dwc.tdwg.org/terms/#dwc:associatedMedia

Term name: **associatedOccurrences**

Definition: A list of identifiers of other occurrence records and their associations to this occurrence

Rationale: Links to other bee or plant occurrences that were observed, detected, or collected around a bee occurrence. This differs from **dwc:associatedTaxa** in that a plant listed here can be another plant in the vicinity of the plant the occurrence was directly interacting with. However, this term can also be used to link to the occurrence of the plant described in **dwc:associatedTaxa**. Use of this term may provide more context for focal species analyses.

Requirement: Optional.

How to use: Use a key:value pair, with the key describing the relationship with the associated occurrence and the value being the unique ID for that occurrence. The unique ID will ideally be a URL link to the occurrence provided on a data portal. We do not provide a controlled vocabulary for the possible relationships; be concise but descriptive when generating these keys. The unique ID can describe for another bee or plant occurrence that a bee occurrence was observed, detected, or collected on. It could also describe the occurrence itself with the use of the "same as" or "same occurrence as" key. If providing multiple key:value pairs, separate them with a comma. Enclose the entire term in curly brackets ({}, see Examples).

Examples:

- {"parasitized by":https://www.gbif.org/occurrence/2851169659}
    - Describes an associated occurrence of a parasitic bee.
- {"observed near": https://www.inaturalist.org/observations/216532139}
    - Describes an associated occurrence of the plant a bee was observed on.
- {"same as": https://www.inaturalist.org/observations/220375291} or {"same occurrence as":https://www.inaturalist.org/observations/220375291}
    - Describes the bee occurrence as posted on iNaturalist. This example can also be used for plant occurrences described in **dwc:associatedTaxa**.

Relevant protocols: All.

For more detail: https://dwc.tdwg.org/terms/#dwc:associatedOccurrences

Term name: **occurrenceRemarks**

Definition: Comments or notes about the occurrence.

Rationale: This term provides additional context for the corresponding occurrence. Here, the term is used to describe how a bee was captured.

Requirement: Optional.

How to use: Provide a brief description of how and where the bee was captured or observed.

Examples: netted in air, netted on the ground

RELEVANT PROTOCOLS: All, particularly the communities protocol (Levenson *et al*., 2025a).
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:occurrenceRemarks

MaterialEntity

TERM NAME: **preparations**
DEFINITION: A list of preparations and preservation methods for material associated with an occurrence.
RATIONALE: Describes procedures taken to preserve material from a physical specimen for molecular or tissue analyses. Can also be used to reference whole specimen preparation.
REQUIREMENT: Core for molecular (López-Uribe *et al*., 2025) and parasite and pathogen (Strange *et al*., 2025) protocols, optional otherwise.
HOW TO USE: Indicate what, if any, material was extracted from the specimen and what that material will be used for. For whole specimens, indicate their final preservation method.
EXAMPLES: DNA extract,–80 freezer, pinned, in alcohol
RELEVANT PROTOCOLS: All, particularly the molecular (López-Uribe *et al*., 2025) and parasite and pathogen (Strange *et al*., 2025) protocols.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:preparations

TERM NAME: **associatedSequences**
DEFINITION: A list of identifiers of genetic sequence information associated with an occurrence.
RATIONALE: Links to genetic sequence data to verify taxonomic identification for a specimen.
REQUIREMENT: Optional.
HOW TO USE: Provide one or multiple means to locate genetic sequence information. Identifiers can include publications, globally unique identifiers, and URLs. Separate identifiers in a list with space vertical bar space (|); this separator is used throughout the Darwin Core standard to concatenate multiple entries in a cell.
EXAMPLES: https://www.boldsystems.org/index.php/Public_RecordView?processid=BEECC462-08, https://www.boldsystems.org/index.php/Public_RecordView?processid=BUSA207-05
RELEVANT PROTOCOLS: All, particularly the molecular protocol (López-Uribe *et al*., 2025).
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:associatedSequences

TERM NAME: **materialEntityRemarks**
DEFINITION: Comments or notes about the MaterialEntity.
RATIONALE: This term provides context for other terms used in the MaterialEntity category. In *The Wild Bee Data Standard*, these terms are **dwc:disposition**, **dwc:preparations**, and **dwc:associatedSequences**.
REQUIREMENT: Core for molecular (López-Uribe *et al*., 2025) and parasite and

pathogen (Strange *et al.*, 2025) protocols, optional otherwise.
How to use: Use this term to provide information related to **dwc:disposition** that is not included in the controlled vocabulary list. This term is also used in the Bee Monitoring RCN protocols to provide more context for any material taken for molecular or tissue analyses for which the final storage conditions are described in **dwc:preparations**.
Examples:

- in lab
    - Example related to **dwc:disposition** that indicates the specimen is in the laboratory awaiting full processing.
- sterilized with 10% bleach | stored on ice between collection and final storage | 0.8 hour between collection and final storage | stored in Sample Lab, Sample Location
    - Example specific to Bee Monitoring RCN protocols for molecular and tissue data analysis.
- Head is missing from specimen
    - Example related to **dwc:disposition** that provides a note about specimen condition.
- Leg removed for molecular analysis
    - Example related to **dwc:disposition** that provides a note about specimen condition.

Relevant protocols: All, particularly the molecular (López-Uribe *et al.*, 2025), and parasite and pathogen (Strange *et al.*, 2025) protocols.
For more detail: https://dwc.tdwg.org/terms/#dwc:materialEntityRemarks

Event

Term name: **fieldNumber**
Definition: An identifier for a sampling event in the field that links field-based or collected information to an occurrence. Examples include a site number or a vial number associated with a bee or group of bees collected at a site. Note that it is possible for multiple vials to be collected at a site during a sampling event. Using this term to indicate site number, vial number, or some other field-based identifier is allowable.
Rationale: Clarifies sampling protocol.
Requirement: Optional.
How to use: Provide any site-identifying information here.
Examples:

- Site numbers: Site 1, 5A-2015, Farm Site 6
- Vial numbers: 2, AM-Site4-08

Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:fieldNumber

Term name: **habitat**
Definition: A category or description of the habitat in which the sampling event occurred.
Rationale: Habitat type has ecological implications on bee community assemblage.
Requirement: Optional.

How to use: Provide any description of the habitat type where the specimen was observed or collected. For a common reference, provide a habitat type and number from either the NRCS Ecological Site Descriptions (ESD) or the EPA Level 3 Ecoregions, specifying which source was used using a key:value pair. If using a key:value pair, enclose the entire term in curly brackets ({}, see Examples).

- More on NRCS ESDs: https://www.nrcs.usda.gov/getting-assistance/technical-assistance/ecological-sciences/ecological-site-descriptions
- More on EPA Ecoregions: https://www.epa.gov/eco-research/level-iii-and-iv-ecoregions-continental-united-states

Examples: oak savanna, steppe, {"EPA Level 3 Ecoregion":"Ozark Highlands (39)"}, {"NRCS ESD":"Snake River Plains (011X)"}
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:habitat

Location

Term name: **county**
Definition: The full, unabbreviated name of the next smaller administrative region than stateProvince (county, department, etc.) in which the sampling location occurs.
Rationale: Providing finer grain location information supports data filtering for analysis.
Requirement: Optional.
How to use: This term uses a controlled vocabulary. See the Getty Thesaurus of Geographic Names (https://www.getty.edu/research/tools/vocabularies/tgn/) for a full controlled vocabulary list.
Examples: Ness, Menominee
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:county

Term name: **locality**
Definition: The specific description of the place.
Rationale: Providing finer grain location information supports data filtering for analysis.
Requirement: Optional.
How to use: This could be any useful collection location name such as: town, park, study site code name, street address, or an amalgamation of other location names in your dataset.
Examples: Grand Staircase-Escalante National Monument, 500 m from Hwy 1 at Old Orchard Rd
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:locality

Term name: **verbatimElevation**
Definition: The original description of the elevation (altitude, usually above sea level) of the sampling location.
Rationale: Elevation has ecological implications on bee community assemblage.

Requirement: Optional.
How to use: Provide an estimate of elevation above sea level in meters. The value can be gathered in the field with GPS or via spatial software tools.
Example: 150 m
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:verbatimElevation

Term name: **coordinatePrecision**
Definition: A decimal representation of the precision of the coordinates given in the **dwc:decimalLatitude** and **dwc:decimalLongitude**.
Rationale: Providing precision is another way of stating uncertainty in the coordinates in conjunction with the core term **dwc:coordinateUncertaintyInMeters**. It can also clarify rounding errors that may occur in computer software when the end of a coordinate value is zero.
Requirement: Optional.
How to use: Provide the appropriate number of decimals in the coordinates of the occurrence record.
Examples:

- 0.00001
    - precise to 5 m; best practice for *The Wild Bee Data Standard*. Associated with GPS-derived coordinates with five decimal places.
- 0.000001
    - precise to 0.11 m; associated with coordinates with six decimal places derived from geographic computer software (*i.e.*, Google Maps, GIS programs).
- 0.01
    - precise to 1 km. The value for **dwc:coordinateUncertaintyInMeters** will be 1000, and the number of decimal places in **dwc:decimalLatitude** and **dwc:decimalLongitude** will be 1. Be sure to indicate location masking in **dwc:informationWithheld**.

Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:coordinatePrecision

Term name: **georeferencedBy**
Definition: A list of names of people, groups, or organizations who determined the georeference (spatial representation) for the sampling location.
Rationale: Providing the names of the georeferencing personnel creates a potential point of contact for more information regarding an occurrence or its collecting event
Requirement: Optional.
How to use: Use full names (First [Middle Initial, if provided] Last) whenever possible. Separate the values in a list with space vertical bar space (|); this separator is used throughout the Darwin Core standard to concatenate multiple entries in a cell.
Example: Amelia Earhart | Harry Manning
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:georeferencedBy

Term name: **georeferenceRemarks**
Definition: Notes or comments about the spatial description determination.

RATIONALE: Some organizations require detailed information regarding the georeference process, including how many satellites triangulated the coordinates or the type of device used to determine the coordinates.
REQUIREMENT: Optional
HOW TO USE: Provide any relevant information to satisfy organization requirements, including the number of satellites or the device type used to record coordinates. To clarify to users outside your organization what information is being provided, describe the information using a key:value pair. Note that numerical values do not need quotation marks. If using multiple key:value pairs, separate them with a comma. Enclose the entire term in curly brackets ({}, see Example).
EXAMPLE: {"number of satellites":5, "device type used to record coordinates": "Garmin eTrex 22x"}
RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:georeferenceRemarks

Identification

TERM NAME: **typeStatus**
DEFINITION: A list of nomenclatural types (type status, typified scientific name, publication) applied to the subject.
RATIONALE: Provides important taxonomic context by allowing for identification verification.
REQUIREMENT: Optional if not a type specimen, but required if the occurrence record refers to a type specimen.
HOW TO USE: Provide any type status information, if applicable.
EXAMPLE: holotype of *Halictus confusus*
RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:typeStatus

TERM NAME: **identificationRemarks**
DEFINITION: Any comments or notes regarding the identification of a specimen.
RATIONALE: Provides context and improves reproducibility for taxonomic identification.
REQUIREMENT: Optional.
HOW TO USE: Provide any ancillary information that may be helpful to others attempting to verify, modify, or study the identification of a specimen.
EXAMPLE: Made determination based on malar space
RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:identificationRemarks

Taxon

TERM NAME: **namePublishedIn**
DEFINITION: A reference for the publication in which the **dwc:scientificName** was originally established.
RATIONALE: Provides important taxonomic context and improves reproducibility for

taxonomic identification by allowing for reference verification by data users.
Requirement: Optional.
How to use: Provide a full citation for a taxonomic reference.
Example: Sandhouse, G.A. 1937. The bees of the genera *Augochlora*, *Augochloropsis*, and *Augochlorella* (Hymenoptera; Apoidea) occurring in the United States. *Journal of the Washington Academy of Sciences* 27: 65–79.
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:namePublishedIn

Term name: **tribe**
Definition: The full scientific name of the tribe in which the occurrence is classified.
Rationale: Provides important taxonomic context. Accurate identification to the lowest taxonomic rank possible creates the most useful data from a set of occurrences.
Requirement: Optional.
How to use: Provide the tribe name.
Examples: Colletini, Perditini, Nomiini
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:tribe

Term name: **subgenus**
Definition: The full scientific name of the subgenus in which the occurrence is classified. Values should include the genus to avoid homonym confusion.
Rationale: Provides important taxonomic context. Accurate identification to the lowest taxonomic rank possible creates the most useful data from a set of occurrences.
Requirement: Optional.
How to use: Provide the subgenus name in parentheses after the genus name.
Examples: *Bombus* (*Cullumanobombus*), *Andrena* (*Melandrena*), *Lasioglossum* (*Dialictus*)
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:subgenus

Term name: **taxonRank**
Definition: The taxonomic rank of the most specific name in the **dwc:scientificName**.
Rationale: Provides important taxonomic context. Accurate identification to the lowest taxonomic rank possible creates the most useful data from a set of occurrences.
Requirement: Optional, but required if **dwc:identificationQualifier** is used.
How to use: Provide the finest resolution of the occurrence species identification.
Examples: genus, species, subspecies
Relevant protocols: All.
For more detail: https://dwc.tdwg.org/terms/#dwc:taxonRank

Term name: **vernacularName**
Definition: A common or vernacular name.
Rationale: Some data collectors, managers, or users may be more familiar with or prefer to use a common name for a species.
Requirement: Optional.
How to use: Provide a common name.

EXAMPLE: Two-spotted bumble bee
RELEVANT PROTOCOLS: All.
FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:vernacularName

APPENDIX 2
Glossary of Terms

ARCHIVE: A data archive can be one of two things: 1) A general data archive for downloading is a snapshot of occurrence data in time, reflecting a dataset at a certain point in history. This type of archive never changes and can be downloaded at any time from a data aggregator, portal, or repository. 2) A Darwin Core archive downloaded from a data aggregator, portal, or repository is a dataset formatted to follow the Darwin Core data standard. A DwC archive can change over time as new records are added by the data provider.

AGGREGATOR: An online source that combines multiple datasets from multiple sources in one place for exploration and download. Examples include GBIF, iDigBio, Symbiota portals, and Discover Life.

CARE: The CARE Principles for Indigenous Data Governance are people and purpose-oriented, reflecting the crucial role of data in advancing Indigenous innovation and self-determination. CARE is an acronym for Collective benefit, Authority to control, Responsibility, and Ethics. (https://www.gida-global.org/care; Carroll *et al*., 2020).

COLLECTIONS MANAGEMENT SYSTEM (CMS): Software used to catalog items in a collection; in natural history, a CMS can be used to organize organismal specimens. Examples include Arctos, Specify, and Symbiota. Data from these systems can be uploaded to the Internet and made openly available.

CONTROLLED VOCABULARY: An accepted list of entries for a type of information (see Term). Controlled vocabulary lists are intended to reduce ambiguity in term use and can be modified if needed.

DARWIN CORE: Darwin Core is a data standard intended to facilitate the sharing of information about biological diversity by providing identifiers, labels, and definitions. Darwin Core is primarily based on taxa, their occurrence in nature as documented by observations, specimens, or samples, and related information. (https://www.tdwg.org/standards/dwc/; Wieczorek *et al*., 2012).

DATA AGREEMENT: A contract describing the appropriate use conditions and crediting practices of a dataset. Also referred to as data use or data sharing agreements.

DATA ASSURANCE: A document verifying that a dataset is of high quality and contains accurate information.

DATA ETHICS: Describes proper use and protection of openly accessible data to develop and maintain trust between data generators, managers, and users.

DATA LIFE CYCLE: Eight steps that describe how to work with data throughout and beyond its use in a particular project: Plan, Collect, Assure, Describe, Preserve, Discover, Integrate, and Analyze. (https://escholarship.org/uc/item/7tf5q7n3; Strasser *et al*., 2012).

DATA MODEL: Formal, codified relationships between types of information. When based on an ontology, it is called a semantic model.

Data sovereignty: The idea that data are subject to the laws of the place they were collected.

Data standard: Guidelines to describe and record data (https://www.usgs.gov/data-management/data-standards).

Digital specimen: A digitized record of a physical specimen.

Digital Object Identifier (DOI): A digital identifier of a physical, digital, or abstract object, designed to be both human-usable and machine readable, that allows the persistent, unique identification of and reliable tracking and access to that object (https://www.doi.org/the-identifier/what-is-a-doi/).

Ecological Metadata Language (EML): A metadata standard that describes ecological data (https://eml.ecoinformatics.org/; Jones *et al.*, 2019).

Extended specimen: A digital specimen along with additional ancillary data describing that specimen, including imagery, phenology, molecular information, environmental surroundings, and more (Lendemer *et al.*, 2020).

FAIR: Describes data that is Findable, Accessible, Interoperable, and Reproducible (https://www.go-fair.org/fair-principles/; Wilkinson *et al.*, 2016).

Identifiers: Machine-readable: Identifiers meant for use by computer software. Universally unique: A machine-readable identifier consisting of a 128-bit label that should only ever be created once. Human-usable: Identifiers that people use to manage data. Unique: a human-usable, usually human-created identifier for a specific purpose.

Integrated Publishing Toolkit (IPT): Software used to publish data to GBIF (https://www.gbif.org/ipt; Robertson *et al.*, 2014).

Key:value pair: A means of providing complex information in a machine-readable manner. A key is the type of information being provided, and the value is the actual information.

License: A document that describes conditions of acceptable use of openly shared data. Assigning a license to a dataset promotes proper crediting. Creative Commons licenses are commonly used; beyond the public domain license, there are six other licenses that can be applied to occurrence datasets: https://creativecommons.org/share-your-work/cclicenses/

Mapping: Translating data column headings to Darwin Core terms.

Metadata: Data that describes other data, including authorship, date created, date published, and license restrictions.

Occurrence data: Records of organisms that include the date collected, collector identification, geographic location, and other ancillary information.

Openly available: Data is considered openly available if it can be downloaded freely without explicit permission from the provider (*i.e.*, no email exchange is required to obtain a dataset) and the conditions for using the data are made clear by the provider. Use conditions are typically provided by applying a license (see License).

Ontology: A description of how various concepts within an area of information relate to each other. An ontology can be used to create a data model.

ORCID iD: A unique identifier used by scientists to link their output across the Internet, obtained and recorded at the Open Research and Contributor ID registry (https://orcid.org/; Haak *et al*., 2012).

PORTAL: A place where data or datasets can be downloaded. Portals provide downloadable access to data.

RECORD: A row of data in a digitized file.

REPOSITORY: A place where data are stored but not aggregated. Datasets can be downloaded individually from individual providers. Repositories can serve as an archive, and archived data are never changed. Examples: Zenodo (https://zenodo.org/), FigShare (https://figshare.com/), the Environmental Data Initiative repository (EDI; https://portal.edirepository.org/nis/home.jsp), and Dryad (https://datadryad.org/stash).

THEMATIC COLLECTIONS NETWORK (TCN): A Thematic Collections Network is a network of institutions with a strategy for digitizing information that addresses a particular research theme. Once digitized, data are easily accessed and available for other research and educational use. (https://www.idigbio.org/content/thematic-collections-networks). Current TCNs that are digitizing information about wild bees are iDigBees (DBI#2216927; https://idigbees.org) and Big-Bee (DBI#2102006; https://big-bee.net).

TDWG: Once known as the Taxonomic Databases Working Group, the Biodiversity Information Standards (TDWG) works to establish international collaboration among the creators, managers and users of biodiversity information and to promote the wider and more effective dissemination and sharing of knowledge about the world's heritage of biological organisms. https://www.tdwg.org/

TERM: In Darwin Core, a term is a label for a type of information and is used as a column heading in a digitized file of occurrence data. The full list of Darwin Core terms is found at https://dwc.tdwg.org/terms/

APPENDIX 3
Additional Resources

Native Bee Monitoring Rcn Data Management Workshop:

- Agenda: https://www.nativebeemonitoring.org/news/workshop-data-management
- Videos:
  - Workshop presentations Day 1: https://youtube.com/playlist?list=PLh3NEUAQ4ng7eQF_xnDYgreNjazdNXiQG&si=bhsF6MhMPKIu7fkw
  - Workshop presentations Day 2: https://youtube.com/playlist?list=PLh3NEUAQ4ng63v-hUamq1lEpLaUvg2JAF&si=vEvF1NYL6fIUaPCP
  - Data management and digitization: examples and resources: https://youtube.com/playlist?list=PLh3NEUAQ4ng5IgHQHZnftYtNZzPzdz0gr&si=3U_VSxfYdbj92gdl
  - Data management with different types of data: https://youtube.com/playlist?list=PLh3NEUAQ4ng6GXVYe2xJHQVVvWkbglVdZ&si=bRRe8UGHCllIF5NV

Links Referenced In This Manuscript:

- Darwin Core term list: https://dwc.tdwg.org/terms/
- GBIF: https://www.gbif.org/
  - Citation guidelines: https://www.gbif.org/citation-guidelines
  - Global Registry of Scientific Collections (GrSciColl): https://scientific-collections.gbif.org/
  - GBIF North America: https://www.gbif-north-america.org/community/
  - Templates to map occurrence data to Darwin Core terms:
- For occurrence data: https://ipt.gbif.org/manual/en/ipt/latest/occurrence-data#templates
- For sampling event data: https://ipt.gbif.org/manual/en/ipt/latest/sampling-event-data#templates
- Symbiota: https://symbiota.org/
  - Bee Library: https://library.big-bee.net/portal/
  - SCAN: https://scan-bugs.org/portal/
  - Ecdysis: https://ecdysis.org/index.php
  - Symbiota Documentation: https://biokic.github.io/symbiota-docs/
- Citation guidelines: https://biokic.github.io/symbiota-docs/coll_manager/citation/

- BeeBDC:
  - Homepage: https://jbdorey.github.io/BeeBDC/index.html
  - GitHub Repository: https://github.com/jbdorey/BeeBDC
- Codes of Conduct or Norms for Data Use:
  - USGS Bird Banding Laboratory Data Release Policy: https://www.usgs.gov/labs/bird-banding-laboratory/science/data-release-policy
  - CARE Principles for Indigenous Data Governance (Carroll *et al.*, 2020): https://www.gida-global.org/care
  - US Federal Data Strategy Data Ethics Framework: https://resources.data.gov/assets/documents/fds-data-ethics-framework.pdf
  - Canadensys Norms for Data Use: https://github.com/Canadensys/norms-for-data-use
  - VertNet Norms for Data Use: https://vertnet.org/resources/norms.html
- Creative Commons: https://creativecommons.org/share-your-work/cclicenses/
- UUID generator tools:
  - UUID R Package: https://www.rforge.net/uuid/, https://cran.r-project.org/web/packages/uuid/uuid.pdf
  - UUID Generator web application: https://www.uuidgenerator.net/
  - Guidance from iDigBio on generating UUIDs in Excel: https://www.idigbio.org/wiki/images/0/03/GUIDgeneration.pdf

OTHER RELEVANT DATA STANDARDS: https://www.gbif.org/standards

- Ecological Metadata Language (EML): https://eml.ecoinformatics.org/
- Developing standards
  - Humboldt Extension to Darwin Core to incorporate inventory and monitoring information, including sampling protocol and effort: https://eco.tdwg.org/
  - Plant-pollinator terms
- REBIPP: https://ppi.rebipp.org.br/
- Term list: https://ppi.rebipp.org.br/terms/
- WorldFAIR: https://worldfair-project.eu/agricultural-biodiversity/

OTHER TOOLS OR DATA SHARING PLATFORMS

- iDigBio: https://www.idigbio.org/
- USDA Plants: https://plants.usda.gov/home
- Discover Life: https://www.discoverlife.org/
- Global Biotic Interactions (GloBI): https://www.globalbioticinteractions.org/

Other Options For Collections Management Systems:

- Specify: https://www.specifysoftware.org/
- Arctos: https://arctosdb.org/

Learning Opportunities:

- iDigBio Digitization Academy: https://digitizationacademy.org/
- TDWG YouTube channel: https://www.youtube.com/@tdwg/featured
- Environmental Data Initiative: https://edirepository.org/
- Entomological Collections Network listserv https://ecnweb.net/resources/listserv/

Further Reading On Sharing And Using Occurrence Data:

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Standardized protocol for collecting community-level bee data

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Abstract. A key component of assessing bee biodiversity patterns and supporting bee conservation is documenting bee communities. When integrated with additional ecological data, community-level data help reveal the relative impact of local- and landscape-scale factors on bee taxa. As such, these data can inform management decisions to support bee diversity and mitigate environmental drivers of decline. However, methods for sampling bee communities vary greatly across projects, making it difficult to compare existing datasets or design new, interoperable studies. Here, we provide a standardized protocol for collecting community-level bee biodiversity data and offer guidance on inventorying, surveying, and monitoring of bee communities. We also present case studies to illustrate how different components of the protocol could be implemented. Although we discuss the benefits of collecting physical specimens, we emphasize the importance of responsible collecting and highlight key strategies to minimize environmental impact while maximizing the value of the work in new projects. This protocol is part of a series developed in association with the U.S. National Native Bee Monitoring Network to standardize bee monitoring practices.

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INTRODUCTION

As the desire to support pollinators (in particular wild bees) has increased across the globe, efforts have begun to focus on documenting trends in bee populations and how they change over time and across their range (LeBuhn *et al*., 2016; Woodard *et al*., 2020; Potts *et al*., 2021; UK Pollinator Monitoring Scheme 2024). In many cases, efforts to document these trends focus on gathering data on particular species that are likely vulnerable to environmental stressors, such as landscape-level modifications (*e.g*., Boone *et al*., 2023) and climate change (Weaver & Mallinger, 2022). There is, however, also a need to assess bee communities, emphasizing the entire assemblage of bee species present in an area, rather than a single species in all its areas.

Studying communities rather than single species shifts the focus to a more comprehensive understanding of bee biodiversity, including richness, relative abundances, species turnover (*e.g.*, beta-diversity), and diversity trends across space and time (Winfree *et al*., 2018; Kammerer *et al*., 2021). Community-level data also provide insights into potential interactions among bee species, such as the relationship between kleptoparasitic and overall bee diversity in a community (Sheffield *et al*., 2013). Comparing community metrics, such as species richness, evenness, and compositional similarity across sites, while accounting for environmental drivers can help address questions about community resilience. For example, how landscape change affects the similarity of bee species in communities in different areas (Harrison *et al*., 2018). Community-level data also inform management decisions aimed at preserving species richness or community structure rather than focusing solely on individual species. For instance, they can be used to compare bee community diversity between forest plots with moderate disturbance from prescribed burns or thinning versus unburned or unthinned plots (Davies *et al*., 2023; Gelles *et al*., 2023), or to examine whether an invasive plant species increases or decreases bee species richness (Tepedino *et al*., 2008). Community-level data are particularly important because diverse bee communities benefit crop and wild plant pollination and promote pollination service resilience in the face of environmental change (Hoehn *et al*., 2008; Oliver *et al*., 2015; Lemanski *et al*., 2022). Moreover, integrating community-level data with bee trait data (Ostwald *et al*., 2024), such as nesting substrate, body size, or trophic specialization, can help identify general patterns in bee responses (Williams *et al*., 2010). For example, determining whether large- or small-bodied bees are more susceptible to landscape change (Larsen *et al*., 2005) or which bees are more sensitive to agricultural land transformation based on their nesting requirements (Forrest *et al*., 2015). When conducted effectively, community-level data collection can also provide valuable insights for studying single species.

Community-level bee data have been collected using a wide range of protocols and strategies (Westphal *et al*., 2008; Klaus *et al*., 2024) that vary in sampling effort and method as well as recorded and reported metadata. These differences can have significant consequences for the data generated (Levenson *et al*., 2025) and can also make it difficult for those less experienced in bee community sampling to know how best to design their sampling plan. This lack of a unified protocol increases the barrier to entry by new researchers exploring bee communities. Thus, to promote a foundation for uniformity in bee community data collection, encourage greater participation in such efforts, and increase data interoperability, we provide a protocol for gathering standardized data that can be used for synthetic assessments of wild bee communities. Although this protocol provides useful guidance for sampling design, certain aspects of a project's sampling framework will necessarily be dictated by each project's unique question(s) and goal(s); thus, it is crucial to define these prior to data collection. In this protocol we provide guidance for three data collecting strategies, which require differing levels of effort: *inventory*, *survey*, and *monitoring* (Table 1). We summarize the data to be recorded (Table 2) and the necessary protocol components to meet the *core*, *recommended*, and *optional* practices of the protocol (Table 1, Table S1). We also provide detailed examples of how each strategy

could be implemented in Case Studies I–III, below. Although the guidelines outlined in this protocol are intended to be embedded within a broader sampling framework, they can also be used to collect data for independent projects, assuming data reporting standards are met (Du Clos *et al*., 2025).

Table 1. This protocol is part of a series developed in association with the U.S. National Native Bee Monitoring Network to standardize bee monitoring practices. These protocols include three levels of data (*Core, Recommended*, and *Optional*), which are outlined for three strategies of data collection (*Inventory, Survey*, and *Monitoring*). Details in Levenson *et al*. (2025).

Levels of Data Collection and Reporting		
Core	*Recommended*	*Optional*
Practices that are essential for achieving one's objective(s) and need to be used to meet the purpose of the protocol	Practices that are extremely beneficial, but not essential, to the specific objective(s) of the protocol	Practices that can be followed and may be worth the additional effort required, depending on one's objective(s)
Strategies of Data Collection		
Inventory	*Survey*	*Monitoring*
An attempt to build a species list for an area, not standardized for space or time	An attempt to record data of an area, standardized over space and/or time	An attempt to record changes in community measures over time, employing a consistent and repeated protocol, standardized over space and time

Table 2. *Core* data fields to be recorded when implementing the community-level protocol to adhere to *The Wild Bee Data Standard* (Du Clos *et al*., 2025).

***Core* Data field**	**Description**	**Darwin Core Term**
Protocol used	Cite this protocol and any additional protocol(s) used	dwc:samplingProtocol
Latitude	Precise location where sampling occurred, reported in decimal degrees (see dwc:geodeticDatum for recommended spatial reference system). Use the geographic center of the sampling location	dwc:decimalLatitude
Longitude	Precise location where sampling occurred, reported in decimal degrees. Use the geographic center of the sampling location	dwc:decimalLongitude
Area of sampling	Size of plot or length of transect used (in metric units). Specify whether a transect or a plot was used for netting or bowl traps	dwc:samplingEffort
Length of time traps were deployed	Start and end date and time (*e.g.*, 9:00–16:00h), and duration traps were deployed (*e.g.*, 6h)	dwc:eventTime, dwc:samplingEffort
Number of traps successfully collected	Number of traps successfully collected (*i.e*., bowls that were not knocked over, damaged, missing, or devoid of liquid)	dwc:sampleSizeValue, dwc:sampleSizeUnit
Length of time spent netting	Start and end date and time (*e.g.*, 11:00– 12:00h), duration of netting (*e.g.*, 1h)	dwc:eventTime, dwc:samplingEffort
Number of net collectors	Number of people who collected bees by net during a sampling event (optimally record collectors' collections separately)	dwc:sampleSizeValue, dwc:sampleSizeUnit
Details of sampling event	Additional context regarding sampling event, including but not limited to weather and field conditions, additional bowl trap details, and field notes	dwc:eventRemarks

PROTOCOL SAMPLING METHODS

Throughout this protocol, we provide guidance on two of many possible sampling methods: sampling bees passively using bowl traps with soapy water, referred to as bowl traps, and actively using handheld nets. We focus on these two sampling methods as they are widely used to sample bee communities effectively (Packer & Darla-West, 2021) and require minimal supplies, making them most easily adopted in a wide variety of contexts. We combine both passive and active methods to capture a more complete representation of the bee community (Cane *et al*., 2000; Roulston *et al*., 2007; Wilson *et al*., 2008). All collection methods have inherent biases (Rhoades *et al*., 2017; Campbell *et al*., 2023; Mathis *et al*., 2024). In netting, factors such as collector experience, dexterity, and timing of sampling can impact sample collection and resulting community measures (Westphal *et al*., 2008; Levenson & Tarpy, 2023; Larson *et al*., 2024). Moreover, some bees are crepuscular, active at only short periods of the day, not easily recognized as bees (*e.g*., wasp-like *Nomada* Scopoli*, Hylaeus* Fabricius), or otherwise less likely to be collected by hand netting. Although the use of passive traps removes collector bias (Westphal *et al*., 2008; Wilson *et al*., 2008), it also introduces its own biases due to trap type (Westphal *et al*., 2008; Tronstad *et al*., 2022; Campbell *et al*., 2023) and size (Wilson *et al*., 2016; Gonzalez *et al*., 2020), surrounding habitat and bloom availability (Wilson *et al*., 2008; Rhoades *et al*., 2017; Kuhlman *et al*., 2021; Mathis *et al*., 2024), differential attractiveness among bee taxa (Wilson *et al*., 2008; O'Connor *et al*., 2019; Briggs *et al*., 2022; Campbell *et al*., 2023; Larson *et al*., 2024), and the overcollection of certain taxa (Gibbs *et al*., 2017). As such, when designing a sampling plan, one will need to balance the biases of different sampling methods with input costs and overall project goals (Schlesinger *et al*., 2023; Levenson *et al*., 2024). It may be worth exploring some of the many other passive sampling techniques used for assessing bee communities that are not included here (see Packer & Darla-West, 2021; Table 3, Supplemental Material). When implementing lethal collections, other insects will also be collected, referred to as 'bycatch'. Preserving and properly processing this bycatch is part of responsible collecting (Trietsch & Deans, 2018), but can be time-intensive; therefore, a plan to manage bycatch should be developed prior to sample collection.

We do not provide information in our protocol for non-lethal, community-level data collection, although see Cariveau *et al.* (2025) for one possible image-based method. When the goal of a project is to assess bee communities, identification to species is required to describe the community as precisely as feasible. At present, without intimate prior knowledge of the local fauna, most bees in most parts of the world can only be reliably identified to species with physical specimens, which requires lethal collection. We advise using our lethal sampling protocol to develop the most comprehensive baseline information for determining future sampling, monitoring, or conservation action. Once baseline information is established with lethal methods, non-lethal methods (*e.g.*, DNA barcodes, high-quality reference photos, eDNA) can then be vetted for accuracy and explored for future data collection.

In sum, our suggested community-level sampling methods are designed to sample as much of the bee community as possible while providing relative abundance measures, with an eye towards not oversampling.

COMMUNITY-LEVEL BEE DATA PROTOCOL

Sampling scheme: A sampling site is defined here as the extent of the area in which sampling occurs, and may contain multiple plots, transects, and habitat types (see Cariveau *et al*., 2025 for more details). We provide two basic approaches for how community-level data are collected

Table 3. Summary of additional passive sampling techniques that are not included in this protocol. See Supplemental Material for details and references.

Method	Specific Uses	Reasons for exclusion from protocol
Glycol traps	Long-term deployment in remote, hot, dry, or low-resource environments	Specimens are harder to process; risk of losing unattended traps; risk of large sampling impact on insect assemblages
Blue vane traps	Passive trapping of larger-bodied bees. See glycol traps	Risk of overharvesting sensitive species, particularly bumble bees and bumble bee queens; indiscriminate sampling in areas with protected species or species of concern
Malaise or flight intercept traps	Non-attracting passive trap for intercepting bees in flight. See glycol traps	Do capture bees, but also capture large volumes of bycatch; more expensive per unit capture
Emergence traps	Passive trapping of ground-nesting bees from nest sites	Very low capture rates; only amenable to ground-nesting bees
Trap nests	Passive trapping of cavity-nesting bees. Examination of nest construction behavior and nest contents	Variable capture rates; only amenable to cavity-nesting bees

within a sampling site: along a belt transect or within a plot. A belt transect (hereafter referred to simply as a transect) is defined here as a sampling route. Transects may be along a straight line or in a meandering line (see Cariveau *et al.*, 2025 for more details). Transects can be sampled passively using bowl traps or actively using nets; we provide details of both approaches. With bowl traps, traps are placed linearly along the transect line. With nets, samples are collected within a standardized distance on either side of the transect line. Regardless of the specifics, all transects within a sampling site should fall within one habitat type. Sampling plots within sites are defined here as a sampling area of standard size that falls within one habitat type. Transects and plots, thus, both emphasize standardizing a unit of area within which samples are collected but differ in the spatial arrangement of data collection. Generally, transects allow for greater precision of the exact area sampled as they better confine the collector within the sampling site, whereas plots allow the collector freedom to cover areas within the sampling site that might be missed in a classic transect. Plots often result in higher documented bee richness (Nielsen *et al*., 2011) and they have been shown to better sample highly mobile organisms in some settings (Ambrose, 2002).

Establishing and sampling within at least one plot or transect, in each sampling site, is a *core* practice for *survey* and *monitoring*, but only a *recommended* practice for *inventory* where sampling may be done in undefined areas. To make *inventory* data more interoperable, however, it can be beneficial to more closely follow the *survey* or *monitoring* protocol practices. For transects, we *recommend* surveying within 1 m on all sides of the transect line during sampling. Surveying within a standardized area on all sides of the transect line allows for data to be matched reasonably to those collected using plots because the sampling area is known. Further, at distances beyond 1 m, small taxa will not be visible, which introduces sampling bias. Transects may be any length and can be tailored to the sampling site, but we *recommend* a minimum of 25 m for small plots and 200 m for large plots, unless otherwise limited by habitat area. Regardless of length, a *core* practice is reporting the length and width of the transect used and the time spent sampling. *The Very Handy Bee Manual* (A Collective, 2024) provides additional useful guidance on transect protocols. For plots, the size used should be standardized

across the project so that all plots used for a study are the same dimensions. We *recommend* picking a size that falls in one of two bins: small (ranging from 0.01–0.24 hectare, *e.g.*, 10 x 10 m to 49 x 49 m) or large (0.25–1.0 hectare, *e.g.*, 50 x 50 m to 100 x 100 m), as it is difficult to fully sample areas greater than 1 hectare with a single plot. In some environments, habitats may be organized linearly (*e.g.*, riverine), requiring elongation for a given size (*e.g.*, 50 x 200 m to match square 1 ha plots). Further, using these bins increases the interoperability of data across studies. Regardless of size, a *core* practice is measuring, recording, and reporting the exact plot area used. As an *optional* practice, GPS can be used to record the sampling area as well as the precise locations of the transects or sampling plots used.

A *core* practice of the protocol is that the entire plot or transect must not cross an ecotone (a transition area between two biological communities) and must be situated entirely within one habitat (*e.g.*, upland prairie, wet prairie, oak woodland, chaparral, riparian grassland, early succession old field, wet alpine meadow, aspen forest), which should be recorded. This is because habitat type can greatly influence the portion of the bee community that is sampled (Hung *et al*., 2017; Du Clos *et al*., 2020), which can bias results. Thus, if the sampling site contains multiple habitats, and the intent of the study is to capture data across multiple habitat types, then separate plots or transects would need to be established per habitat type.

The level of plot replication for *inventory* and *survey* will depend on project goals, which may require consideration of statistical power (LeBuhn *et al*., 2012; LeBuhn *et al*., 2016; Breeze *et al.*, 2020), although, in general, more locations sampled will increase the completeness of the species list. For *monitoring*, the number of sampled plots or transects, and the number of repeated sampling events, are important components of a statistically defensible monitoring scheme, both of which are heavily impacted by the goals of monitoring. Power analyses and other assessments, focused on determining the sampling structure that would be required to detect changes of a defined magnitude through time, need to be performed to identify the appropriate spatial and temporal extent of sampling (number of plots or transects and number of sampling events at those locations; LeBuhn *et al*., 2012; LeBuhn *et al*., 2016; Breeze *et al.*, 2020); too few samples, and statistically rigorous comparisons will not be possible. We recognize, however, that in many cases the data required to perform full power analyses may not be available; in these cases, it may be necessary to reevaluate and update sampling designs later, when more rigorous power analyses are possible.

Many studies of wild bee communities geographically distribute plots and transects to avoid sampling within the estimated flight distance of bee species or based on the spatial scale at which bee community turnover occurs, to achieve statistical independence of plots or transects. For flight distance, a separation of at least 2 km is considered sufficient to avoid encountering the same individual bees in different sites (Greenleaf *et al*., 2007). For community turnover, change in bee community composition has been demonstrated to occur both within and beyond 2 km (Messinger, 2006; Rollin *et al*., 2015; Dorchin *et al*., 2018; Reverté *et al*., 2019); furthermore, local- and landscape-level habitat characteristics can also influence patterns of species turnover (Rubene *et al*., 2015; Martins *et al*., 2017; Beduschi *et al*., 2018; Christman *et al*., 2022). Thus, the geographic distribution of plots and transects will depend on specific project question(s) and goal(s). For example, sampling at more sites spaced farther apart from each other would provide information on the bee community across ecoregions or land uses, whereas sampling more frequently at fewer sites spaced closer together would provide more information on temporal turnover of species and species interactions. We advise seeking guidance from experts for establishing criteria of spatial independence for each project's unique specifications prior to sampling.

SAMPLING FREQUENCY: Bee community composition significantly changes across the bee flight season (Leong *et al*. 2016; Hung *et al*. 2017; Neave *et al*., 2020; Turley *et al*., 2022; Levenson & Tarpy, 2023), so visiting the same site multiple times during the season is important for documenting as much of the community present at a site as possible (Levenson *et al*., 2024). For *inventory* and *survey*, the *core* practice is to conduct a single sampling event, but it is *recommended* that sites are visited multiple times across the season to account for phenological differences among bee species. For *inventory*, multiple sampling events in a season would be needed to generate a complete list of species in an area, whereas for *survey,* multiple sampling events may be important to gain a more comprehensive understanding of the bee community and how it changes across the season. For both *inventory* and *survey*, we *recommend* at a minimum of two sampling events that attempt to capture data at two distinct periods of time within the peak of the bee flight season (*i.e.*, while floral resources are available). More frequent sampling, however, such as every 2–3 weeks, will allow one to capture seasonal differences in the bee community. Note that site seasonality and species turnover through time may dictate the specific interval and number of sampling events that are needed to achieve a project's objective(s). Also note that in some parts of the world there are two discrete seasons; for example, in the southwestern US, one season is driven by winter precipitation and temperature, and the second the result of monsoons, with a midsummer hiatus in bloom. This should be considered when developing sampling plans in these areas.

For *monitoring*, the timescale over which sites are visited within each season and across years will depend on each project's goal(s) as these will be influenced by within-season dynamics, bee population dynamics, land use change, desired statistical rigor, and other variables (LeBuhn *et al*., 2012; Aldercotte *et al*., 2022), including available survey resources and costs (Breeze *et al*., 2020). Nevertheless, it is *recommended* that for *monitoring*, samples are collected during approximately the same time or part of the season each year.

APPROPRIATE CONDITIONS FOR SAMPLING: *Recommended* conditions for sampling bees are warm temperatures, clear skies, and no or minimal winds (Beneder, 1976; Kevan & Baker, 1983; Vicens & Bosch, 2000; Abrol, 2006; also see Mahon & Hodge, 2022), although this is not always achievable in certain environments or conditions (*e.g.*, coastal, alpine, prairie, desert, Arctic, early spring). Recording these elements at each collecting event is a *core* practice of the protocol as it provides users of the data the ability to evaluate what data to use. In general, we advise sampling when temperatures are above 50° F (10° C) or below 110° F (~43° C), with minimal cloud cover (no more than lightly overcast), and low winds (no more than a 3 on the Beaufort scale or 12 kph). We do not advise sampling if precipitation is occurring (or expected to occur while bowl traps are deployed) or when air quality (*e.g.*, smoke haze) causes conditions similar to extensive cloud cover.

SAMPLE COLLECTION: We *recommend* two methods of lethally sampling bees: bowl traps and net collecting. For guidance on supplies and preparation of sampling materials, including the preparation of bowl traps, *The Very Handy Bee Manual* (A Collective, 2024), Packer & Darla-West (2021), and LeBuhn *et al*. (2016) provide relevant information. Prior to sample collection, a plan should be made for how samples will be processed after collection; see Table 4 and *The Very Handy Bee Manual* (A Collective, 2024) for guidance. For *inventory*, which is not necessarily standardized, the following methods do not need to be adhered to in such detail, but we *recommend* deploying all three bowl colors to maximize species richness captured.

Table 4. Additional, *optional* practices to consider when developing a sampling design, beyond what is outlined in this protocol. While each of these practices can provide valuable data, they also require additional time and resources. It is important to balance data collection with logistical constraints for each project.

Additional Practice	Considerations
Site documentation	Photographing the sampling site and bowl trap arrangement can aid future reference. Plan where and how photos will be stored for usability
Plant-pollinator interactions	While the protocol separates netted samples by plot or transect, further separation by host plant provides insight into bee ecology and plant-pollinator networks. However, this increases specimen handling time. See Cariveau *et al*. (2025) for guidance
Incrementation of collection time	For finer-scale sampling effort calculations, netting duration can be recorded in smaller increments (*e.g*., 10- or 15-min bins), pausing the timer during specimen handling. This increases processing time and requires more collection containers
Recording and reporting bowl trap details	Optional bowl trap details, such as deployment height, arrangement, size, color, and liquid medium, help assess potential biases but add to data management
Sample storage	Storage conditions in the field and during transport can affect specimens' suitability for molecular, parasite, and pathogen analyses (see López-Uribe *et al*., 2025, and Strange *et al*., 2025)

For *survey* and *monitoring*, we *recommend* that bowl traps be deployed along transects that form a single line (Fig. 1). For plots, bowls may be deployed in two lines, crossing the plot in an "X". Although it is more time consuming to deploy and retrieve traps in an "X" configuration, this is one reasonable way to deploy 30 traps in a one-hectare plot, using appropriate spacing; other configurations, such as a "Z" could also be used. We *recommend* placing bowls five meters apart, alternating among fluorescent blue, fluorescent yellow, and white bowls (Droege *et al*., 2010). The number of bowls deployed will vary based on plot size and project goal(s). A *core* practice of the protocol is that an equal number of each color is deployed with a minimum of nine bowls (3 bowls per color) used per plot or transect; this will aid in making data comparable to other studies. We note, however, that nine bowls is likely an insufficient number to estimate the bee community in many habitat types and plot sizes; thus, many data collectors will use a greater number than this. We *recommend* deploying a maximum of 30 bowls (10 of each color), when sampling plot or transect area allows, as Shapiro *et al*. (2014) estimate that this number adequately samples most communities while maximizing sampling efficiency.

Placing bowl traps on the ground is logistically easiest and most effective in open areas. If vegetation is thick or tall, however, it may be best to elevate bowls to the top of vegetation. To maximize bowl trap effectiveness, we advise placing the bowls so that they are just above the densest part of the vegetation, not towering over the sparser upper vegetation. In general, bowls should not be placed under brush or in significant shade, but rather in open areas where they can be easily detected by bees and seen by data collectors. Spacing bowls apart (versus clustering them together) maximizes bee capture (Droege *et al*., 2010). In some conditions (*e.g*., when vegetation is tall and bowls are elevated), clustering bowls together may make them easier to deploy and retrieve, but we *recommend* not clustering bowls whenever possible. For examples of implementing bowl traps, see LeBuhn *et al*. (2003), Wilson *et al*. (2008), and Meiners *et al*. (2019).

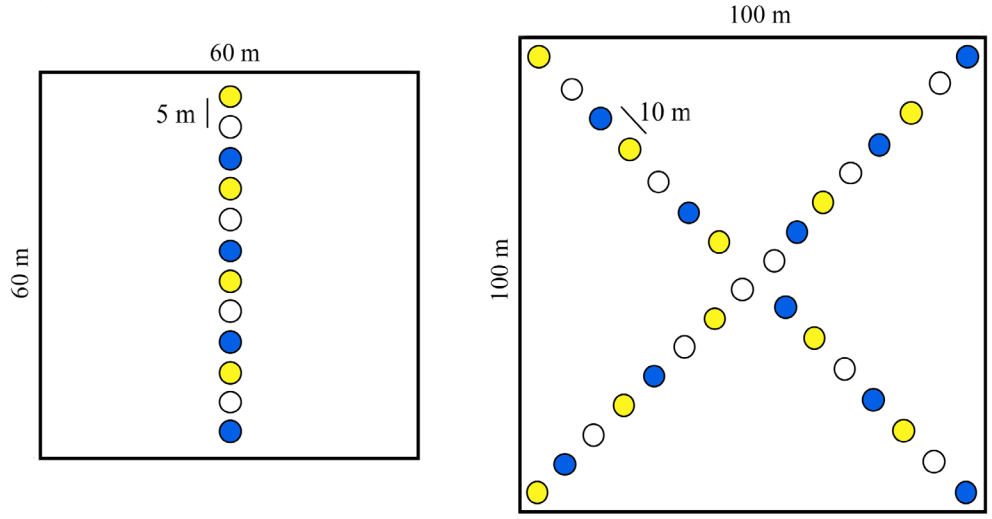

Figure 1. Possible layouts of bee bowls include a transect of 12 traps in a small plot (left) and a "X" configuration of 30 traps in a large plot (right). These are just two examples of how bee bowls can be arranged for sampling. Diagrams are not to scale.

The data to be recorded when using bowls traps to meet the *core* practices of *survey* and *monitoring* include latitude, longitude, plot size, the starting and finishing times that bowls are deployed (see below), and the number of bowls successfully retrieved (*i.e.*, bowls that were not knocked over, damaged, missing, or devoid of liquid). The latter includes bowls that did not collect any bees; the null data from bowls that were successfully retrieved but did not contain any bees are important for calculating sampling effort. Recording of these data fields is *recommended* for *inventory* as recording measures of effort greatly improves the usefulness of the data.

Active netting is inherently less standardized than deploying bowl traps because sample collection is heavily impacted by the skill and approach of the individual collector. Differences among collectors, however, can be measured and considered in data analysis if enough intra- and inter-individual replication has occurred (Cane *et al*., 2006). Netting at small sites can be conducted by a single collector, whereas netting at larger sites may require multiple collectors to ensure a more complete sampling of the community during an allotted period of time. When netting in a plot, we *recommend* searching for and collecting bees foraging on flowers (*i.e.*, targeted netting) along a meandering path throughout the plot boundaries. When netting along a transect, cover its entire length during the time period. Note that although most bees might be collected from flowers, bees can also be collected from the air and on the ground; these often include kleptoparasites and males. It is a *core* practice that all bees, of any species unless protected, be collected through targeted active netting (not 'sweep' netting) during a sampling event (regardless of whether they are observed on flowers or not) to avoid biased data. This includes honey bees. Although honey bees are feral or managed (not wild) in North America, they are frequently encountered in many regions and habitat types and can influence wild bee community composition (Mallinger *et al*., 2017; Page & Williams, 2023). Another *core* practice for *survey* and *monitoring*, and a *recommendation* for *inventory*, is to document sampling events when no bees are collected. These negative data are important for quantifying effort and can provide critical information for conservation decisions. When netting, documenting the number of collectors and the time spent sampling is a *core* practice of *survey* and *monitoring*.

For *inventory*, netting can be done opportunistically and haphazardly rather than being constrained within plots. Even though an *inventory* is not necessarily standardized for space and time, it is still important to collect relevant metadata, including location data.

Timing and duration of sampling event: Regardless of whether using passive traps or active netting, we advise collecting samples between 09:00–16:00 h (Vicens & Bosch, 2000) unless the specific habitat being sampled or project goal(s) require sampling outside of this time frame. Most bees are active during this period of the day; however, there are bee species that only forage at specific times of day–*e.g.*, matinal, crepuscular, xeric species–and may require different sampling timeframes. If project logistics allow, there are advantages to sampling a site in both morning and afternoon; this increases the likelihood of collecting species that are active at different times of the day.

For passive sampling, we *recommend* deploying traps for a minimum of 6 h (during peak bee flight activity) and a maximum of 24 h. For active netting, a *core* practice of the protocol is to sample a plot or transect for a minimum of 10 min; however, sampling time can be any length beyond this, especially when sampling in larger sized plots or transects. Regardless of how long each timed sampling event is determined to last, the entire plot or transect should be covered within that time period. To ensure that an entire plot is sampled, more than one transect may be needed; pace may vary depending on location and density of blooming plants. When a bee is successfully netted, the collector should immediately pause the timer, then transfer the bee into a collecting vessel. When the specimen has been securely transferred and appropriately labeled, resume timing and continue netting, starting and stopping the timer to process additional bees as they are collected. In some situations, multiple bees may be netted at once; if project goals allow, these can be collected into the same container.

For *survey* and *monitoring*, a *core* practice of the protocol (whether using passive or active sampling) is to record start and stop time so that sampling effort can be calculated. For passive traps, this would equate to the times that traps are deployed and retrieved, whereas for netting, this refers to the start and stop times for netting (including stopping of the timer during field specimen processing). For *inventory*, recording time is not a *core* practice of the protocol, but is still *recommended*.

Data recording: An important aspect of standardizing data collection is properly recording data. We provide descriptions of data fields to record and report when using this protocol in Table 2, which align with *The Wild Bee Data Standard* (Du Clos *et al*., 2025; this issue). *The Wild Bee Data Standard* uses Darwin Core terms (Wieczorek *et al*., 2012) and describes their application to wild bee occurrence data. Darwin Core is a widely accepted biodiversity data standard used by leading biodiversity data providers, including the Global Biodiversity Information Facility (GBIF; https://www.gbif.org/), Integrated Digitized Biocollections (iDigBio; https://www.idigbio.org/portal/search), and iNaturalist (https://www.inaturalist.org/). Applying Darwin Core terms to wild bee occurrence data following *The Wild Bee Data Standard* increases interoperability of data across studies. Follow the case studies, below, and *The Wild Bee Data Standard* for guidance on full data reporting requirements. Additionally, examples of recorded data associated with the collecting events for each case study presented below can be found in worksheet and workbook templates provided with *The Wild Bee Data Standard* (Du Clos *et al.*, 2024). Although we outline the *core* data requirements in Table 2, one should consider documenting data beyond what is outlined in this protocol if capacity allows (examples in Table 4).

EXAMPLES OF IMPLEMENTING COMMUNITY-LEVEL PROTOCOL

Case Study I. Bee Inventory for Conservation

A land conservancy group is interested in identifying what bee species occur on their properties, with the future goal of documenting the impacts that their land conservation efforts have on wild bee communities to inform future conservation decisions. To begin with the foundational step of discovering the bee species on their properties, the group would like to implement a single-year *inventory* of the wild bee species.

Before the *inventory* begins, an identification expert who will identify bee specimens is contacted and compensation is agreed upon for the work. Supplies are prepared based on the number of sites that will be visited in a day. Permitting and permissions are established, data worksheets are prepared, and sites for collection are decided upon and visited. A plan for bycatch is put in place: a local institution that specializes in outdoor education will use them for teaching.

The group will visit 25 sample sites at various dates across one year. Sites are selected to include as many habitats as possible to capture bees that may be habitat specialists, and areas with high floral abundance and diversity as these areas are expected to have high bee diversity. Each site will be in a distinct habitat so that bees collected in one place can be associated with that habitat. Tangentially, they will also pick sites that show contrasting management efforts, because these data may help determine what questions they want to try to answer with their future *survey* and *monitoring* efforts. Given that their immediate goal is to complete an *inventory*, rather than a more standardized *survey* or *monitoring* effort, selecting sites that will yield them the most bee occurrence data is the optimal approach. They will collect haphazardly and opportunistically, rather than setting up plots or transects.

The group wants their sampling effort to cover as much of the bloom period as possible in the area and have the capacity to sample monthly. They will sample once per month for the eight months during which most flowering plant species are blooming. They will use both bowl traps and netting for sample collection. For bowl traps they will set up 60-m transects at each site, which will include 12 bowl traps (4 each of white, yellow, and blue), placed in a line, spaced every five meters, in consecutive order to make it easier to find the traps (Fig. 1). The traps will be filled with soapy water and deployed for 7 h from 09:00 to 16:00 h.

The group will also have two collectors go to each site and net bees on the same day that bowl traps are out each month. On each of the eight visits, two collectors will wander for as long as scheduling allows, searching for areas with blooms or with bee nesting activity. Given that plants are important to this study, they will also record the plant on which each bee specimen is found.

The specimens collected from bowl traps are processed into storage containers (in this case WhirlPaks®) and stored in 95% EtOH (ethanol) (López-Uribe *et al.*, 2025). Netted specimens are euthanized in the field, also using ethanol. Because the collecting day is long, and there are 25 sites to visit each month, pinning is saved for one day out of each month. In the interim, netted bees are temporarily labeled with the date of collection, the site name, GPS coordinates, the hours during which collecting occurred, the collector's name, and the plant on which that container of bees was collected. Specimens from both collection methods are stored in a standard freezer (-10 to–20° C) until 'pinning days' occur. Specimens are pinned and labeled appropriately so that important information–such as date, coordinates, and name(s)–are recorded, but that anatomy can still be accessed for identification (see Burrows *et al*., 2021;

A Collective, 2024; Du Clos *et al*., 2025). After, all specimens will be sent to experts for identification and accession into a university insect museum collection.

The group follows *The Wild Bee Data Standard* (Du Clos *et al*., 2025) and uses either the worksheet or workbook data template to organize their data (Du Clos *et al*., 2024). In their template, each specimen collected is assigned a unique **dwc:occurrenceID** and the following information is provided for each specimen record, or row, in the digitized data: the date on which sampling took place (**dwc:eventDate**), the method used to capture the specimen (**dwc:samplingProtocol**), the location at which the specimen was found (**dwc:decimalLatitude**, **dwc:decimalLongitude**, **dwc:fieldNumber**), the full name of the person who collected the specimen (**dwc:recordedBy**), and the start and stop time of the sampling event in which the specimen was collected (**dwc:eventTime**). For specimens netted on a flower, the plant species is recorded (**dwc:associatedTaxa**); for those netted on the ground or in the air, this too is recorded (**dwc:occurrenceRemarks**). To fully document sampling effort, each specimen record will provide additional details about the sampling event in which the specimen was collected, including the length of the transect for bowl traps or plot size for active netting (**dwc:samplingEffort**), the number of bowls successfully retrieved or the number of net collectors (**dwc:sampleSizeValue** and **dwc:sampleSizeUnit**), and the total duration of the sampling event (**dwc:samplingEffort**). Details of their bowl trap methods are provided, including the number of traps deployed, colors used, shape, height, and trap medium (**dwc:eventRemarks**). Finally, weather notes (**dwc:dynamicProperties**), habitat type (**dwc:habitat**), and accuracy of georeferenced site locations are provided (**dwc:coordinateUncertaintyInMeters**, **dwc:coordinatePrecision**). Example entries for this case study are provided in both the worksheet and workbook templates available for use through Zenodo (Du Clos *et al*., 2024).

Case Study II. Surveying a Local Park

A researcher is interested in understanding how change in land use impacts the bee community in a local park. Several previous research projects have been conducted in the area and so they have some ideas of what species are present. It is not well understood, however, how different bee species within the community will respond to future, ongoing land use change. To understand the impacts on the bee community, the researcher would like to implement a *survey* of several sites along a nearby land use gradient.

The researcher will visit four replicates of three land use types for a total of 12 plots. At each plot, two one-hectare (100 m x 100 m), fixed sampling areas (one for each collector, see below) will be laid out, contained within a single habitat type, that best represents the land use change. Plots will be placed at least five kilometers apart. They will visit each plot at six different time points across three months of peak bee activity, sampling each plot at a regular two-week interval. Sampling will be repeated for these same plots across three consecutive years.

Before collecting begins, the researcher marks the corner of each sampling area with a GPS unit, as well as the center of the plot. They get permission from a local land-owner whose property must be crossed to get to one plot. Data fields to record are determined following guidance from *The Wild Bee Data Standard* (Du Clos *et al*., 2025) and data sheets are prepared. A conversation is had with the in-house bee taxonomist or formally trained professional in bee identification to ensure time can be set aside to identify these specimens. No takers for bycatch can be found, and funding is not available to pin and label non-bee specimens. A plan is made to store the bycatch specimens in 95% EtOH (Marquina *et al.*, 2021; López-Uribe *et al.*, 2025)

with appropriate label information until an institution and funding are secured; while it may take time to find an institution and funding, having a developed plan for when this does occur is still important.

The researcher will use both bowl traps and netting for sample collection. Thirty bowl traps will be used in each plot (10 each of white, yellow, and blue). They will be placed in an "X" from corner to corner of the one-hectare plot, with 15 traps running along each leg of the "X" (Fig. 1). They will be spaced 10 m apart to span the corner-to-corner distance of the square. The vegetation is not very high, so the traps will be placed directly on the ground. The traps will be filled with soapy water and deployed for eight hours.

The researcher will have two collectors visit each plot to conduct netting on the same day that bowl traps are laid out. Each pair of collectors will sample one of the one-hectare sampling areas for 30 min, twice, for a total of 120 person-minutes of sampling per plot. Collectors will cover the entire sampling area during netting using meandering transects. As the researchers may consider using these specimens for genetic analyses in the future, both collectors wear a waist pack with a small ice pack in it. Each time a bee is netted, the timer is paused until the bee is collected into an individual tube; each tube is held in the waist pack, next to the ice pack to ensure that DNA quality is preserved and that the specimens are humanely handled during the field day. Although not essential to the study, the researcher opts to document the plants that the bees are found visiting as this supplemental information is potentially relevant to the land use types that are being documented. To do this, the researcher separates the tubed bees into Ziplock bags, one per plant species, and carries all Ziplock bags in the waist pack, next to the ice pack, for the duration of the sampling event. After collection is complete, the small plant-specific Ziplock bags are all placed in a large gallon zip-lock bag labeled with the site information, the date, the subplot, whether it was the first or second collection event, and the collector's name. Because the two sampling areas are relatively close together, netting for both will happen on the same day, and all plots can be covered in six field days.

The collectors transport the labeled bags from the field in a small cooler with ice, when back at the lab the specimens are placed at–20° C in a freezer until further processing. All specimens collected in the bowl traps are processed in the field, with bycatch separated from bees, moved into labeled containers filled with 95% EtOH, and transported back to the lab, also in the cooler, where they will be stored at–20° C in a freezer until further processing. Prior to pinning the specimens, the researcher removes a mesothoracic leg from each to preserve DNA for future use; these legs are held in cold storage following López-Uribe *et al*. (2025).

When ready to be pinned, each specimen will be given proper identification labels, including specimen numbers, so that the data can be added to the in-house lab collection and eventually added to public data aggregators, such as GBIF.

The researcher follows *The Wild Bee Data Standard* (Du Clos *et al*., 2025) and uses either the worksheet or workbook data template to organize their data (Du Clos *et al.*, 2024). In their template, each specimen collected is assigned a unique **dwc:occurrenceID** and the following information is provided for each specimen record, or row, in the digitized data: the corresponding specimen number from the identification label (**dwc:catalogNumber**), the taxonomic identification of the specimen (**dwc:genus**, **dwc:specificEpithet**, **dwc:scientificName**), the full name of the person who made the taxonomic identification (**dwc:identifiedBy**), the date on which that specimen was collected (**dwc:eventDate**), the method used to capture the specimen (**dwc:samplingProtocol**), the location at which the specimen was found (**dwc:decimalLatitude**, **dwc:decimalLongitude**, **dwc:fieldNumber**), the full name of the person who collected the specimen (**dwc:recordedBy**), the start and stop times of the sampling event in which the specimen was collected (**dwc:eventTime**), and the plant on which each netted specimen was collected (**dwc:associatedTaxa**). Specimen handling details, including field and lab storage on ice,

will also be provided (**dwc:preparations**, **dwc:materialEntityRemarks**). To fully document sampling effort, each specimen record will provide additional details about the sampling event in which the specimen was collected, including the size of the plot (**dwc:samplingEffort**), the number of bowl traps deployed (**dwc:eventRemarks**) and number successfully retrieved (**dwc:sampleSizeUnit**), and the total duration of the sampling event (**dwc:samplingEffort**). Further information is provided to describe sampling methods and conditions, including the land use type associated with each plot (**dwc:habitat**), weather notes (**dwc:dynamicProperties**) specifics about the bowl trap height and liquid medium (**dwc:eventRemarks**), and the GPS unit used to mark the plot center and corners (**dwc:georeferenceRemarks**). Example entries for this case study are provided in both the worksheet and workbook templates available for use through Zenodo (Du Clos *et al*., 2024).

Case Study III. Monitoring Bees and Pesticide Use

A government agency needs information on the bee community within a specific state and how it might be impacted by a new pesticide, to inform new policy development. The agency decides to establish a *monitoring* program for the state, with funding secured for the next ten years.

As collecting long-term data could be used to address many future questions beyond the current focus, the agency wants to ensure they establish a robust sampling scheme that will collect high-quality, standardized data. To do this, the agency meets with a group of statisticians to decide where, when, and to what extent data will be collected to ensure they can detect what they consider meaningful changes through time. To address the current focus, their sampling framework also incorporates information about where the new pesticide will be deployed, allowing them to test hypotheses about how it will impact bee communities. They select 50 sites across the state that they will visit eight times each year, once per month. The sites are selected to represent a diversity of habitat types, focusing on those where policy may be most impactful. Sites are separated by statistically relevant distances and there are a range of sites with different pesticide schedules. In some sites, pesticide implementation is planned for the second and third years of the study, so an effort is being made to collect solid baseline data prior to pesticide use so that immediate and long-term effects can be assessed. Some sites will receive pesticide application annually, and others less frequently. A few sites have already received applications for many years prior to the beginning of this study.

Before bee sampling begins, permits are secured for bee collections happening in sites that are under special state and federal jurisdiction. Bycatch is to be housed in the land grant university of the state and funding is being secured to assess the impact of the pesticide on other insect groups collected during the bee surveys. A government employed bee taxonomist has agreed to identify bee specimens quickly to genus each year, and over the course of the ten-year project, will identify bees to species. The identified insects will be housed together at the government facility and given proper labels so that the data can be used for future, larger scale analyses that are combined with datasets from other states. All eight collectors who will be spending the season visiting sites will spend two weeks practicing bee collecting. This two-week training will involve learning to observe and sample bees on flowers or on the ground, recognizing different kinds of bees, and learning different netting techniques.

At each site, the plan is to use bowl traps and netting for sample collection. At each site, a 0.5-hectare plot is established for sampling. Since this plot is only 100 m from corner to corner, 18 bowl traps will be used (6 each of white, yellow, and blue), spaced 5 m apart, and deployed in an “X”. The traps will be deployed for 24 h, once per month, from March through October.

Teams of two collectors are employed for each quadrant of the state, with each team responsible for 12–13 of the collection sites.

Two collectors will conduct netting surveys when trap contents are collected, for efficiency. Each 0.5-hectare plot will be collected for 30 min by both collectors, for a total of 60 person-minutes of sampling per site per month. Even with two weeks of training, collectors are not fully trained melittologists, and so to ensure that the samples are as complete as possible, collectors are instructed to collect all "bee-like" insects actively visiting flowers, hovering in the air, or along the ground; by collecting all "bee-like" insects, the risk of missing unique or rare bees is reduced. Each collector will have a timer that starts at the beginning of netting but is stopped during specimen handling; this is especially important because new collectors take longer to process specimens, and also because all "bee-like" insects are being collected, which may slow down processing. Collectors net insects opportunistically within the plot.

Netted specimens are euthanized in soapy water due to limitations of ethanol accessibility while in the field (the use of soapy water is but one example of a collection method, see *The Very Handy Bee Manual* (A Collective, 2024) for other options; collectors should balance ease of collection with project goals when selecting collection methods). Specimens are stored in small sample vials with screw-on lids and detailed labels describing the date, collector, location, method, and time of collection. At the end of each day, the soapy water is drained from the vials and replaced with alcohol to prevent specimen rot. The collected specimens will not be pinned until the end of the season. With crews in four locations throughout the state, a central processing location is not feasible. All specimens, collected by both net and bowl trap, are stored locally in a freezer until they can be transferred to the government facility. In October, all specimens are relaxed and pinned and labeled for identification.

The agency follows *The Wild Bee Data Standard* (Du Clos *et al*., 2025) and uses either the worksheet or workbook data template to organize their data (Du Clos *et al.*, 2024). In their template, each specimen collected is assigned a unique **dwc:occurrenceID** and the following information is provided for each specimen record, or row, in the digitized data: the corresponding specimen number from the identification label (**dwc:catalogNumber**), the initial taxonomic identification of the specimen (**dwc:genus**), the full name of the person who made the taxonomic identification (**dwc:identifiedBy**), the date on which sampling took place (**dwc:eventDate**), the method used to capture each specimen (bowl trap or netting, **dwc:samplingProtocol**), the location at which each specimen was collected (**dwc:decimalLatitude**, **dwc:decimalLongitude**, **dwc:fieldNumber**), the full name of person who collected the specimen (**dwc:recordedBy**), the start and stop times of the sampling event in which the specimen was collected (for netting, **dwc:eventTime**; 24 hour bowl trap events are provided in **dwc:eventDate**). For specimens netted on a flower, the plant species is recorded (**dwc:associatedTaxa**); for those netted on the ground or in the air, this, too, is recorded (**dwc:occurrenceRemarks**). Specimen handling and storage details will also be provided (**dwc:materialEntityRemarks**). To fully document sampling effort, each specimen record will provide additional details about the sampling event in which the specimen was collected, including the size of the plot (**dwc:samplingEffort**), the number of bowl traps successfully retrieved (**dwc:sampleSizeValue**, **dwc:sampleSizeUnit**), the total duration of the sampling events (**dwc:samplingEffort**), and weather notes (**dwc:dynamicProperties**). Details about pesticide application schedules, bowl trap deployment, and collector experience are provided (**dwc:eventRemarks**) along with the habitat associated with each sampling location (**dwc:habitat**). Example entries for this case study are provided in both the worksheet and workbook templates available for use through Zenodo (Du Clos *et al.*, 2024).

DISCUSSION

Our intention with this protocol is to provide the bee research, monitoring, and conservation community with standardized methods for collecting comprehensive bee community-level data, including data standards, that can be used for the *inventory*, *survey*, and *monitoring* of wild bee communities. Carrying out the protocol outlined here for community-level bee data has the potential to produce large, interoperable datasets that can be analyzed together to understand patterns in bee communities at scales far beyond individual projects or programs. To date, our ability to answer questions about bee communities and how they change over space and time has been severely hindered by a lack of historic data collected using statistically rigorous, standardized approaches. This has left our research community to find creative approaches to understanding bee community change (*e.g.*, Colla *et al*., 2012; Burkle *et al.*, 2013; Mathiasson & Rehan, 2019; Chesshire *et al*., 2023; Ruzi *et al*., 2023). Although these approaches have given us the only insights possible into historical change, they have taxonomic, spatial, or other limitations that ultimately undermine our ability to detect and understand true changes in bee communities as distinct from changes in recording effort over time (Bowler *et al.*, 2024). A standardized, reproducible, and widely-shared protocol will give us the ability, moving forward, to overcome many of the limitations that currently exist. Properly collected, identified, stored, and digitized specimens, with appropriately reported sampling effort and protocols, can be utilized repeatedly to answer future, unexpected research questions (Meineke *et al*., 2018; Vaudo *et al*., 2018; Nachman *et al*., 2023) with diverse foci. Moreover, with standardized data, collections from multiple years and sites will be interoperable, even if collection efforts change from year to year. There are precedents for research, monitoring, and conservation communities coming together to develop standardized practices for their mutual benefit. Projects such as the North American Bat Monitoring Program (NABat; Loeb *et al*., 2015; see https://www.nabatmonitoring.org/) show us what is possible for wild bee data, if improved collection and data standards are implemented.

Currently, our protocol only includes lethal methods for data collection as bee species identities must be known to understand community composition, enabling informed conservation decisions (Breeze *et al*., 2020), and because most bees can only be reliably identified to species using physical specimens under a microscope. We acknowledge that data can be collected for subsets of the entire bee community (*e.g.*, bumble bees) using non-lethal, catch-and-release methods; at present these methods cannot be deployed for projects attempting to capture data on entire bee communities. All indications are that, in the future, the bee research, monitoring, and conservation community will have more opportunities to use non-lethal methods to collect data on wild bees, such as using photos (Flaminio *et al*., 2021; Armistead, 2023; Schlesinger *et al*., 2023) and eDNA (Thomsen & Sigsgaard, 2019; Sickle *et al*., 2023) as evidence of occurrence. We welcome these approaches to minimize lethal collection, but note that at present, they are still undergoing the processes of thorough vetting, validation, and development for deployment at larger scales. Moreover, some of these methods may not ever provide abundance data, which are needed to estimate some of the key parameters of communities and may only be suited to sample a portion of the bee community (Turley *et al*., 2024). We also recognize the inestimable value of continuing to collect some physical specimens and properly stewarding them in natural history collections (Lane, 1996; Holmes *et al*., 2016; Hilton *et al*., 2021), as this provides a wealth of ecological and evolutionary information that cannot be retroactively obtained, if specimens are not collected.

In the meantime, as we move towards more non-lethal approaches, we need to ensure that collections are conducted mindfully to limit harm to the very organisms we hope to conserve (Fischer & Larson, 2019; Barrett *et al*., 2022). This includes using collection methods that

reduce the negative experiences of individual bees (Drinkwater *et al*., 2019; Gelperin, 2019) and minimize potential harm to bee populations. For the latter, it is important to fully articulate the goals of a project and optimize the sampling design to best meet those goals (LeBuhn *et al*., 2016; Schlesinger *et al*., 2023; Levenson *et al*., 2024), while minimizing collection whenever possible (Drinkwater *et al*., 2019). Even when implementing this protocol, care will still need to be taken to minimize the multiple risks of lethal collection and difficulties of specimen stewardship, especially when moving toward the establishment of large-scale (*e.g.*, national) projects. Projects should estimate whether the scale of intended collection might have negative impacts on populations, although, in truth, this is challenging because we have so little information about how bee population sizes change through time (Williams *et al*., 2001; Aldercotte *et al*., 2022; but see Gezon *et al*., 2015) and what processes regulate wild bee population dynamics (Roulston & Goddell, 2011). We should also consider that as more bee species are protected under state and federal laws, certain sampling methods may become more restricted. Further, as population status can change rapidly, expeditious data access will be critical for conservation analyses and decision-making (Rousseau *et al*., 2024). Before a sampling plan is implemented, we advise reviewing the guidelines outlined in Drinkwater *et al*. (2019), Montgomery *et al*. (2021), and Trietsch & Deans (2018). As a summary of these guidelines, we suggest the following practices:

1. Select the sampling method and effort that will cause the least harm to bee populations, estimated to the researcher's best ability, while also collecting sufficient data to answer the project questions.
2. Review one's plan with experts in experimental design and statistics to confirm that the plan will address the project's needs.
3. Ensure the appropriate expertise is in place for identification of collected specimens, prior to initiating sample collection.
4. Properly store physical specimens, including labeling and depositing at an institution, to maximize the value of lethally-collected specimens.
5. Collect detailed data in association with physical specimens and deposit the data in an appropriate repository so that they may be used for future projects (see Du Clos *et al*., 2025).
6. Make specimen-related data publicly available as soon as possible in light of institutional or other limitations.
7. Reduce bycatch of non-target species while sampling, properly preserve any collected bycatch, and arrange for these additional specimens to be provided to other researchers or maintain them securely for future use.

We would also add to this list that projects might consider involving volunteers in participatory science projects to engage and train the public, as this can generate support for bee conservation. Large-scale community-level monitoring programs can be designed to provide opportunities for public involvement in data collection (Best *et al*., 2022; Rondeau *et al*., 2023; Turley *et al*., 2024). These programs benefit all parties as they provide training to participants and result in large-scale datasets that would be otherwise unattainable due to labor and resource constraints.

As we navigate this time of unprecedented biodiversity loss (Ceballos *et al*., 2015) it is critical that we document bee communities in a standardized, interoperable manner. Whether a project's goal is to *inventory*, *survey*, or *monitor* bee communities, standardized data are incredibly valuable and support both our foundational understanding of bee communities and the conservation of wild bees and other insects. In the case of bee community monitoring, we hope to see a greater shift towards sampling designs that allow for hypothesis testing (Breeze *et al*., 2020) and the establishment of explicit thresholds of community change (*e.g.*, percent

reductions in species richness, evenness, functional group breadth) that would trigger specific conservation actions. This would also require projects or institutions (or their partners) to have the capacity to then take on those conservation actions through large-scale collaboration across the science-policy interface as well as effective dissemination of results and information to a wide range of stakeholders.

By using standardized protocols, as outlined here and in the other protocols included in this special issue, there will be the opportunity for the bee research community to come together on a scale not yet seen, so that we can better address current, pressing, and future needs for bee conservation.

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SUPPLEMENTAL MATERIAL

Table S1. Summary of the *core*, *recommended*, and *optional* practices for following the community-level bee data protocol, specifically regarding site set up and data recording.

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Standardized protocols for collecting data on bee-flower interactions and the associated floral community

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Abstract. Pollen and nectar from flowers constitute the primary food resources of bees, inextricably linking bee and flowering plant communities in space and time. Thus, our understanding of bee biology and distribution can be greatly enhanced by documenting interactions between bees and their host plant species. Plant-pollinator interaction data are routinely collected in studies with diverse research goals, but the lack of standardization in data collection has limited our ability to integrate datasets and address outstanding questions in bee ecology, conservation, and pollination biology. Here, we provide standardized protocols for (A) documenting bee-flower interactions and (B) quantifying associated floral resources available to foraging bees. These protocols can be combined for a more detailed understanding of bee-flower interactions and can be applied in *inventories*, *surveys*, and *monitoring* programs of bees. We also provide case studies demonstrating their application. We discuss tradeoffs that are inevitable in any methodological approach, including the use of lethal versus non-lethal sampling approaches, and highlight the need to prioritize rigorous testing of the scalability and generalizability of current methodologies. These protocols are part of a series developed in association with the U.S. National Native Bee Monitoring Network to standardize bee monitoring practices.

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INTRODUCTION

Quantifying interactions among bee species and the flowers on which they forage is critical for understanding and advancing bee conservation and pollination biology alike. Flowers provide bees with nectar and pollen necessary for survival and reproduction. Thus, knowing which plant species individual bee species use and prefer across their flight seasons is central to supporting bee populations. Matching floral use to bee species can also inform how generalized a species is in its diet and reveal the identities of alternative floral resources. Both of these aspects determine species' resilience to landscape transformation, habitat loss, competition, and climate change. In addition to the importance of flowers for supporting bees, bees provide flowers with essential pollination services. Bees' functional role as pollinators of wild plants and managed crops is a primary justification driving bee conservation worldwide (Ollerton *et al*., 2011; Hanley *et al*., 2015; Siopa *et al*., 2024). Quantifying the frequency and timing of bee visitation to flowers allows us to make inferences regarding the importance of different bee species for the pollination of plant species of interest (*e.g*., Winfree *et al*., 2007). Currently, due to the relative paucity of empirical studies providing detailed measures such as pollen deposition from single bee visits, patterns of floral visitation form the foundation for understanding bees' functional roles as pollinators (Vázquez *et al*., 2005). Thus, direct observation of plant-pollinator interactions provides a pathway for understanding a variety of ecological and evolutionary processes, including pollination, resource partitioning, trait matching, phenology of communities and their interactions, community robustness, and biodiversity maintenance, which in turn serve as foundational knowledge for evidence-based conservation and management efforts.

Historically, data on the interactions between bees and flowers have been obtained through largely opportunistic, or otherwise unstandardized, collections of bees on flowers (Burkle *et al*., 2013). These methods provide important insights that, when accumulated, can be used to infer general host associations (Hurd *et al*., 1980; Fowler, 2016; Fowler & Droege, 2020; Smith *et al*., 2023). Such opportunistic collections, however, often lead to biased representation of certain interactions depending on factors such as the season of collection, and thus may result in over- or under-reporting of some species and their functional importance as either hosts or pollinators. Additionally, even datasets collected using more standardized methods, such as those in the recent proliferation of studies of plant-pollinator network structure (*e.g*., Bascompte & Scheffer, 2023), often lack quantitative measurements of the abundance of flowering plants available to bees (Vázquez *et al*., 2007). Floral abundance and diversity often show strong relationships to bee community metrics (Potts *et al*., 2003; Lane *et al*., 2020; Gerner & Sargent, 2022; Torresani *et al*., 2023). Furthermore, quantifying floral abundance for each plant species at the time bees are collected allows for interpretation of host plant preferences that underlie bee-host plant associations (Vázquez & Aizen, 2003; Williams *et al*., 2011). Thus, standardized assessment of floral communities, combined with characterizing flower use by bees, provide fundamental information to land managers selecting plant species for conservation, management, and restoration efforts (Harmon-Threatt & Hendrix, 2015; Williams *et al*., 2015).

Here, we present standardized protocols for collecting bee-plant interaction data. We recognize that individual research teams may work in different ecological contexts and have diverse goals for documenting patterns of floral visitation by bees, and therefore we do not prescribe rigid parameters for study design. Rather, we

propose a set of *core* metrics for which to record how data collection is performed, such that future researchers can utilize the data to the fullest extent. In particular, it is necessary to report metrics such as floral resource abundance and survey effort (*e.g.*, size of search area, amount of time spent searching) so that those wishing to combine multiple independent datasets in meta-analytic or synthetic frameworks may do so without having to make assumptions that may lead to incorrect inferences. Properly documenting the *core* metrics we propose will allow researchers, managers, and agencies to achieve their specific goals (*e.g.*, evaluate the importance of different host plants and bloom phenology) while simultaneously generating interoperable data across collections to understand plant-pollinator interactions better over greater spatial and temporal scales. In the face of declining pollinator populations, the ability to combine robust data on floral host use among studies is fundamental to understanding broader-scale changes of species and communities in responses to climate and land use and other persistent environmental drivers. Moreover, documenting patterns of interactions informs strategies for how we can help mitigate these impacts.

Below, we present two standardized protocols to be used in combination:

Protocol A: Collecting bee-flower interaction data, specifically the species identities and relative abundances of interactions among blooming flowers and bees at a given location. Here, an interaction between a bee species and a plant species is inferred when a bee has been collected from (or observed on) a flower.

Protocol B: Collecting community-level flower data. This involves recording blooming flower species at the location where bee sampling took place, including estimated flower abundances (in floral units), which can be used to estimate floral resource availability for bees and other pollinators at the location, and also their relative preferences among resources standardized by resource abundance.

These protocols assist in the design and implementation of *inventory*, *survey*, or *monitoring* projects of bees with the goal of generating standardized, interoperable data on bee interactions with floral resources (Protocol A) and the availability of floral resources for bees at the same location (Protocol B) (Du Clos *et al*., 2025; Levenson *et al*., 2025). We summarize *core, recommended,* and *optional* data collection and practices of these protocols (Table 1, Appendices 1–3). We define a bee-flower interaction as occurring when a bee contacts the reproductive parts of the flower or is extracting resources through behaviors such as nectar robbing. Time permitting, it is *optional* for the collector also to record more detailed behavior of the bee when visiting the flower (*e.g.*, collecting pollen, imbibing nectar).

Depending on sampling design, information generated by following these protocols can be used to make ecological inferences, including individual bee species' diet breadth, floral choices and preference, and the phenology of bee-flower interactions. Note that the bee-flower interaction protocol (Protocol A) addresses individual visits and cannot be used to calculate the rate of visitation from either the bee's or the plant's perspectives, which may be important variables for some studies. Protocol A will generate bee community-level data, but these data will be specific to bees actively visiting flowers; for sampling entire bee communities, irrespective of whether bees are visiting flowers, a protocol is provided in Levenson *et al*. (2025b; this special issue). Protocol A can also be used to generate lists of bee visitors to flowers in an area. Although we focus on bee visitors to flowers, this protocol can be used in studies that aim to sample broader groups of insect flower-visitors (flies, butterflies, etc.) by modifying it to meet taxon-specific differences in data collection. Protocol B is

Table 1. This protocol is part of a series developed in association with the U.S. National Native Bee Monitoring Network to standardize bee monitoring practices. These protocols include three components of data (*Core, Recommended*, and *Optional*), which are outlined for three strategies of data collection (*Inventory, Survey*, and *Monitoring*). Details in Levenson *et al*. (2025a).

Levels of Data Collection and Reporting		
Core	*Recommended*	*Optional*
Practices that are essential for achieving one's objective(s) and need to be used to meet the purpose of the protocol.	Practices that are extremely beneficial, but not essential, to the specific objective(s) of the protocol.	Practices that can be followed and may be worth the additional effort required, depending on one's objective(s).
Strategies of Data Collection		
Inventory	*Survey*	*Monitoring*
An attempt to build a bee-flower interaction list for an area, not standardized for space or time.	An attempt to record data of an area, standardized over space and/or time.	An attempt to record changes in community measures over time, employing a consistent and repeated protocol, standardized over space and time.

meant to estimate food resources available to bees (*i.e.*, floral abundance and diversity) within the immediate area in which Protocol A is carried out. As such, Protocol B may not be appropriate for estimating overall floral resource availability at the level of the site in which Protocol A is embedded (unless coupled with robust methods such as stratified random sampling of quadrats or transects distributed at the site level), since Protocol A focuses effort on flower patches or other areas enriched with floral resources.

PROTOCOL METHODS

Protocol A: Bee Sampling

Sampling scheme. Where to sample: For these protocols, as in the protocol for collecting community-level bee data (see Levenson *et al*., 2025b), we are defining terms as follows. A *site* is an area of interest of any size, containing one or more plots or transects (Fig. 1), that may contain multiple habitat types. The site may be, for example, an entire location to which a treatment was applied (*e.g.*, hedgerow planting, an area managed through grazing or burning, or restoration site). Site selection is among the most important and time-consuming steps of sampling design if a researcher is interested in ultimately using their data to make general inferences (*e.g.*, the effect of logging on plant-pollinator interactions), as poor site choice can limit or even negate study findings (Eigenbrod *et al*., 2011). Details of site selection are beyond the scope of these protocols and are highly dependent upon the goal(s) of the study. It is critical, however, to ensure sites are independent, not spatially autocorrelated (*e.g.*, sites assigned to specific treatments are not clumped in a specific area), encompass the range of variation in predictor variables appropriate to the specific questions (*e.g.*, site size,

surrounding landscape) while not significantly varying in factors that may impede meaningful comparison across sites (*e.g.*, underlying geology or hydrology), and are numerous enough to have the power to detect changes within or differences among sites (Eigenbrod *et al*., 2011; Williams, 2011; Pasher *et al*., 2013; Hung *et al*., 2019a; Bowler *et al*., 2022). Further, because Protocol A calls for hand-netting bees from blooming flowers (see below), sites without blooming flowers at the time of data collection will not have bee-flower interaction data. In these cases, it is still important to document clearly that the site lacks floral resources during the sampling time in question, as it allows for comparison among types of sites, times of season, state of disturbance, *etc*., and thus context for understanding key goals of monitoring bee-flower interactions. In these cases, researchers can report a sampling event at that site with no bee occurrences recorded (Du Clos *et al*., 2025). In some instances, a land manager may be interested in the bee-flower interactions or floral resources at a specific location, rather than making general inferences, and thus can dispense with explicit consideration of site selection protocols. In these cases, however, researchers should refrain from making general inferences over large areas based on these location-specific findings.

A *plot* is an area within a site that could be sampled via linear or meandering *transects* (Fig. 1; Westphal *et al*., 2008) and is located within one habitat type. A *transect* is a sampling path (including length and width), located within one habitat type, that falls within a plot or site (Fig. 1, A versus B). Thus, using plots, transects, or the two in combination (*i.e.*, transects within plots), are alternative ways of organizing data collection with the goal of characterizing the bee and/or floral communities at a site. Establishing and sampling at least one standardized plot and/or transect at each sampling site is a *core* practice for Protocols A and B for *surveys* and *monitoring*, and *recommended* for *inventories*. Importantly, this means that for the goal of *inventory* for Protocol A, single bee-flower interactions provide valuable information where the *core* data fields are bee identity, plant identity, date, and geographic location of the interaction, but without the requirement of documenting sampling effort within

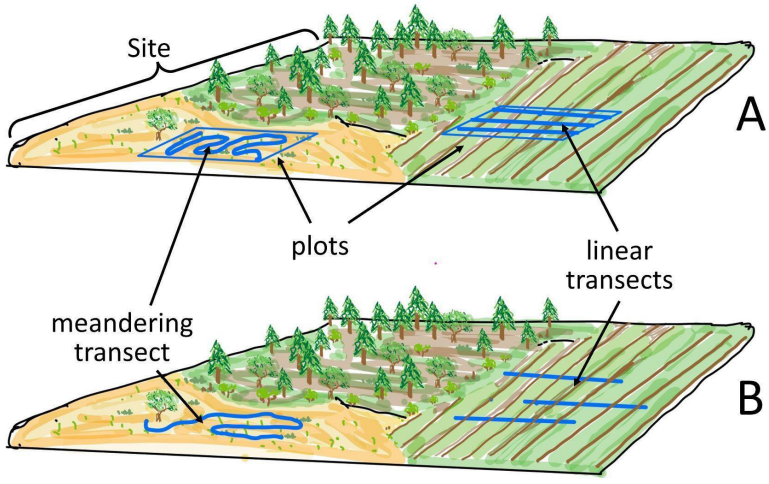

Figure 1. Schematic of sampling scheme showing (A) plot-based approaches with embedded transects and (B) transect based approaches. In both cases these sampling frames fall within single habitat types within the larger site.

delimited spatial areas or time frames. The majority of Protocols A and B generally pertain to methods related to *survey* and *monitoring*, which are plot- or transect-based.

To select plots within a site, we *recommend* following a stratified random sampling design across the site. Stratification involves placing plots across a known gradient or underlying distribution of habitats or environmental conditions (*e.g.*, wetland to upland, wooded versus open areas) within the site. This protocol allows for a deliberate, unbiased representation of the site. Completely random plot placement, in contrast, could also capture the range of environmental conditions, but might require a larger sample size. As long as the choice of exact plot locations within a stratum is random, samples will avoid bias. The appropriate number and distribution of plots within a site will depend on available resources and the question being asked. Theoretically, the number of plots should increase in more heterogeneous sites, but in practice the number employed is often dictated by the amount of time and effort that can be invested. We *recommend* using two categories of plot sizes (see also Levenson *et al*., 2025a): *small plots* (0.01–0.24 h), which can be surveyed in their entirety or nearly so; or *large plots* (0.25–1 h), where researchers can derive informative and representative samples of the overall area using a number of transects (see below). While admittedly somewhat arbitrary, these recommendations are consistent with plot sizes used in the existing literature and represent workable spatial scales for the data collection protocols we outline here. Although it is not a *core* practice of the protocols, for most purposes, keeping plot size consistent across sites within a study is critical for making robust comparisons.

Standard transects are fixed lengths and often (but not always) linear. Typically, standard transects maintain the same location across sampling rounds, although this is not a *core* practice. For meandering transects, observers meander within a plot among floral resources. Meandering transects may sample a greater proportion of the bee community than linear transects (Westphal *et al*., 2008). If a transect is not bounded within an established plot, a *core* practice is to record the length and width of the transect being used and the nature of the transect (*i.e.*, linear *vs.* meandering, randomly placed *vs.* directed). The flexibility that meandering transects allow for may be particularly beneficial in habitats where floral resources have a heterogeneous distribution, as they allow researchers to avoid areas without flowers and thus maximize the amount of time spent sampling from actively flowering plants. Regardless of whether transects are linear or meandering, we *recommend* that within a study, the length and width of transects be kept constant across sites/plots and sampling rounds to facilitate statistical comparison of data. We also *recommend* that time of sampling either remains consistent and/or is recorded to facilitate comparisons across study sites.

It is *recommended* that for small plots (see above) the transect minimum length is 25 m and sampling is performed within 1 m on all sides of the transect for a total minimum sampling area of 50 m^2. For large plots we *recommend* a minimum transect length of 100 m, with sampling performed within 1 m on all sides of the transect for a total minimum sampling area of 200 m^2. Longer transects are *recommended* when possible and necessary (*e.g.*, to capture a representative set of blooming plant species in highly heterogeneous habitats). Splitting a long transect into smaller sections and keeping data separated by section will allow for easier comparison of data with studies and sites that have shorter transects or effort, and calculation of measures of variation.

Transects can be used to sample sites, and the habitats within them, without defined plots. It is a *core* practice of these protocols that regardless of transect type, total transect distance be contained in one general habitat type and that the transect length

or plot area be recorded to allow for standardization of effort and interoperability of the data. For meandering transects, length can be determined using various mobile phone-based GPS applications or more technical GPS receivers.

In some cases, research goals may be better served by allocating approximately equal sampling effort across all blooming plant species within a transect or plot, *e.g.*, when it is important to document the bees associated with rare or rarely visited plant species (Gibson *et al.*, 2011). In Appendix 4, we provide guidance on converting data collected in that fashion into data that are interoperable with our *core* practices.

WHEN TO SAMPLE: The timing and frequency of sampling events will depend on the specific project goal(s) but should consider ecological characteristics relevant to the bee-flower interactions, such as the duration of bloom periods and bee flight periods, environmental conditions that influence when bees would be observed at flowers, and the research and conservation goal(s) of the project. A *core* practice of these protocols is that each plot or transect is sampled a minimum of one time. Sampling more sites less intensively in close temporal proximity better characterizes regional or large site-level patterns of plant use (Bruninga-Socolar *et al*., 2023), whereas repeated sampling within a growing season will be more informative to assess the quality of a site and temporal turnover of bee-flower interactions (Levenson & Tarpy, 2023). Floral resource availability can change over short timescales (on the order of days or weeks). Therefore, if a goal is to compare visitation and/or resources between sites, data collection should happen ideally over a time period that minimizes temporal turnover among bee and floral communities.

We *recommend* including sufficient sampling rounds (temporal replication) required to capture within-season turnovers of bee and blooming flower communities and their interactions within a habitat type. Whether these samples are implemented across replicated sites, or replicated rounds within a site, will depend on geographic region, elevation, season length, and specific project goals. For example, in areas with a shorter active bee flight season, fewer sampling rounds may be required than in areas with a longer active season. If the goal is characterizing the entire bee community, for example, then sampling events are *recommended* across the active flight season of all bee species to capture seasonal differences in the bee and flower communities. If the sampling goal is examining between-year phenological change, for example, the timing of sampling can be selected to coincide with the peak active flight season (if known) or can coincide with phenological events, such as snowmelt or the bloom of a particular plant species. Alternatively, holding the calendar date constant across sampling years may provide information on how bee and plant communities shift their phenologies in response to interannual climatic variation.

Consider that sampling at different times of day at the same site can affect the resulting data as different bee species have different daily activity windows (Fründ *et al*., 2011; Danforth *et al*., 2019). Furthermore, bee activity can be affected by biotic factors such as pollen and nectar availability, and abiotic factors, such as temperature, wind, and moisture on flowers. Thus, it is a *recommended* practice that each site be sampled twice in a sampling round (single day or sequential days), once in the morning and once in the afternoon. Doing so can help to account for this variability and allow one to capture a more complete snapshot of the interactions between bees and flowers.

Recommended conditions for bee data collection are on warm days with clear skies and low to no wind (see Levenson *et al*., 2025b for more details). Practitioners will determine the specific details about sampling site, plot size, transect type, and transect

length for each study, and record these metrics prior to data collection. Although the duration of sampling necessary to obtain sufficient data may vary across contexts, we *recommend* establishing a consistent, predetermined sampling duration for each event prior to data collection to facilitate comparisons across sampling events within the same study. For example, 10 min of active sampling along a 100-m transect has been effective in grasslands (Lane *et al*., 2020). It is a *core* practice, however, to record the sampling duration as a metric of search effort. It is important that the recorded sampling effort only includes the time spent searching for bees; the timer must be stopped after netting and while processing bees or recording data. Therefore, transects with high bee and flower abundance may take much longer to sample compared to transects with low bee and flower abundance. Due to this variation in total elapsed time among sampling events, it is also a *core* practice to record the start and end time of the entire sampling event so that appropriate inferences may be made regarding the activity patterns and foraging choices of the bees that were documented. When sampling, move at a slow, even pace from one end towards the other end of the transect (for both linear and meandering transects). The pace must allow the entire transect to be sampled within the established sampling duration. The observer scans all flowers within a 180-degree radius that are within one meter on either side and one meter in front of the observer.

Type of sampling, lethal and non-lethal: Prior to lethal or non-lethal sampling, researchers need to decide whether to collect honey bees. It is a *core* practice to document whether honey bees are to be collected or not. If honey bees are not collected, collectors must be able to distinguish honey bees from other bee species. In general, we *recommend* netting wild bees only, as processing honey bees (*i.e.*, netting, pinning/photographing, and labeling) can increase the amount of time spent in the field and lab. Furthermore, honey bees can be highly abundant in some areas and thus may constitute a large proportion of sampling effort. If honey bees will not be collected, we *recommend* tallying the number of honey bees seen along each transect, making sure to note the flowers on which the honey bees were observed. Record these numbers on the data sheet by listing the flower species followed by the number of honey bees seen on that plant species. Such data allow researchers and others interested in directly comparing honey bee visits to wild bees to use the data. Time permitting, researchers might want to mark honey bees to ensure that individuals are not recounted. A *recommended* alternative practice would be to collect honey bees, record the plants they were foraging on, keep them in a cooler, and then release them when sampling is complete. This would eliminate the potential of double counting honey bees within a sampling event. Note that some other insects (*e.g.*, some flies and wasps) closely resemble bees; thus, we *recommend* netting or tallying all insects suspected to be wild bees.

Lethal sampling: One of the most critical considerations when implementing lethal collection is ensuring specimens are accurately identified and properly curated. A *core* practice of this protocol is that a plan for bee specimen identification and storage is established *prior* to starting data collection. This includes ensuring the identification expertise, funding, and resources required to identify, curate, and maintain collected specimens are all in place (see Packer *et al*., 2018). This plan should be reported with bee records following *The Wild Bee Data Standard* (Du Clos *et al.*, 2025).

When a bee is observed on a plant, the observer captures the bee, immediately pauses the timer, and transfers the bee into a collecting vessel (*e.g.*, a jar or vial containing ethyl acetate or another euthanizing agent). Once transferred, the vessel is labeled with the plant species from which the bee was collected. All bees caught from that plant species within the plot or transect during the same sampling event can be placed in the same collecting vessel for temporary storage, if project goal(s) allow. A *core* practice is to record the most precise taxonomic rank possible for plants. Typically, this would be plant genus and plant species. For each plant species from which bees are collected, we *recommend* taking four photos of one representative plant as a voucher: one photograph of a single flower looking down on the petals, one photograph from the underside of the flower, one capturing details of the stem and leaf, and one of the whole plant. This series of photos can be used to identify most plants to the level of species. We *recommend* adding photo vouchers to established online platforms (*e.g.*, iNaturalist, observation.org). For an example of how to use iNaturalist to document this information, refer to The Oregon State University Master Melittologist program (https://extension.oregonstate.edu/master-melittologist).

We suggest using the following workflow for processing specimens in the field when following this lethal-sampling approach:

First, fill out a sample label and place one in each collecting vessel. The information should include site, date, plot and/or transect number, site, start and stop time of the sampling event, and collector's initials. We note that most of this information can be pre-printed onto small paper labels ahead of the collecting date for more efficient labeling in the field.

Second, once all individual specimen containers are labeled with plant data, collect and transfer them into a labeled plastic bag (representing one sampling event).

Third, in the plastic bag place a card with the following information: date, site, capture method (netting), and initials of the collector(s). If more collecting will occur, place the bag in a cooler with ice or an ice pack and repeat this process.

An *optional* practice is to handle specimens in a way that will allow them to be used for studying pollen carried on or adhering to bee bodies, or for ectoparasites; in these cases, the bees must be individually collected into separate containers to avoid cross-contamination from one bee to another. Samples that are not collected in this way cannot be used to study pollen or ectoparasites because of the potential for transfer when specimens come in contact with each other in collecting vials (see Strange *et al*., 2025; this issue).

NON-LETHAL APPROACH: For non-lethal data collection, methods may emerge with new technologies and wider adoption among the community of bee enthusiasts and researchers. At present, our non-lethal protocol mirrors the structure of the lethal approach and requires stringent approaches to photography (digital imaging) to ensure photo vouchers are of a standard as comparable as possible to physical specimens. It is not a protocol that creates data as coarse morphological groupings but rather is geared at species / morphospecies identification. Nonetheless it is important to recognize there are many bees that cannot be identified to species based on photographs; such species will thus go unrepresented in datasets generated using this approach despite being photographed (Turley *et al*., 2024). This will limit inference regarding some measures of community change (*e.g.*, diversity metrics, turnover, etc.) and will be biased towards bees that can be identified from photographs or on the wing. For a number of goals, a

non-lethal image-based approach might be best suited for certain bee groups such as bumble bees and other groups that can be identified accurately by sight. It is possible to combine lethal and non-lethal approaches within the same study (See Case study 1). Further, some bee species are distinct enough to be identified on the wing and can be treated in a manner similar to honey bees (see above).

When a bee is observed on a plant, the observer captures the bee, immediately pauses the timer, and then transfers the bee into a clean collecting vessel. In cases where multiple bees are visiting the same plant species in a transect or site, if not collecting specimens for pollen or ectoparasites (Strange *et al.*, 2025), it is an *optional* practice to capture multiple individuals in the same net sweep and chill them together in a larger container. Once transferred, the vial is labeled with the plant name (as outlined above) and placed into a cooler for a minimum of 10 min to immobilize the bees. In our experience, long periods on ice of even two hours will not harm bees (see Oyen *et al.*, 2021). Bee species inhabiting different environments vary in their cold tolerance (Gonzalez *et al*., 2022), and some species may be more prone to chill-induced injury or mortality than others. Since thermal tolerances are unknown for most bee species, and even more so their responses to and recovery from cold immobilization (*e.g.*, Wilson *et al*., 2006; Frost *et al*., 2011), we *recommend* that researchers perform pilot observations of how species in their targeted bee communities respond to cold immobilization before subjecting large numbers of bees to this treatment in full-scale studies. When using a non-lethal approach, a *core* practice is that all handled specimens must be photographed, either singly or arranged in neat groups on a plain surface (*e.g.*, ideally neutral, off-white matte background, with a known-sized printed grid), after which they can be released. We *recommend* using established protocols for photographing bees, such as the protocol developed for the Xerces Society of Invertebrate Conservation's Bumble Bee Atlas projects (available at https://www.bumblebeeatlas.org/pages/photography-tips). Note that this protocol was developed and is effective for bumble bees (Colgan *et al*., 2024), but may not be sufficient for other bee groups. As non-lethal methods continue to develop, we expect that protocols will be tailored to specific groups of bees to aid in identification. It is a *core* practice to label any photo vouchers taken in the field to ensure alignment with sampling event data once digitized (*e.g.*, by recording the image filename in a datasheet, or placing a written or printed sampling event identifier next to each bee being photographed).

Once bees are chilled enough to be immobile, an *optional* practice is to hold all bees in a cooler and release them at the end of a sampling event. Another *optional* practice is for collectors to mark their thoraces with a small dot of non-toxic ink and then release them. The ink dot ensures that individual bees are not resampled. After an individual bee has been processed, the timer is started again, and the observer continues toward the opposite end of the transect, repeating the process outlined above if and when another bee is encountered. We *recommend* treating the "digital specimens" (*i.e.*, photographs) generated using this protocol with the same standard of curation as with physical specimens generated from lethal sampling protocols–*i.e.*, reporting information regarding who provided the taxonomic identification of each specimen and where the images are digitally archived. Uploading the images to iNaturalist.org and adding the identification using the platform provides a streamlined approach to accomplish this goal.

Protocol B: Plant Sampling Methods

A *core* practice for *surveys* and *monitoring* is estimating the amount of blooms for all flowering species occurring in the area where bee sampling is performed (*i.e.*, along transects or throughout a plot). Another *core* practice is to collect floral data around the same time (ideally, on the same day) that bee data have been collected using Protocol A. Doing so provides information regarding floral resource composition and availability at the same spatial and temporal scales as the bee sampling. Importantly, if *site-level* floral resources need to be characterized, additional floral data must also be collected at locations where bees are not sampled. In either case, floral units are estimated separately for each flowering species, in logarithmic or quasi-logarithmic quantity bins (Table 2), to enable rapid and interoperable quantification of the diversity and relative abundance of floral resources in the sampled area. An *optional* practice is to assess floral abundance that yields specific density-based estimates of floral units in the sampled area. The appropriate methodology to accomplish this latter task may vary across study systems and research goals, and may include censusing floral units in plots, transects, or quadrats (Appendix 5).

Table 2. Example quasi-logarithmic floral unit bins in a transect-based survey, with corresponding description-based categories provided for comparative purposes. For longer transects, additional categories with higher floral unit quantities may be added.

Categories for a 50–100m transect	Categories for a 100m + transect	Alternative description-based categories	Alternative category definitions
1–5	1–10	Sparse	Seldom occurring and usually occurring as an isolated plant; few total individuals observed
10–50	10–100	Occasional	Scattered plants in low number; sometimes occur in small clumps
50–250	100–1000	Frequent	Many plants observed; species is regularly seen but rarely becomes dominant
200+	1000 +	Very Common	Species occurring in large numbers; can be dominant

To quantify floral units, it is a *core* practice for researchers to walk along the entire bee sampling area (transect or plot) and estimate the floral units encountered in the area. It is a *core* practice that all species in flower be documented regardless of whether bees are observed visiting them or not, since data on the identity and relative abundance of flowers that are not visited are crucial for elucidating foraging decisions and preferences of bees. Floral unit estimation can be done at any time of day but note that some flowers may wilt or close by midday or may not open until mid-morning, making them more difficult to observe depending on the time of day of flower sampling. It is an *optional* practice to record sampling time and sampling effort (*i.e.*, sampling duration and transect or plot area) as doing so may help in planning for how much labor is required for future sampling. If bee sampling methods may cut or trample flowers, we *recommend* estimating floral abundance first, before bees are sampled.

Documenting the unit of measurement constituting a floral unit for each species is also a *core* practice. A floral unit may consist of a single floret (*i.e.*, morphologically distinct flower) or intuitive clusters of florets (parts of inflorescences or whole inflorescences, for example, "flat" inflorescences of certain Apiaceae and panicles of *Lupinus* and *Solidago* spp.). As a guide, we suggest considering these seven flower shape categories, defined and depicted in Appendix 6: Distinct, Spike, Catkin, Composite, Clustered, Flat, and Paniculate. Decisions on what a floral unit consists of depends on practicality–estimating individual florets may be preferable when a plant species presents distinct, unclustered flowers (*e.g.*, *Argemone* spp.) or when it is rare, whereas estimating compound units (*i.e.*, spikes, clusters, panicles) may be necessary when the same species is overly abundant. To ensure interoperability across surveyors and datasets, it is a *core* practice to record floral data that allow for cross conversion—for example, recording the average number of open florets on a spike or panicle when using these aggregate units of floral abundance. Consider the following scenario: a surveyor might estimate the number of *Lupinus* flowers as individual flowers when fewer than 20 individual blooming plants are encountered in a transect, but estimate the number of blooming spikes at a site where several hundred are encountered in a transect; in this latter case, the surveyor would also record the number of individual flowers borne on 5–10 spikes such that the number of individual flowers at the transect might be estimated. It is a *recommended* practice to predetermine the floral units for each species of a specific project prior to data collection. Detailed photographs of representative units of floral measurement associated with each data collection event may also facilitate interoperability. It is important to note that this protocol yields simple estimates of floral abundance for each plant species, and thus generally cannot be used to parameterize some plant-focused metrics, such as plant density or number of flowers per plant, without the collection of additional data outside the scope of this protocol.

A *core* practice of this protocol is that all recorded plant species are vouchered; this can be done with photo vouchers as described in Protocol A, but physical specimen voucher collection is *recommended* for species-level identification. Regardless, it is a *core* practice to report the type of voucher collected and where the voucher can be accessed for verification. Another *core* practice is to report any sources used in plant identification (*e.g.*, *The Jepson Manual* (Baldwin *et al.*, 2012) or a research-grade iNaturalist photo voucher). The taxonomic resolution for plant identification will depend on project goals. Monolecty (specialization on a single plant species) is rare in bees with most specialist (*i.e.*, oligolectic) bee species not distinguishing among congeners (Wcislo & Cane, 1996); therefore, taxonomic resolution at the genus-level is a *core* practice for identifying flowering plants, but we *recommend* species-level identification.

Data recording: The data to record for this protocol include information on bee species, plant species, and floral units. The complexity of bee-flower interaction data presents challenges to establishing universal standards. This is a rapidly changing area and we expect new protocols to emerge. Two recent, ongoing projects working on such standards are the Brazilian Network of Plant-Pollinator Interactions (REBIPP, Salim *et al.*, 2022) and the WorldFAIR Agricultural Biodiversity Standards (Trekels *et al.*, 2023; Drucker *et al.*, 2024). Both initiatives aim to modify the Darwin Core data standard to incorporate terms that describe plant-pollinator interactions. Darwin Core (Wieczorek *et al.*, 2012) is a widely accepted biodiversity data standard used by leading biodiversity

data providers, including the Global Biodiversity Information Facility (GBIF; https://www.gbif.org/), Integrated Digitized Biocollections (iDigBio; https://www.idigbio.org/portal/search), and iNaturalist (https://www.inaturalist.org/). *The Wild Bee Data Standard* (Du Clos *et al*., 2025; this issue) uses Darwin Core terms and describes their application to wild bee occurrence data, with modifications to existing ratified terms to report bee-flower interactions (Table 3). Applying Darwin Core terms to wild bee occurrence data following *The Wild Bee Data Standard* increases interoperability of data across studies. Examples of recorded data associated with the collecting events for the case studies presented below can be found in worksheet and workbook templates provided with *The Wild Bee Data Standard* (Du Clos *et al*., 2024). Although we outline the *core* data requirements in Table 3 (but also see Appendices 1–3), additional data fields can be collected beyond what is outlined if capacity allows.

Table 3. *Core* data fields to be recorded when implementing the bee-flower interaction and floral community context protocols to adhere to *The Wild Bee Data Standard* (Du Clos *et al*., 2025). *These terms also relate to plant data for Protocol B.

***Core* Data field**	**Description**	**Corresponding Darwin Core Term**
	Protocol A	
Protocol used*	Cite this protocol, as well as others used, and note any modifications	**dwc:samplingProtocol**
Latitude/ Longitude*	Location in decimal degrees of where sampling occurred. Use the center of sampling location (*e.g.*, transect or plot)	**dwc:decimalLatitude dwc:decimalLongitude**
Sample Area*	Plot size or transect area in square meters	**dwc:samplingEffort**
Duration of sampling event	Start date/time, end date/time, duration of active sampling	**dwc:eventTime, dwc:samplingEffort**
Number of collectors	The number of people who collected bees by net during a sampling event (optimally record collectors' collections separately)	**dwc:sampleSizeValue, dwc:sampleSizeUnit**
Basis of record	Document whether the record is a physical specimen or a photographic voucher. Can relate to a bee record or a plant record depending on which protocol component is being used	**dwc:basisOfRecord**
Details of the sampling event*	Report transect type (linear or meandering), length, and width, along with other contextual event information. This includes any site treatment and how honey bees were handled	**dwc:eventRemarks**
Bee physical specimen identification information	For lethally collected specimens, report the identity of the specimen, and the personnel and reference sources involved in the identification	**dwc:scientificName, dwc:identifiedBy, dwc:identificationResources**

Bee physical specimen curation information	Provide identifiers (links or codes) for the institution and collection where the specimen is permanently stored. May report in one or multiple terms	**dwc:institutionID, dwc: collectionID, dwc:institutionCode, dwc:collectionCode**
Bee photo voucher information	Provide links or identifiers of photo vouchers, separated by a vertical bar if necessary. For non-publicly held media, please provide the name of the institution that manages the media data	**dwc:associatedMedia**
Plant association	The plant species on which a bee was collected or observed. Report the species ID and the nature of the interaction (Appendix 7)	**dwc:associatedTaxa**
Plant photo voucher information, if applicable	Provide links or identifiers of photo vouchers, separated by a vertical bar if necessary. For non-publicly held media, please provide the name of the institution that manages the media data. This field is core only if the plant a bee occurrence was collected on was photographed as a representative voucher	**dwc:associatedOccurrences**
	Protocol B	
Plant photo voucher information	Provide links or identifiers of photo vouchers, separated by a vertical bar if necessary. For non-publicly held media, please provide the name of the institution that manages the media data	**dwc:associatedMedia**
Plant identification source(s)	Provide citations for any references used to identify a plant record. Additional context for the taxon name may be provided in **dwc:namePublishedIn** or **dwc:nameAccordingTo**.	**dwc:identificationReferences**
Number of floral units	Provides a count for the number of floral units of a species observed at a sampling site; note that these are reported as ranges as data are binned into categories based on counts (Table 3)	**dwc:organismQuantity**
Type of floral unit	Provides the type of floral unit of a species observed at a sampling site (Appendix 6)	**dwc:organismQuantityType**
Details on measuring floral units	Provides context for arriving at floral unit measurements for each plant species for reproducibility	**dwc:occurrenceRemarks**

EXAMPLES OF IMPLEMENTING BEE-FLOWER INTERACTION AND FLORAL COMMUNITY PROTOCOL

Case Study 1. Inventory of Plant-Pollinator Interactions at Federal Sites

A government agency requests an inventory of plant-pollinator interactions (specifically, wild bee floral visitors) in different habitats within the boundaries of their properties. The agency would like to begin with implementing a single-year *inventory*. The agency has restrictions in which, for certain key bee groups (in particular, at-risk bumble bees), lethal collection should be minimized, and any take must be carried out under permit. As a result, the inventory team is preparing a hybrid *lethal-* and *non-lethal* approach to reduce sampling biases.

Before the *inventory* begins, a plan is established for bee physical specimens and photo voucher identification, curation, and storage. A taxon expert who will identify physical specimens is contacted and compensation is agreed to for the work. An accession agreement for the identified specimens is established with a local museum. An iNaturalist project is created to share photo vouchers of both bees and plants, which will allow for verification of field-based identifications. Supplies are prepared based on the number of sites that will be visited in a day. Permitting and permissions are established for each property and protocols are developed in collaboration with staff at each property.

A set of priority sites has been determined in collaboration with the agency that are expected to have high bee diversity, diverse regionally important native plants, and include multiple habitat types. This approach will advance the agency's interest in using the data to inform vegetation management and selection of plant species to support bees at the properties.

A team of two researchers will visit sites on four different sampling rounds distributed over the main growing season of the region to capture phenological turnover of wild bee floral visitors, their floral host plants, and patterns of interaction. During each sampling round, the team will visit two sites per day, sampling at each site in both the morning and afternoon. To estimate relative abundances among wild bee floral visitors, the team will use a meandering transect approach and record the transect length and width. Most sites contain a single habitat type (*e.g.*, montane wet meadow) but some sites have two habitats (*e.g.*, open woodland adjacent to a meadow). In this case, each habitat will be inventoried separately using separate transects. The team will spend one person-hour walking a 400-m meandering transect, netting any bees observed within 1-m on each side in each habitat type. The team will record the start and end times for each sampling transect and will stop the timer when processing netted bees.

All sampling during the visits will be conducted using an aerial net, for which honey bees will be tallied on a datasheet but not netted due to known high abundances at some sites near apiaries. Bumble bees will be assessed using a non-lethal photographic method, and other bee species will be lethally collected. The team has received extensive training on bumble bee visual identification and there is a high degree of confidence in separating them from other bee and flower-visiting insect taxa. Each collector will net bees from flowers. The flower and foliage of one representative of each plant that bees are collected from will be photographed as a voucher from four different views: (i) a single flower looking down on the petals, (ii) the underside of the

flower, (iii) details of the stem and leaf, and (iv) the whole plant. During the morning sampling, while one team member begins collecting bees, the other will quantify floral abundance along the transect. For efficiency and because of time constraints, the team will use categorical estimates of floral units in $\log_{10}$ bins. Exact floral units (spikes, florets, panicles, etc.) will be determined before each sample event and will be kept consistent within a plant species among the four sample rounds. While quantifying floral abundance, one representative of each plant species in bloom, including those from which no bees are observed, will be photographed as a voucher from four different views as described above. All plant photo vouchers will be uploaded to the team's iNaturalist project.

Lethal approach: When a bee is collected from a new blooming plant species along a sampling transect, a plant-specific collection vial will be created and labeled with a unique event identifier containing the date, site and time of sample; the flower species name; and collector initials using masking tape (*e.g.*, AM-SITE1-Date, Plant species, INITIALS). Note that the unique event identifier created here can be used when digitizing the data after field sampling. Each vial will contain a rectangular strip of paper towel (~3 x 6 cm) inserted as a liner to absorb moisture. If the bee is not a bumble bee, it will be euthanized in the field using a cyanide kill vial and transferred to a labeled plant-specific vial. All non-bumble bees subsequently collected from that same flower species along the same transect will be euthanized and placed in this plant-specific vial.

Non-lethal approach: Bumble bee specimens will be handled differently after netting. Here, each bumble bee is transferred to a vial with air holes bearing a number on the cap. A photo of the vial cap is taken next to the flower the bee was collected on, allowing the vial number, bumble bee identity (as visually assessed in the field), and plant identity to be transcribed onto a datasheet. The vial containing the bumble bee is then placed into a wearable cooler carried by the surveyor. Vial caps have a 1-mm air hole in them to allow for air flow. At 10–15 min intervals during the transect walk, the timer will be paused and bumble bees will be removed from the cooler one at a time and placed in a simple light box, or a grooved tray painted flat white, that allows the bee to be quickly manipulated and photographed from (i) top, (ii) front-on-head, (iii) back-of-abdomen, (iv) side, and (v) underside-of-abdomen views. The numbered vial cap associated with each bee will be included in each photo to allow unambiguous association of the photos with the flower interaction data. The bee will then be released after imaging. After completing the sampling day, all photos of bees will be uploaded to the team's iNaturalist project. Photo sets from each specimen will be grouped based on the datasheet.

The team will follow *The Wild Bee Data Standard* (Du Clos *et al.*, 2025) and start with either the worksheet or workbook data template to organize their data, adding in any additional Darwin Core terms needed for their specific project (Du Clos *et al.*, 2024). In their template, each bee specimen collected is assigned a unique **dwc:occurrenceID** and reported as either a physical specimen if lethally collected or a photo voucher if non-lethally collected in **dwc:basisOfRecord**. The following information is provided for each specimen record, or row, in the digitized data: the unique event identifier used to label the collecting vessels (**dwc:eventID**), the date on which sampling took place **(dwc:eventDate)**, the method used to capture the specimen **(dwc:samplingProtocol)**, the location at which the specimen was found

(dwc:decimalLatitude, dwc:decimalLongitude, dwc:fieldNumber) based on the coordinates from a handheld GPS, the full name of the person who collected the specimen **(dwc:recordedBy)**, and the start and end time of the sampling event in which the specimen was collected **(dwc:eventTime).** To document sampling effort fully, each specimen record will provide additional details about the sampling event in which the specimen was collected, including the total sampling area (length * width of the transect) (**dwc:samplingEffort**) and the predetermined duration of active sampling along the meandering transect, reported in person-hours or decimals of person-hours (**dwc**:**samplingEffort**). Ecological context is provided by reporting weather conditions during the sampling event (**dwc:dynamicProperties**) and the habitat type each bee was collected in (**dwc:habitat**). The team reports that honey bees were tallied but not collected in **dwc:eventRemarks**.

The interaction between a blooming plant and a bee will be described with the term **dwc:associatedTaxa**. This term uses a key:value pair to describe the nature of the interaction and the plant species identification. The interaction is described using two controlled vocabularies, one describing the collection or observation of the bee, the other describing the part of the plant where the bee was collected or observed. While *The Wild Bee Data Standard* allows for interactions to be recorded on leaves and stems, all interactions recorded following this protocol will use "flowers of" here. The plant species identification is described with the taxonomic name and any sources used in making the identification. Examples and controlled vocabulary lists for **dwc:associatedTaxa** are provided in Appendix 7, and these details are also provided in *The Wild Bee Data Standard* (Du Clos *et al*., 2025). If the bee was collected on a photographed plant voucher, the link to the voucher plant on the team's iNaturalist project page should be provided in the term **dwc:associatedOccurrences**. If the plant the bee was collected on was not photographed, do not report anything in **dwc:associatedOccurrences**; the relationship established in **dwc:associatedTaxa** is sufficient. To document floral abundance, report the number of floral units in **dwc:organismQuantity**, report the type of floral unit in **dwc:organismQuantityType**, and report any details on measuring floral units in **dwc:occurrenceRemarks**. Example entries for this case study are provided in both the worksheet and workbook templates accompanying *The Wild Bee Data Standard* (Du Clos *et al*., 2024).

Case Study 2. Monitoring of Plant-Bee Interactions to Determine Effect of Prescribed Fire

A graduate student is examining whether prescribed fire affects floral resource abundance and floral use by wild bee communities. The current funding will allow the student to sample 20 sites for three years, hire a crew of three field technicians, contract with taxonomists for accurate bee species identification, and curate bee specimens for long-term storage. There are no protected bee species in the area, and the student will thus use a *lethal sampling* approach for all bee species.

The student works with various land management agencies to select 10 sites that will be burned in the spring every other year and 10 sites that will not receive burn treatment. A burned site will be paired with a nearby unburned site to create distinct site pairs. Sites within pairs will be at least 1000 m apart but within 5000 m. The student ensures that important characteristics (*e.g*., surrounding landscape, soil type, etc.) are relatively similar across all 20 sites. Further, the sites are evenly distributed across the landscape with respect to burn category (burned *vs*. unburned) and thus treatments

are not clumped in one location of study area. The sites are on average 5 ha in size and the habitat type is relatively similar across sites. The student decides to place two 0.5-ha plots randomly in each site. The sites will be sampled four times throughout the year to yield inference representative of distinct floral communities across the growing season. Before the first round of data collection starts, all four researchers will perform the study protocol together at two burned and two unburned sites, and compare their individually collected data (*e.g.*, estimated floral abundances, size distribution of collected bees) to verify that there are no systematic differences across the four datasets that would result in biased interpretations.

Sites within each pair will always be sampled simultaneously, with each site sampled by a set of two technicians, totaling four personnel working on each sampling date. Both plots at each site are sampled twice on each sampling date, once in the morning and once in the afternoon, totaling eight sampling events, four per site, on each sampling date. The date, sampling start time, and sampling end time will be recorded for each sampling event for each plot. During a sampling event, one technician will walk along a 200-m meandering transect for 10 minutes and collect all bees observed visiting flowers within 1-m on either side of the center of the transect. Once a bee is collected, the technician will stop the timer and transfer the bee into a plant-specific collecting vessel (a 50-ml centrifuge tube charged with ethyl acetate). They will record the plant species the bee was collected on, what part of the plant the bee was collected on, and the nature of the interaction. If this is the first time a bee has been collected from a plant species, a plant-specific collecting vessel will be created by writing the name of the flower species from which the bee was collected and the initials of the collecting technician onto a small cardstock label preprinted with a unique event identifier comprised of the site and plot numbers, sampling date, and sampling period (*i.e.*, AM or PM), then placing the label into the collecting vessel before restarting the timer and returning to netting. When another bee is collected from that same flower species during the same sampling event, it is also placed in that labeled plant-specific collecting vessel. When a bee is collected from a new flower species, another plant-specific collecting vessel is labeled. This approach is being used because the student will not be performing any analyses of pollen or ectoparasites on the collected bees. During this time, the other technician will follow this same protocol at the other plot at that site. Once a sampling event has been completed, the technicians transfer all bee specimens collected from each flower species, along with their associated host plant labels, from plant-specific collecting vessels into plastic vials for storage. All the vials are then placed in a cooler. This protocol is repeated in the afternoon following the floral data collection (see below).

Following the morning collection event, the technicians will briskly walk throughout their respective plots and document the abundance of all blooming plant species, at the level of the 0.5-ha plots, in log10-based bins. Whenever possible, they will record floral units as compound inflorescences (spikes, panicles, etc.), taking five photos of haphazardly selected inflorescences so that the number of florets within each floral unit may be calculated, for interoperability across sites. These photos, along with photographs of the foliage and the entire plant, will be uploaded to an iNaturalist project set up for this study to act as digital vouchers to establish plant identity. Additionally, as one of the planned analyses involves examining how host plant density influences bee foraging decisions, the team will also record a more precise, density-based estimate of floral abundance by laying out four 50-m transects after estimating floral abundances at the plot level. Along each transect, they will place a

1x1-m quadrat at 0 m, 10 m, 20 m, 30 m, 40 m, and 50 m, alternating quadrat placement on either side of the transect. This will lead to a total of 20 quadrats per plot. In each quadrat, the observer will count the total number of floral units for each species within the quadrat. Floral units for each species will be determined prior to collecting plant data. In addition, the technicians will measure the dimensions of 10 floral units for each plant species in the study, haphazardly chosen from within the plot. This will then be used to calculate the total floral area for each plant species for each quadrat (number of floral units x mean area of each floral unit).

The team will follow *The Wild Bee Data Standard* (Du Clos *et al*., 2025) and start with either the worksheet or workbook data template to organize their data, adding in any additional Darwin Core terms needed for their specific project (Du Clos *et al*., 2024). In their template, each bee specimen collected is assigned a unique **dwc:occurrenceID** and is reported as a physical specimen in **dwc:basisOfRecord**. The following information is provided for each specimen record, or row, in the digitized data: the unique event identifier used to label the collecting vessels (**dwc:eventID**), the date on which sampling took place **(dwc:eventDate)**, the method used to capture the specimen **(dwc:samplingProtocol)**, the location at which the specimen was found **(dwc:decimalLatitude, dwc:decimalLongitude, dwc:fieldNumber)**, the full name of the person who collected the specimen **(dwc:recordedBy)**, and the start and end time of the sampling event in which the specimen was collected **(dwc:eventTime)**. The plant species the specimen was collected on, and the nature of the interaction is provided in **dwc:associatedTaxa** (see Appendix 7 for full details). If the bee was collected on a photographed plant voucher, the link to the voucher plant on the team's iNaturalist project page should be provided in the term **dwc:associatedOccurrences**. If the plant the bee was collected on was not photographed, do not report anything in **dwc:associatedOccurrences**; the relationship established in **dwc:associatedTaxa** is sufficient. To document sampling effort fully, each specimen record will provide additional details about the sampling event in which the specimen was collected, including the total sampling area (length * width of the transect) (**dwc:samplingEffort**) and the predetermined duration of active sampling along the meandering transect, reported in person-hours or decimals of person-hours (**dwc**:**samplingEffort**). Report the site type (burned or unburned) each bee specimen was collected in in **dwc:eventRemarks**. To document floral abundance, report the number of floral units in **dwc:organismQuantity**, report the type of floral unit in **dwc:organismQuantityType**, and report any details on measuring floral units in **dwc:occurrenceRemarks**.

DISCUSSION

The scientific literature presents a long and rich history of documenting interactions between communities of co-occurring plants and pollinators. The methodologies used in previous studies have ranged from visual observations on single plant taxa with pollinators identified only to coarse taxonomic groupings (*e.g.*, Albano *et al*., 2009; Watts *et al*., 2012), to collection of all floral visitors of an entire blooming plant assemblage (*e.g.*, Alarcón *et al*., 2008; Williams, 2011; Lane *et al*., 2020; Levenson & Tarpy, 2023), with methods tailored variously to address research questions from the plants' or the pollinators' perspective, or both. Many of these studies are couched in the context of examining the mathematical properties of plant-pollinator interactions in an interaction network context (*e.g.*, Carstensen *et al*., 2016; Cirtwill *et al*., 2018). Our intention with these protocols is not to provide guidance on the "correct" way to construct bee-

flower interaction networks, or to dictate aspects of sampling design that can only be decided based on the goals of a particular project. Rather, we provide the bee research, monitoring, and conservation community with fundamental standardized methods and data standards for documenting interactions between bees and their floral host plants, primarily from the bee community's perspective, but also with guidance on better integrating the plant's perspective (Appendix 4). These practices are designed to support existing and future efforts to contribute interoperable floral visitation (and floral abundance) datasets across the diverse disciplines that routinely involve the collection or observation of bees on flowers, and for *inventory*, *survey*, and *monitoring* projects with diverse goals. When separate datasets are collected using the *core* practices we present, we can combine them to elucidate the nature of bee-flower interactions over large spatial and temporal scales and address research questions that range from fundamental natural history (*e.g.*, the list of preferred host plants for a particular bee species over its geographic range) to applications in evolutionary biology (*e.g.*, conservatism in host plant use across congeners) and conservation biology (*e.g.*, key floral communities associated with persistence of threatened bee species), regardless of the initial objectives of the study in question. In addition to data interoperability across studies, documenting the *core* metrics we propose is crucial for establishing the most robust and actionable comparative data. For instance, Thorp *et al*. (1994) had meticulously documented floral visitation patterns and qualitatively scored host-plant preferences of native bees and introduced European honey bees on Santa Cruz Island, California, and were able to draw some qualitative inferences on the impact of partial honey bee eradication on the island (Thorp *et al*., 2000). However, because we lack information on aspects of their methodology that are *core* to the protocols we presented, we are unable to assess quantitatively at the species level—for either plants or pollinators—the repercussions of one of the only successful large-scale European honey bee eradications ever performed (Wenner *et al*., 2009).

One challenge of research on bee-flower interactions is the tradeoff between lethal and non-lethal data collection methodologies. Non-lethal methods often will yield taxonomically imprecise data, which preclude the use of such data for assessing the floral host associations of the full suite of individual bee species in a study system. In contrast, lethal methods may adversely impact bee populations and/or pollination services rendered to plants, potentially altering the pattern of interactions being documented even as individual bees are removed during the data collection period (Brosi & Briggs, 2013). Here, we provide standardized guidelines for non-lethal documentation of bee-flower interactions in a manner that yields enhanced taxonomic resolution compared to observation-based protocols but acknowledge that these non-lethal methods are still in their infancy. At the present, they are time-intensive relative to lethal collecting and may not be practical or feasible in all regions and for all taxa. Photographic vouchers may be sufficient for certain taxa, such as bumble and carpenter bees, but will yield imprecise identification for taxa that traditionally require scrutiny of morphological minutiae—though resolution may improve with advances in both imaging technology and image classification assisted by deep-learning computer vision (Spiesman *et al*., 2024). As such technologies continue to improve, validation of non-lethal methods and vigorous testing of their scalability should be a research priority. More broadly, few studies to date have evaluated whether different methodologies for documenting bee-flower interactions yield different conclusions (*e.g.*, Gibson *et al.*, 2011). Studies to evaluate the degree to which protocols with different sampling

intensity (*e.g.*, sampling duration and frequency, area of coverage), effort allocation decision (*e.g.*, across plant species, transects, sites), and data precision (*e.g.*, floral unit quantification) yield comparable patterns are very much needed.

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APPENDIX 1

Summary of the *core*, *recommended*, and *optional* practices for establishing study sites and sampling timeframes following the plant-pollinator interaction protocol (*i.e.*, both A and B components) in a *survey* or *monitoring* context. Each project will need to decide the specific details used under each component.

Protocol Component	***Core* Practices**	***Recommended* Practices**	***Optional* Practices**
Sampling scheme	Use a sampling plot or transect Sites are spatially independent		
Transects and Plots	Transects and plots are entirely located in one site in one habitat type (Levenson *et al.*, 2025b) Use at least one standardized plot or transect per site and sample event	Select plots or transects within a site following a stratified random sampling design At least one standardized plot or transect for *inventories*	Completely randomized plot or transect placement can be used but may require larger sample sizes to capture the range of environmental conditions
Plot size	Record the plot size	Establish a small plot (0.01–0.24 h) or a large plot (0.25–1 h) (Levenson *et al.*, 2025b) Keep plot sizes consistent across sites	
Transect size	Record transect length and width Record transect type (linear or meandering) and placement (random or fixed location)	A minimum of 25 meters for small plots and 200 meters for large plots Fixed length across sites/plots	Record meandering transect length with a phone-based GPS application or a GPS receiver
Sample frequency	Sample each plot or transect one time at minimum	Sample enough times to capture within-season turnover of bee and blooming flower communities If the goal is to characterize the entire bee community, sample across the active bee flight season Sample each site once in the morning and once in the afternoon in each sampling round	

APPENDIX 2

Summary of the *core*, *recommended*, and *optional* practices for the plant-pollinator interaction protocol specifically relating to bee sampling methods (Protocol A). Each project will need to decide the specific details used under each component.

Protocol Component	***Core* Practices**	***Recommended* Practices**	***Optional* Practices**
		For lethal and non-lethal	
Sampling conditions	Record weather conditions during sampling	Sample on warm days with clear skies and little to no wind (Levenson *et al.*, 2025b)	
Plant interactions	Document the plant species a bee specimen was collected on	Take four photo vouchers of each plant species: one of a single flower looking down on the petals, one from the underside of the flower, one of the stem and leaf details, and one of the whole plant Upload photo vouchers to iNaturalist	
Sampling time frame (for *survey* and *monitoring* only but recommended for *inventory*)	Record start time, end time, and total search time (*i.e.*, excluding specimen handling / data recording time) Pause the timer when netting and processing bees or recording data	Standardize total search time across sampling events	
Targeted taxa	Record how data on honey bees, if present, were collected. Also record if other species were not collected. If a bee species was collected differently from others, detail the method used (*e.g*, tallied on flowers, netted and released after temporary confinement, etc.). For taxa that are released, record sex when possible	Tally the numbers and identities of non-collected bees (*e.g.*, honey bees) observed foraging on each plant species Capture all insects suspected to be bees	

		For lethal	
Physical specimen collection	Once captured, specimens need to be accompanied by labels unambiguously tied to sampling event data in all vessels until pinned in the laboratory Identify specimens to the finest taxonomic resolution possible and deposit them in a collection capable of long-term archival	If project goals allow, place all specimens collected from the same plant species in the same collecting vessel	If specimens will be used to study pollen or ectoparasites, place each specimen in separate containers to avoid cross-contamination
		For non-lethal	
Digital specimen collection (image-based)	Take at least one photograph of all handled bee individual specimens Each photograph needs to be unambiguously tied to sampling event data (write down photo filename in datasheet, or include event data within image frame) Identify photographed specimens to the finest taxonomic resolution possible and safely archive the image files	Use a developed photography protocol, such as those from Xerces Bumble Bee Atlas, to increase likelihood and certainty of species-level identification Upload photo vouchers to iNaturalist	Chill all specimens collected on the same plant species together To reduce double counting, ink dot bees or hold specimens in a cooler until the end of the sampling event (including honey bees) Collect only wild bees

APPENDIX 3

Summary of the *core, recommended,* and *optional* practices for following the plant-pollinator interaction protocol specifically relating to plant sampling methods (Protocol B). Each project will need to decide the specific details used under each component.

Protocol Component	***Core* Practices**	***Recommended* Practices**	***Optional* Practices**
Floral units	For *survey* and *monitoring*, estimate the amount of blooms for all flowering species in a plot or transect, regardless of whether a bee was collected on that species or not Walk the entire plot or transect Use quantity bins outlined in Table 2 Document the measurement constituting each floral unit following Appendix 6 Record floral data to allow for cross-conversion such as average number of open florets on a spike, for example	Record floral abundance before bees are sampled to avoid cutting or trampling blooms Photograph a representative unit of floral measurements associated with each data collection event	Follow methodology outlined in Appendix 5 to perform more detailed floral abundance assessments Record sampling effort
Plant vouchers	Voucher all plant species included in data collection Report if a physical or photograph voucher is used Identify plants to genus-level	Physical specimens may be needed for species-level identification Identify plants to species-level	

APPENDIX 4

An alternative to documenting bee-flower interactions using transects is to spend a standardized, predetermined length of time observing patches of each blooming plant species within a plot (*e.g.*, Gibson *et al.*, 2011; Spiesman & Inouye, 2013; Traveset *et al.*, 2018). This approach may be useful when plots where bees are sampled are highly heterogeneous such that no transect layout would cover all plant species, or when documenting the bees associated with rarer plant species is an important goal (Gibson *et al.*, 2011). We *recommend* spending the same amount of time observing each plant species in bloom and observing multiple patches of each species in intervals of 1 to 10 min per patch. An observation patch should be large enough that pollinator visits to the patch are likely within the observation interval (*e.g.*, a single flower may not be visited within 10 min), but small enough that any bee visiting flowers of the patch can be readily detected and collected without losing track of other bees visiting the same patch. The size of the patch would thus depend on the context of the bee-flower interactions—species with large flowers that experience low visitation rates may have larger patches, whereas densely packed inflorescences that experience high visitation rates may need to have smaller patches. We highly *recommend* keeping the patch size approximately consistent within the species during each sampling event at each site (but not necessarily across sampling events and/or sites). As with the transect-centered protocol, each bee that lands in the patch being monitored is collected and placed in a lethal or non-lethal collecting vessel while the timer is paused.

This equal-effort observation approach results in pollinator data that do not accurately reflect plot-level relative abundances of visitors to rare versus abundant plant species. However, it is possible to correct for the bias towards rarer plants introduced by this approach. To do so, it is necessary to record the number of floral units in each species' observation patches, as well as a more precise estimate of the number of floral units of each plant species within the plot (*i.e.*, more precise than logarithmic-based quantity bins; see Appendix 5). The process for the bias correction is as follows:

First, average across the N rounds of observations at patches of a particular plant species to estimate the average number of blooming floral units (*e.g.*, individual flowers, capitula, panicles) observed in each round (or alternatively, choose a set number of floral units and consistently observe a patch with that number of floral units for each round of observations).

Second, average across the N rounds of observations of the plant species to estimate the average number of individuals of each pollinator taxon visiting an observed patch of that species per observation interval within the study plot.

Third, estimate the number of observation patches of the plant species blooming within the study plot (*i.e.*, divide the plot-level floral unit count by the observation patch-level floral unit count), and multiply this number by the pollinator abundance estimates calculated in the second step. The resulting value represents the estimated number of individuals of each pollinator taxon expected to be visiting all flowers of the plant species per observation interval over the entire study plot.

Fourth, repeat steps above for each plant species in bloom at the study plot to derive corrected relative frequencies of bee-flower interactions at the plot.

APPENDIX 5

The *core* methodology for documenting floral abundance involves estimating the number of floral units within the sampled area in logarithmic or quasi-logarithmic bins. However, certain research questions would benefit from additionally obtaining more precise measures of floral density over the sampled area. The most efficacious method for obtaining these more precise measures may depend on the context, and here we offer two possible methods.

METHOD 1. If there are blooming plant species, one may count floral units in regularly (or randomly) placed quadrats or transects dispersed throughout the study area. For example, consider a 50m x 50m plot where a field technician walks along a meandering transect to collect bees. One way to sample the floral community would be to create two ~71m transects running diagonally across the plot from corner to corner. Along the transect, the field team places a 1m x 1m quadrat every 7m for 20 total quadrats. The field team alternates the placement of each quadrat on either side of the transect. For each quadrat, the team counts the number of floral units that are contained within the quadrats. As much as possible, the team should agree on how to characterize species based on their floral units. If a new species of flowering plant is encountered, the field team should all agree on how the new species will be recorded. The field team also measures the floral units so as to be able to calculate the total area per floral unit. For example, for circular flowers or inflorescences, they will measure the diameter to estimate area per unit. Measurements should be conducted for at least 10 floral units. After the data are collected, entered, and cleaned the number of floral units per species can be multiplied by the average area for that species to calculate the total floral area per quadrat per species. This method provides transect-level estimates for the total floral area as well as each species individually.

METHOD 2. In study systems with highly patchy distribution of blooming plant species, it may not be possible to capture the relative abundance of all plant species using transects or quadrats. In such cases, we *recommend* counting replicates of increasingly larger components of floral units, then multiplying across the averages of all components (*e.g.*, see Hung *et al*., 2019b). For example, count 5 replicates of the number of flowers on a *Lupinus* stalk, 5 replicates of the number of stalks on a *Lupinus* plant, 5 replicates of the number of *Lupinus* in a 1-m^2 patch of *Lupinus*, and the number of 1-m^2 patch of *Lupinus* in the entire sampled area. Then, average the replicate counts and multiply the averages together to derive the estimated number of *Lupinus* flowers at the entire plot. There can be as many nested levels of components as necessary, and the organization of the levels may depend on the context (*e.g.*, number of individuals might be estimated if floral abundance is relatively uniform across individuals, but number of stems or racemes might be estimated instead if individuals differ widely in how many stems or racemes they bear). It may be helpful to divide the plot into quadrants or sectors to facilitate counting plot-level components, and to use a click counter when tracking large numbers.

APPENDIX 6

Example floral morphologies and arrangements, and recommendations for documenting their abundance.

DISTINCT
Example: *Chamaecrista fasciculata*

Each flower has its own pollen structures, is fairly large and easily countable.

Count each individual flower as one floral unit.

Other examples include *Rosa*, *Papaver*, *Potentilla*, and *Penstemon*

SPIKE
Example: *Verbena hastata*

Each spike is a tall structure composed of many smaller, distinct flowers.

Count each independent spike structure as one floral unit.

Other examples include *Melilotus*, *Lupinus*, and *Astragalus*.

COMPOSITE
Example: *Rudbeckia hirta*

Each composite is composed of a central disk of many small florets surrounded by ray petals.

Count the entire composite head as one floral unit.

Note that composite blooms often hold onto their ray petals after they stop producing pollen. Be sure to check the pollen structures in the central disk for pollen before recording it as "blooming".

Other examples include *Helianthus*, *Heliopsis*, *Ratibida*, *Grindelia*, *Madia*, and *Taraxacum*.

CLUSTERED
Example: *Trifolium repens*

Each cluster is composed of many small, often irregular florets. Clusters are most often round or semi-circular. In some cases, these will be hanging down.

Count each cluster as one floral unit.

Other examples include *Securigera*, *Monarda*, *Medicago*, *Lotus*, and *Eriogonum*

FLAT
Example: *Zizia aurea*

Each flat unit is composed of many small, difficult-to-count florets arrayed on a single plane, called an umbel. Since each umbel can have varying numbers of florets, count this type of flower as the number of circles with a 5 cm diameter (about the size of a fist).

Other examples include *Vernonia*, *Achillea*, *Lomatium*, and *Pycnanthemum*.

PANICULATE
Example: *Solidago canadensis*

Each paniculate unit is composed of many small, difficult-to-count florets arrayed on irregularly sized branches, called a panicle, along a single rooted stalk.

Count each individual rooted stalk as one floral unit.

Note that panicle blooms may need to be further categorized into distinct size categories when there is large variation in individual panicle sizes, such that a plant species would occupy multiple entries on the datasheet, where panicles belonging to separate size classes are recorded separately (*e.g.*, recording small panicles ≤ 15 cm, medium panicles ≤ 50 cm, and large panicles > 50 cm as distinct entries).

Other examples include *Symphyotrichum*, *Euphorbia*, and *Hypericum*.

APPENDIX 7

Details for using the term **dwc:associatedTaxa** as described in *The Wild Bee Data Standard* (Du Clos *et al.*, 2025).

DEFINITION: A list of identifiers or names of taxa (in this case, plants) and the associations of this occurrence (in this case, a bee) to each of them.

HOW TO USE: *This term uses a controlled vocabulary.* Using a key:value pair, provide the appropriate relationship from the following list, using a combination of an action and a part of the plant where the bee was found. If using both the plant species and the authority key:value pairs, separate them with a comma. Enclose the entire term with curly brackets ({}, see Examples):

- Controlled vocabulary list for **dwc:associatedTaxa**:
  - Action vocabulary: "Caught on", "observed on", "visits"
  - Plant part vocabulary: "flowers of", "leaves of", "stem of"

Provide at least the genus name of the plant, though the full plant scientific name (*Genus species*) is preferred. We advise reporting the source for the taxonomic name with the authority key:value pair.

- The authority should be a full citation of the source used to identify the plant. Examples include:
  - Flora Novae Angliae. 2011. Yale University Press https://plants.usda.gov/home/plantProfile?symbol=SOCA6
  - The Jepson Manual: Vascular Plants of California. Second Edition, 2012. University of California Press

EXAMPLES:

- {"visits flowers of":"*Rubus*"}
  - For reporting plant interaction only and identifying plant to genus level
- {"observed on flowers of":"*Solidago canadensis*", "authority":"The Jepson Manual: Vascular Plants of California. Second Edition, 2012. University of California Press"}
  - For reporting plant interaction, full scientific name of the plant, and the source of the taxonomic identification of the plant

FOR MORE DETAIL: https://dwc.tdwg.org/terms/#dwc:associatedTaxa

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Estimating occupancy of focal bee species

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Abstract. Current bee monitoring efforts have a limited capacity for understanding factors affecting wild bee population changes, including the effects of management. To improve the effectiveness of wild bee monitoring, we first discuss principles of biological monitoring and provide a framework to design monitoring projects to estimate species occupancy, where occupancy is defined as the probability that a Sampling Unit or site is occupied by the focal species. Monitoring practitioners should first define the desired goal or question of monitoring and secondly select the appropriate state variable for monitoring (*e.g.*, species richness, occupancy, abundance). These represent two critical, yet often overlooked, steps in the development of wild bee monitoring projects. As with all forms of demographic monitoring, practitioners who are interested in estimating species occupancy will need to develop a sampling scheme tailored to meet their monitoring objectives. Defining key sampling terms will provide the architecture of their scheme, including the Area of Interest, Sampling Unit, Season, and Replicate Survey. We also highlight data standards, including *core* data fields that must be collected during Surveys for bee occupancy data and additional, *recommended* data fields. We illustrate how these monitoring concepts are being applied to the design of a real-world monitoring project for the federally endangered rusty patched bumble bee (*Bombus affinis* Cresson). This framework was developed in association with the U.S. National Native Bee Monitoring Network.

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INTRODUCTION

Occupancy, defined as the probability that a Sampling Unit (*i.e.,* site, patch, etc., Table 1) is occupied by one or more focal species, is a primary variable of interest for many biological monitoring programs in the United States, including the Amphibian Research and Monitoring Initiative and North American Bat Monitoring Program. It is selected as a state variable (*i.e.,* quantities that describe a state of a dynamic system, at a specific time) for biological monitoring because of its effectiveness in informing management (Weller, 2008; Hamer *et al.,* 2021), understanding species distribution dynamics (Adams *et al.,* 2013), and evaluating species responses to environmental stressors (Grant *et al.,* 2016; Janousek *et al.,* 2023). In addition, the U.S. Fish and Wildlife Service (USFWS) often uses occupancy when establishing demographic goals for species recovery under the Endangered Species Act. More pragmatically, occupancy is often used in wildlife monitoring because it is less costly and time consuming than collecting species abundance data yet also provides meaningful information on species demographic dynamics (MacKenzie & Nichols, 2004; Noon *et al.,* 2012).

Here, we provide bee monitoring practitioners with a framework to design a sampling scheme for estimating species' occupancy across space and time, while also outlining some more general principles required for robust monitoring projects. We provide guidance on monitoring design and assist practitioners with defining key terms that are important for conducting occupancy monitoring. We describe *core* (*i.e.,* required for achieving monitoring objectives) and *recommended* (*i.e.,* additional, beneficial) data fields, though we do not provide specific parameters for these fields, such as recommended Sampling Unit size or Survey duration, because these should be based on individual project goals (Du Clos *et al.,* 2025). For many bee species, relatively little is known about their baseline distribution and natural history, which makes it challenging or impossible to implement formalized monitoring. Some information on the focal species' natural history is required before more formalized monitoring can be initiated (Levenson *et al.,* 2025a). Our target audience thus consists of people or organizations interested in developing monitoring projects for focal wild bee species to understand changes in species occupancy through time or the effect of management or stressors on species occupancy. We recognize that holistic monitoring of wild bees should also include other state variables such as species diversity, population size, and vital rate parameters associated with changes in diversity and population size (Yoccoz *et al.,* 2001). In fact, we note that occupancy often serves as the foundation of other biological monitoring programs in the United States, but these programs also include monitoring of other variables such as species richness, abundance, and survival (Corn *et al.,* 2005; Muths *et al.,* 2005). Practitioners should review additional protocols in this special issue and other published bee monitoring protocols (*e.g.,* Droege *et al.,* 2016) to decide which best fit their monitoring objectives.

Much has been written about designing biological monitoring projects (Yoccoz *et al.,* 2001; Nichols & Williams, 2006; Marsh & Trenham, 2008) and there is a pressing need to incorporate this guidance into wild bee monitoring to generate actionable information for conservation. Otto *et al.* (2025) highlight the broad importance of identifying bee monitoring objectives and state variables and discuss the advantages of integrating occupancy estimation into bee monitoring. Here, we build upon this approach to provide a framework to design a sampling scheme for bee monitoring for estimating species occupancy. This framework consists of the following steps: 1) Identify monitoring objectives; 2) Select the state variable(s) of interest; 3) Design a sampling scheme and define key sampling terms (Table 1); 4) Select field sampling methods; and 5) Select data fields (Fig. 1).

Table 1. Key terms for designing an occupancy monitoring project.

Term	Definition
Area of interest	The space over which monitoring practitioners hope to make inference
Detection	An unambiguous record of the focal species observed or collected during a Survey. A positive Detection may include a physical or photographic voucher
Sampling unit	Discrete location or patch, located within the Area of Interest, where occupancy of the focal species will be evaluated (*i.e.*, a monitoring site)
Season	A time period when the state variable (e.g., occupancy, abundance, species richness) is assumed to be static or unchanged. For occupancy monitoring, a Season is a period when Units are closed to changes in occupancy (*i.e.*, unoccupied Units remain unoccupied and occupied Units remain occupied)
State variable	One or more quantities that describe the state of a dynamic system, at a specific time. For biological monitoring, State Variables include occupancy, abundance, and species richness
Survey	A single sampling event conducted at a Sampling Unit where detection/non-detection data of the focal species are recorded. Multiple Surveys are conducted within a single Season to estimate species detection probability
Target population	All Sampling Units that exist within the Area of Interest. Probabilistic sampling is used to select a subset of Sampling Units for data collection

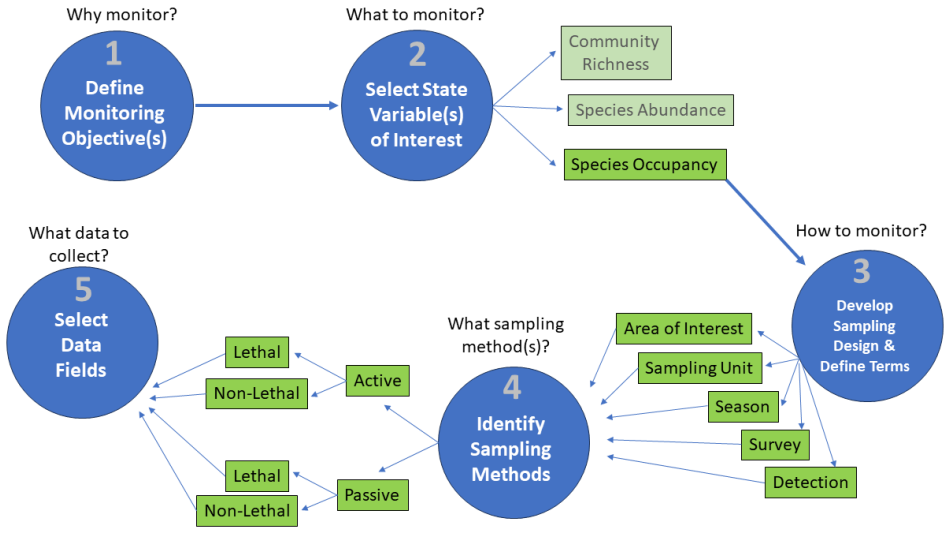

Figure 1. Flow chart for designing a monitoring effort for estimating occupancy dynamics of focal bee species.

We provide practitioners with specific guidance at each step of the framework and address common issues practitioners are likely to encounter along the way. To further illustrate the necessary processes, we also provide a Case Study describing a long-term monitoring project being developed for the federally endangered rusty patched bumble bee (*Bombus affinis* Cresson, Fig. 2), where occupancy is a state variable of interest for monitoring.

Figure 2. The federally endangered rusty patched bumble bee (*Bombus affinis* Cresson) visiting butterfly milkweed (*Asclepias tuberosa* L., Apocynaceae) in eastern Minnesota. Photograph by Clint Otto, USGS.

STEP 1. IDENTIFY MONITORING OBJECTIVES

Before designing protocols for occupancy monitoring (or any form of monitoring), it is important to establish monitoring objectives. Developers of wildlife monitoring programs have stressed that monitoring has its greatest utility when the objectives are clearly defined, the data collection is hypothesis-driven, and it is clear what decisions will be influenced, or what uncertainty will be addressed, through monitoring (Yoccoz *et al.*, 2001; Nichols & Williams, 2006; Sutherland *et al.*, 2009). Experts have challenged practitioners to develop monitoring objectives that either address scientific uncertainty surrounding species demography or assess the impact of management (Yoccoz *et al.*, 2001), as opposed to conducting surveillance monitoring that is not driven by specific objectives. Monitoring objectives can also be strengthened if the desired future state of the system can be identified, such as a desired minimum population size. Whereas general "trend detection" is often used as the impetus for initiating monitoring, once a trend is detected, it often leaves decision-makers wanting to know more detailed, actionable information, such as the ecological drivers of the observed trend, or what population vital rates are associated with the observed trend (*e.g.*, local colonization/extinction for occupancy, individual survivorship, fecundity, and movement for abundance). Thinking hard about monitoring objectives during the early phases of wild

bee monitoring can help ensure that priority information needs are met and that years of monitoring effort are not wasted on the collection of data that have little value for achieving specific monitoring goals. This is especially important for rare or declining species that often have time-sensitive monitoring needs. Otto *et al.* (2025) provide working examples of how to develop wild bee monitoring objectives that improve scientific understanding of demographic processes and/or inform management actions. The importance of defining monitoring objectives will become readily apparent when it comes time to design the sampling scheme. This is because decisions about where and when to sample and what data to collect are highly conditional on the monitoring objectives (Fig. 1). Defining monitoring objectives also helps practitioners determine the state variable(s) to monitor and the demographic quantities to estimate. Note that monitoring objectives can be formulated to address multiple areas of uncertainty and will often be accomplished in phases, such as in an adaptive management framework. The multiple phases of monitoring are evident in our Case Study, provided below, where practitioners are interested in first learning about factors that bias estimates of *B. affinis* occupancy, specifically false absences, so that a more robust monitoring project is designed to understand long-term changes in species occupancy.

STEP 2. SELECT THE STATE VARIABLES

Identifying the focal state variable(s) of a monitoring project is the second step in our monitoring framework and is informed by the monitoring objectives identified in Step 1 (Fig. 1). For demographic monitoring, state variables of interest include abundance (*i.e.*, population size), species occupancy, species diversity, and species richness (Yoccoz *et al.*, 2001). Monitoring protocols for estimating bee community properties are published elsewhere in this special issue (Levenson *et al.*, 2025b). Occupancy is often selected as a state variable for species experiencing rapid distributional changes (*e.g.*, range contractions) or for situations where local population size varies dramatically based on life history (Noon *et al.*, 2012). For these species, estimating local abundance or change in local abundance may not be practical or necessary for understanding population changes across broad geographic landscapes. Practitioners may also be interested in drawing inferences about system vital rates that are responsible for affecting change in the chosen state variable. For example, the vital rates responsible for changes in abundance are survival, fecundity, and movement. In contrast, the vital rates that are responsible for changes in species occupancy are local colonization and extirpation. Colonization represents a situation where a Sampling Unit that was not occupied in an earlier period becomes occupied. Systematic colonization of unoccupied Units could, in time, be interpreted as a range expansion. Extirpation, also referred to as local extinction, is when a Sampling Unit that was occupied in an earlier period becomes unoccupied. Systematic extirpation could eventually lead to range reduction, such as in the case of *B. affinis, B. franklini* (Frison), and *B. occidentalis* (Greene) (Cameron *et al.*, 2011; Graves *et al.*, 2020). The remainder of this framework will focus on occupancy as a state variable of interest and the vital rates associated with occupancy (colonization and extirpation).

What is Occupancy?: As mentioned above, occupancy is the probability that a Sampling Unit, patch, or site is occupied by one or more focal species. Occupancy estimates are generated from detection and non-detection data of the focal species (*i.e.*, observed/not observed) during standardized Surveys. These data are commonly referred to as "presence-absence" data; however, inferring absence when a species is

undetected is problematic. It is challenging to distinguish between genuine absence and failing to detect the species during one or more Surveys when it is present at a Unit (*i.e.,* false negative). This dichotomy reflects the two processes that affect the outcome of whether a bee species is detected at a Sampling Unit (MacKenzie *et al.,* 2017). The first is the biological process: the Unit is either occupied or unoccupied by the focal species. The second is the sampling or observational process: if the Unit is occupied, what is the likelihood the bee species will be detected during a given Survey or sampling event? Accounting for "false absences" or "false negatives" is a widely understood problem in ecology and biological monitoring (refer to MacKenzie *et al.,* 2017). The solution to this problem is to incorporate detection probabilities in models used to estimate changes in species occupancy across space and time. Occupancy models, fortunately, allow practitioners to estimate occupancy while accounting for imperfect detection of focal species (MacKenzie *et al.,* 2017). For example, occupancy models have been used to estimate occupancy dynamics of Northern Spotted Owls (*Strix occidentalis*) to inform recovery efforts of this federally Threatened species that is also difficult to find in the wild (Olson *et al.* 2005). Occupancy models integrate two conditional logistic regression sub-models to estimate occupancy and detection parameters from detection and non-detection data collected during Replicate Surveys (Royle & Dorazio, 2006).

The sequence of detection/non-detection data recorded for the target bee species is represented as a detection history consisting of multiple (*j*) Surveys conducted at *i = 1, 2, …N* Sampling Units. For example, detection histories for N=10 Sampling Units (*e.g.*, restored prairies) that were each surveyed *j*=4 times during the summer for *B. affinis* may appear as:

Prairie 1: 1011
Prairie 2: 1100
Prairie 3: 1011
Prairie 4: 0000
Prairie 5: 0011
Prairie 6: 1-10
Prairie 7: 00-0
Prairie 8: 0000
Prairie 9: 1000
Prairie 10: 1100

Here, a '1' in a detection history represents a detection of at least one *B. affinis* during a single Survey, '0' represents non-detection, and '-' represents a missing value, indicating the Sampling Unit was not surveyed during a particular Survey or event. For example, at Prairie 2, *B. affinis* was detected during the first and second Surveys but not during the third and fourth Surveys. This detection history is used to estimate occupancy and detection probabilities.

STEP 3. DESIGN A SAMPLING SCHEME AND DEFINE KEY SAMPLING TERMS

Here, we provide practitioners with a generalized approach for designing a monitoring project where occupancy is the state variable of interest. We avoid specific recommendations of sample size (*i.e.,* number of Sampling Units), effort (*i.e.,* area of Sampling Units and Survey duration), and sampling protocol (*i.e.*, employing passive or active methods) because there is no prescriptive, one-size-fits-all approach to

monitoring occupancy or other state variables. In fact, particular details of monitoring project design are going to be driven by monitoring objectives, the unique biology of the focal species and study area, and logistical constraints. Our guidance incorporates recommendations associated with estimating species occupancy (MacKenzie *et al.,* 2017) and recommendations from experts who have developed guidance for other wildlife monitoring programs (Yoccoz *et al.,* 2001; Williams *et al.,* 2002; Nichols & Williams, 2006). The Case Study we provide below for *B. affinis* monitoring is an example of using our framework (steps 1-5, Fig. 1) to design a sampling scheme for a monitoring project, but we caution readers that this design will likely not be appropriate for the specific needs of their species or system. Practitioners interested in monitoring species occupancy should review additional concepts and occupancy model assumptions during the monitoring project design phase (MacKenzie *et al.,* 2017).

Defining the Area of Interest: The Area of Interest is the space over which monitoring practitioners hope to make inference, recognizing that only a subset of locations within the Area of Interest can likely be selected for monitoring and be surveyed. Virtually all biological monitoring programs lack the ability to census large areas, and there is a near-universal need for drawing inference about these large areas based on sampling a subset of locations within these areas (Yoccoz *et al.,* 2001). Defining the Area of Interest differs with different monitoring objectives. For example, the Area of Interest may be potential habitat(s) in the species' current or historical range or within geopolitical boundaries (*e.g.*, county park network, or state forest lands). MacKenzie *et al.* (2017) provide the following considerations for defining the Area of Interest: 1) Ensure the Area of Interest is consistent with monitoring objectives (objectives will outright define the Area of Interest, or help bound it), 2) Address logistical issues (site access or remoteness), and 3) Eliminate areas of 'non-habitat' (impervious surface cover, water bodies, etc.). Once the Area of Interest is defined, then practitioners must define additional key sampling terms, namely the Sampling Units and the Season (or time frame) over which the species is available for detection at occupied Units (Table 1). These definitions will help practitioners make decisions about sample size and sampling effort. Figure 3 provides an example of an Area of Interest for monitoring *B. affinis.*

Defining a Sample Unit: Sampling Unit is a general term used to represent a location or patch, located within the Area of Interest, where occupancy of the focal species will be evaluated (Table 1). Sampling Units are defined by practitioners developing a monitoring project and are informed by the monitoring objectives, species biology, and practical constraints such as logistics and cost. A Unit may be as small as a patch of flowers in a desert matrix or as large as forest stands. Units may vary in size (*e.g.*, farm fields, forest patches, city parks) or be uniform in size (grid cell, habitat plot, or transect). The area of each Sampling Unit must be reported to calculate sampling effort, a *core* data field for this framework. Yoccoz *et al.* (2001) defines all Units that exist within the Area of Interest as the Target Population, from which a subset of Sampling Units is selected for monitoring and data collection. Importantly, defining the Unit implies the spatial scale at which occupancy will be estimated from the resulting data. For example, the U.S. Forest Service may wish to understand how occupancy of a declining bee species is affected by forest clearcutting and subsequent forest regeneration. Here, the Sampling Units may be defined as a discrete number of timber stands, and the Target Population is all timber stands found within the Area of Interest, which may be all National Forest Lands owned by the U.S. Forest Service, across the known range of the species. Harvested stands could be stratified among

Figure 3. Defining the Area of Interest and Sampling Units for a monitoring effort for the federally endangered rusty patched bumble bee (*Bombus affinis* Cresson). The left figure shows the species' historic range, divided into five Conservation Units (USFWS, 2021). The Area of Interest for Objective 1 includes Conservation Units 1, 2, and 5, focusing on areas where *B. affinis* has been detected since 2017 (dark shade). The Area of Interest for Objective 2 will include all five Conservation Units. The center figure shows an example Sampling Unit consisting of grassland, forest, or developed land that is also public land. The right figure depicts a Sampling Unit, defined as a 3.14 ha circle (100-m radius) where Replicate Surveys will be conducted for *B. affinis*.

relevant focal age classes (*e.g.*, 1–3, 6–9, and 12–15 years post-harvest) and a stratified random sample of stands could be selected to ensure replication across a range of stand ages. Additionally, a subset of unharvested stands should be included as 'controls'.

Ideally, all of the Units within the Area of Interest (Williams *et al.*, 2002, Chapter 5) would be sampled, yet this is rarely achieved due to practical and logistical constraints. Instead, nearly all existing biological monitoring programs stress the need for probabilistic selection of Sampling Units to ensure that inferences drawn from the Units are representative of the Target Population. Non-probabilistic or ad hoc approaches to selecting Sampling Units (*i.e.*, selecting only the most florally diverse native prairies, sampling exclusively along roadsides or in cities because they are easily accessible) may be necessary in some cases, but practitioners should strive for probabilistic sampling whenever possible. If the Sampling Units are not representative of the Target Population, then insights gleaned from monitoring data are not applicable to the entire Area of Interest. Probabilistic sampling designs are important components of biological monitoring (Yoccoz *et al.*, 2001), and practitioners should develop a Unit selection process prior to initiation of monitoring. MacKenzie *et al.* (2017) provide examples of several probabilistic sampling schemes that can be used when monitoring occupancy. As with all other forms of biological monitoring, convenience sampling should be generally avoided as it does not represent a probabilistic sampling scheme. In addition, it is generally inadvisable to select Units based on knowledge of their likely occupancy state, such as Units that were known to be occupied in the recent past. Using prior knowledge of occupancy status to select Units typically does not result in a representative sample of the Target Population and has the potential to bias estimates of occupancy for the entire population (Fournier *et al.*, 2019). If there is interest in selecting Units where the focal species is known to occur, then practitioners

must recognize that the estimated level of occupancy is likely to be higher than for a random sample of study Units throughout the Area of Interest. If practitioners have interest in Sampling Units where the species is known to occur, these Units should be treated as a different stratum. For example, our Case Study describing *B. affinis* monitoring includes Sampling Units selected across two strata: one where prior knowledge of occupancy was used to select Units and another stratum where no prior knowledge was used.

The number of Sampling Units selected for monitoring will be driven by monitoring objectives, species biology, Area of Interest, and time availability of monitoring practitioners. Although there is no general rule as to the minimum or optimal number of Sampling Units for estimating occupancy, we note that practitioners should expect to include tens or even hundreds of Sampling Units within their monitoring project. When estimating occupancy, we often sacrifice sampling depth (*e.g.*, detailed data collection at a few Units) for sampling breadth (*e.g.*, collecting a modicum of data across multiple Units). While sampling this many Units may seem daunting to individuals familiar with traditional bee sampling techniques, we note that collecting detection and non-detection data does not often require the level of effort required by other bee monitoring protocols (see Replicate Survey, below). Bailey *et al.* (2007) provide guidance on how to determine the appropriate number of Sampling Units to meet the desired objectives of an occupancy monitoring project, subject to economic and logistical constraints.

Defining the Season: Season is a term often used by ecologists to define a time period when the state variable (*e.g.*, occupancy, abundance, species richness) is assumed to be static or unchanged (Table 1). For occupancy, a Season should be a period when a Unit is either unoccupied by the focal species, or the Unit is occupied by the focal species and the species is available for detection (*i.e.*, Surveys have a greater than zero chance of detecting the species at occupied Units). Across multiple Seasons, occupancy status may change (*i.e.*, unoccupied Units may become occupied and occupied Units may become unoccupied), but within a Season the occupancy status is assumed static (*i.e.* occupancy state is assumed closed to changes). Often monitoring practitioners will be interested in understanding how the occupancy status changes across multiple Seasons and what environmental factors are driving the observed changes. A single year or growing season is often used as a starting point for defining a Season; however, species phenological information can be useful for honing the definition. For example, adult Mojave poppy bees (*Perdita meconis* Griswold; Andrenidae) are actively flying and available for detection during the brief bloom periods of their host plants, the prickly- and bear-poppies (Papaveraceae, *Argemone* sp. *and Arctemecon* sp.) (Chanprame *et al.*, 2024). Here, it may be appropriate to define a Season as a two-week period when the poppies are blooming and poppy bees are actively foraging, as opposed to other times in the year when they are in other life stages and nesting underground. Similar to defining a Sampling Unit, a Season is defined by practitioners developing a monitoring project and is informed by the monitoring objectives and species biology. Typically, a Season is defined as a period when the species is available for detection, which is often going to be when adult bees are actively flying and foraging. For example, our Case Study provided below on *B. affinis* monitoring has a 3-month Season from late June to early September, reflecting the active flight period of the focal species. Importantly, defining the Season implies the temporal scale at which occupancy will be estimated from the resulting data and the time periods between which occupancy status may change. Highly specialized survey methods and design considerations will need to be

implemented if practitioners wish to make inference of bees during non-flight periods of the species' life cycle, such as the overwintering stage.

DEFINING A SURVEY AND REPLICATE SURVEYS: A Survey is a single sampling event conducted at a Unit (Table 1). Replicate Surveys should be conducted during a defined Season, when the occupancy state of a Sampling Unit is static. Occupancy analysis is dependent on multiple, repeated Surveys. These Replicate Surveys will be used to estimate species detection probability, so that practitioners can disentangle false absences from true absence. Replicate Surveys are achieved by conducting Surveys during multiple points in time within a Season, by having multiple, independent observers, or even multiple, independent sampling protocols. It is important that practitioners define what constitutes a Replicate Survey and strive to maintain this definition for all sampled Units. Practitioners should seek to avoid situations where Replicate Surveys are conducted in an inconsistent manner, or where duration varies across Surveys (*e.g.*, some visual encounter surveys last 10 minutes where others last 60 minutes). Data generated during Replicate Surveys will be used to account for species' imperfect detection.

A Survey could include a visual encounter survey, netting, eDNA sampling, camera traps, trap nests (MacIvor & Packer, 2016), or any other method of detection. We recognize that most surveyors are likely to use some form of active, in-field survey and therefore provide guidance below that focuses primarily on active surveys. There is no universal rule dictating the number of Replicate Surveys that should be conducted at a Sampling Unit, but the general recommendation is a minimum of three Surveys during the defined Season (i.e., flight period of the focal species) when detection probability of the focal species is high (>0.5 per Survey; MacKenzie & Royle, 2005). Three Surveys should be considered a minimum and additional Surveys may be needed to understand factors contributing to variation in detection probability. If practitioners have interest in obtaining precise estimates of species detection probability, or in understanding factors that influence species detection, then the sampling design will often be weighted towards having multiple Replicate Surveys at fewer Sampling Units. This approach can be highly advantageous during the initial phase of monitoring and can help inform the design of longer-term occupancy monitoring (Boone *et al.* 2023 a,b; Otto *et al.*, 2023). Once the detection process is better understood, the sampling design can be altered to focus more on occupancy estimation, which typically involves sampling additional Units with fewer Replicate Surveys at each Sample Unit. MacKenzie *et al.* (2017) provide detailed guidance on design tradeoffs for balancing the number of Sampling Units versus the number of Replicate Surveys conducted at each Sampling Unit. Bailey *et al.* (2007) provide working examples of how to evaluate project design tradeoffs within an occupancy framework. Practitioners can use simulations and pilot data to evaluate whether a given design is sufficient for achieving the desired monitoring objectives.

DEFINING CRITERIA FOR DETECTION: Practitioners should also define what constitutes a Positive Detection of the focal species to avoid ambiguous detection/non-detection data. This may include collection of a physical specimen, a photographic voucher, or visual confirmation by well-trained observers. Given the difficulties of identifying most wild bee species without handling them, we recommend some form of physical or digital vouchering for Positive Detections. Note that photographic vouchers can be reliably used to identify some bee genera (*e.g.*, *Bombus*), but are less reliable for other

genera. Ambiguous detections can be recorded but should not be considered Positive Detections during analysis of monitoring data.

STEP 4. SELECT FIELD SAMPLING METHODS

Once the key sampling terms have been defined and a probabilistic sampling scheme has been developed, the next step is selection of field sampling methods for the monitoring project (Fig. 1). Various sampling methods can be employed for the collection of detection and non-detection data of bees [*e.g.*, haphazard walks, passive traps, active netting on hosts, camera traps, environmental DNA (eDNA)]. Regardless of whether a single individual or several dozen individuals are detected within a single Survey, the Unit is occupied. Thus, occupancy Surveys can often be shorter durations relative to traditional abundance surveys where observers need time to collect multiple individuals. For all monitoring projects, details of the sampling protocol (*e.g.*, detection method, such as active netting) and sampling effort (*e.g.*, the Survey duration and the area of the Sampling Unit) are *core* data fields that must be reported (Rousseau *et al.*, 2024; Du Clos *et al.*, 2025). Whenever possible, sampling protocol and effort should be decided upon prior to data collection and standardized across Replicate Surveys (refer to Step 3: Monitoring Design). Regardless of the sampling method used, it is important to maintain associations between the detection and non-detection data by recording the *core* data fields: Sampling Unit name/ID, sampling location, date, time, observer name, duration of the Survey and Sampling Unit Area (Table 2). *Recommended* and *optional* data fields, and any other relevant information following *The Wild Bee Data Standard* (Du Clos *et al.*, 2025) can also be recorded to maintain the long-term viability of these data (Table 2).

Active Surveys: Active Surveys involve methods where one or more observers are actively engaged in looking for one or more focal species within a Sampling Unit (*e.g.*, haphazard walking, active netting on floral hosts). Active methods are highly advised, especially when the monitoring is limited to one or several focal species. Duration of active Surveys will vary widely based on factors such as monitoring objectives, project logistics, and the size of the Sampling Unit. In general, practitioners should ensure the Survey duration provides the field observers with a reasonable chance of detecting the focal species, assuming it is present and available for sampling within the Unit. Most active sampling protocols range from 10 to 60 min, but needs may vary depending on the biology of the focal species or the size of the Sampling Unit. We recommend standardizing Survey duration for all occupancy monitoring projects. Having Survey duration standardized (*e.g.*, defining a Survey as a 30-minute search) will make it easier to interpret Survey-specific estimate of detection probability. Shorter durations may serve to increase the number of Sampling Units that can be visited in a given time period but should not be so short that the focal species has an extremely low likelihood of being detected, when present. In the Case Study provided below, a Survey is a 30-minute period where a single observer is actively looking for *B. affinis* within the Sampling Unit at a time of day when the focal species is active.

Non-lethal: Non-lethal Active Surveys can be conducted for a limited number of bee species that are easily identified in the field or from photographic vouchers. Non-lethal methods with photographic vouchers may be required for protected species. In this case, at least one representative voucher of each species should be photographed. It is advisable to use established protocols for photographing bees, such as the protocol developed for the Xerces Society for Invertebrate Conservation's Bumble Bee

Table 2. *Core*, *recommended* and *optional* data fields to be recorded during Replicate Surveys following this occupancy monitoring framework and *The Wild Bee Data Standard* (Du Clos *et al*., 2025). We note this is not an exhaustive list and practitioners will likely add/remove additional data fields based on the specific objectives of their monitoring effort. A full list of potential data fields (including many Sampling Unit covariates) is provided in *The Wild Bee Data Standard* (Du Clos *et al*., 2025).

Data Field	Level of requirement	Darwin Core Term(s)
Sampling unit location (Lat/Long)	Core	dwc:decimalLatitude, dwc:decimalLongitude
Sampling unit Name/Identifier	Core	dwc:fieldNumber
Survey date	Core	dwc:eventDate
Detection / Non-detection of focal species	Core	dwc:occurrenceStatus
Field observer name/Identifier	Core	dwc:recordedBy, dwc:identifiedBy
Survey start/End time	Core	dwc:eventTime
Survey duration	Core	dwc:samplingEffort
Area of sampling unit	Core	dwc:samplingEffort
Survey-specific covariates (e.g., weather)	Recommended	dwc:dynamicProperties
Habitat quality metrics	Recommended	dwc:habitat, dwc:eventRemarks
Geographically-specific stressors (*e.g.*, pesticide use)	Recommended	dwc:dynamicProperties
Floral host plant	Recommended	dwc:associatedTaxa
Non-target bee species detections	Optional	dwc:associatedOccurrences

Atlas projects (available at https://www.bumblebeeatlas.org/pages/survey-protocol). Note, however, that this protocol was developed and is very effective for bumble bees (Colgan *et al*., 2024) but may not be appropriate for other bee groups. Indeed, some bee groups are difficult or impossible to identify to species even with extensive photographs. Appropriate species for field or photographic identification should be determined in advance of data collection by consultation with regional bee experts. During data collection, observers should indicate when voucher photographs are taken so that photographs can be linked with specific Sampling Units and Surveys. In practice, it is often beneficial to photograph a partially completed datasheet before and after a Survey so that any bee photos taken during a Survey can be easily cataloged. Photographic vouchers should be organized in a database and curated in a similar manner to specimen vouchers so that each photograph or set of photographs is permanently associated with detection data including the *core* data fields Sampling Unit name/ID, geographic location, and area; date, time, and duration of the Survey;

the *recommended* data field floral association, and any other relevant information following *The Wild Bee Data Standard* (Du Clos *et al.,* 2025).

Lethal: Active Surveys involving active lethal capture will be functionally similar to non-lethal methods, except that individual bees will be removed from the Sampling Unit and typically identified in the laboratory at a later date (refer to Levenson *et al*., 2025b in this issue for more information). Observers should keep detailed records of sampling events, effort, and methods following *The Wild Bee Data Standard* (Du Clos *et al*., 2025). For lethal collection, we advise euthanizing in a way that maintains tissue for molecular and parasite and pathogen analyses (refer to Strange *et al.,* 2025 and López-Uribe *et al.,* 2025 in this issue for more information). Lethal collection may not be authorized, or may require a permit, for some protected species (*e.g.*, state or federally Threatened or Endangered species).

Passive Surveys: Passive Surveys involve methods where devices are deployed within the Sampling Unit to collect detection and non-detection data. Bee bowls and vane traps are passive devices that are typically deployed for many hours or even days and are better suited for gathering species richness data (Portman *et al*., 2020; Levenson *et al*., 2025b). These Passive Surveys also require significant processing time for handling and identifying the multitude of bees collected, thereby negating the time savings compared to active detection/non-detection Surveys. In addition, Passive Surveys with long sampling windows make it more challenging to understand how factors such as time of day, weather, and local habitat quality influence species detection probability. Where the species of interest is especially difficult to detect with Active Surveys, or there are numerous species of interest that co-occur spatially and temporally, Passive Surveys may be a more appropriate method to employ.

Most of the Passive Surveys done when monitoring bees have involved lethal sampling (Droege *et al.,* 2016), but other biological monitoring efforts have successfully used non-lethal passive sampling for estimating occupancy of vertebrate wildlife (Strickland & Roberts, 2019; Kays *et al.,* 2020). Technological improvements with camera traps and eDNA methods will lead to increased adoption of these techniques into wild bee monitoring in the future. The deployment duration of Passive Surveys varies by method, with some, such as soapy water traps, being appropriate for shorter periods (24 h or less) and others, such as camera traps, being appropriate for long time periods. As with Active Surveys, practitioners should select a Survey duration that provides a reasonable chance of detecting the focal species, assuming it is present and available for sampling within the Unit and given the known limitations of the chosen method. Having a standardized definition of a Passive Survey is important for interpreting detection estimates when analyzing data within an occupancy framework. The number of trapping devices, arrangement, and duration should be held constant across all Surveys. For example, a Survey may consist of a trap line of 6 bee bowls, spaced 5 meters apart, activated for a 24-hour period.

Non-lethal: Non-lethal Passive Surveys are increasingly available with the development of machine-learning-based image processing for video and photographic devices and the development of molecular methods including environmental barcoding (Montero-Castaño *et al.,* 2022). The use of eDNA for detecting focal bee species seems to hold promise for bee monitoring in the future (Newton *et al.,* 2023), but most eDNA studies have yet to achieve species-specific resolution in bee identification, which limits current applicability to focal species monitoring. For some species, non-lethal passive traps may be effective, but additional research on camera traps and eDNA could help determine the benefits of widely integrating these tools into formal bee monitoring.

Lethal: Lethal Passive Surveys involve the deployment of one or more trapping devices such as bee bowls or vane traps that collect and kill target and non-target insects. Protocols for Lethal Passive Surveys are well established and often deployed for bees (Droege *et al.,* 2016; Packer & Darla-West, 2021). Given the history of Lethal Passive Surveys in bee monitoring, there are many existing data sets collected using these methods that could be used to provide historical estimates of species occupancy, which could be compared with estimates from more contemporary monitoring data. With passive lethal sampling, practitioners have flexibility in defining what constitutes a single Survey (Levenson *et al*., 2025b). For example, a Survey may be defined as a single bee bowl deployed at a Unit for a 6-h period, or an entire array of 30 bee bowls deployed over 24 hours. In many cases, Lethal Passive Surveys will not be necessary to examine occupancy of focal species. From the standpoint of estimating species occupancy and detection probabilities, a positive detection is confirmed when a single individual of the focal species is detected; detection of >1 individuals is not required, nor are counts of individuals easily incorporated into an occupancy analysis. Lethal collection may not be authorized, or may require a permit, for some protected species.

STEP 5. SELECT DATA FIELDS

Once monitoring objectives have been established, the state variables selected, the sampling scheme developed, and field sampling methods have been chosen, the last step in the monitoring project design framework is to decide what data to collect (Fig. 1). Du Clos *et al.* (2025) define *core*, *recommended*, and *optional* data fields to be recorded during data collection. For occupancy, we emphasize both *core* (*i.e.,* data required for achieving the stated objectives) and *recommended* (*i.e.,* nonessential data that are likely to provide additional benefit) data fields and provide brief examples of *optional* data fields. Table 2 provides a list of *core* data fields that are universal for any occupancy monitoring project. It is likely that other *core* data fields will need to be included, based on the objectives of each monitoring project. For example, if the objective of a monitoring project is to understand how the presence of the non-native honey bee (*Apis mellifera* Linnaeus) affects occupancy of a focal wild bee, then recording detection and non-detection data of honey bees would be a *core* data field "Non-target Bee Species Detections". For other monitoring projects, detections of *A. mellifera* may be merely *recommended, optional,* or omitted. Using monitoring objectives to guide data collection will ensure the most relevant data are collected and time is not wasted collecting extraneous information.

Data recording and reporting for this framework follows *The Wild Bee Data Standard* (Du Clos *et al*., 2025; this issue). *The Wild Bee Data Standard* uses Darwin Core (dwc) terms (Wieczorek *et al*., 2012) and describes their application to wild bee occurrence data (and associated ecological data) such as those collected through this framework. Darwin Core is a widely accepted biodiversity data standard used by leading biodiversity data providers, including the Global Biodiversity Information Facility, (GBIF; https://www.gbif.org), Integrated Digitized Biocollections (iDigBio, https://www.idigbio.org/portal/search), and iNaturalist (https://www.inaturalist.org). Data recorded following *The Wild Bee Data Standard* will be suitable for publication on any of these platforms. To record data using this framework in alignment with *The Wild Bee Data Standard*, bee detection and non-detection data should be reported in **dwc:occurrenceStatus**. If bee counts were recorded, they should be reported

in **dwc:individualCount**. *Core* site location information should be reported in **dwc:decimalLatitude**, **dwc:decimalLongitude**, and **dwc:FieldNumber**. If habitat type was recorded, it should be reported in **dwc:habitat**. *Core* sampling event information (*i.e.*, Survey time and date) should be reported in **dwc:eventTime** and **dwc:eventDate**. Practitioners should report the observer(s) and identifier(s) in **dwc:recordedBy** and **dwc:identifiedBy**, respectively. Any information specific to a Replicate Survey (*e.g.*, observer experience, site condition, method details) should be recorded in **dwc:eventRemarks**. Weather conditions for each Replicate Survey should be reported in **dwc:dynamicProperties**. Sampling effort, which includes the Survey duration and the area of the Sampling Unit, should be reported in **dwc:samplingEffort**. If photo vouchers are generated, their location should be reported in **dwc:associatedMedia.** For non-publicly held photo vouchers, please provide the name of the institution that manages the photograph database, or if photographic vouchers are shared online, please provide URLs where they can be accessed. When applicable, the flower a bee was observed on should be reported in **dwc:associatedTaxa**. Other bee species observed can be reported in **dwc:associatedOccurrences**. When these data are reported to an online data provider, all records should be recorded as human observations if non-lethally sampled or preserved specimens if lethally sampled in **dwc:basisOfRecord**. Lastly, this framework should be cited in **dwc:samplingProtocol** along with the specific methods employed (*i.e.*, active netting or passive sampling). Full details on using these Darwin Core terms are provided in *The Wild Bee Data Standard* and its associated templates (Du Clos *et al.*, 2024; 2025) and a summary table is provided in Table 2.

Covariates: Occupancy models allow incorporating covariates to account for variability in occupancy and detection and to test specific hypotheses related to monitoring objectives. Covariates may be collected both *in situ* and *ex situ*. Collecting environmental data at each Sampling Unit is important for understanding spatial patterns in occupancy and occupancy dynamics. For example, practitioners may choose to collect information on local habitat quality, land cover, or the prevalence of a biological threat, such as pesticides. Similarly, practitioners should consider collecting Survey-specific data associated with factors expected to influence detection of the focal species, such as observer experience, local weather in addition to time of day. Whether these data fields are *core* or *recommended* is largely determined by the objectives of the monitoring project. Furthermore, the spatial and temporal scale of covariate collection will largely be informed by monitoring objectives.

Guidance on incorporating and reporting these covariates is provided in *The Wild Bee Data Standard* (Du Clos *et al.*, 2025; terms: **dwc:dynamicProperties**, **dwc:eventRemarks**). Unmodeled variation (heterogeneity) in detection probability leads to biased occupancy estimates (MacKenzie *et al.*, 2017). Our Case Study below showcases specific detection and occupancy covariates that are collected during a Survey. *Ex situ* data, such as land cover characteristics, can also be collected via GIS before or after Surveys are complete. These data have the added benefit that they do not require time spent in the field that might be better spent visiting and collecting data at a greater number of Sampling Units.

CASE STUDY

Developing a Monitoring Project for the US Federally Endangered Rusty Patched Bumble Bee (*Bombus affinis*), Where Occupancy is the State Variable of Interest

The rusty patched bumble bee (*B. affinis,* Fig. 2) was listed as federally endangered under the U.S. Endangered Species Act in 2017 due to an estimated ~90% reduction in its distribution. Although the causes of *B. affinis* declines are not fully known, detrimental pathogens, small population genetics, habitat degradation, the effects of climate change (*e.g.*, prolonged drought), and pesticides may be responsible (Grixti *et al*., 2009; Cameron *et al.,* 2011; USFWS, 2016). The current distribution of *B. affinis* is confined to just a few Midwestern and Mid-Atlantic states in the United States (USFWS, 2016; Hepner *et al*., 2024). The *B. affinis* Recovery Plan developed by the U.S. Fish and Wildlife Service lists specific criteria for downlisting or delisting the species and it is understood that monitoring will play a primary role in evaluating progress towards recovery goals (USFWS, 2021). To consider downlisting the species from endangered to threatened, the Recovery Plan stipulates two criteria that must be met: 1) evidence of a minimum number of healthy populations and 2) a stable or increasing trend in occupancy over a minimum of five to ten years within each of the five Conservation Units identified in the recovery plan (USFWS, 2021).

One critical short-term need is to understand the factors associated with *B. affinis* detection, so that long-term monitoring efforts (>5years) can minimize false absences. Understanding species detectability will help optimize the monitoring design, which is especially important for efforts that operate on limited funding and volunteer-based effort.

We applied the framework (steps 1–5) discussed above to the design of a monitoring project for *B. affinis*, which was developed during a January 2024 *B. affinis* stakeholder meeting held in Bloomington, Minnesota. Participants (which included members of the U.S. National Native Bee Monitoring Network) agreed that a long-term monitoring project should estimate occupancy trends of *B. affinis* to inform the second downlisting recovery criteria in the *B. affinis* Recovery Plan (USFWS, 2021). Participants also discussed the need for monitoring to understand location-specific stressors and ecological information influencing *B. affinis* occupancy dynamics (*i.e.*, local colonization and extirpation that governs occupancy trends).

STEP 1. IDENTIFY MONITORING OBJECTIVES: Objective 1 of this project, intended to be a short-term objective accomplished over one year of sampling, is to understand environmental factors that influence *B. affinis* detection. Knowledge gained from Objective 1 will help optimize long-term, larger-scale monitoring project associated with Objective 2. Objective 2 is aimed at estimating occupancy dynamics across the five Conservation Units and understanding location-specific stressors and environmental factors influencing *B. affinis* vital rates (*i.e.*, local colonization and extirpation). Objective 2 will also allow practitioners to estimate occupancy trends through time, allowing for direct evaluation of a recovery goal stated in the USFWS Recovery Plan (USFWS, 2021; Ellis *et al.,* 2025). Understanding *B. affinis* floral host plant use is also important for informing recovery efforts, so surveyors will also record flower visitation records while occupancy Surveys are being conducted.

STEP 2. DEFINE STATE VARIABLE(S) OF INTEREST: The state variable of interest for this monitoring project is occupancy.

Step 3. Design sampling scheme and define key sampling terms: The sampling scheme for Objective 1 is designed to understand factors influencing *B. affinis* detection. As such, Sampling Units will need to be in areas where the species is likely to occur. Accordingly, the Area of Interest during the first year of monitoring will be confined to the three Conservation Units (CUs) with known extant populations of *B. affinis* and further confined to areas that have been modeled by USFWS as having a high likelihood of extant *B. affinis*, with at least one known *B. affinis* detection since its listing in 2017 (Fig. 3). By selecting Sampling Units with a high likelihood of *B. affinis* occupancy, we know our occupancy estimates for Objective 1 will be biased high, relative to Units with no prior occupancy information. However, selecting Sampling Units with a high likelihood of occupancy is necessary for achieving Objective 1, so we can understand factors that influence *B. affinis* detectability.

Most Surveys will be conducted by volunteers, so Sampling Units predominantly occur on public lands, though private lands will also be incorporated when possible (Fig. 3). Adult *B. affinis* use a diversity of habitats, thus we define a Sampling Unit as a 3.14 ha patch (100-m radius circle) within a grassland, forest, roadside, or urban area within our Area of Interest (Fig. 3). Ideally, Sampling Units within this Area of Interest (public lands with known *B. affinis* detection since 2017) would be chosen in a probabilistic manner, stratified by number of known detections or annual frequency of detection (*i.e.,* number of years with detections since 2017). For practical purposes, the Units selected for Objective 1 will be an ad hoc sample (non-probabilistically drawn), selected on a voluntary basis, to ensure each Unit is surveyed multiple times within a Season. Sampling Unit selection will be modified for Objective 2, which we describe below. The Season for Objective 1 will correspond to a 3–4-month window (late June - early September) in a single year when *B. affinis* workers tend to be numerically abundant and actively flying. During this period, it is assumed the occupancy status of the sampled Units does not change (*i.e.,* occupied Units remain occupied and unoccupied Units remain unoccupied). This is a reasonable assumption given that by mid-June, *B. affinis* queens will have already established nests, so the locations of colonies are unlikely to change during this period. While occupancy is unlikely to change during the Season and is likely high based on our chosen Sampling Units, detectability is likely to change over Surveys (Boone *et al.* 2023a, b, Otto *et al.,* 2023); we aim to understand these changes in Objective 1. Following one year of data collection, analyses will be conducted to understand how *B. affinis* detection probability is influenced by time of day, day of year, local weather, and local habitat quality to achieve Objective 1 and inform future sampling for Objective 2. A Replicate Survey will consist of a 30-min non-lethal active visual encounter survey during daylight hours (between 900 and 1700), when *B. affinis* has a reasonable chance of actively foraging. We aim for a total of six replicate Surveys over the Season, though any Sampling Unit with at least two Surveys will be included in the subsequent analysis. A Positive Detection occurs when a single observer finds and vouchers a *B. affinis* worker, drone, or queen within the 30-min Survey. A photographic voucher is required to confirm a Positive Detection of *B. affinis* during a Survey. Physical voucher specimens of *B. affinis* are not allowed unless permitted to do so. Detection of other bumble bee species may be recorded and vouchered whenever possible but are not required.

The sampling scheme for Objective 2 expands on that of Objective 1. The Objective 2 sampling scheme includes all five Conservation Units, with each defined as a separate Area of Interest, as *B. affinis* downlisting criteria applies to each CU individually. Sampling Units within these Areas of Interest are defined identically to those for Objective 1: a 3.14 ha patch (100 m radius circle) within a grassland, forest,

roadside, or urban area. However, for Objective 2, Sampling Units will be separated into two groups. One set of Sampling Units will be locations where *B. affinis* has been detected within the recent past (since its federal listing in 2017) and have a higher likelihood of being initially occupied. The second set consists of Units within the Areas of Interest that lack recent (2017–2024) *B. affinis* detections. Units within these groups will be selected probabilistically to achieve (1) ~66% historically occupied and ~33% historical unknown status units, and (2) spatially balanced coverage among the Areas of Interest. Selected Units that do not harbor flowers or have accessibility issues will be removed from the sampling pool. A Season for Objective 2 will correspond to a 3–4 month window (late June - early September) annually, but the duration of the Season may be adjusted based on findings from Objective 1. A Replicate Survey and Positive Detection are the same for Objectives 1 and 2. However, sampling schemes and key sampling terms are allowed to change based on what is learned from monitoring for Objective 1.

STEP 4. SELECT FIELD SAMPLING METHODS: A single observer will conduct a meandering walk within a Sampling Unit, actively searching for bumble bees on flowers, and record detection or non-detection information for *B. affinis*. Multiple observers can conduct simultaneous Surveys within a Sampling Unit, but the Surveys must be conducted independently (*i.e.,* no information shared between surveyors), and data records (detections and non-detections) kept separate for each observer. Surveys should not be conducted during rain events, during high wind (>20 kph), or temperatures < 15.5 °C. Survey-specific weather data will be collected at the onset of each Survey. Observers will wait at least one hour after rain subsides before conducting a Survey. Partially cloudy days or overcast conditions are permissible if observers can see their own shadow. *In situ* habitat data will be collected in the form of quantitative floral resource abundance and richness once per Sampling Unit, per Season. Protocols for collecting habitat data will be developed in the future.

STEP 5. SELECT DATA FIELDS: Objective 1 has several *core* and *recommended* data fields (Table 3). Upon the completion of sampling for Objective 1, *B. affinis* detection and non-detection data will be analyzed using a single-species, single-season occupancy model to determine how time of year, time of day, local weather, and local habitat quality affect *B. affinis* detection probability. Detection heterogeneity across different observers will also be explored. Results from Objective 1 will be used to evaluate design tradeoffs (Bailey *et al*., 2007) and to refine survey protocols for Objective 2. Note that for *B. affinis*, data requirements deviate (*e.g.*, floral host is *core* data) from this framework, largely due to permit reporting requirements of this federally endangered species. An example of recorded data that describes a Survey for this monitoring project can be found in *The Wild Bee Data Standard* and its associated templates (Du Clos *et al.,* 2024; 2025).

Core and *recommended* data fields for Objective 2 will likely be similar to Objective 1 (Table 3), but these data fields are subject to change given what practitioners learn upon the completion of Objective 1. Results from Objective 1 will be used to determine which detection covariate information for explaining variation in detection probabilities are important for collecting to achieve Objective 2. One unique aspect of Objective 2 is the focus on estimating occupancy dynamics and understanding environmental stressors that are associated with these dynamics. There are myriad potential stressors impacting *B. affinis* occupancy dynamics, including detrimental pathogens, the effects of small population genetics, habitat degradation, pesticide use, competition, drought, and climate change. Table 3 provides coarse-level examples of

Table 3. Data fields for the *Bombus affinis* monitoring project. Each of the *core* or project-specific data fields should be collected and recorded during each 30-min Survey following the case study sampling scheme and *The Wild Bee Data Standard* (Du Clos *et al.*, 2025).

Data Field	Level of requirement	Darwin Core Term(s)
Sampling unit location (Lat/Long)	Core	dwc:decimalLatitude, dwc:decimalLongitude
Sampling unit name/Identifier	Core	dwc:fieldNumber
Survey date	Core	dwc:eventDate
Detection / Non-detection of *B. affinis*	Core	dwc:occurrenceStatus
Field observer name/Identifier	Core	dwc:recordedBy, dwc:identifiedBy
Survey start/End time	Core	dwc:eventTime
Survey duration	Core	dwc:samplingEffort
Area of sampling unit	Core	dwc:samplingEffort
Survey-specific weather (wind, temp, humidity, cloud cover)	Core	dwc:dynamicProperties
Land cover covariates	Core	dwc:dynamicProperties
B. affinis floral host plant	Core	dwc:associatedTaxa
Habitat quality/Degradation & land cover metrics	Core	dwc:habitat
Pesticide treatments	Recommended	dwc:dynamicProperties
Bombus pathogen detection	Recommended	dwc:associatedOccurrences
Spatially-specific drought & climate indices	Recommended	dwc:dynamicProperties
Non-target *Bombus* species detections	Optional	dwc:associatedOccurrences
Floral host plants of non-target *Bombus*	Optional	dwc:associatedOccurrences

environmental threat data (*e.g.*, pesticides and pathogens) that could also be collected at each Sampling Unit, to understand their effects on *B. affinis* occupancy dynamics. For example, protocols for pathogen sampling could be adapted from Strange *et al*. (2025) and incorporated into this monitoring project. These threats are currently listed as *Recommended* data fields because they are important for understanding *B. affinis* occupancy dynamics; however, protocols for incorporating them into a monitoring design are currently unavailable. Although there is value in collecting data on all potential stressors, the monitoring project will primarily focus on the habitat quality affecting local colonization and extirpation rates. Specifically, data will be collected so that local colonization and extirpation rates can be modeled as a function of changes in floral resource diversity and abundance and changes in land cover through time. Floral resource data will be collected *in-situ* once per Season. Land cover will be quantified annually in a GIS at 250, 500, and 1000m from the Sampling Unit location, derived from the National Land Cover Database (https://www.mrlc.gov/data) and Cropscape - Cropland Data Layer (https://nassgeodata.gmu.edu/CropScape/). As the monitoring project matures, data collection on additional stressors (*e.g.*, pesticide use, pathogens, drought) will be added so that region-specific stressors can be investigated.

CONCLUSIONS

In this article, we provide a framework for focal species monitoring where occupancy is the state variable of interest. Establishing objectives is an important first step when developing a new biological monitoring project (Yoccoz *et al*., 2001); clearly defined objectives are critical for monitoring wild bees (Otto *et al*., 2025). Once monitoring objectives have been established, then practitioners can work with biologists and quantitative ecologists to design a sampling scheme, define key terms, select sampling methods, and determine *core* and *recommended* data fields.

Although there is a lot of interest in collecting bee data in the name of monitoring, we caution against a rush to data collection without first answering two questions: 1) *Why are we monitoring?* and 2) *What demographic properties are we monitoring?* Careful thinking during the initial phase of monitoring project development will ensure that years of field sampling will lead to desired outcomes and measurable gains of information. As demonstrated by more established vertebrate monitoring programs, occupancy has several inherent advantages for bee monitoring (Otto *et al*., 2025), and we hope this article provides practitioners with a useful framework for designing their own bee monitoring projects where occupancy is a state variable of interest.

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Standardized protocol for collecting bee samples to generate molecular data

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Abstract. This protocol provides guidance on the appropriate collection of bee specimens or tissue samples for molecular analysis, with an emphasis on generating genetic and genomic data while ensuring tissue integrity. Specifically, the protocol focuses on tissue collection and storage methods, including relevant specimen metadata recording and reporting, but does not cover any downstream handling or analyses, which vary depending on the aims of a given project or study. This protocol is specifically designed for freshly collected, individual bee specimens intended for genetic, genomic, or other molecular analyses. While molecular approaches to bee monitoring are not the primary focus, we emphasize their promising role for future applications. This protocol is part of a series developed in association with the U.S. National Native Bee Monitoring Network to standardize bee monitoring practices.

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INTRODUCTION

Molecular data provide critical information for bee conservation and monitoring efforts (Zayed, 2009; López-Uribe *et al*., 2017; Lozier & Zayed, 2017; Kelemen & Rehan, 2021). Characterizing genetic variation in individuals and populations enables the estimation of colony density for social species (McGrady *et al*., 2021), effective population sizes (Lozier *et al*., 2023), adaptive processes (Theodorou *et al*., 2018; Jaffé *et al*., 2019; Pope *et al*., 2023), levels of genetic diversity and inbreeding (López-Uribe *et al*., 2019; Mola *et al*., 2024), signatures of environmental stressors (Tsvetkov *et al*., 2021), and other types of information that are cornerstones of population management and conservation. These types of information are essential for identifying how bee populations and species have responded to past environmental changes, whether they are adapting to ongoing changes, and if there is genetic variation available for them to adapt (López-Uribe *et al*., 2025). Additionally, DNA-barcoding is a standard approach for molecular-based bee identification (Packer *et al*., 2009). New methods that implement non-lethal collections of tissue (Herrera-Mesías *et al*., 2022) or environmental DNA (eDNA; Thomsen & Sigsgaard, 2019) hold promise for a future role in bee monitoring, although at present they are still in the earlier stages of testing and implementation. Molecular data also aid in discovering and delimiting previously uncharacterized cryptic species and lineages, as well as distinguishing between intra-specific (*i.e*., polymorphic) and inter-specific variation (Gueuning *et al*., 2020; Andrade *et al*., 2022; Sandoval-Arango *et al*., 2023). This helps to establish and differentiate species and subspecies, which are the fundamental units of conservation action.

With increasing bee survey and monitoring efforts, and the resulting increase in the number of bee collections (Woodard *et al*., 2020; Tepedino & Portman, 2021), it is critical to establish standards for how to preserve biological material to maximize its utility for genetic, genomic, and other molecular analyses. Although most bee monitoring efforts do not explicitly address the characterization of genetic or genomic diversity at the moment, this has been proposed as a critical component of more comprehensive future monitoring, especially given the accelerated rate of species and genetic loss across taxa worldwide (Sánchez-Bayo & Wyckhuys, 2019; Exposito-Alonso *et al*., 2022; van Klink *et al*., 2022). The ways that samples are collected and stored directly impact whether they can be used for molecular analyses, with the general pattern that the more effort that is devoted to handling samples, the greater the number of molecular analyses that can be subsequently performed. Although samples that were not collected using this protocol, or any specific tissue preservation methods, can still be used to acquire molecular data (*e.g*., through museomics), some limitations (outlined below) cannot be overcome if samples are not collected appropriately.

Here, we provide general guidelines for the collection of material (including tissue samples or entire organisms, referred to as tissue hereafter) intended for genetic, genomic, transcriptomic, and other molecular types of datasets. This protocol is designed to address specifically how tissues should be collected, rather than downstream handling or analyses, the specifics of which depend on the aims of a given project or study (see Schweizer *et al*., 2021). The protocol is focused specifically on freshly collected, individual bee specimens and associated data that are collected with the intention of use for genetic, genomic, or other molecular analyses. We provide examples of studies that used different types of methods and molecular markers to answer questions about population structure, demography, inbreeding, and colony abundance.

We recognize that many other methods are used to generate molecular data to answer some of the above questions (*e.g.*, use of museum specimens, bees collected from passive traps), and that there is considerable interest in the future role of molecular methods of monitoring through eDNA and DNA metabarcoding (Levenson *et al.*, 2025). Therefore, we offer some general recommendations for best practices outside of our specific protocol, such as collection methods if specimens will be pinned and stored in collections. We also provide a brief treatment of the future role of molecular methods of bee monitoring that are on the horizon.

SAMPLING DESIGN

The sampling and experimental design employed for generating different types of molecular data is dependent on the goals of a study or project. Before carrying out any sampling, we highly recommend consulting with the specific research groups performing subsequent bioinformatic and statistical analyses to design a sampling scheme that will best support your monitoring or other goals. Some aspects to take into consideration include establishing a well-defined question that determines whether neutral or adaptive (or both) DNA markers are needed, or whether expression data based on RNA are required. The genetic marker needed for the study will determine what tissue sampling protocol is necessary. We also urge investigators to consider potential future uses of the tissues, because the samples could have value well beyond the focal study if extra effort to appropriately collect and store the tissue is taken. Currently, a variety of genetic markers—defined as sequences in DNA or RNA that can be used to identify specific regions of a genome or transcriptome—are available (Schiebelhut *et al.*, 2024) and their suitability will depend on the question and budget available for the study (Table 1).

Similarly, the choice of sampling effort related to the number of individuals per population, and number of populations, depends heavily on the specific questions of a study or project. There is generally a tradeoff between the number of samples and the number of markers that must be generated for genetic analyses (Schweizer *et al.*, 2021). For example, if you are using a dozen microsatellite markers to determine population genetic structure, you will need a larger number of samples per population, whereas if you are using thousands of markers across the genome, fewer than 10 individuals per population may be sufficient (see Case Study I). Likewise, if you need to screen a very large number of individuals (*e.g.*, many hundreds) for in-depth parentage or colony density analyses, screening fewer markers per individual may be a more economical approach (see Case Study II). If the objective of a study is to examine lineage survival through time for social species such as bumble bees (*Bombus* Latreille) (Carvell *et al.*, 2017), note that sample sizes must be particularly large to account for the attempt to recapture the same lineages at multiple time points.

SAMPLE COLLECTION AND STORAGE

Tissue collection methods (and the level of rigor and effort required) are dependent on what type(s) of molecular data the samples will be used to generate and what types of questions will be answered (Fig. 1). Methods for tissue sampling can be categorized by their ability to preserve the highest quality tissue that can be used to recover different types of markers (Table 2). The best available method is to flash-freeze (defined as placing into ultra-cold temperatures < -80 ºC) individuals in liquid

Table 1. Summary of modern genetic markers commonly used for population genetics, phylogenetics, genomics, and transcriptomic analyses for questions related to pollinator monitoring and conservation.

Type of Marker or Method	Descriptions	Examples
Microsatellites	Short, repetitive sequences of DNA, typically consisting of 1-6 base pairs, that are scattered throughout the genome and are highly polymorphic	Jha & Kremen (2013), Mola *et al.* (2024), Pope *et al.* (2023)
Mitochondrial DNA (mtDNA)	Represents the maternal lineage of a species and can be analyzed either by individual loci or by sequencing the entire genome	Landaverde-González *et al.* (2017), Praz *et al.* (2022)
Restriction-site approaches (*e.g.*, RAD-seq)	Approaches that use restriction enzymes to cut DNA at specific sites, allowing for the sequencing of adjacent regions to identify genetic variations across the genome	Lozier (2014), Jackson *et al.* (2018), Theodorou *et al.* (2018), Pope *et al.* (2023), Samad-Zada *et al.* (2023)
Hybridization approaches (*e.g.*, UCEs, AHEs, RAD capture)	Approaches that involve using probes to enrich and sequence specific regions of the genome selectively, allowing for targeted genetic analysis and comparison across individuals and species	Gueuning *et al.* (2020), Andrade *et al.* (2022), Samad-Zada *et al.* (2023), Sandoval-Arango *et al.* (2023)
Whole genome sequencing	Determines the complete DNA sequence of an organism's genome; depending on the sequencing technology used, its quality and completeness can vary from tens of thousands of scaffolds to chromosomal-level resolution	Lozier *et al.* (2023), Pope *et al.* (2023)
Transcriptomics and other gene expression analyses	Involve the study of the complete set of RNA transcripts, or targeted regions, expressed by organisms under specific conditions	Tsvetkov *et al.* (2021), French *et al.* (2024)

nitrogen immediately after collection to preserve the best quality tissue that allows you to recover most molecular markers. Alternatively, individuals can be brought to the laboratory alive for flash freezing. If the recommended flash-freezing cannot happen immediately, then tissue or whole bees can be maintained in a nucleic acid stabilizer such as RNA*later* (Ambion, Invitrogen), DNA/RNA Shield (Zymo Research), or ATL Buffer (Qiagen). These stabilizers preserve both RNA and DNA without ultra-cold storage, although further testing is needed to understand fully how these stabilizers ultimately influence molecular quality through time (*e.g.*, Passow *et al.*, 2019). When using this approach, collect the bee specimens and immediately place them into the solution, ensuring that the sample is completely submerged to stabilize the RNA and DNA in all tissues of the specimen. Follow manufacturers' protocols for specimen storage specific to the stabilizing solution. For example, when using RNA*later*, allow the specimens to incubate at room temperature (20 to 25 °C) for at least 24 hours; after

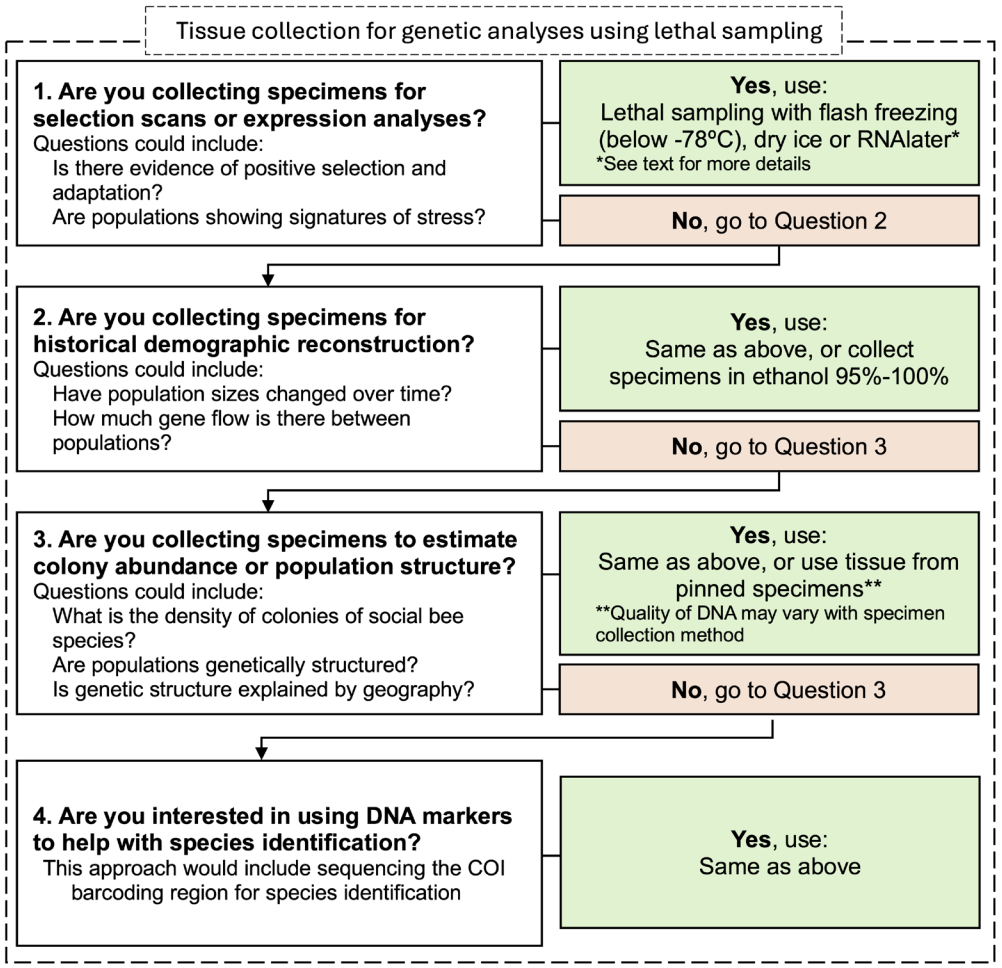

Figure 1. Flowchart guiding the selection of preservation methods based on specific research questions. Note that methods in figure are the minimum effort that can be used for samples intended for a specific purpose.

that, it is recommended to store them at -20 ºC. Specimens can be stored in RNA*later* at room temperature for one week or at -4 ºC for up to one month. Alternatively, tissue or specimens can be preserved in 95–100% ethanol at room temperature for a couple of weeks and then transferred to ultra-cold storage without significantly impacting DNA quality for some applications (Table 2). Note, however, that tissue that is not immediately flash-frozen cannot be used for some molecular analyses, including transcriptomic and proteomic analyses, because RNA and proteins quickly degrade at room temperature unless tissue is preserved in a stabilizing buffer (*e.g.*, RNA*later*).

If you plan to use the samples to generate high-quality genomes (see Case Study III), transcriptomes (Tsvetkov *et al.*, 2021), or proteomes, immediate flash-freezing is necessary for optimal tissue preservation. We also recommend flash-freezing because it minimizes the suffering of the bees collected and, in situations where you are unsure how samples will be used, it preserves high-molecular weight (HMW) DNA that is

Table 2. Summary of tissue preservation methods categorized from best to worst, in terms of quality of the molecules preserved and the type(s) of molecular marker recovered.

Preservation method	Molecule quality	Molecules	Type(s) of marker recovered	Notes
Flash freezing (below -78 ºC)	Best	DNA, RNA, Proteins	All markers	Requires access to liquid nitrogen or dry ice and long-term storage in ultralow freezers
RNA*later*	Very good	DNA, RNA	Microsatellites, mtDNA, genomics, transcriptomics	Less suitable for reference genomes
Ethanol 95–100%	Good	DNA	Microsatellites, mtDNA, genomics	Lower-quality DNA
Ethanol <95% or ethyl acetate	Poor	DNA	Microsatellites, mtDNA, and possibly genomics	Preserves fragmented DNA

usable for any subsequent purpose. It also preserves RNA and proteins and helps maintain DNA structure, which is critical for building reference-quality genomes. In the field, flash-freezing can be performed by placing tubes on dry ice in a cryogenic cooler (~-80 ºC; be sure that tubes come in direct contact with ice) or into an ultra-cold dry shipper charged with liquid nitrogen (-196 ºC).

Samples that will be used for purposes that do not require RNA or higher-quality DNA, such as for the generation of microsatellite data (see Case Study II), ddRAD, ultraconserved elements (UCEs), or whole genome resequencing, can alternatively be stored in a stabilizing liquid such as 95–100% ethanol at room temperature (Marquina *et al.*, 2021) or on ice for an extended period of time (>12 hours) without significant loss of DNA quality. Samples should be stored at -20 ºC or below as soon as possible when using these approaches. Note that repeated freezing and thawing of specimens (or of their extracted DNA) reduces their quality for molecular use (Shao *et al.*, 2012) and should be avoided as much as possible. Other preservatives have also been shown to store high-quality DNA safely (Mulcahy *et al.*, 2016), but these have not been tested extensively in bees.

Passive traps, such as bee bowls, that capture multiple individuals of a species or multiple species may negatively impact the quality of specimens for genetic or genomic studies (Ballare *et al.*, 2019); therefore, we recommend caution when using passive traps for collecting tissue for these types of analyses. We note, however, that the degree of degradation depends on a variety of factors, such as the duration of time until specimens are placed in storage and the preservative used. Additionally, the collection of specimens in propylene glycol or ethyl acetate as a killing agent can result in the degradation of genetic material and thus these substances are not acceptable for use with this protocol (Vaudo *et al.*, 2018). For active collection methods such as netting, cyanide is an acceptable alternative as cyanide-killed bees consistently have higher-quality DNA (inferred from a higher molecular weight) than samples collected in ethyl acetate (Ballare *et al.*, 2019).

A core component of this protocol is that individually captured bees be placed into unique, prelabeled, sterilized tubes for transfer and storage. We recommend using

labeling systems with unique catalog numbers that begin with acronyms of collections or projects followed by consecutive numbers (*e.g.*, USDA-ARS:BBSL0511821 for a specimen that will be deposited in the USDA ARS Bee Lab, Logan, UT, USA). These numbers should be associated with all other metadata required to follow best data management practices (Du Clos *et al.*, 2024; 2025). When handling specimens, it is recommended to use sterilized forceps, to minimize the accidental transfer of DNA or other materials among samples. It is worth noting, however, that complete sterilization of handling tools may be impractical in some situations. If non-sterilized materials are used, the transfer of contaminant DNA or RNA can be filtered out of data bioinformatically, but it is better to avoid cross-contamination at the time that samples are collected. When possible, we also advise transferring specimens into cryogenic vials, as these are specially designed to withstand ultra-cold conditions (< -80 ºC), and direct exposure to liquid nitrogen, for long-term storage. Regardless of their intended use, once samples are collected and transferred to the laboratory, we advise storage in a -80 ºC freezer. DNA, RNA and proteins are well-preserved at this ultra-cold temperature for long periods of time. Note also that specimens stored in ethanol or RNA*later* may require additional processing if the remaining specimen is to be pin mounted and deposited in a museum collection as a voucher specimen (see Strange *et al.*, 2024 for additional information).

ADDITIONAL BEST PRACTICES

Non-lethal tissue collection should be considered as an alternative to lethal collection when possible (Oi *et al.*, 2013; Scriven *et al.*, 2013). Tissue samples, such as parts of individual legs (Holehouse *et al.*, 2003), hairs (Rongstock *et al.*, 2024), and fecal samples (Scriven *et al.*, 2013), can be used to generate genetic and genomic data (see Case Study IV). Antennal tissue can also be used (Oi *et al.*, 2013) but is not preferred above leg or fecal samples because it may be more likely to impact bee flight and foraging. Overall, additional testing is needed to characterize the effects of non-lethal tissue sampling on bee survival and fitness (Mola *et al.*, 2021). Additionally, most studies that have tested these approaches have focused on bumble bees and orchid bees (Apidae: Euglossini), which are larger-bodied; additional testing may be needed to determine whether enough DNA can be extracted from specific tissue types from other bee species. If the quality and quantity of DNA is not sufficient for the intended application, it may be necessary to implement lethal techniques, but this should be determined on a case-by-case manner. For the implementation of these non-lethal sampling approaches, live bees can be briefly immobilized on ice or with CO_2, tissue can be dissected or removed, and the tissue can be treated and stored in the same ways described above for entire bee specimens. We recommend wiping dissection tools with 70-95% ethanol between specimen handling to avoid transferring DNA (or parasites or pathogens) between specimens, although contaminant DNA can be bioinformatically filtered out from samples if needed. Swabbing specimens or washing plant surfaces (*e.g.*, eDNA) may be another way to sample bees non-lethally and detect the presence of pathogens (see Strange *et al.*, 2025), but these approaches are largely untested and mainly yield very low quality DNA or RNA that has more limited utility (but see Johnson *et al.*, 2023; Newton *et al.*, 2023; Avalos *et al.*, 2024).

Vouchering is important to corroborate the species identity of the samples being analyzed (Monckton *et al.*, 2020). As such, we discuss several ways to voucher specimens properly depending on the collection method. For each of these methods,

we recommend storing extracted DNA as a secondary voucher for determining species identity.

If samples are collected non-lethally (see Case Study IV), photographic vouchers can be used instead. In this case, we advise collecting photographs of the entire individual and diagnostic parts of the body that can be used to confirm identification. If diagnostic characters are uncertain, we recommend taking face, lateral, dorsal, and ventral images as standard.

If specimens are sampled lethally but non-destructively (*e.g.*, a single body part or tissue type is removed and used for molecular analysis, but the remainder of the sampled specimen is maintained), the remaining specimen can become the voucher to confirm species identification (see Case Study II). When possible, vouchers should be pinned and clearly associated with the tissue sample used in molecular analysis through a clear labeling system. Imaging the voucher is also valuable in case of specimen damage.

If the protocols require destructive sampling of entire specimens, we recommend collecting an additional series of individuals of the same putative species, to be maintained as voucher specimens that are representatives of the particular collection event and that can be associated with downstream analysis (see Case Study III). If the species is social, vouchers can be collected by taking individuals from the same nest. Otherwise, vouchers that are putatively the same species should ideally be from the same location and date as the destroyed specimen.

We also encourage the sequencing and deposition of DNA barcodes as molecular vouchers, especially for non-lethal samples. The COI barcode gene is a standard marker for species ID in bees and is likely to be a more useful tool for verifying species than other markers, like microsatellites. There are limitations, however, to the broad applicability of DNA barcodes for species identification including a lack of existing reference libraries and absence of genetic divergence among evolutionary units with clear morphological differentiation (*e.g.*, Janko *et al.*, 2024).

METADATA SPECIFIC TO THIS PROTOCOL

Core metadata to record for samples that will be analyzed for molecular data include information about sample handling conditions prior to final storage, time until final storage, final storage conditions, and final storage location. It is valuable to record this type of information at the time samples are collected. This allows you to know, later, whether they can be used for different molecular analyses, even if these analyses were not originally considered at the time of collection. There are ways to test the quality of samples, such as DNA fragmentation analysis, so that decisions can be made about whether samples can and should be used for different molecular analyses, regardless of whether metadata about sample handling conditions were recorded. We note, however, that it is more efficient to record these metadata at the time of collection, so this information is readily available. We are also making these recommendations so that more formal sampling schemes, such as monitoring programs, are aware of the value of preserving samples for molecular analysis even if they are not originally integrated into the program design, and have the information in-hand for doing so in the most efficient and effective ways possible.

The final storage conditions, particularly the temperature at which the sample is stored, are reported in the Darwin Core protocol field **dwc:preparations**. All other information on how the sample was handled is reported together in the term **dwc:materialEntityRemarks**. Genetic sequence identifiers can be provided in the term **dwc:associatedSequences** (Table 3). When providing multiple pieces of information for one Darwin Core term, separate them with a vertical bar; for example: "sample stored on ice between collection and final storage | 0.5 hour between collection and final storage | stored in the USDA ARS Bee Lab, Logan, UT, USA" is an appropriate entry for **dwc:materialEntityRemarks**. Although it may seem counterintuitive to provide this much text in one spreadsheet cell, adhering to these practices aligns with the Darwin Core standard (Wieczorek *et al.*, 2012; Du Clos *et al.*, 2025) and promotes data reproducibility and utility. Lastly, please be sure to cite this protocol in **dwc:samplingProtocol**. Full details on using these Darwin Core terms and templates to enter this information into a spreadsheet or workbook are provided with *The Wild Bee Data Standard* (Du Clos *et al.*, 2024; 2025). Optionally, provide any online repository (*e.g.*, GenBank submission number) or other identifying information for the sequence data generated from the samples.

Table 3. List of core metadata to be recorded from specimens collected for genetic data to adhere to The Wild Bee Data Standard (Du Clos *et al.*, 2025).

Core Metadata	Description	Darwin Core Term
Sample conditions prior to final storage	Report how the specimen was handled between collection and final storage	dwc:materialEntityRemarks
Time until final storage	Report duration between specimen collection and final storage	dwc:materialEntityRemarks
Final storage conditions	Report how the specimen is stored, particularly the temperature	dwc:preparations
Final storage location	Report where the specimen is stored	dwc:materialEntityRemarks
Genetic sequence identifiers	Provide one or more means to locate genetic sequence information, including publications, URLs, or any other type of unique identifier	dwc:associatedSequences

EXAMPLES OF MOLECULAR METHODS AND MARKERS IN BEE RESEARCH

Case Study I. Demographic History and Signatures of Adaptation of an Agricultural Pollinator

Pope *et al.* (2023) reconstructed the demographic history of the squash bee *Xenoglossa pruinosa* (Say) (formerly *Eucera pruinosa*) (Apidae: Eucerini), which is a pollen specialist and important agricultural pollinator of *Cucurbita* L. (Cucurbitacae)

crops (Fig. 2). This study used a combination of microsatellites, ddRAD markers, and whole genome resequencing to characterize the population structure of the species, reconstruct its historical demography, and investigate signatures of positive selection. For the investigation of population structure, 938 individuals from 26 populations were genotyped for five microsatellite loci, and a subset of 142 individuals were genotyped for >110k SNPs from a ddRAD library. After characterizing population structure, a subset of 44 individuals from the main five lineages of the species were selected for whole genome sequencing (about eight individuals per lineage). This smaller dataset was used for demographic inference using ancestral recombination graphs, and inference of purifying and positive selection. With this hierarchical sampling scheme, the study identified five lineages within the species, a recent superexponential demographic expansion across lineages during the past 2,000 years, and signatures of positive selection in 20% of the protein coding genes.

Case Study II. Colony Density Quantification of an Agricultural Pollinator

To estimate accurately the abundance of social species, it is necessary to calculate the number of colonies instead of using the abundance of individual bees as a proxy. McGrady *et al.* (2021) quantified the number of colonies of the bumble bee *Bombus impatiens* Cresson (Apidae: Bombini), which provide pollination services to cucurbit crops (Fig. 3). To estimate this, ~6,000 individuals were collected from 30 cucurbit fields (with an average of 200 worker bees per field) and genotyped for eleven microsatellite markers. All specimens were collected and pinned, and then a mesothoracic leg was removed from each individual and used for DNA extractions to multiplex microsatellite genotyping. Using sibship analysis reconstruction (Jones & Wang, 2013), which assesses individual specimen relatedness, the study concluded that, on average, workers from an estimated 540 colonies were providing pollination services to each cucurbit field.

Case Study III. Reference Genome of a Specialist Pollinator of Conservation Concern

Schweizer *et al.* (2024) built a high-quality reference genome for *Perdita meconis* Griswold (Andrenidae), commonly known as the Mojave poppy bee (Fig. 4). This desert bee specializes in the pollen collection of plants in the genera *Arctomecon* Torrey & Frémont and *Argemone* L. (Papaveraceae). The primary host plant for this bee in Utah (USA) is *Arctomecon humilis* Coville, which is a federally protected plant under the U.S. Endangered Species Act. As a result of habitat loss and the decline of the host plant, *P. meconis* is also a species of conservation concern. The development of a reference genome for *P. meconis*, combined with resequencing data, will facilitate an understanding of the levels of genetic diversity, genetic structure, and isolation of the remaining populations of this species of conservation concern. To collect specimens for this study, the team sampled a small series of individuals of this bee and kept them chilled but alive while transported to the lab. The bees were warmed up to keep a photographic record of the specimens. After that, specimens were kept in a -20 ºC freezer. DNA was successfully extracted from a single male individual (whole-body) despite its small body size, which ranges between 5 to 7 mm in length. Despite the lack of flash freezing after collections, the quality of this genome was high with a N50 of

17.5 and a BUSCO score of 95.5% for the Hymenoptera genes. A reference genome was successfully generated and annotated from the specimen.

Case Study IV. Population Structure and Inbreeding of an Endangered Bee Pollinator

Bombus affinis Cresson (Apidae: Bombini), commonly known as the rusty patched bumble bee, was the first Federally Endangered bee species in the continental United States (Fig. 5). This species began declining in abundance during the late 1990s and has lost an estimated ~70% to 90% of its historical range. Mola *et al.* (2024) investigated the population structure and patterns of extant genetic diversity in this Federally Endangered species. To avoid lethally collecting specimens of this endangered species, the team opportunistically collected tarsal tissue from 470 individuals from 59 sites that corresponded to 13 extant populations. A total of 15 microsatellite loci were amplified in two multiplex sets. The study identified three main genetic clusters that are now being distinctly prioritized for conservation. The estimated number of colonies per site varied between 4 and 70, indicating that the abundance of this species is significantly lower than the observed abundance of common species such as *B. impatiens* (see Case Study II).

Figures 2–5. Bees featured in case studies using molecular methods and markers. **2.** Squash bee, *Xenoglossa pruinosa* (Say). Photo credit: Nash Turley. **3.** Common eastern bumble bee, *Bombus impatiens* Cresson. Photo credit: Laura Jones. **4.** Mojave poppy bee, *Perdita meconis* Griswold. Photo credit: Collen Meidt. **5.** Rusty patched bumble bee, *Bombus affinis* Cresson. Photo credit: Clay Bolt.

DISCUSSION

Although the preservation of tissue for molecular data analyses is beyond the current scope of many wild bee monitoring efforts, it has been proposed as a critical component of more comprehensive future monitoring (van Klink *et al.*, 2022). Outside of monitoring, genetic, genomic, and other molecular approaches are also routinely used in bee research, but to the best of our knowledge, there are no standardized methods for these approaches that are available for the wild bee research community. Standardized protocols and data standards will help to ensure that samples are collected and stewarded properly for subsequent use for molecular analyses. This protocol is especially timely because technology is continuing to advance, resulting in improved molecular capabilities, while also reducing its cost. With these advances, members of the bee research, monitoring, and conservation communities will likely become increasingly interested in adding these types of analyses to their work. Thus, it is critical to develop standards for how tissue is collected, processed, and stored to ensure high-quality genetic, genomic, transcriptomic and other types of molecular data.

Molecular approaches not only aid in understanding historical population dynamics but also provide insights into the evolutionary responses of species to past environmental changes (*e.g.*, López-Uribe *et al.*, 2014; Černá *et al.*, 2017). As such, these methods are invaluable for guiding current and future conservation strategies, ensuring the preservation of biodiversity in the face of ongoing environmental challenges. Traditionally, genetic data have been used to address critical conservation issues such as effective population sizes (Lozier *et al.*, 2023), adaptive processes (Theodorou *et al.*, 2018; Pope *et al.*, 2023), and levels of genetic diversity and inbreeding (López-Uribe *et al.*, 2019; Mola *et al.*, 2024); issues that would otherwise be unanswerable. Genomic and transcriptomic tools are particularly valuable in assessing the recent demographic history of declining and endangered bee species (Kent *et al.*, 2018; Mola *et al.*, 2024). One of the most exciting avenues in this field is the development of protocols that use tissue from pinned museum specimens (Grewe *et al.*, 2021; Brasil *et al.*, 2023; Samad-Zada & Rehan, 2023). Advances in sequencing technologies are enabling the extraction of valuable genetic information from even the smallest and oldest specimens, further expanding the scope of genetic studies (Blaimer *et al.*, 2016). The proper storage of tissue for genetic analysis will open the potential to answer future questions not yet imagined (Nachman *et al.*, 2023) and aid efforts like the Earth Biogenome Project (Lewin *et al.*, 2018), which aims to sequence genomes for all species on Earth.

Molecular approaches such as megabarcoding, DNA metabarcoding, and environmental DNA (eDNA) are promising for advancing insect monitoring, limiting lethal collection, and overcoming the bottleneck of taxonomic identification (Piper *et al.*, 2019; Roger *et al.*, 2022; Avalos *et al.*, 2024). DNA megabarcoding relies on the ability to generate molecular data for a large number of samples quickly and cheaply and to use the data to sort specimens into species more quickly than traditional approaches (Caterino & Recuero, 2023). DNA metabarcoding technology allows researchers to pool hundreds of individuals for targeted sequencing of one genomic region (*e.g.*, the barcode region of the cytochrome oxidase I (COI) gene), thus it can be integrated into already ongoing monitoring efforts to facilitate species identification. eDNA approaches aim to detect the presence of DNA from focal taxa in air, soil, or water. Several recent studies have shown that bee DNA deposited on flowers can be extracted

and species reliably identified from the DNA (Thomsen & Sigsgaard, 2019; Harper *et al.*, 2023). How these approaches compare to traditional monitoring efforts is an area of active research, but eDNA approaches show promise for the discovery and monitoring of biodiversity including plant-bee interactions (Ruppert *et al.*, 2019). Additionally, transcriptomes offer valuable insights into gene expression patterns in response to environmental stressors, providing a deeper understanding of mechanisms underlying stress and drivers of insect decline (Tsvetkov *et al.*, 2021). These tools collectively enhance our ability to monitor bee populations more efficiently and accurately, leading to more informed conservation decisions. The integration of these advanced molecular techniques into traditional monitoring frameworks holds great promise for addressing the challenges of biodiversity loss and ecosystem management.

We close with the argument that once the integrity of specimens for molecular analyses is compromised, it is not possible to go back in time to recover it. Therefore, we encourage the wild bee monitoring community to use a forward-thinking approach and consider making, when possible, the additional effort needed to maximize the uses of their collected specimens in the future. Although insect collections are undeniably extremely valuable for conservation, dry specimens collected using traditional approaches have limited use for some of the approaches discussed in this protocol. We argue that the value of molecular data that can be extracted from specimens in the future is worth the extra time and effort associated with the preservation of tissue for genetic markers, particularly for formal monitoring approaches that rely on lethal sampling. Lastly, if storage space or cryogenic facilities are limiting factors, consider reaching out to other researchers or museums who may specifically maintain repositories of genetic material. We hope this protocol will motivate the community to implement these approaches and move forward with bee monitoring efforts in a more holistic manner.

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Standardized protocol for collecting bee samples for internal parasite and pathogen data

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Abstract. Internal parasites and pathogens have not been a focus of wild bee systematic data collection efforts to-date but are important to document because they have been strongly linked to bee declines. Here, we provide a standardized protocol for collecting fresh bee tissue samples for generating parasite and pathogen data. The protocol emphasizes appropriate handling and storage conditions and data standards. It can be embedded within bee health monitoring projects or used by individual data collection efforts that aim to generate parasite and pathogen data now and in the future. This protocol is part of a series developed in association with the U.S. National Native Bee Monitoring Network to standardize bee monitoring practices.

INTRODUCTION

A wide diversity of parasites and pathogens infect bees (Fünfhaus *et al.*, 2018; Hristov *et al.*, 2020; Evans *et al.*, 2023; Figueroa *et al.*, 2023;) and there is increasing interest in the roles they play in influencing wild bee population dynamics, including decline (López-Uribe *et al.*, 2020). Parasite and pathogen population dynamics are also closely aligned with host population dynamics; thus, co-monitoring of bee hosts and

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their parasites and pathogens can bring about a fuller understanding of changes in populations. In addition to wild bee species-specific parasites and pathogens, disease outbreaks in commercially managed bees in North America (including the non-native honey bee, *Apis mellifera* L., and native bee species such as *Bombus occidentalis* Greene) have raised concerns regarding pathogen spillover into wild bee populations (Colla *et al.*, 2006; Arbetman *et al.*, 2013: Fürst *et al.*, 2014; Deutsch *et al.*, 2023; Strange *et al.*, 2023). Although the connection is not fully understood, higher prevalence of parasites and pathogens have been detected in declining bee species (Cameron *et al.*, 2011; Cordes *et al.*, 2012; Hristov *et al.*, 2020; Figueroa *et al.*, 2023).

Here, we first briefly outline the diversity and natural history of common internal macro- and micro- bee parasites and pathogens that occur across a broad diversity of bee taxa. We emphasize that future work is warranted on this topic, specifically on how particular parasites and pathogens impact wild species, for which there is a paucity of data. We provide a protocol and associated data standards to aid with collecting individual bee tissue for parasite and pathogen analysis. The protocol specifically addresses sample collection and storage methods, rather than sampling design or downstream handling or analyses, as these details can differ greatly depending on the aims of a specific project or study. Although it can be used as part of any wild bee data collection effort, the protocol is specifically provided with an eye towards wild native bee monitoring and not for sampling managed bees where disease monitoring protocols already exist (*e.g.*, Dietemann *et al.*, 2013). Similarly, we focus on primarily internal parasites and not kleptoparasites or social parasites in detail as these are often handled as individual specimens.

OVERVIEW OF PATHOGENS AND PARASITES AFFLICTING WILD BEES

Viruses: To date, nearly all bee-associated viruses were first described in honey bees (Grozinger & Flenniken, 2019; Figueroa *et al.*, 2023). Although detections of these viruses frequently occur in other bee species, there is little information regarding the route of transmission, symptoms, or consequences of infection for most non-*Apis* species (McArt *et al.*, 2014; Figueroa *et al.*, 2019). Indeed, non-*Apis* bees generally show significantly lower prevalence and titers of viruses than honey bees (Evison *et al.*, 2012; Jones *et al.*, 2021; Levenson & Tarpy, 2022). Cross-transmission is likely, given that co-occurring bee species share similar viral profiles (McMahon *et al.*, 2015; Tehel *et al.*, 2020), and transmission dynamics within and among species are still being discovered (Alger *et al.*, 2019a,b; Burnham *et al.*, 2021). Common bee viruses found in both honey bees and wild bees include deformed wing virus, sacbrood virus, and black queen cell virus. Because many of the viruses are single-stranded RNA viruses that break down quickly and can become undetectable in a deceased host (Grozinger & Flenniken, 2019), particular care must be taken when sampling bees for viral presence (see Sample Collection and Storage below).

Fungal parasites: Several groups of fungal symbionts can form pathogenic relationships with bees (Evison *et al.*, 2012; Evison & Jensen, 2018). Two primary groups have received the most attention in bees. The Microsporidian genus *Nosema* (Microsporidia: Nosematidae) is an important group of pathogens found in both commercial (*Apis* Linneaus, *Bombus* Latreille, etc.) and wild bees. A recent generic name change to *Vairimorpha* was proposed; however, we refer to this group as *Nosema* in this document following the suggestion of the Society for Invertebrate Pathology

(Bartolomé *et al.,* 2024). Several *Nosema* species are known to infect bees, chiefly *N. bombi* Fantham & Porter, *N. apis* Zander, and *N. ceranae* Fries (Grupe & Quandt, 2020; Deutsch *et al.,* 2023; Figueroa *et al.,* 2023). Another microsporidian, *Antonospora scoticae* Fries *et al.,* has been isolated from *Andrena scotica* Perkins, underscoring the potential for continued discovery of novel parasites and limited knowledge of parasite diversity across bee taxa (Fries *et al.,* 1999). The genus *Ascosphaera* (Ascomycota: Eurotiomycetes: Ascosphaerales) has several members with associations with numerous bee species (Klinger *et al.,* 2013; Evison & Jensen, 2018). Both *Nosema* and *Ascosphaera* are primarily known from studies of managed bees, but research into associations with and impacts on wild bees is growing (Deutsch *et al.,* 2023; Figueroa *et al.,* 2023; LeCroy *et al.,* 2023). *Nosema* spp. are primarily detected through dissection of gut tissues followed by microscopic observation, PCR based screening, or qPCR quantification. *Ascosphaera* spp. infections largely impact developing brood (Klinger *et al.,* 2013), thus detections are generally made via inspection of the nest; however, PCR detection has been implemented with adult bees (Evison *et al.,* 2012).

BACTERIAL PARASITES: Bee-associated bacteria appear to be largely commensal or beneficial; however, some important diseases of honey bees are bacterial and thus it is reasonable to expect that other bee species encounter pathogenic bacteria. American and European Foulbrood (*Paenibacillus larvae* White and *Melissococcus plutonius* White, respectively) are devastating bacterial infections of honey bees (Fünfhaus *et al.,* 2018) and the causative agents have recently been reported in other bees, although disease has not (Deutsch *et al.,* 2023). *Spiroplasma* spp. have been described in honey bees, bumble bees, mason bees, and squash bees (Schwartz *et al.,* 2014; Fünfhaus *et al.,* 2018; Jones *et al.,* 2022). These bacteria may occur intra- or extracellularly with corresponding differences in pathology. Detection is generally done with a combination of microscopy, PCR-based detection, or qPCR quantification (Schwartz *et al.,* 2014).

PROTOZOAN PARASITES: Several groups of Protozoa impact bee populations. *Apicystis bombi* (Liu, Macfarlane & Pengelly) (Apicomplexa: Neogregarinorda: Lipotrophidae) is highly virulent and occurs in all life stages of bumble bees (Lipa & Triggiani, 1996). Introduced in South America by commercial *Bombus terrestris* L. colonies, it spilled over to wild *B. dahlbomii* Guérin-Méneville populations, contributing to their rapid decline (Rutrecht & Brown, 2008; Arbetman *et al*., 2013). Furthermore, undetermined Neogregarines have been described in a diversity of wild bees in North America (Figueroa *et al.,* 2021), emphasizing the need for new species discovery in a diversity of host taxa. Three genera of trypanosomes, *Crithidia* Léger, *Leptomonas* W. S. Kent, and *Lotmaria* spp. (Euglenozoa: Kinetoplastea: Trypanosomatidae), are highly prevalent in bees viscera (Jones *et al.,* 2022; Figueroa *et al*., 2023). Detection of protozoan parasites is typically done with microscopy, PCR-based detection, or qPCR quantification.

OTHER PARASITES: A variety of multicellular organisms are known to cause pathology in bees (Sammataro *et al.,* 2000; Evans *et al.,* 2023). A rich fauna of mites, both internal and external, is known to inhabit bees and their nests. Several parasitic wasps, nematodes, and flies have been recorded from across bee taxa (Evans *et al.,* 2023). Detection varies, but is generally through microscopic examination, either of the external cuticle of the bee or the bee nest, or through dissection and microscopic examination. PCR is frequently used to verify species identity of immature parasitoids.

SAMPLING DESIGN

The sampling design employed for generating parasite and pathogen data is dependent on the goals of a study or project. Consultation with both an insect pathologist and the laboratory performing subsequent analyses is highly recommended prior to carrying out any sampling. For example, sample sizes are dependent on the prevalence of a pathogen within the study population, which should be estimated prior to collecting because this will influence the depth of recommended sampling. Low prevalence pathogens may require large sample sizes for detection; for example, if prevalence is low (*e.g.*, < 5%), numbers of individuals in the hundreds would be required to quantify parasite or pathogen prevalence accurately. Pathogens and parasites can also be life stage- (Klinger *et al.*, 2013), caste- (Poinar & Van der Laan, 1972; Kapheim *et al.*, 2015), and tissue-specific (Larsson, 2007; Otti & Schmid-Hempel, 2007), making it important to collect the appropriate samples for the target pathogen. The time of year in which samples are collected is also important when designing studies to include pathogen monitoring. This is especially true for social or semi-social species with discrete brood cycles (Graystock *et al.*, 2020). Due to the dynamic nature of host-parasite interactions, pathogen and parasite monitoring, paired with host-population monitoring, using repeated longitudinal sampling (*e.g.*, sampling of a population at regular temporal intervals across a season) is necessary to reveal true patterns of prevalence and host choice over time (Moussy *et al.*, 2022; Cardoso *et al.*, 2022). A single sampling event is a snapshot that offers little context; regular sampling events provide finer resolution to the host-parasite dynamic. Moreover, individual laboratory protocols for pathogen or parasite analysis can vary (Levenson & Tarpy, 2022) and may require special handling considerations in the field to ensure data quality. Note that there are also important considerations about the functional significance of pathogens that require guidance from insect pathologists. For example, detection of a parasite does not necessarily equate to a fitness effect on the host (Tehel *et al.*, 2020), and this needs to be considered when interpreting the findings of pathogen quantification studies based on prevalence data.

SAMPLE COLLECTION AND STORAGE

Lethal sampling: Proper handling and storage of specimens is critical to achieve accurate detection and quantification of pathogens and parasites. Passive traps, such as bowl traps, which often collect multiple individual bees, should not be used for studies focused on pathology. This is because these traps create conditions that do not adhere to the standards outlined in this protocol, which are the minimum standards for treating tissue intended for generating high-quality parasite and pathogen data. Moreover, traps that capture multiple individuals of a species or multiple different species create a risk of contamination for pathology work, if the goal is to quantify pathogens per individual. A core component of this protocol is that individual bees are collected with tubes, vials, or forceps that are sterilized using 10% bleach solution, > 70% ethanol, flame, or another appropriate method of sterilization. Freshly sterilized tools need to be used for each bee specimen to avoid cross-contamination, and all samples (whole bees or tissue) collected into plastic bags or sterile tubes or vials (*e.g.*, glass scintillation vials for ease of observation and storage). Repeated use of uncleaned nets is a potential source of contamination of specimens, although no specific evidence of this exists. We recommend disinfecting nets (*e.g.*, bleach, hot water, detergent)

regularly to avoid pathogen spread between sites and to minimize potential specimen contamination; a simple method for this is spraying ethanol on nets and laundering nets between site visits. This is also a best practice for minimizing the spread of invasive weeds among sites.

Most tissue collection methods for parasite and pathogen analysis involve collecting live tissue, maintaining it under some temporary storage conditions, then processing it immediately with microscopy, nucleic acid (DNA/RNA) extraction, or placing it at ultra-cold (*e.g.*, frozen at—80°C or below) temperatures for long-term storage. Diseased tissue may be collected from nests and care should be taken to limit transfer of disease to healthy brood in the nest site. Ultra-cold temperatures can be achieved by placing tissue on dry ice (~-78°C), directly into liquid nitrogen (~-196°C), into a liquid nitrogen-charged dry shipper, or placed directly into an ultra-cold freezer (~-80°C). The time between when samples are first collected and subsequently transferred to their long-term storage conditions, and the temperature at which they are kept during this intermediate time, are especially important for parasite and pathogen studies. A core component of this protocol is to record and report this information. As a rule of thumb, the more one reduces the time to freezing and the temperature of storage, the more accurate detection and quantification are both with microscopy and PCR-based techniques. The optimal method, when using a lethal sampling approach, is to flash-freeze the entire bee as early as possible so that there is no time between field collection and long-term storage. This minimizes the suffering of the bees (Gibbons *et al.*, 2022) and results in tissue that can be used for the maximum number of purposes (*e.g.*, isolation of high-quality DNA, RNA, and RNA viruses). A notable exception is the detection and study of trypanosomes using microscopy, which is best done with fresh, unfrozen tissue because the movement of live trypanosomes greatly aids in detection and quantification. If immediate freezing is not possible, bees can be kept alive between 0–10°C for up to 24 hours before long-term storage. For bees that have been collected and are temporarily stored at room temperature the maximum is 12 hours until they enter long-term storage; note that in warmer temperature conditions, or in direct sunlight, bees can perish quickly (< 1 hour) in collection vials if they are not kept on ice.

As an alternative to handling and storing tissue at cold temperatures, tissue can also be collected and stored in fixing substances that preserve them for parasite and pathogen analyses. These other methods can be more practical in some situations, such as remote fieldwork, where ultra-cold temperatures are not accessible. Ethanol (> 95%) can be used for long-term storage, but samples stored in ethanol cannot be reliably used for RNA extraction, visualization of some, or culturing of most pathogens in the future, whereas flash-freezing followed by maintenance at or below—80°C would allow for the future use of these methods. Additionally, specimens stored in ethanol for microscopy benefit from cold storage at—20°C or below to ensure high quality tissue for dissections. As an alternative to ethanol, tissues can be collected into and stored in quaternary ammonium salt solutions such as RNA*later*™ (Ambion, Applied Biosystems), which preserves RNA for one day at 37°C, one week at 25°C, one month at 4°C, or indefinitely at—20°C. RNA*later* also preserves DNA for a longer duration than RNA and is compatible with microscopy and potentially cell culture (Van Eijsden *et al.*, 2013). Note that when entire bees are collected into or stored in these fixing substances (ethanol, RNA*later*), specimen curation and species identification can be difficult because these substances can alter tissue integrity over time. Ethanol storage can make tissues brittle and indistinguishable, whereas RNA*later* will precipitate salt

crystals onto the bee cuticle in storage and may make subsequent identification difficult (Strange *pers. obvs.*). Crystals can be dissolved again by heating to 37°C, but this may impact downstream molecular analyses of pathogens.

Non-lethal sampling: Effective, high-throughput methods are being developed for collecting tissue non-lethally for parasite and pathogen analyses (Tissier *et al.*, 2024). At this time, however, these non-lethal methods are still in development and are not field-ready for most projects, and there are some costs that must be considered. First, sampling time will be much greater than if collecting whole bee specimens and may be prohibitive based on sampling design and objectives. Second, the methodology for non-lethal pathogen sampling is not fully developed, although active research is being conducted (Tissier *et al.*, 2024). Equipment for sampling non-lethally may also vary from studies collecting lethal samples. The utility of fecal samples to detect parasitism by nematodes, parasitic wasps, and parasitoid flies is unknown; thus non-lethal samples may provide an incomplete picture of parasitism. Finally, while pathogens have been detected in non-lethal samples, correlation of pathogen loads in fecal samples to pathogen loads in the gut tissue is not known. Given the overwhelming evidence that parasites and pathogens can be key regulators of bee population dynamics, including those in decline (Cameron *et al.*, 2011; Cordes *et al.*, 2012; Hristov *et al.*, 2020; Figueroa *et al.*, 2023), we advise that protocol users consider balancing the considerable value of collecting samples lethally for parasite and pathogen analysis with any downsides of lethal collection, such as unintentionally over-collecting and causing harm to wild populations.

If used, non-lethal tissue sampling should follow the sample collection and storage requirements outlined above, with the exception that the live bee being sampled is released once the non-lethal sample (*e.g.*, tissue, fecal matter) is collected. Upon collection, non-lethal tissue samples should be processed for microscopy or DNA/RNA extraction or placed in storage (frozen, ethanol, RNA*later*) as directed for lethal sampling.

Vouchering: Vouchering is especially important for studies where bees are not maintained as specimens in their entirety both in lethal and non-lethal sampling. If specimens are sampled "non-destructively" (*i.e.*, if a single body part or tissue type is removed and destroyed, but the remainder of the sampled specimen has been maintained), and can still be used to confirm species identification, then the remaining specimen can become the voucher. In this case, vouchers should be pinned and labeled to be clearly associated with the tissue sample used in the analysis and their deposition information reported in publications (Montero-Castaño *et al.*, 2022). Alternatively, extracted DNA can be stored as a voucher that can be used to determine species identity. If samples are used destructively or tissue samples are collected non-lethally (see above), photographic vouchers can be used instead. In this case, collecting photographs of the entire individual and parts of the body that will confirm identification is critical (see Cariveau *et al.*, 2025). We also recommend collecting a set of individuals of the same species to be maintained as pinned voucher specimens that are representatives of the species sampled during the collection event.

ADDITIONAL BEST PRACTICES

Where possible, we recommend 'banking' a subset of samples in ultra-cold storage (at or below −80°C) for potential future use, rather than using all samples destructively.

This is because novel pathogens can be difficult to detect in historical samples that are not stored appropriately.

We also recommend collecting and reporting information about honey bees or other managed bees from any sites included in wild bee pathogen studies. This may include the presence or density of managed bees, or the quantification of shared resource use (as per Page & Williams, 2023). Additionally, we recommend collecting a sample of managed bees present at a site, as these can be used for pathogen or parasite detection.

METADATA SPECIFIC TO THIS PROTOCOL

Metadata to record for pathogen samples include information about the sterilization methods of collecting equipment, type of tissue(s) sampled, sample handling conditions prior to final storage, time until final storage, final storage conditions, and final storage location (Table 1). The final storage conditions, particularly the temperature at which the sample is stored, should be provided in **dwc:preparations**. All other information can be provided together in the term **dwc:materialEntityRemarks**. When providing multiple pieces of information for one Darwin Core term, separate them with a vertical bar; for example: "collecting equipment sterilized with 10% bleach | sample stored on ice between collection and final storage | 0.8 hour between collection and final storage | stored in Sample Lab" is an appropriate entry for **dwc:materialEntityRemarks**. Although it may seem counterintuitive to provide this much text in one spreadsheet cell, adhering to these practices aligns with the Darwin Core standard (Wieczorek *et al.*, 2012) and promotes reproducibility and utility of the data. Lastly, please be sure to cite this protocol in **dwc:samplingProtocol**. Full details on using these Darwin Core terms are provided in The Wild Bee Data Standard (Du Clos *et al.*, 2025); examples of proper data entry in spreadsheet templates can be found on Zenodo (Du Clos *et al.*, 2024).

Table 1. Required data to be recorded when implementing the protocol to adhere to the Wild Bee Data Standard (Du Clos *et al.*, 2025).

Required Data	Description	Darwin Core Term
Sterilization method	Method used to sterilize equipment between samples. Methods can include bleach (10% is recommended), ethanol (>70% recommended), or another appropriate method of sterilization	dwc:materialEntityRemarks
Sample conditions prior to final storage	Report how the specimen was handled between collection and final storage	dwc:materialEntityRemarks
Time until final storage	Report how long between specimen collection and final storage	dwc:materialEntityRemarks
Final storage conditions	Report how the specimen is stored, particularly the temperature	dwc:preparations
Final storage location	Report where the specimen is stored	dwc:materialEntityRemarks
Type of tissue stored	Report the type of stored tissue (whole body, abdomen, gut, brain, etc.)	dwc:preparations

DISCUSSION

Disease monitoring is a major focus of wildlife monitoring efforts (Morner *et al.*, 2002), and has been performed in managed honey bees (Lee *et al.*, 2015), but has not yet been a focus in wild bee monitoring. This is despite concerns of pathogen spillover (Colla *et al.*, 2006; Strange *et al.*, 2023) and implications of disease in species declines (Cameron *et al.*, 2011; Cordes *et al.*, 2012; Cameron & Sadd, 2020). As interactions between managed bees and wild bees continue to increase, and documented declines of wild bees continue, the urgency for understanding the underlying mechanisms of pathogen and parasite dynamics in bee communities grows. To facilitate this understanding, disease monitoring becomes most powerful when it is paired with population monitoring (Cardoso *et al.*, 2022) and fully integrated into comprehensive bee monitoring programs. Effective monitoring should consider a more targeted approach that prioritizes monitoring wild bee parasites and pathogens based on their ease of transmission and virulence for a given focal bee species, if this is known. Note, however, that surveillance monitoring, which can detect emerging and lesser-understood parasites and pathogens, is also an important component of comprehensive disease monitoring programs.

The urgency of expanding our knowledge and increasing baseline data on pathogens and parasites in bee communities is underscored by past declines in some wild bee species (Cameron *et al.*, 2011). Specifically, declines in several North American bumble bee species in the late 1990s and early 2000s are associated with the pathogen outbreaks in commercial bumble bees during that time (Flanders *et al.*, 2003; Cameron *et al.*, 2011). Despite intensive efforts to link directly the declines to these pathogens (Cordes *et al.*, 2012; Cameron *et al.*, 2016), the lack of baseline data prior to the population declines has prevented definitive answers to the cause of decline. Given that many additional bee species are threatened, or potentially declining, there is an urgent need to collect tissue samples from other bee groups to obtain the information needed to link parasites and pathogens better to declines in these species, if these relationships exist.

There are also foundational knowledge gaps in our understanding of bee symbionts, their functions and/or pathologies, and their dynamics in wild bee populations (Figueroa *et al.*, 2023). For example, recent studies have shown that many parasites and pathogens move among species in bee communities. Yet, little is known about these types of transfers outside of a few case studies (Evison *et al.*, 2012; McArt *et al.*, 2014; McMahon *et al.*, 2015; Evison & Jensen, 2018; Figueroa *et al.*, 2019; Deutsch *et al.*, 2023), and a few well-studied, managed bee species (*A. mellifera*, *B. terrestris*, *B. impatiens* Cresson, *Megachile rotundata* (Fabricius), and *Osmia* spp.) (Graystock *et al.*, 2013; Grupe & Quandt, 2020). Other valuable pieces of information, such as the geographic distribution, favorable environmental conditions, preferred suite of hosts, and impacts of infection, are also unknown for most pathogens found in wild bees. This information is essential to understand population dynamics properly, manage recovery of endangered species, or implement habitat restoration for most bee species. This further underscores the need for more research on parasites and pathogens in wild bees, and greater integration of the sampling approaches we outline into wild bee monitoring projects.

In the future, we anticipate that wild bee monitoring programs will increasingly incorporate pathogen and parasite monitoring. We provide this protocol to support

those efforts by giving researchers information about the best ways to sample tissue to maximize its use for parasite and pathogen analyses. We note also that although our protocol was developed with the goal of advancing wild bee monitoring, it holds equal value for any data collection effort aimed at generating data on wild bee parasites and pathogens. We also foresee an increasing emphasis on non-lethal sampling approaches for the study of wild bee parasites and pathogens, although at present we urge caution using these methods because of their current efficacy and practicality. Ultimately, the goal is to predict and prepare for potential disease outbreaks in at-risk populations and to reduce the role pathogens play in wild bee population declines.

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