Arthropods at the center: Expanding the all-taxa net

SysEB Section Symposium at the Entomological Society of America annual meeting
Columbus, OH – November 8–11, 2026 | Wednesday, 1:30 PM - 5:30 PM | GCCC room A114-115
Co-organized by Heather Stehle, Crane Hollow Preserve & Will Kuhn, Discover Life in America

Large-scale All Taxa Biodiversity Inventories are transforming how insect diversity is documented across landscapes. This symposium convenes leaders of multiple efforts to compare approaches, share best practices, and examine arthropods' central role in comprehensive biodiversity assessment, fostering collaboration and future coordination in inventory-driven systematics and biodiversity research.

Schedule

Presenting author listed here; see abstracts for co-authors and affiliations

Introductory Remarks	**Heather, Will**	1:30–1:35
Diversity at every scale: What two eastern ATBIs reveal about discovering the unknown fauna of North America	**Will Kuhn**	1:35–1:55
The Vermont Atlas of Life as a model for a regional All-Taxa Biodiversity Inventory	**Susan Hindinger**	1:55–2:15
Developing a statewide all-taxa inventory with a focus on arthropod checklists	**Jim Brighton**	2:15–2:35
From a million specimens to ten million: developing an in-house barcoding pipeline for the California Insect Barcoding Initiative	**Austin Baker**	2:35–2:55
Break - 10 mins		2:55–3:05
Hidden in the hollows: Documenting and preserving the biodiversity of Appalachian Ohio	**Heather Stehle**	3:05–3:25
Cataloging biodiversity at Powdermill Nature Reserve: A natural history museum's field station approach	**Andrea Kautz**	3:25–3:45
An ad hoc and self-organizing ATBI for a northern Michigan natural area	**Kerry Woods**	3:45–4:05
Island biodiversity: Surveying all taxa when expertise is limited	**Sarah Bois**	4:05–4:25
Break - 10 mins		4:25–4:35
Panel Discussion - 50 mins		4:35–5:25
Closing Remarks	**Heather, Will**	5:25–5:30

Abstracts

From a million specimens to ten million: developing an in-house barcoding pipeline for the California Insect Barcoding Initiative

Austin Baker, Sean Jungbluth & Michelle Jungbluth – BioKEA, Berkeley, CA

Large-scale all-taxa biodiversity inventories (ATBIs) of insects increasingly rely on DNA barcoding to match the pace of specimen accumulation. Last year, we presented results from the California Insect Barcoding Initiative (CIBI) at one million specimens, including biodiversity patterns, sampling completeness, and species richness estimates across the state. Scaling to several million specimens, however, requires laboratory and informatics infrastructure capable of sustained high throughput at low cost. Here, we describe progress toward a fully in-house specimen-to-sequence pipeline under development at BioKEA, integrating automated specimen plating, DNA extraction, COI sequencing, and bioinformatic processing within a single tracked workflow. We present preliminary throughput metrics from our first months of operation and discuss lessons learned about which components transfer cleanly from research- to production-scale. We aim to offer a candid template for other groups building sustainable infrastructure for ATBI-scale invertebrate barcoding.

Island biodiversity: Surveying all taxa when expertise is limited

Sarah T. Bois – Linda Loring Nature Foundation, Nantucket, MA

A high proportion of regional biodiversity occurs in hotspots of species richness that can cover relatively small, sometimes isolated areas. Islands and other isolated communities often act as such regional hotspots. However, remote areas often have a limited supply of experts and a lack of access to appropriate repositories to catalog such diversity. Biodiversity data are often skewed towards the scientific expertise available. Taxa that require particular expertise (e.g. Lepidoptera, arachnids, sedges) are often underrepresented in the known biodiversity data for such places. One method to increase research on underrepresented species is through visiting scientists; however, their visits tend to be for a short duration and may not capture the complete phenology or lifecycle of target species. Using Nantucket Island as an example, an island 28 miles from mainland Massachusetts, we highlight various ways that local scientists use available community science programs and bioblitz events to catalog island-wide biodiversity. These programs leverage modern digital tools with deep, localized, year-round ecological knowledge. We will highlight the importance of engaging both community participation and potential experts when available to cast a broad biodiversity net. Coupled with a global network of taxa experts that are able to identify records via iNaturalist, eBird, and other platforms, we have built on the known biodiversity information for the island. It is through collaboration, and sometimes friendly competition, that new discoveries are still being made today.

Developing a statewide all-taxa inventory with a focus on arthropod checklists

Jim Brighton, Bill Hubick – Maryland Biodiversity Project, Cambridge, MD

The Maryland Biodiversity Project (MBP) is a nonprofit initiative dedicated to documenting all living organisms in Maryland through a collaboratively curated, publicly accessible biodiversity archive. This presentation will explore the origins and growth of MBP, with particular emphasis on the challenges of building and maintaining comprehensive arthropod checklists, engaging regional taxonomic experts, resolving taxonomic and identification issues, and curating large-scale biodiversity data for public use.

Over the past fourteen years, the MBP community has documented more than 22,200 species across the state, including over 14,600 species supported by photographic vouchers. The database now contains more than 1.39 million records and 1.47 million photographs, making it one of the most comprehensive regional biodiversity resources in North America. MBP data have been utilized by a wide range of scientific, educational, and conservation organizations, from the Smithsonian Institution to local environmental groups. New state records are added regularly, and the continued growth of the MBP community has significantly expanded our understanding of Maryland's biodiversity and natural history.

The Vermont Atlas of Life as a model for a regional All-Taxa Biodiversity Inventory

Susan Hindinger, Kent McFarland, Michael Hallworth, Jason Loomis, Spencer Hardy, Megan Massa & Dana Williams – Vermont Center for Ecostudies, White River Junction, VT

Arthropods constitute the vast majority of animal diversity yet remain disproportionately under-documented in biodiversity assessments. The Vermont Atlas of Life (VAL) addresses this challenge through a statewide All Taxa Biodiversity Inventory that integrates community science, traditional research, and long-term monitoring methods, with a focus on arthropods because they are traditionally under-surveyed. VAL leverages existing open-source informatics infrastructure, including the Global Biodiversity Information Facility (GBIF) network and crowd-sourced biodiversity platforms — such as iNaturalist, eBird, and eButterfly — to aggregate, curate, and share georeferenced occurrence records at minimal, direct cost. Nearly 12 million primary biodiversity records representing more than 16,500 species currently populate the repository. Arthropods account for approximately 44% of recorded species; most are categorized as data-deficient, revealing substantial knowledge gaps that guide targeted survey efforts. VAL's approach supports diverse methodologies (from passive collecting and bioblitzes to statewide atlasing with expert-verified digital and physical vouchers), lowers barriers to participation, and expands areal and taxonomic coverage. These data are increasingly informing conservation applications including state conservation status rankings, conservation priority-setting, protected area gap analyses, and climate adaptation planning. Using species distribution modeling under current and future climate scenarios, VAL has identified areas harboring unique communities critical for maintaining biodiversity and assessed how well existing protected lands conserve them. This presentation will share VAL's approach, infrastructure, and lessons learned, highlighting how building on shared informatics platforms makes a comprehensive all-taxa inventory achievable for any region and how arthropod diversity drives both the scientific value and practical utility of the effort.

Cataloging biodiversity at Powdermill Nature Reserve: A natural history museum's field station approach

Andrea Kautz – Powdermill Nature Reserve, Carnegie Museum of Natural History, Rector, PA

Established in 1956 and encompassing 2,200 acres of Appalachian forest in the Laurel Highlands of southwestern Pennsylvania, Powdermill Nature Reserve serves as the environmental research station for the Carnegie Museum of Natural History in Pittsburgh, supporting both museum staff and visiting researchers from all over. During the last 70 years, Powdermill has amassed numerous biodiversity datasets and species lists, spanning the web of life, from plants and mushrooms to birds and crane flies. Efforts have included independent research projects, multi-agency collaborations, and public-facing bioblitz events. These data are not only valuable from an ATBI perspective, but also serve as critical baselines for documenting changes in community composition over time, particularly in relation to climate change, ecological invasions, and other disturbances. As a highly diverse taxon, arthropods are an especially important piece of this complex puzzle and should not be overlooked. Partnering with other similar efforts elsewhere to help streamline and standardize the data collection, storage, and management aspects of these studies would be highly beneficial for studying patterns of biodiversity across geographic areas and over time.

Diversity at every scale: What two eastern ATBIs reveal about discovering the unknown fauna of North America

Will Kuhn – Discover Life in America, Gatlinburg, TN; Brent Steury – George Washington Memorial Parkway, National Park Service, McLean, VA

All taxa biodiversity inventories (ATBIs) rest on the simple premise that sustained, taxonomically comprehensive effort in one place reveals far more life than anyone expects, including species new to science. Two long-running ATBIs in the eastern US test that premise at opposite ends of the landscape spectrum. In Great Smoky Mountains National Park—522,000 acres of montane wilderness—the inventory coordinated since 1998 by Discover Life in America has approximately doubled the known biota to more than 22,000 species, adding over 11,000 park records and more than 1,000 species new to science. Along the George Washington Memorial Parkway—a 6,700-acre corridor of protected land threaded through metropolitan Washington, DC—a parallel effort started in 2006 has documented over 7,000 species, including at least 122 confirmed or likely new to science, 385 new state records, and 5 new to North America. Many are arthropods: springtails, mites, flies, and beetles uncovered within sight of the nation's capital.

Rather than ranking these projects, we consider what they reveal in tandem. Despite a hundredfold difference in area and contrasting governance models—a nonprofit–agency partnership versus an inventory led from within the National Park Service—both converge on the same lessons: that hyperdiverse, under-studied invertebrate groups hold most undescribed diversity; that comprehensive inventory is itself an act of conservation; and that discovery is limited less by how wild a place is than by how closely we look. Together, the Smokies and the Parkway make the case for ATBIs across the full gradient of protected lands.

Hidden in the hollows: Documenting and preserving the biodiversity of Appalachian Ohio

Heather Stehle – Crane Hollow Preserve, Rockbridge, OH

Crane Hollow Preserve, a 1,988-acre dedicated state nature preserve in southeastern Ohio, has served as a focal point for long-term biodiversity research, specimen collection, and natural history documentation for nearly 50 years. This presentation will highlight the evolution and integration of three complementary efforts: the Crane Hollow Preserve All Taxa Biodiversity Inventory (ATBI), the Crane Hollow natural history collection housed at Ohio University, and an ongoing project to digitize historical field notes and collection records.

The Crane Hollow ATBI seeks to document the biodiversity within the preserve, generating valuable baseline data on plants, animals, fungi, and other organisms. These inventory efforts have resulted in over 120,000 specimens and observations that contribute to our understanding of species distributions, ecological communities, and long-term environmental change. The associated natural history collection preserves these records and provides an important resource for research, education, and conservation.

A major challenge has been unlocking 25 years of handwritten field notes and collection records for integration into a biodiversity database. To address this issue, we are undertaking a comprehensive digitization effort using FileMaker to transcribe, standardize, and organize these records. This work creates a bridge from paper field notes to contemporary collection management practices by preparing records for migration into the Specify database platform.

Here, we'll discuss workflows, lessons learned, and opportunities for collaboration while demonstrating how digitization and data mobilization can enhance the long-term value of inventories and collections. Ultimately, this project ensures that decades of biological knowledge remain accessible for future research, conservation, and public engagement.

An ad hoc and self-organizing ATBI for a northern Michigan natural area

Kerry Woods – Bennington College, Bennington, VT; Huron Mt. Wildlife Foundation, Big Bay, MI

The Huron Mountains are an ecologically diverse landscape on the Michigan shore of Lake Superior. The private Huron Mt. Club holds a large (ca. 10,000 ha) and particularly pristine tract, with habitats ranging from several lakes and wetlands, to dry bedrock glades, to large tracts of old-growth forest. These holdings have drawn researchers for over a century, with research overseen for the last 70+ years by the non-profit Huron Mt. Wildlife Foundation. Many early researchers focused on biodiversity documentation and, in 2007, we compiled all existing records to arrive at a ‘first version’ ATBI listing about 4,000 species across all kingdoms. Since then, new species have been added at a rate of over 100/yr, and the current working version of the ATBI approaches 6,500 species (arthropods accounting for about half). HMWF’s ‘low-overhead’ model does not support systematic solicitation of specific research projects, so the ATBI has relied on researcher-initiated proposals. Of about 25 research projects sponsored annually by HMWF, typically five or six focus on biodiversity documentation. This means that, while some groups are extremely thoroughly documented, others have been largely (or entirely) neglected. Compilation and updating of diversity data remains an ad hoc effort and, going forward, maintaining and managing an increasingly large and complex data-set will be a challenge for a small organization with no permanent scientific staff, but we hope the HMWF ATBI can serve as an example for other smaller, regional initiatives.