

# The value of museums in the production, sharing, and use of entomological data to document hyperdiversity of the changing North<sup>1</sup>

Derek S. Sikes, Matthew Bowser, Kathryn Daly, Toke T. Høye, Sarah Meierotto, Logan Mullen, Jozef Slowik, and Jill Stockbridge

**Abstract:** If the current rate of climate change continues, the composition, distribution, and relative population sizes of species in the higher latitudes of the Northern Hemisphere are likely to change considerably. Understanding the magnitude of this change requires a well-documented baseline against which to compare. Although specimen-less observations can help augment such a baseline for the minority of organisms that can be confidently identified in the field or from photographs, the vast majority of species are small-bodied invertebrates, primarily arthropods, that can only be identified from preserved specimens and (or) their tissues. Museum staff archive specimens and make them and their data available for research. This paper describes a number of challenges to the goal of thorough documentation of high-latitude arthropod biodiversity and their potential solutions. Examples are provided from ongoing and recently completed research that demonstrates the value of museum specimens and the sharing of their data via global portals like GBIF.org.

*Key words:* Arctic, biodiversity, Arthropoda, monitoring, inventory, taxonomic bottleneck.

**Résumé :** Si le taux actuel du changement climatique se maintient, la composition, la répartition et les tailles de population relatives d'espèces dans les latitudes plus hautes de l'hémisphère nord sont susceptibles de changer considérablement. Pour comprendre l'ampleur de ce changement, il faut une ligne de référence bien documentée contre laquelle on peut comparer. Bien que les observations sans spécimens puissent aider à augmenter une telle ligne de référence pour la minorité d'organismes qui peuvent être identifiés avec assurance sur le terrain ou à partir de photographies, la grande majorité d'espèces est composée d'invertébrés à petit corps, principalement des arthropodes, qui ne peuvent être identifiés qu'à partir de spécimens préservés et (ou) de leurs tissus. Le personnel de musées archive les spécimens et les rend disponibles ainsi que les données connexes aux fins de recherche. Dans cet article, on décrit un certain nombre de défis à l'encontre du but de la documentation minutieuse de la biodiversité d'arthropodes à hautes latitudes et les solutions potentielles à ces défis. On fournit des exemples de recherche en cours et récemment complétée qui démontrent la valeur de spécimens de musée et le partage de données via des portails mondiaux comme le Système mondial d'informations sur la biodiversité (GBIF.org).

*Mots-clés :* Arctique, biodiversité, Arthropoda, surveillance, inventaire, goulot d'étranglement taxonomique.

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**D.S. Sikes, K. Daly, S. Meierotto, L. Mullen, J. Slowik, and J. Stockbridge.** University of Alaska Museum, University of Alaska Fairbanks, 907 Yukon Drive, Fairbanks, AK 99775, USA.

**M. Bowser.** US Fish and Wildlife Service, Kenai National Wildlife Refuge, P.O. Box 2139, Soldotna, AK 99669, USA.

**T.T. Høye.** Arctic Research Center, Aarhus University, 114, Bldg. 1540, DK-8000 Aarhus, Denmark; Department of Bioscience, Kalø, Aarhus University, Grenåvej 14, DK-8410 Rønne, Denmark.

**Corresponding author:** Derek S. Sikes (email: dssikes@alaska.edu).

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## Introduction

The Arctic and subarctic are regions of intense ecological interest due to the rapid changes resulting from global warming, the biogeographic uniqueness of these regions' biota, and how well adapted the biota is to a cold climate (Danks 1981; Meltofte et al. 2013; Sikes and Allen 2016). As high temperature records continue to be broken, with the 10 months prior to and including July 2016 being the warmest globally since recording began in 1880 (NASA 2016), we are transitioning into a different world. Research has documented a variety of alarming changes associated with high-latitude warming, which is more rapid than that seen in lower latitudes. For instance, Alaska has warmed about 3.5 °C in the interior during the winter and 2 °C overall since the 1950s (Melillo et al. 2014). Shrubs are expanding into Arctic tundra and alpine zones, fire frequency and intensity have increased, the growing season has lengthened by about 2 weeks, sea ice, alpine snowfields, permafrost, and glaciers are thawing and shrinking, nonnative organisms such as ticks are establishing, and the climate is shifting beyond the physiological optimum of a dominant boreal forest species white spruce, *Picea glauca* (Veblen and Alaback 1996; Stone et al. 2002; Lawrence and Slater 2005; Sturm et al. 2005; McGuire et al. 2009; Beck et al. 2011; Bret-Harte et al. 2013; Juday et al. 2015; Durden et al. 2016; Phoenix and Bjerke 2016). The National Science Foundation (NSF), the premier science funding agency of the United States, has recently prepared a list of 10 major research foci for future NSF investment (NSF 2016). Among these 10, "Navigating the new Arctic" is listed, demonstrating the high priority the NSF places on the documentation of "these rapid biological, physical, chemical and social changes." The international Conservation of Arctic Fauna and Flora (CAFF) has established the Circumpolar Biodiversity Monitoring Program (CBMP), the goal of which is to monitor arctic biodiversity to provide decision makers relevant information about the changing Arctic. Their 2013 Arctic Biodiversity Assessment report (Meltofte et al. 2013) includes a chapter on terrestrial invertebrates (Hodkinson et al. 2013) that stresses the importance of increasing our understanding of past, current, and potential future Arctic terrestrial invertebrate biodiversity.

Although the Arctic contains fewer arthropod species per unit area than environments at lower latitudes, arthropod diversity is still high and makes up the largest component of multicellular biodiversity in the region (Hodkinson et al. 2013; Høye and Sikes 2013; Sikes et al. 2013; Ernst and Buddle 2015). Arthropods respond rapidly to environmental changes and are deeply entwined in Arctic food webs (Høye and Forchhammer 2008). However, the consequences of climate warming remain understudied across the Arctic and subarctic.

Within the Arctic and subarctic biogeographical zones, Alaska's arthropod fauna is unique. Unlike most of what is now Canada, Alaska's lower elevations were mostly glacier-free during the Neogene and Pleistocene (Ives 1974; Matthews 1975; Behan 1978; Pielou 1991; Elias and Brigham-Grette 2013). This allowed organisms to survive in ice-free refugia (e.g., Beringia) (Abbott and Brochmann 2003; Behan-Pelletier and Schatz 2011; Elias and Brigham-Grette 2013; Pringle 2014). This is thought to be a primary explanation for Alaska's hundreds of potentially endemic arthropod species (Sikes and Allen 2016). Due to changes in climate and sea levels, the region acted alternatively as a passageway or a barrier, which has resulted in multiple dispersal events between the Palearctic and Nearctic across the Bering Land Bridge (Sanmartín et al. 2001; Vila et al. 2011; Sikes and Venables 2013). This has created many complex and interesting biogeographic patterns between the Nearctic and Palearctic.

We, and others before us (e.g., Hodkinson et al. 2013), consider it an urgent priority to establish a well-documented baseline for the Arctic's unique biodiversity, before these ecosystems are greatly altered by predicted radical changes due to climate change.

This baseline will allow future assessment of the magnitude of change and enable detection of range shifts, extirpations, extinctions, invasions, and novel species assemblages. The best data are based on vouchered specimens — physical bodies of organisms (Winker 2004; Rocha et al. 2014) and associated environmental data from their collection events. To promote global collaboration, specimens and these data are ideally held for the public trust in well-maintained research collections, such as the University of Alaska Museum, which share specimen data freely online. Museum collections have always served as references for historical conditions. In recent years, technological advances in museum record digitization, along with increased sampling, have made it possible to infer broad trends of ecological and spatial abundance of terrestrial invertebrates in the Arctic. In addition to a specimen-based assessment of the biota, funding for taxonomic revisions is necessary (Wheeler et al. 2012; Høye and Sikes 2013). Descriptions of new species, new synonymies, and new identification keys are needed desperately — all of which require large research collections to provide adequate sample sizes.

Voucher specimens are particularly important for organisms that are hard to identify, which most invertebrates are. Accurate identification of organisms of high economic or ecological concern is enormously important. Examples include species that threaten agriculture (e.g., *Lygus* spp. on peony crops), subsistence (e.g., winter ticks, *Dermacentor albipictus* Packard, 1869, on moose), and human health (e.g., the brown recluse, *Loxosceles reclusa* Gertsch and Mulaik, 1940, or *Aedes* mosquito vectors of Zika virus). Specimens vouchered in a museum allow verification of identifications and enable multiple forms of identification — both traditional and molecular.

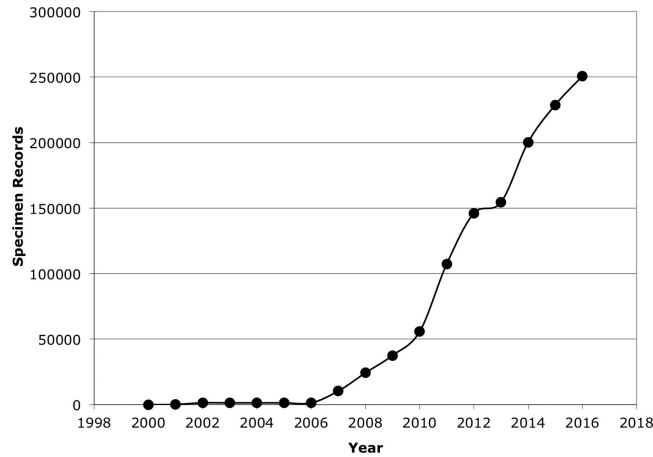
In this paper, we focus on the role that research collections play in the study of Arctic ecosystems and describe the short history of the University of Alaska Museum Insect Collection. We outline major challenges faced in the discovery and documentation of Alaska's Arctic and subarctic biodiversity, along with solutions we have tried, and provide examples of key research projects in Alaska, Canada, Iceland, and Greenland. Throughout, we stress the importance of research collections to the entire Arctic research community and argue for their continued and increased funding.

### History and status of the University of Alaska Museum Insect Collection

Established as part of a NSF-funded Arctic Archival Observatory grant (DEB-9981915), the University of Alaska Museum (UAM) Insect Collection began in late 2000. An Interim Curator of Insects was appointed on a 3 year postdoctoral position to establish the collection. Three large collections of Alaskan material were acquired: ~50 000 specimens of Alaskan aquatic insects (Ephemeroptera, Diptera, Plecoptera, Trichoptera, etc.) stored in glass vials and preserved in ethanol, ~30 000 biting fly specimens (mostly Culicidae and Simuliidae) on pins and in vials of alcohol collected by K.M. Sommerman during the Northern Biting Fly survey of 1947–1958, and ~75 000 pinned terrestrial insect specimens collected between 1940 and the mid-1970s for a US Department of Agriculture collection in Palmer, Alaska.

The first author was hired in 2006 as Curator of Insects and began a vigorous digitization and collection-building program with support from various funding agencies (see Acknowledgements) and help from students and volunteers. Since 2012 the UAM Insect Collection has been using the online specimen database Arctos (<https://arctosdb.org/>). Arctos is an entirely web-based collection management system serving ~2.7 million museum records from 95 collections to end users and data distributors such as GBIF.org and iDigBio.org. As a centralized web application, Arctos integrates other internet resources, calls appropriate web services such as GeoLocate and BerkeleyMapper, and is indefinitely scalable. Arctos is hosted by the Texas Advanced Computing Center, a member of the NSF-sponsored

**Fig. 1.** University of Alaska Museum Insect Collection digital specimen records since the origin of the collection in the year 2000.



TeraGrid network of supercomputing centers. Arctos developers are thoroughly familiar with developing standards for georeferencing, the Darwin Core (<http://rs.tdwg.org/dwc/>), and other data-sharing protocols. With the exception of electively encumbered sensitive data, all data are accessible in real time to the public. Daily backups are stored on three separate tectonic plates. This solution affords great stability and makes the biodiversity data in Arctos among the most securely archived and publicly accessible on the planet.

The UAM Insect Collection now serves data online for over 1.5 million nonmarine invertebrate specimens in 3260 species (23% are apparent new records for the state), represented by over 250 000 georeferenced specimen records (Fig. 1) that cover a date range of 1883–2016. More than 80% of the specimens have been collected since the year 2000. This averages to about 2000 specimen records created per month. Over 75% of the pinned collection and approximately 10% of the wet collection have been databased. At least one specimen of every lowest identification, in both the pinned and wet collections, has been databased, creating a complete online taxon inventory of the collection; 70 601 of these specimen records have been cited or otherwise used in support of 59 peer-reviewed publications ([http://arctos.database.museum/info/publicationbycollection.cfm?collection\\_id=4andcitationonly=trueandpeerr=true](http://arctos.database.museum/info/publicationbycollection.cfm?collection_id=4andcitationonly=trueandpeerr=true)).

Part of the success of the UAM Insect Collection is due to our modern, high-efficiency databasing protocol. Only about 10% (153 692 specimens) of the digitized collection has been identified to the species level. However, the remaining 90% has already been databased and georeferenced. Wheeler et al. (2012) stated “While exciting technologies and projects are being conceived to address these huge backlogs, there is absolutely no excuse for adding to them. All species described from this point forward and every specimen added to a collection from this point forward should be done in a way that is part of the solution and not part of the problem.” Specimens should be digitized prospectively: at the earliest, and easiest stage possible — before labeling and before sorting or identification. Retroactive digitization proceeds at a pace of between 5 and 30 specimens per hour, per technician. Prospective digitization can proceed at a pace of 5–30 collecting events (samples) per hour, per technician, and each collecting event can contain thousands of specimens. The key to this approach is the use of scannable barcode labels linking specimens to their digital records. Once specimens have been prepared, sorted, and identified, the barcode labels allow technicians to rapidly search for long series of specimen records and update their taxonomic identifications — the final step in the process (Table 1).

**Table 1.** Rapid, prospective DBYL (Database Before You Label) protocol.

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1. Collect specimens from  $X$  collection events
  2. Prepare specimens, but keep sorted by  $X$  collection events, and allocate 1 barcode label per pinned specimen or vial ( $n$  barcodes)
  3. Digitize by collection event with all members sharing the same taxonomic identification (e.g., “Arthropoda”).  
Duplicates of this record differing only in barcode number can be generated rapidly (thousands in a few seconds), one matching each of the  $n$  barcodes assigned in step 2
  4. Print labels from database and place on specimens with barcode labels
  5. Sort and identify specimens taxonomically
  6. Scan all barcode labels for each lowest identification, and update records in database to taxon identification
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Unfortunately, this method is not standard, and many research projects, including those administered by museum staff, add thousands of specimens annually to the backlog of specimens awaiting costly retroactive digitization.

### The taxonomic bottleneck

Even in the relatively species-poor Arctic, it is easier to collect invertebrate specimens than it is to identify them. This is one aspect of the so-called “Taxonomic Bottleneck” (Kim and Byrne 2006) that describes the problem of Earth’s biodiversity being too large for the limited, and possibly declining, taxonomic workforce available to describe and identify it. Alaska, a region one fifth the size of the contiguous 48 US states, and estimated to hold over 8200 species (<http://arctos.database.museum/saved/AK-Arthropoda-checklist-2016-01-14>) of nonmarine arthropods (Sikes et al. 2017), currently has one Ph.D.-level insect taxonomist. There are fewer than 10 people in Alaska who regularly identify arthropods to species level and whose combined taxonomic expertise covers less than 25% of the state’s species. Thus, a large backlog of incompletely identified specimens accumulates quickly, which explains why 90% of the digitized specimens in the UAM Insect Collection are not yet identified to species level.

To mitigate this problem, we have collaborated with taxonomists in Canada, Europe, and other US states to whom we loan specimens (or invite to visit UAM). Currently, we have 53 010 specimens on loan and send out an average of 30 loans per year. This helps reduce our backlog but is not a comprehensive solution for various reasons: often no funding is available for these identifications, and they are generally performed as a favor in exchange for the option to retain specimens of interest (and data) for later use. Loans sometimes take much longer than the expected 1 year to return or, in some cases, are lost. There are orphan taxa for which no specialist exists or specialists are too busy with their own backlogs to take additional loans. Also, mailing specimens in alcohol has become increasingly challenging.

### Identification keys

One solution to this issue is the production of identification resources, such as keys and guides, to the Alaskan fauna (preferably user-friendly and well-illustrated) to enable in-house identifications. Since 2006 there has been a slow but steady increase in such Alaska-specific resources; these treat stoneflies (Stewart and Oswood 2006), common insects of southcentral Alaska (Collet 2008), dragonflies (Hudson and Armstrong 2010), and butterflies (Philip and Ferris 2016). However, these cover only 515 species — 6% of the state’s arthropod fauna. There are numerous taxonomic works with a larger geographic scope that include keys to species that are useful for Alaska, such as Darsie and Ward’s (2005) monograph on mosquitoes of North America, the excellent “Insects and arachnids of Canada” series (e.g., Anderson and Peck 1985), and the *Canadian Journal of Arthropod Identification* (e.g., Knee and Proctor 2010), although this latter resource is focused primarily on

northeastern Canada. We have yet to assess how many Alaskan species are in unrevised taxa, for which no reliable keys exist, but the number is likely to be substantial.

However, most keys are written for taxonomists who specialize on a particular family, or order, which makes their use by generalists more challenging and error-prone. A recently published monograph with keys to the entomofauna of Greenland holds promise for the future (Böcher et al. 2015). Ideally, the largest insect collection in each state or province would employ a minimum of one Ph.D.-level taxonomist for each of the five largest orders (Coleoptera, Diptera, Hymenoptera, Lepidoptera, and Hemiptera), one for Araneae, one for Acariformes/Parasitiformes, and one (or more) for the minor orders. Thus, to properly inventory and monitor a region as large as Alaska, a team of at least eight arthropod curators would be ideal.

### DNA barcoding

Another solution to address the taxonomic bottleneck is the use of DNA barcodes to obtain routine identifications of specimens. However, to obtain Linnaean names in this manner, the DNA barcode library, which holds identified DNA sequences against which one can query with unidentified sequences, must be reasonably complete. Towards this goal, the UAM Insect Collection has partnered with the US Fish and Wildlife Service's Alaska Region National Wildlife Refuge System Inventory and Monitoring Initiative to build an Alaska-specific DNA barcode library of nonmarine arthropods (Sikes et al. 2017). The UAM Insect Collection has, to date, contributed DNA barcodes for 1662 Alaskan species, which, combined with DNA barcodes for species that occur in Alaska that were already in the Barcode of Life Datasystems database (BOLD) (Ratnasingham and Hebert 2007), has yielded a total of 4020 species, or 48.5% of the known Alaskan nonmarine arthropod fauna. Thus, approximately half of the known arthropod species in Alaska should be identifiable via DNA barcodes. However, a recent analysis of arthropod diversity in Canada (Hebert et al. 2016) based on analysis of formally defined molecular operational taxonomic units termed Barcode Index Numbers (BINs) (Ratnasingham and Hebert 2013) implies that the Alaskan fauna, like Canada's, may be much more diverse than previously thought.

One challenge to the regular use of DNA barcoding to obtain identifications is the cost of sequencing. Traditional Sanger sequencing currently costs about \$12 USD per specimen per sequencing attempt, but sequencing success is not 100%. Thus, the cost per successful amplification is often much higher and can quickly become quite prohibitive. Next-Generation Sequencing (NGS) methods are being developed to generate barcodes that can be traced to their specimen of origin for less than \$1 USD per specimen (Meier et al. 2015).

Although NGS can produce sequences more cheaply than Sanger sequencing, current NGS sequence read lengths are typically 200–400 bp, shorter than the standard 658 bp DNA barcoding region, limiting their utility for species-resolution identifications (Liu et al. 2013). This limitation is being overcome as newly available platforms employing single molecule real time (SMRT) sequencing technology now yield read lengths of 3000–20 000 bp (Roberts et al. 2013), covering the entire DNA barcoding region. Full-length 650+ bp DNA barcodes were recently obtained from arthropod specimens using an SMRT platform (M. Bowser et al., unpublished data). Recently developed nondestructive techniques enable sequencing without destroying specimen tissues (Hajibabaei et al. 2012; Wong et al. 2014) so that undamaged morphological voucher specimens can be associated with DNA barcodes.

Other challenges to the use of the DNA barcoding to obtain identifications, aside from the cost, and the rapidly changing and improving protocols, include the many ways that things can go wrong and prevent positive identification (or cause misidentification). Contamination, laboratory errors, differently spelled but synonymous names, different taxonomic classifications, misidentifications, young/incipient species (haplotype sharing,

introgression), *Wolbachia* infection, taxonomic oversplitting (species that should be synonymized), and taxonomic undersplitting (species that should be split) can all cause this approach to fail to various degrees. Cognato (2006), Trewick (2008), Collins and Cruickshank (2013), and Goldstein and DeSalle (2011) described these and other limitations of DNA barcoding. Of course, traditional identification methods are not cost- or error-free either.

For the purpose of biomonitoring to address the threats described in our introduction, morphological identifications are simply inadequate due to cost, time required, and inability to identify many specimens that are damaged, immature, or otherwise unidentifiable. Metagenomic analysis of environmental samples via NGS is now being implemented as a way to overcome this taxonomic bottleneck in biomonitoring applications (Gibson et al. 2015; Hajibabaei et al. 2016; Bowser et al. 2017), but these methods require an adequate DNA barcode library to link observed operational taxonomic units to Linnaean names. The role of the museum in this biomonitoring context is to husband the physical specimens that make possible improvements in our taxonomic understanding and the resulting molecular libraries.

Ideally, these two approaches, production of well-illustrated guides or keys and DNA barcoding, will be synergistic and complementary. The recently published guide to North American bumblebees (Williams et al. 2014) is an excellent example of how DNA barcoding and shared online specimen data (see below) can help with production of a valuable identification resource.

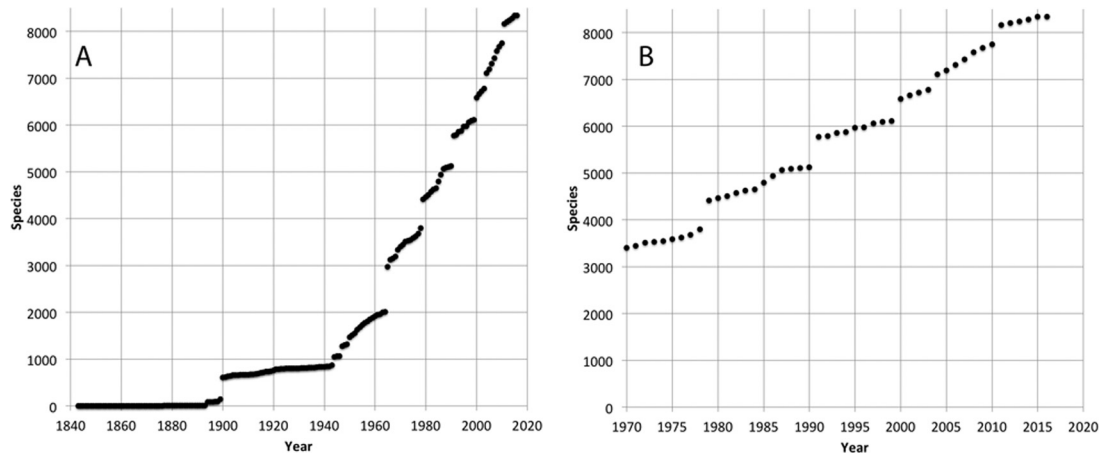
### Historic versus modern data — bees and butterflies

Museum specimen data can be used to understand ecological changes among extant organisms over a long time span, sometimes as long as a century (Bartomeus et al. 2011; Kerr et al. 2015). However, few taxa are sampled densely enough across time and space to allow rigorous analyses that provide reliable answers to climate change questions. In the Arctic, which is logistically more costly and difficult to sample than lower latitudes, long-term data for rigorous time-series analyses are particularly rare. Due to their popularity among researchers and amateur enthusiasts, butterflies are often among the most well-sampled taxa in most regions, Alaska being no exception.

The Alaska Lepidoptera Survey (ALS), founded by the late Dr. Kenelm W. Philip, was a citizen science initiative to document butterfly and moth species across Beringia. Through the support of the NSF, National Park Service, and other entities, collecting kits were sent out to over 600 volunteers who captured specimens for Dr. Philip. Through this effort, along with Dr. Philip's personal collecting across Alaska, western Canada, and eastern Russia, over 111 000 specimens of Beringian Lepidoptera were obtained from 1966 to 2013. The majority of butterfly specimens were identified and recorded in a private database maintained by Dr. Philip. His death in March of 2014 ended the survey, but the specimens and data remain as the most complete representation of Beringian lepidopteran fauna in existence. After Dr. Philip's death, the collection was moved from his private laboratory to the UAM. Much of the collection will eventually be transferred to the National Museum of Natural History, but the ALS specimen data are now publicly available through Arctos ([http://arctos.database.museum/kwp\\_ento](http://arctos.database.museum/kwp_ento)) and have been used in the production of a field guide to the butterflies of Alaska (Philip and Ferris 2016).

The records produced by the ALS have great potential for use in future studies. Museum records have been used to assess geographic (Parmesan et al. 1999) and phenological (Thackeray et al. 2010; Polgar et al. 2013) changes in butterfly species over time in response to climate warming. The ALS butterfly data are currently being used to analyze seasonal flight periods of interior Alaska butterfly species (K. Daly, in preparation). Museum records can also reveal species that may have declined or gone extinct through time-series analyses

**Fig. 2.** Cumulative number of nonmarine Alaskan arthropod species by year of earliest Alaskan record in the UAM, UAMOBs, KWP, and KNWR data sets in the Arctos database ([http://arctos.database.museum/uam\\_ento\\_all](http://arctos.database.museum/uam_ento_all)). Earliest year based on either earliest known specimen or earliest known publication, whichever was earliest. (A) 1843–2016; (B) 1970–2016.



(Solow 1993). Bias may be present in records if collectors favored certain species or regions over others or if collecting effort was not equal across years (Burgman et al. 1995; Shaffer et al. 1998). However, technology is rapidly evolving to address these issues during data analysis of natural history collection records (Graham et al. 2004; ESKILDSEN et al. 2015). Museum records are undeniably a critical resource for detecting species responses to climate warming.

Because the UAM Insect Collection shares its data online via iDigBio.org and GBIF.org, Alaskan data on bumblebees (*Bombus* spp.) were available for inclusion in a cross-continental analysis of bumblebee distributional change over a 110 year time span (Kerr et al. 2015). This study found that bumblebees were disappearing from the southernmost regions of their distributions, but unlike many organisms that track climate change were not dispersing farther north; thus, their ranges were being compressed. These long-term data sets are not only valuable for illuminating the past, but if built upon now, they will allow us to understand the present into the future.

### New records, new species, and discovery analysis for Alaska

“A prerequisite to making any decisions concerning the preservation of populations, species, or higher taxa is knowledge of their existence.” — George Barrowclough, Ornithology Curator of the AMNH (Eldredge 1992, p. 124). The discovery of species, documenting the nonmarine arthropod fauna of Alaska, began with Russian naturalists in the early to mid-1800s (Eschscholtz 1822; Mannerheim 1843) and accelerated in the 1940s, resulting in about 1000 new species discovered in Alaska every 20 years (Fig. 2A), with over 1700 species added to the list between 2000 and 2016 (Fig. 2). There is no sign of a plateau in recent decades, although the rate of discovery has slowed somewhat in recent years (2011–2016) (Fig. 2B). This possible deceleration in species discovery is somewhat surprising, given that this period has seen a great increase in collecting effort (Fig. 1).

Comparing the rapid increase in specimens collected into the UAM Insect Collection during the 21st century (Fig. 1) to the discovery curve for the same time period (Fig. 2B), it is remarkable that no similarly dramatic increase in discovery rate is evident. We suspect this may be due to the time lag between collection and identification and thus a consequence of the taxonomic impediment described above. Bebbler et al. (2007) were critical



of the use of such species discovery curves to interpret inventory completeness. Their analysis indicates that a plateau in new discoveries would have to extend for a long time, with continuing effort expended, before one could confidently conclude that an inventory had neared completion. Figure 2 was assembled from data in Arctos, limited to nonmarine arthropods of Alaska with species-level identifications, and based on the earliest records we have from either specimens or the literature. Jumps in the data, such as that around 1900, result from addition of many records from a single publication or series of closely spaced publications, in this case those of the Harriman Expedition (Banks 1900; Caudell 1900; Coquillett 1900; Dyar 1900; Heidemann 1900; Kincaid 1900; Pergande 1900; Schwarz 1900; Currie 1901; Folsom 1902; Ashmead 1902, 1904; Cook 1904; Richardson 1904). Since each publication we used to compile this list summarized records from years or decades prior to its publication, and no special effort was made to document all earliest records from the literature (more recent checklists were favored over older, original works), this graph is only an approximation of the actual discovery curve.

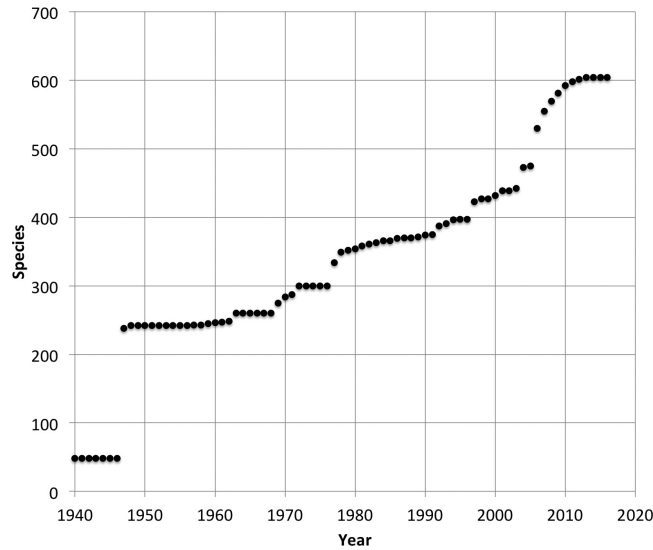
However, it is clear that new regional records (Scudder and Sikes 2014; Sikes and Allen 2016) and species new to science (e.g. Sikes and Stockbridge 2013; Williams et al. 2016) are continually being found on an annual basis, suggesting that the inventory of the entomofauna is far from complete. It is, therefore, important to continue with basic inventory and taxonomic revisionary work of arthropod taxa in the rapidly changing north.

#### **Taxonomic research on climate-sensitive species: *Phlaeopterus* (Coleoptera: Staphylinidae: Omaliinae)**

A phylogeny and revision of the omaliine rove beetle genus *Phlaeopterus* Motschulsky 1853 is currently being prepared (L.J. Mullen, J.M. Campbell, and D.S. Sikes, in preparation). The genus contains multiple undescribed species that may be threatened by a warming North. These beetles are found at elevations up to 3830 m (1100 m in Alaska) at the edges of snowfields and alpine streams and lakes. *Phlaeopterus* have been observed feeding on arthropod fallout, or windblown allochthonous insects, which become lethargic with cold and may become stranded on snowfield surfaces (Swan 1963; Edwards and Banko 1976; Edwards 1987). The unique niche occupied by these beetles renders them particularly sensitive to a warming climate. There are three snowfield-associated *Phlaeopterus* species that have not been recollected since the 1970s, despite targeted sampling efforts in the same locations since then. These three species may be extinct or endangered (L.J. Mullen, J.M. Campbell, and D.S. Sikes, in preparation).

A similar fate has been suggested for snowfield- and glacier-associated ground beetles (Carabidae) (Kavanaugh and Schoville 2009), ice crawlers (Grylloblattodea) (Wipfler et al. 2014), and a glacial meltwater stonefly (Plecoptera) (Muhlfeld et al. 2011; Jordan et al. 2016). Snowfields, glaciers, and cold meltwater are often isolated habitats and function as alpine islands for such taxa. The disappearance of such habitats can leave alpine insects stranded, with the nearest suitable habitat prohibitively far away, especially for flightless taxa such as some *Phlaeopterus* species. This genus may also serve as an example of a glacial refugia distribution, with an Alaskan population of one soon-to-be-described species isolated by over 1000 km from a larger population in British Columbia and Alberta (L.J. Mullen, J.M. Campbell, and D.S. Sikes, in preparation). The UAM Insect Collection is a key resource for this project. We have georeferenced and databased 2577 *Phlaeopterus* specimens, belonging to the UAM Insect Collection and on loan from 36 other insect collections, in Arctos and shared these with GBIF.org (<http://www.gbif.org/species/3262329>) to aid in the taxonomic revision of the genus. These records create dynamic and data-rich species distributions. Digitization of these specimens also allows for the association of specimen data and DNA sequence data, which will be archived in GenBank and BOLD once the project is complete.

**Fig. 3.** Cumulative number of Alaskan spider (Araneae) species by year of earliest Alaskan record in the UAM, UAMOBs, KWP, and KNWR data sets in the Arctos database ([http://arctos.database.museum/uam\\_ento\\_all](http://arctos.database.museum/uam_ento_all)). Earliest year based on either earliest known specimen or earliest known publication, whichever was earliest. The large jump in species in 1947 was due to the publication of Chamberlin and Ivie (1947). Earliest records of spiders in Alaska dating from 1900 (38 species) are not shown.



### Spider research in Alaska

Studies of the Alaskan arachnid fauna have generally been included as a byproduct of other research. Early surveys were often not arachnid-specific and of limited geographic scope (Banks 1900; Chamberlin 1921; Holm 1960). There have been few spider-specific Alaskan surveys. The first was by Chamberlin and Ivie (1947) who collected across the state and also worked to identify any Alaskan specimens they could find in museums to establish the first comprehensive treatment of Alaskan spiders (Fig. 3). More recent spider-focused work (Slowik 2006; Slowik and Blagoev 2012) concentrated on two islands in Southeast Alaska and attempted to establish diversity levels for the area as well as add species records. Additionally, Wyant et al. (2011) and Sikes et al. (2013) studied spiders from the Toolik Field Station on the north slope of the Brooks Range, the only spider-specific studies done in the Alaskan Arctic. They discovered that among-habitat spider diversity was much higher than expected. Since then, similar high local variation in spider assemblages have also been documented in Greenland (Hansen et al. 2016a, 2016b).

Spiders suffer from a taxonomic impediment common to other arthropods — there are many undescribed species and poor descriptions in obscure journals that make identification difficult. Historically, taxonomists working with Alaska specimens relied heavily on the “Insects and arachnids of Canada” series, intermittently published, which tackled one family at a time (Dondale and Redner 1978, 1982, 1990; Platnick and Dondale 1992; Dondale et al. 2003). Today, this problem is being mitigated through the online World Spider Catalog ([www.wsc.nmbe.ch/](http://www.wsc.nmbe.ch/)), which not only lists all taxonomically valid species but also allows for authors and institutions to deposit taxonomic publications. This facilitates cumbersome identifications and aids in new species descriptions. Additionally, online databases such as BOLD ([www.boldsystems.org/](http://www.boldsystems.org/)), MorphoBank ([www.morphobank.org/](http://www.morphobank.org/)), MorphBank ([www.morphbank.net/](http://www.morphbank.net/)), and Arctos (e.g., <http://arctos.database.museum/saved/Susan-Wise-Eagle-spiders>) allow for images of specimens to be included with either the DNA or specimen data.

The most recently published species list of Alaskan spiders is the Canada and Alaska checklist of Paquin et al. (2010) based on records from literature sources and the Canadian National Collection. However, published works lag behind dynamic databases. For example, Chamberlin and Ivie (1947) listed 247 Alaskan spider species and Paquin et al. (2010) listed 382 species. Through the Arctos portal, the UAM now lists 604 named species for the state, an increase from 592 species in 2010 (Fig. 3). All of these records are vouchered by specimens or the literature. This number is still low, as there are many specimens awaiting identification as well as known but still undescribed species. There are also many large unsurveyed regions of the state. However, there has been a decline in new spider records for Alaska in recent years (Fig. 3). Between 2010 and 2016, only 12 species have been added, in contrast with the 6 years prior (2004–2009) that saw the addition of 119 species. It is too early to tell if this is a true plateau indicating nearly complete documentation of the fauna — it most likely is not.

### Arctic long-term monitoring

Systematic collections of Arctic arthropods have yielded detailed insights into the spatial and temporal variation in diversity and trophic structure as well as in key life history traits like phenology and body size. Three of the most notable long-term studies are yellow pitfall trapping at Zackenberg, northeast Greenland (Høye et al. 2007; Høye and Forchhammer 2008; Høye et al. 2013), the repeated Northern Insect Survey in Canada (Fernandez-Triana et al. 2011; Ernst and Buddle 2015; Ernst et al. 2016), and the spectacular long-term time series at Lake Myvatn in Iceland (Ives et al. 2008). The monitoring program at Zackenberg is part of the Greenland Ecosystem Monitoring Program, nationally funded by Denmark. It has been operating for 20 years, monitoring arthropods for the full duration of the growing season every year since 1996 (Jensen et al. 2014). As part of this monitoring program, tens of thousands of pitfall trap samples are sorted to the family level, specimens are counted, and the samples are carefully curated at the Natural History Museum Aarhus in Denmark. Some families of arthropods are represented by a single species at the site, e.g., Lycosidae: *Pardosa glacialis* (Thorell 1872) and Lygaeidae: *Nysius groenlandicus* (Zetterstedt 1838), but for most samples, species identification has progressed slowly through individual research projects.

One example is the collection of butterfly specimens, which were recently identified to species level and sexed. A total of four species of butterflies are known from the Zackenberg area across three families, so the identification task was limited to the separation of *Boloria chariclea* (Schneider 1794) and *Boloria polaris* (Boisduval 1828). The systematic collection allowed for a unique and detailed assessment of the timing and duration of the flight time of the two most abundant species of butterflies, *Boloria chariclea* and *Colias hecla* Lefèbvre, 1836 (Høye et al. 2014). Morphological variation could also be studied because contrary to conventional butterfly census schemes based on observational transect counts, the specimens were available for detailed study and measurements. Exploiting this opportunity led to recent documentation of warming-induced body size declines in both males and females of *Boloria chariclea* and *Colias hecla* from Zackenberg (Bowden et al. 2015a). These studies follow up on earlier studies of body size variation in spiders collected in the same pitfall traps. In the High Arctic crab spider (*Xysticus deichmanni* Sørensen 1898), body size varied among habitats (Bowden et al. 2015b), while in a more mobile wolf spider (*Pardosa glacialis*), body size was positively associated with interannual variation in the length of the growing season (Høye et al. 2009). The pattern of temporal variation in wolf spider body sizes was corroborated by similar variation along an elevational gradient for two of three wolf spider species studied at Disko Island in West Greenland (Høye and Hammel 2010).

Such findings would not have been possible without the curation of specimen samples over the entire 20 year monitoring period.

### Conclusions and vision

Careful investigation, mapping, and description of all species on Earth in under 50 years, as envisioned by Wheeler et al. (2012), may exceed our ability unless we can generate a human-genome or mars-landing-like effort. However, an effort focused on the rapidly changing Arctic, with its much smaller pool of species, and potentially endangered cold ecosystems, is more likely to succeed. A first step in this direction is the recent accomplishment to describe the nonmarine arthropod fauna of the archipelagoes of the Barents Sea (Coulson et al. 2014). To accomplish broader Arctic coverage including regions with considerably higher taxonomic diversity, nations conducting research in the Arctic must expand, curate, identify, and fully digitize their biological collections (e.g., via high-efficiency processing protocols such as DBYL “Database Before You Label”) and share these open-access data online with GBIF.org (Ivanova and Shashkov 2017), e.g., through international initiatives such as the Circumpolar Biodiversity Monitoring Programme ([www.caff.is/monitoring](http://www.caff.is/monitoring)) and the Network for Arthropods of the Tundra ([tundraarthropods.wordpress.com](http://tundraarthropods.wordpress.com)). Increased funding for museum positions in entomology and invertebrate zoology is needed to produce taxonomic revisions and faunistic treatments of northern taxa. Given the effort that the Canadian Centre for DNA Barcoding has spent on documenting the Canadian fauna (Hebert et al. 2016), that of Sikes et al. (2017) in Alaska, and that of Wirta et al. (2015) in Zackenberg, it would be ideal if Arctic nations globally collaborated to DNA barcode Arctic biodiversity, making not only millions of georeferenced taxon-occurrence data available but also genetic data available that could be used for both identifications and taxonomy. DNA barcoding efforts such as Norway’s NorBOL project ([www.norbol.org/en/](http://www.norbol.org/en/)), which has a focus on polar biodiversity and plans to DNA barcode 20 000 species by the end of 2018 (Ekrem et al. 2015), and Finland’s FinBOL (<http://www.finbol.org>) are encouraging. Continued collaborative monitoring of long-term research sites in the Arctic (Friedhuber 2016), through either traditional means or NGS metabarcoding methods, with consequent vouchering of resulting specimens and environmental data (Urban et al. 2016), is also a high priority. Such long-term and highly structured data sets, as demonstrated by the research in Iceland and Greenland, will provide us great confidence in our assessment of the inevitable changes to Arctic ecosystems.

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