

# Natural History Collections as Emerging Resources for Innovative Education

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*There is an emerging consensus that undergraduate biology education in the United States is at a crucial juncture, especially as we acknowledge the need to train a new generation of scientists to meet looming environmental and health crises. Digital resources for biology now available online provide an opportunity to transform biology curricula to include more authentic and inquiry-driven educational experiences. Digitized natural history collections have become tremendous assets for research in environmental and health sciences, but, to date, these data remain largely untapped by educators. Natural history collections have the potential to help transform undergraduate science education from passive learning into an active exploration of the natural world, including the exploration of the complex relationships among environmental conditions, biodiversity, and human well-being. By incorporating natural history specimens and their associated data into undergraduate curricula, educators can promote participatory learning and foster an understanding of essential interactions between organisms and their environments.*

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**C**limate change, the loss of biodiversity, emerging pathogens, threats to food security, environmentally induced health issues: These are the crucial challenges that confront scientists, policymakers, and the public today. Responding to these challenges requires that biologists be trained to ask penetrating questions, to think critically, to collect and analyze relevant data, and to interpret those data with an eye toward crafting creative solutions. The physical resources and digital data associated with natural history museums provide a superb but underused platform for innovative, relevant, and significant educational experiences that engage students in the processes of learning and enable them to become effective solvers of global problems. Natural history collections and their associated online databases, along with new tools that support innovative uses of these data, provide educators and students with unparalleled opportunities to explore the factors that give rise to and maintain biological diversity (figure 1). By capturing variation in real-world phenotypes, natural history collections are ideally suited to promote the type of direct discovery of relationships between patterns and processes that are fundamental to today's biology education.

## The challenges

We are now at a crucial juncture in science education in the United States. As the challenges to humanity increase, our literacy in science, technology, engineering, and mathematics (STEM) continues to decline relative to that of nearly all other industrialized countries. This alarming trend in STEM education has been documented in multiple recent publications, including Brewer and Smith (2011) and PCAST (2012). As awareness of this crisis has grown, both public and private funding sources have been directed toward undergraduate education, including National Science Foundation (NSF) programs, such as Improving Undergraduate STEM Education ([www.nsf.gov/funding/pgm\\_summ.jsp?pims\\_id=504976](http://www.nsf.gov/funding/pgm_summ.jsp?pims_id=504976)), which are aimed at revising STEM curricula and implementing best practices, and the Partnership for Undergraduate Life Sciences Education ([www.pulsecommunity.org](http://www.pulsecommunity.org)), which is intended to foster broadscale change at institutions of higher learning by engaging college and university administrators nationwide (Musante 2013). A fundamental question that remains, however, is how best to use such funds to enact meaningful changes in undergraduate science education.



**Figure 1.** Undergraduate students at Harvard use specimens and associated data to explore speciation and molecular evolution in spring 2013. Photograph: Scott V. Edwards.

A central theme that has emerged from recent discussions of science education is the need for authentic, inquiry-driven experiences in which active—rather than passive—learning is emphasized (NRC 2003, Brewer and Smith 2011). Such experiences serve to internalize and personalize information, so that students take ownership of the knowledge they acquire. At the same time, because students participate directly in shaping the outcomes of learning activities, they gain crucial experience with the process of discovery. Developing and implementing these types of experiences,

however, is challenging because of constraints (e.g., economic) that favor passive forms of learning that can be broadcast to massive audiences, thereby minimizing classroom costs (Deneen 2013). Indeed, at some institutions, such concerns have led to the reduction or removal of laboratory exercises from basic biology courses. Resolving the current decline in STEM literacy in the United States requires enhancements to the pedagogy of undergraduate education and creative solutions to the practical challenges faced by undergraduate institutions.

### Natural history collections as innovative resources for STEM education

An estimated 2–4 billion specimens are contained in natural history collections worldwide (Ariño 2010). These specimens and their associated data represent the foundation of our understanding of biodiversity, including the morphological, genetic, ecological, and behavioral variation among organisms. As an irreplaceable record of past biodiversity, specimens have emerged as a key indicator of the impact of anthropogenic activity on environmental conditions. Given the accelerating rate of environmental change, museum specimens and their associated data provide valuable sources of information for understanding the ecological and evolutionary processes underlying biotic responses (Suarez and Tsutsui 2004, Winker 2004, Wandeler et al. 2007). Therefore, collections offer unparalleled opportunities for students to investigate some of the most pressing societal challenges that we face.

Traditionally, the use of natural history specimens in undergraduate education was limited to campuses fortunate enough to house such collections and

to courses focused on the diversity and evolution of specific groups of organisms. For example, in many courses in organismal biology (e.g., botany, ornithology), specimens are used to introduce undergraduates to the key morphological features used to distinguish taxonomic units. Although such courses are invaluable for immersing students in the biology of a given subset of organisms, they fall short of harnessing the full potential of natural history collections in two important ways: (1) They do not typically cross major taxonomic lineages to provide integrative perspectives on biodiversity,

and (2) they cannot be extended to students enrolled at institutions that lack appropriate collections. Now, however, the growing availability of digital technology and Internet access in the classroom, coupled with international efforts to make museum data available in a digital format, offers new and powerful ways to create active learning opportunities based on natural history specimens (e.g., Bookman and Malone 2006, Carle et al. 2009). Such efforts enable the use of the vast stores of information held in natural history museums to provide innovative, inquiry-based instructional experiences that can engage all students in important, topical issues spanning multiple scientific disciplines.

### The digital revolution: Museum specimens, bioinformatics and big data

A crucial roadblock to the use of natural history collections in undergraduate education has been the challenge of unlocking—in many cases, literally—the cabinet drawers housing specimens and their associated data. This challenge and the collaborative efforts to address it have become a key example of innovation at the nexus of bioinformatics and emerging database technologies (*big data*). Natural history collections are not typically born digital. They can encompass several centuries of research effort and are often highly idiosyncratic with regard to methods and formats for data storage. As a result, the barriers to developing user-friendly, efficient systems for sharing specimen data have been substantial and, accordingly, have required a variety of creative solutions for making such information widely available to researchers, educators, and the public.

The resources developed to improve accessibility to the information contained in natural history collections include multiple networked databases and a constellation of services and tools that allow users to search the holdings of numerous museums simultaneously, including MaNIS (mammal collections), ORNIS (ornithology collections), HerpNet (herpetological collections), and FishNet 2 (fish collections); all of these are now part of the larger VertNet project (all vertebrate collections; [www.vertnet.org](http://www.vertnet.org)). In concert with the creation of these databases, new approaches have been developed for standardizing terminology (e.g., the Darwin Core; Wicczorek et al. 2012) and for publishing specimen data online (e.g., the Integrated Publishing Toolkit). The primary international repository for such information, the Global Biodiversity Information Facility (GBIF; [www.gbif.org](http://www.gbif.org)), currently contains about 440 million specimen and observation records, all of which can be searched and downloaded by anyone with Internet access. The number of online data available is impressive, but these data represent only about 10%–20% of the natural history specimens housed worldwide and include only the recorded information associated with each specimen.

Full mobilization of specimen data is perhaps the most fundamental challenge for natural history collections over the next 10 years. Underscoring the importance of this endeavor are the considerable financial resources being

directed toward the digitization of specimen records, including the NSF's Advancing Digitization of Biodiversity Collections program, which represents a significant federal commitment to making collections data publicly available. The potential increase in the availability of online resources is tremendous, but no data set is perfect, and data quality issues (e.g., incorrect specimen identifications, errors in locality records) continue to be of concern. However, a key advantage of specimen-based data sets is that putative errors in individual records can be evaluated through an examination of the specimens from which the data are derived. The digitization of records accelerates this process by making it easier for experts to identify questionable records, and data annotation services are becoming more sophisticated in addressing some of these issues (Dou et al. 2012, Morris et al. 2013). In summary, digitization is facilitating efforts to produce high-quality specimen data. In concert with the digitization effort is the equally monumental challenge to continue documenting diversity before it is lost. Just as previous generations of museum scientists had the foresight to build collections that make it possible for us to address important biodiversity-related questions today, so, too, must we work to improve the associated collections infrastructure. Additional support for field exploration is essential if we are to provide crucial data for the next generation of researchers.

As a result of these unprecedented efforts at digitization, the fundamental nature of the natural history collections enterprise is in flux, mirroring broader societal opportunities and concerns emerging from the digital revolution. New workflows are being developed for all aspects of museum curation, beginning with specimen collection, continuing through data digitization, and culminating in the integration of the diverse outcomes of specimen-based research. These new procedures allow multiple types of data to be filtered efficiently into networks capable of handling online publishing rates of tens or hundreds of records per second, with download rates that are an order of magnitude higher and that are likely to increase. As data records are used, the resultant products (e.g., publications) must be tracked, and all newly created information (e.g., species distribution maps) that arises from these data must be digitally linked to the original records to allow future replication, refinement, and advancement of science. Associated with these processes is a series of additional challenges related to intellectual property rights, licensing, credit models, and the sociology of science.

Concordant with the shift to digital data, the nature of collection vouchers and natural history specimens is changing dramatically. Present-day collections go far beyond traditional specimen preparations such as skins and skeletons, fluid-preserved animals, pinned arthropods, and pressed plants and fungi; they now include diverse specimens, including eggs and embryos, nests and recordings of vocalizations, frozen tissues, and associated parasites. Modern museum-based collecting expeditions often involve integrated sampling across multiple elements of biological communities and thereby offer insight into ecological associations

(e.g., host–parasite or plant–pollinator relationships) that would be missed by more traditional, taxon-specific efforts. The merger of molecular genetics with specimen-based research has revealed that collections can also store information about aspects of natural history that may not be immediately apparent. For example, DNA sequencing can be used to identify symbionts, including parasites and pathogens, in preserved specimens (Sumbicay et al. 2012). At the same time, genome-level surveys of specimens can be used to estimate historical population sizes (Bi et al. 2013), identify genes that appear to be subject to selection (Barrett and Hoekstra 2011), and reconstruct phylogenetic relationships (Stull et al. 2013). Similarly, human-driven ecosystem changes attributable to microbial dynamics can be traced by sequencing preserved virus fossils from herbarium specimens (Malmstrom et al. 2007, 2011).

The future of natural history collections is crucially dependent on not only preserving physical specimens but also capitalizing on the broader potential of those specimens in a digital age (Graham et al. 2004). In summary, nearly all future collections-based research will involve community-shared and -owned digital repositories, regardless of whether those repositories store images, sounds, or sequences. Particularly exciting are the biological insights that will emerge from the integration of diverse data sources; some of the most stimulating research programs that are emerging in evolutionary biology come from interdisciplinary groups that combine phenotypic, geographic, phylogenetic, paleontological, developmental, and ecological information to explore the basis for biodiversity. Data portals such as GBIF and VertNet are facilitating such efforts by employing novel computational approaches to manage and to visualize ever-growing data sets, thereby permitting investigators to explore huge quantities of data in order to quickly detect global patterns that would have historically required decades of tedious labor to reveal. The ambitious role of the Integrated Digitized Biocollections initiative (Matsunaga et al. 2013; [www.idigbio.org](http://www.idigbio.org)) in aggregating and serving specimen data, including images, for nonfederal collections in the United States attests to the growing importance of the developing digital museum framework. The training of not just the next generation of museum scientists but of all undergraduates must be expanded to encompass the crucial role of natural history data in addressing global challenges.

### **Integrating educational needs and museum bioinformatics resources**

The exciting transformations taking place within natural history collections are ideally suited to promoting reforms to undergraduate biology education. As the digitization of collections proceeds and the development of new bioinformatics tools continues to enhance our ability to use the information contained in specimens, images, and their associated records, educators are increasingly able to capitalize on these resources to provide students with significant learning experiences, regardless of their institution (Dunnum

and Cook 2012). The array of biological questions that can be explored is vast and includes important evolutionary themes, such as the patterns of morphological and genetic change over time (Bi et al. 2013), fundamental processes underlying ontogeny (Cooper et al. 2013), individual variation in behavior (Yeakel et al. 2009), patterns of interspecific community assembly (Hoberg et al. 2012), modeling of projected species distributions (Anderson 2012), and human-mediated ecosystem dynamics (Malmstrom et al. 2007, 2011). Natural history collections provide an ideal platform from which to integrate innovative approaches to biology education with cutting-edge science. Accordingly, such collections represent a unique mechanism for addressing the major challenges identified by Brewer and Smith (2011), who included a formal call for reform of undergraduate biology education. Below, we review the key challenges raised by this report and outline how natural history collections can be used to address these pressing needs for change in biology education.

One crucial challenge identified by Brewer and Smith (2011) is the need to better integrate instruction in key concepts and facts with exploration of the process of science. Natural history collections offer important opportunities to address at least three of the more specific goals encompassed by this challenge—namely, (1) to introduce students to the scientific method, (2) to relate abstract concepts to real-world examples, and (3) to stimulate curiosity. Specimens and the associated online databases represent exceptional resources for realizing these goals, because instructors can use these materials to guide students through open-ended activities that employ hypothesis testing and model building to explore selected topics. In other words, students are exposed to key concepts and information while engaging in the process of scientific discovery. By building exercises around museum specimens, a powerful connection can be established between real organisms and more-abstract areas of biological knowledge, such as evolutionary theory. Students typically respond enthusiastically to the opportunity to examine specimens, which provide a tangible focal point for their efforts to integrate questions, concepts, and data. For many students, specimen-based learning invigorates their fundamental fascination with diversity and creates an opening to gain experience using the methods of the naturalist. Such skills are taught with decreasing frequency in undergraduate programs, but they are foundational for many biological disciplines and offer gateways into new realms of discovery. Even in the absence of physical specimens, the online availability of images, field notes, and (for some taxa) recorded vocalizations helps bring these materials to life, thereby providing an immediate and direct connection in the classroom between evidence collected from nature and real-world environmental challenges. Such tangible connections can help stimulate curiosity about how to meet challenges and solve problems.

A second crucial challenge facing undergraduate education in biology is the need to restructure science courses

to emphasize student-centered learning experiences. This includes a fundamental pedagogical shift from standard lecture-format classes to courses that employ active and inquiry-based strategies (NRC 2003). The benefits of this approach have been amply demonstrated in terms of learning gains to all students, as well as to nontraditional students in biology (Haak et al. 2011). Museum collections provide excellent resources for developing inquiry-based learning experiences. The diversity encompassed by such collections inherently gives rise to numerous questions regarding evolutionary patterns and processes. Rather than relying on formulaic exercises with predictable outcomes, students provided with a question (or allowed to develop one of their own) can generate crucial predictions, extract relevant data from either physical specimens or evidence in online databases, and conduct appropriate analyses to test their predictions. Such activities can yield much more salient, transformative learning experiences than do traditional lecture or lab offerings. Because collections data are relevant to numerous biological concepts, the types of questions that can be addressed are limited primarily by the creativity of the instructor. Many excellent exercises for classroom use can be derived from real-world issues regarding biodiversity (e.g., changing species distributions; Pergams and Nyberg 2001, Tingley et al. 2009) and applied conservation needs (e.g., heavy metal contamination; Vo et al. 2011), thereby making the associated learning experiences particularly authentic and underscoring the direct connection between biology education and the solutions to pressing global problems.

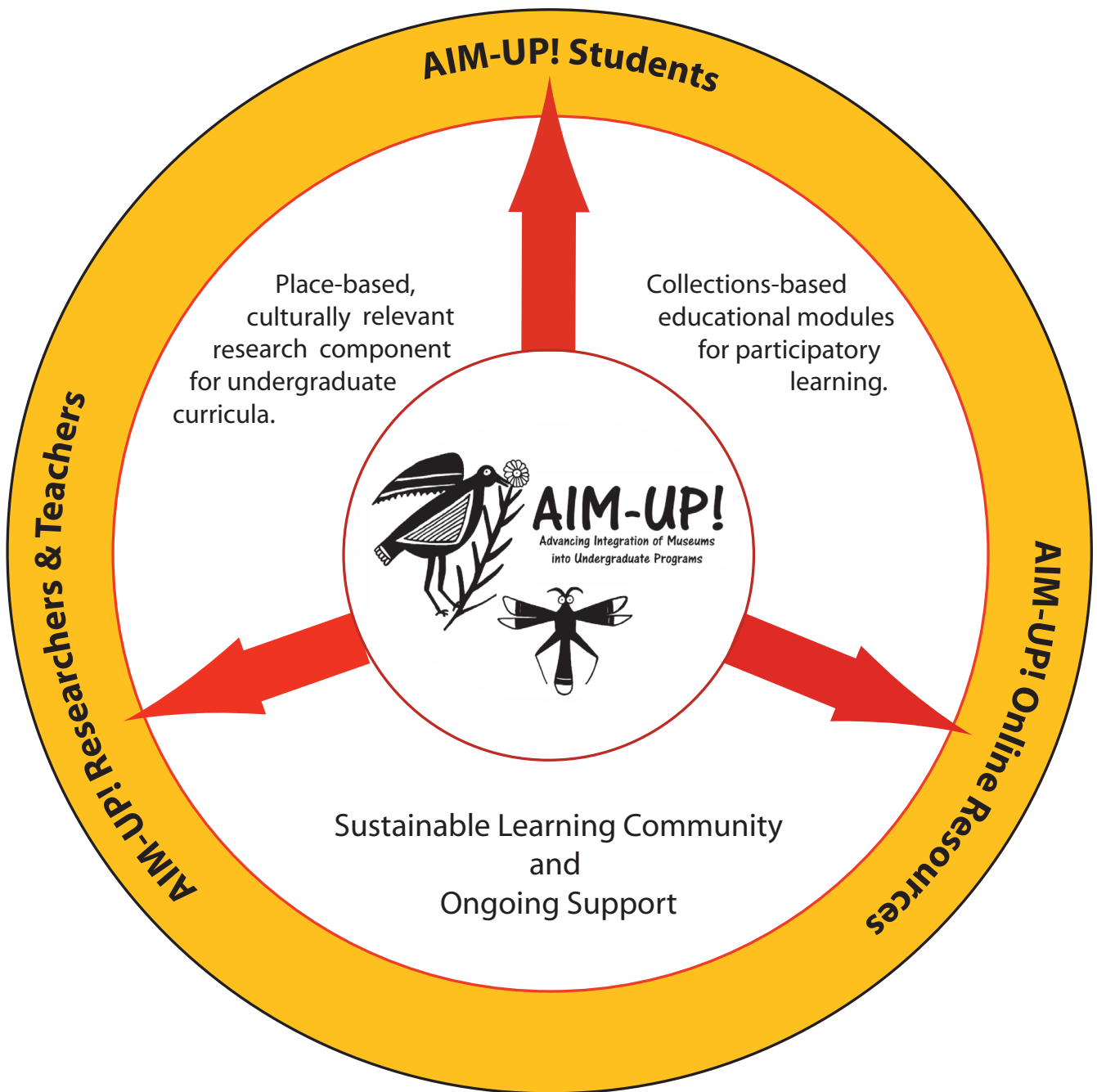
A third major challenge outlined by Brewer and Smith (2011) is to “ensure that all undergraduates have authentic opportunities to experience the processes, nature, and limits of science” (p. xv). Natural history collections provide at least two important means of addressing this challenge. First, as was outlined above, the use of collections data offers students the opportunity to engage directly in the process of science. Biological research is messy, because organisms do not always behave as is expected, data are often less abundant than is ideal, and errors in data collection do occur. As a result, learning how to evaluate the nature and quality of a data set represents an important skill for students. The diversity and real-world complexity of collections data provide ideal opportunities for wrestling with these challenges. Second, natural history collections provide a logical focal point for engaging the larger community of biologists in these efforts. Numerous researchers, many of whom are also educators, already either contribute to or make use of natural history collections. Digitization efforts are now extending access to these resources to all biologists. At the same time, the growing number of collections-based citizen science efforts (e.g., eBird, the USA National Phenology Network, Notes from Nature) allows students to explore and to evaluate data sets to which they may have contributed directly. Collectively, these attributes indicate that natural history collections and collections data have the potential to introduce

large numbers of students from diverse populations to the reality of science and scientific inquiry.

### Using specimens to convey core concepts in biology

Educational activities based on the information contained in natural history collections provide important opportunities to incorporate inquiry-based learning experiences into undergraduate biology courses. With the increasing availability of online specimen data, the potential for such exercises to enhance undergraduate education is growing rapidly. To capitalize on this potential, we are participating in Advancing Integration of Museums into Undergraduate Programs (AIM-UP!), an NSF-funded Research Coordination Network composed of museum scientists and educators (figure 2; [www.aim-up.org](http://www.aim-up.org)). The network was established to explore the use of natural history collections in undergraduate education, with the intent of using these resources to promote the reforms outlined in Brewer and Smith (2011). During an AIM-UP! workshop held at the Museum of Comparative Zoology at Harvard University in April 2013, we identified several conceptual areas in which natural history collections can play a pivotal role in transforming the undergraduate biology experience. Below, we outline these themes, with an emphasis on how each can draw on natural history data to address fundamental conceptual and methodological issues in modern biology.

Patterns of genetic variation are fundamental to the concept of evolutionary change, and understanding how and why genes vary is central to much of modern biology. Rapid advances in DNA technology make it possible to efficiently sequence entire genomes of organisms, thereby creating new opportunities to explore the genetic architecture of evolutionary processes. With the growing use of genetic data sets comes a potential problem: the inability to repeat, validate, or build on results reported in large databases (Longo et al. 2011). Vouchered museum specimens provide excellent opportunities to reproduce and extend previous work, both central tenets of the scientific method, because the specimen is a permanent, physical record of an individual's genotype, and these samples can be studied multiple times by multiple labs. Classroom activities that draw on genomic data from museum specimens allow students to explore the relationships between genetic variation and other variables (e.g., morphological traits) while developing an understanding of data quality and the challenges associated with the use of the extensive digital data sets available online. Furthermore, because individual specimens are georeferenced and the associated sequences are typically accessioned into databases such as GenBank, students can learn how to integrate spatial, ecological, and phenotypic information as they study patterns of genetic variation. In addition, because specimens are time stamped, adding a temporal component to educational exercises is also possible. Collectively, these diverse forms of information can be used to explore a wide range of genetically themed issues, including the reconstruction of evolutionary relationships, interactions between genotype



**Figure 2.** *Advancing Integration of Museums into Undergraduate Programs (AIM-UP!)* is a National Science Foundation Research Coordination Network focused on museums and undergraduate education.

and phenotype, and genotypic and phenotypic responses to environmental change through time.

We live in a period of profound environmental change resulting from anthropogenic modifications to climates, habitats, and species distributions (Parmesan 2006). Understanding and—more important—predicting biotic responses to these changes require using legacy data that document species distributions over time. For example, comparisons of localities for small mammals collected in Yosemite National Park in the early twentieth century with

records for the same taxa collected during the past decade have revealed significant changes in the elevational limits of some species (Moritz et al. 2008), which raises important questions regarding the reasons for these interspecific response differences. At the same time, ecological niche-modeling tools can identify species–habitat associations and can therefore help predict potential future responses to ongoing changes in these parameters (Rubidge et al. 2011). At the core of such analyses are the specimens and the associated field notes required to tie specific organisms to

different habitats. Biodiversity data-sharing platforms allow students to investigate these relationships for themselves using the same thought processes and analytical procedures that professional researchers and conservation managers use. Data sets that can be integrated to explore patterns of species distributions include georeferenced collection localities for multiple animal, fungal, and plant taxa; photos of local habitats; records of abiotic environmental variables generated from *in situ* sensors or from remote sensing; and maps of significant physical features (e.g., geology). The concepts that can be explored include the difference between fundamental and realized niches, habitat specialization, community composition, and phenotypic plasticity and adaptation, all of which are relevant to understanding and predicting responses to environmental change and are crucially dependent on the data held in natural history collections.

The threat of newly emerging pathogens is an applied aspect of biodiversity research that currently receives considerable attention from both scientists and the public, in part because changing climatic conditions are thought to be increasing the potential for pathogens to encounter new hosts, including humans (Hoberg et al. 2008). Museum collections provide a crucial data source for understanding the geographic distributions of pathogens and their hosts, information that is essential to identifying emerging threats. Existing specimens can provide a wealth of information, because macroparasites (e.g., fleas, ticks, fungi, helminths) can often be retrieved directly from the exterior or interior (e.g., tissues, organs) of the specimens. At the same time, the increasing sophistication of molecular-genetic analyses allows the identification of less-visible parasites and pathogens. To maximize the potential for parasite and pathogen detection, many contemporary field efforts now specifically include collection of these organisms and the host specimens, thereby increasing the utility of museum collections in studying host–parasite dynamics. Using these materials, students can explore themes such as coevolutionary relationships, the dynamics of species interactions, pathogen emergence, and disease ecology. Such exercises can be structured around the growing body of literature on the spatial and temporal dynamics of host–pathogen systems, such as avian malaria (Beadell et al. 2006), viral infections in bats (Yob et al. 2001), the distribution of the Ebola virus (Leirs et al. 1999), and human-mediated spread of certain cereal viruses into native grasslands (Malmstrom et al. 2007), which provides concrete links between specimen-based data and real-world medical and societal concerns.

### Bringing it home: Place-based exercises using museum data

Educational activities that are structured around local examples are particularly effective at engaging student interest and establishing connections between concepts and tangible applications of those ideas (Orr 1994). Natural history collections are ideally suited to creating such place-based exercises, which emphasize local organisms. At the same

time, online databases make it easy to extend these activities to multiple spatial scales, thereby underscoring connections between local and global issues. Below, we outline two educational modules currently in development by the AIM-UP! network. Each module requires that students use the vast resources available in natural history museums to explore important, place-based concepts in biology, thereby using active, inquiry-based approaches to introduce students simultaneously to the scientific method, digital information literacy, and key elements of biological theory.

**Floridian flora: From field to phylogeny and beyond.** Relative to most of the continental United States, the flora of much of Florida is unusual and conspicuously tropical. Determining how these plant communities differ from those in more-temperate systems and understanding how they came to exist in what is now the southern United States are fundamental questions in systematics, biogeography, and both physiological and community ecology. At the same time, given the ever-growing human population in Florida, these distinctive floras are increasingly threatened with destruction by a loss of habitat and other forms of anthropogenic change. Accordingly, educational activities that are focused on these plant species provide highly relevant learning experiences for undergraduates at Florida institutions.

Collections-based data regarding the flora of Florida provide numerous opportunities to design such activities. Beginning in the field (including the surrounding campus, local parks, or field stations), students can collect examples of one or a few plant species. Identifications of these taxa can then be confirmed using herbarium specimens or online images of these specimens. Once the species' identities have been established, the students can search GenBank for DNA sequences (e.g., the commonly used *rbcL* locus) associated with these taxa. With this information, the student-collected specimens (figure 3) can be placed in the appropriate phylogenetic context, using tools provided by the Open Tree of Life project (<http://blog.opentreeoflife.org>), thereby connecting these specimens to their closest relatives. By comparing the geographic distributions of these species, the students can draw inferences regarding the biogeographic histories of the focal taxa. In addition, they can use maps of current species distributions in Florida in conjunction with climate data to identify the apparent physical requirements of these species. By comparing this information with data regarding projected future climatic conditions (e.g., from the Intergovernmental Panel on Climate Change; Stocker et al. 2013), the students can generate basic predictions as to how the distributions of these species may change over time.

Collectively, these activities offer critical, inquiry-based exposure to fundamental concepts in evolutionary and conservation biology while also providing essential experience with the process of scientific investigation. The skills acquired include specimen collection, preservation, and digitization; the use of complex, dynamic databases to test hypotheses; and the analysis and interpretation of original



**Figure 3.** University of Florida undergraduate biology students on a museum field trip to collect plant specimens at the Ordway-Swisher Biological Station. Photograph: Pamela S. Soltis.

data. If they desire to do so, instructors can enhance the comparative component of the exercise by having different student groups focus on different plant species or conceptual issues. By coordinating with other instructors to conduct this exercise simultaneously at multiple institutions, students from different programs can interact online to enhance learning, foster interactions, and develop a collective and more collaborative perspective on scientific problem solving.

**Island biogeography: Exploring the Alexander Archipelago of Alaska.** For more than a century, studies of island systems have played a fundamental role in the development of ecological and evolutionary theory (Darwin 1859, Wallace 1880, MacArthur and Wilson 1967), including advances in our understanding of processes related to colonization, extinction, and speciation. Now, as natural areas are diminishing worldwide, island biogeography theory provides an important foundation for the design of conservation programs. Island systems along the coasts of North America and in other regions provide multiple opportunities to use

place-based activities to explore the evolutionary basis and applied outcomes of this body of conceptual and empirical research.

Natural history collections are an ideal source of information for such exercises. Students can explore key concepts regarding island biogeography by posing specific questions about a particular island system and then downloading and examining relevant data. Beginning with georeferenced specimens from well-inventoried sites, the students can construct classic species–area curves to examine the relationships between island size and biotic diversity for an array of plant, fungal, and animal taxa, a process that requires that they also consider crucial issues of sampling bias and data quality. Similarly, the students can explore the effects of distance from other landmasses on biotic diversity or, using specimen records, the relationships between island size and animal body mass (Foster 1964). Using records of the ocean depth between islands or historical changes in sea levels, the students can then test predictions about historical connections among landmasses and their implications for patterns



of colonization and connectivity among the island populations of the focal archipelago. Looking forward, information regarding projected sea level or temperature changes can be used to predict possible future modifications to the biotic diversity of archipelagos.

These ideas underlie a preliminary educational module that we have developed for the Alexander Archipelago, a large system of islands located in the North Pacific, off the southeastern coast of Alaska ([www.aim-up.org/educational-modules/educational-module-1-island-biogeography](http://www.aim-up.org/educational-modules/educational-module-1-island-biogeography)). The module guides students through the concepts and analytical tools required for testing fundamental rules of island biogeography (e.g., species–area relationships) using specimens and associated data from this archipelago. Because a large number of DNA sequences derived from museum specimens from this region are available on GenBank, students can explore this component of biotic diversity across islands. They can predict how genetic variation in a given mammal species should vary with island size or with the distance among islands, after which they can test these predictions using phylogenetic inference tools available online (e.g., the Open Tree of Life). The module was designed for use in a lower-division (freshman or sophomore) biology course but can easily be adapted to suit upper-division courses and advanced high school classes. The underlying principles and procedures are also readily adaptable for use with isolated continental landmasses, such as the sky islands of the southwestern United States or isolated patches of native prairie. Given the simplicity and clarity of many of the predictions deriving from island biogeography theory, the module provides a particularly powerful means of engaging students in the process of scientific discovery through direct participation in the development and testing of evolutionary and ecological hypotheses.

### Future prospects for educators

The prospects for integrating museum collections into a broad array of classroom exercises that can be tailored to diverse audiences (e.g., biology majors and nonmajors) have never been better. The goal of the AIM-UP! network is to help realize this potential by making educators aware of the growing availability of natural history data and by developing initial sets of activities that can subsequently be modified by individual instructors. Natural history collections are vast, irreplaceable repositories of information regarding biodiversity, but, for decades, most students have been unable to access these resources. As the digitization of specimen records and their associated data progresses, biology educators are in an unprecedented position to leverage these sources of information to enhance the learning of students who have been Web savvy from an early age. Indeed, the digitization of museum data is making natural history collections relevant to students in ways that curators and collection managers could not have imagined a decade ago. With so many online tools now available, student scientists anywhere in the world can spend a metaphorical night in

the museum exploring their favorite organisms. Our objective is to increase awareness of how natural history collections could transform undergraduate biology education. We encourage educators to build on these ideas to develop new and creative ways that collections can be used to enhance the understanding of the complex biological processes that shape our rapidly changing world.

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### References cited

- Anderson RP. 2012. Harnessing the world's biodiversity data: Promise and peril in ecological niche modeling of species distributions. *Annals of the New York Academy of Sciences* 1260: 66–80.
- Ariño AH. 2010. Approaches to estimating the universe of natural history collections data. *Biodiversity Informatics* 7: 81–92.
- Barrett RDH, Hoekstra HE. 2011. Molecular spandrels: Tests of adaptation at the genetic level. *Nature Reviews Genetics* 12: 767–780.
- Beadell JS, et al. 2006. Global phylogeographic limits of Hawaii's avian malaria. *Proceedings of the Royal Society B* 273: 2935–2944.
- Bi K, Linderoth T, Vanderpool D, Good JM, Nielsen R, Moritz C. 2013. Unlocking the vault: Next-generation museum population genomics. *Molecular Ecology* 22: 6018–6032.
- Bookman J, Malone D. 2006. Negotiating roles and meaning while learning mathematics in interactive technology-rich environments. *Journal of Scholarship of Teaching and Learning* 6: 41–65.
- Brewer CA, Smith D, eds. 2011. *Vision and Change in Undergraduate Biology Education: A Call to Action*. American Association for the Advancement of Sciences.
- Carle AC, Jaffee D, Miller D. 2009. Engaging college science students and changing academic achievement with technology: A quasi-experimental preliminary investigation. *Computers and Education* 52: 376–380.
- Cooper KL, Oh S, Sung Y, Dasari RR, Kirschner MW, Tabin CJ. 2013. Multiple phases of chondrocyte enlargement underlie differences in skeletal proportions. *Nature* 495: 375–378.
- Darwin C. 1859. *On the Origin of Species by Means of Natural Selection, or the Preservation of Favoured Races in the Struggle for Life*. Murray.
- Deneen PJ. 2013. We're all to blame for MOOCs. *Chronicle of Higher Education* (3 June 2013). (28 May 2014; <http://chronicle.com/article/Were-All-to-Blame-for-MOOCs/139519>)
- Dou L, Cao G, Morris PJ, Morris RA, Ludäscher B, Macklin JA, Hanken J. 2012. Kurator: A Kepler package for data curation workflows. *Procedia Computer Science* 9: 1614–1619.
- Dunnum JL, Cook JA. 2012. Gerrit Smith Miller: His influence on the enduring legacy of natural history collections. *Mammalia* 76: 365–373.
- Foster JB. 1964. The evolution of mammals on islands. *Nature* 202: 234–235.
- Graham CH, Ferrier S, Huettman F, Moritz C, Peterson AT. 2004. New developments in museum-based informatics and applications in biodiversity analysis. *Trends in Ecology and Evolution* 19: 497–503.
- Haak DC, HilleRisLambers J, Pitre E, Freeman S. 2011. Increased structure and active learning reduce the achievement gap in introductory biology. *Science* 332: 1213–1216.

- Hoberg EP, Polley L, Jenkins EJ, Kutz SJ, Veitch AM, Elkin BT. 2008. Integrated approaches and empirical models for investigation of parasitic diseases in northern wildlife. *Emerging Infectious Diseases* 14: 10–17.
- Hoberg EP, Galbreath KE, Cook JA, Kutz SJ, Polley L. 2012. Northern host–parasite assemblages: History and biogeography on the borderlands of episodic climate and environmental transition. *Advances in Parasitology* 79: 1–97.
- Leirs H, Mills JN, Krebs JW, Childs JE, Akaibe D, Woollen N, Ludwig G, Peters CJ, Ksiazek TG. 1999. Search for the Ebola virus reservoir in Kikwit, Democratic Republic of the Congo: Reflections on a vertebrate collection. *Journal of Infectious Diseases* 179 (suppl. 1): S155–S163.
- Longo MS, O'Neill MJ, O'Neill RJ. 2011. Abundant human DNA contamination identified in non-primate genome databases. *PLOS ONE* 6 (art. e16410).
- MacArthur RH, Wilson EO. 1967. *The Theory of Island Biogeography*. Princeton University Press.
- Malmstrom CM, Shu R, Linton EW, Newton LA, Cook MA. 2007. Barley yellow dwarf viruses (BYDVs) preserved in herbarium specimens illuminate historical disease ecology of invasive and native grasses. *Journal of Ecology* 95: 1153–1166.
- Malmstrom CM, Melcher U, Bosque-Pérez NA. 2011. The expanding field of plant virus ecology: Historical foundations, knowledge gaps, and research directions. *Virus Research* 159: 84–94.
- Matsunaga A, et al. 2013. A computational- and storage-cloud for integration of biodiversity collections. Pages 78–87 in *eScience 2013: 2013 IEEE 9th International Conference on e-Science*. IEEE Computer Society. doi:10.1109/eScience.2013.48
- Moritz C, Patton JL, Conroy CJ, Parra JL, White GC, Beissinger SR. 2008. Impact of a century of climate change on small-mammal communities in Yosemite National Park, USA. *Science* 322: 261–264.
- Morris RA, Dou L, Hanken J, Kelly M, Lowery DB, Ludäscher B, Macklin JA, Morris PJ. 2013. Semantic annotation of mutable data. *PLOS ONE* 8 (art. e76093).
- Musante S. 2013. PULSE: Implementing change within and among life science departments. *BioScience* 63: 254.
- [NRC] National Research Council. 2003. *Improving Undergraduate Instruction in Science, Technology, Engineering, and Mathematics: Report of a Workshop*. National Academies Press.
- Orr DW. 1994. *Earth in Mind: On Education, Environment, and the Human Prospect*. Island Press.
- Parmesan C. 2006. Ecological and evolutionary responses to recent climate change. *Annual Review of Ecology, Evolution, and Systematics* 37: 637–669.
- [PCAST] President's Council of Advisors on Science and Technology. 2012. *Engage to Excel: Producing One Million Additional College Graduates with Degrees in Science, Technology, Engineering, and Mathematics*. PCAST.
- Pergams ORW, Nyberg D. 2001. Museum collections of mammals corroborate the exceptional decline of prairie habitat in the Chicago region. *Journal of Mammalogy* 82: 984–992.
- Rubidge EM, Monahan WB, Parra JL, Cameron SE, Brashares JS. 2011. The role of climate, habitat, and species co-occurrence as drivers of change in small mammal distributions over the past century. *Global Change Biology* 17: 696–708.
- Stocker TF, Qin D, Plattner G-K, Tignor MMB, Allen SK, Boschung J, Nauels A, Xia Y, Bex V, Midgeley PM, eds. 2013. *Climate Change 2013: The Physical Science Basis*. Cambridge University Press.
- Stull GW, Moore MJ, Mandala VS, Douglas NA, Kates H-R, Qi X, Brockington SF, Soltis PS, Soltis DE, Gitzendanner MA. 2013. A targeted enrichment strategy for massively parallel sequencing of angiosperm plastid genomes. *Applications in Plant Science* 1 (art. 1200497).
- Suarez AV, Tsutsui ND. 2004. The value of museum collections for research and society. *BioScience* 54: 66–74.
- Sumbicay L, Kadjo B, Gu SH, Kang HJ, Lim BK, Cook JA, Song J-W, Yanagihara R. 2012. Divergent lineage of a novel hantavirus in the banana pipistrelle (*Neoromicia nanus*) in Côte d'Ivoire. *Virology Journal* 9: 34.
- Tingley MW, Monahan WB, Beissinger SR, Moritz C. 2009. Birds track their Grinnellian niche through a century of climate change. *Proceedings of the National Academy of Sciences* 106 (suppl. 2) 19637–19643.
- Vo A-TE, Bank MS, Shine JP, Edwards SV. 2011. Temporal increase in organic mercury in an endangered pelagic seabird assessed by century old museum specimens. *Proceedings of the National Academy of Sciences* 108: 7466–7471.
- Wallace AR. 1880. *Island Life: Or, the Phenomena and Causes of Insular Faunas and Floras, Including a Revision and Attempted Solution of the Problem of Geological Climates*. MacMillan.
- Wandeler P, Hoeck PEA, Keller LF. 2007. Back to the future: Museum specimens in population genetics. *Trends in Ecology and Evolution* 22: 634–642.
- Wieczorek J, Bloom D, Guralnick R, Blum S, Döring M, Giovanni R, Robertson T, Vieglais D. 2012. Darwin Core: An evolving community-developed biodiversity data standard. *PLOS ONE* 7 (art. e29715).
- Winker K. 2004. Natural history museums in a postbiodiversity era. *BioScience* 54: 455–459.
- Yeakel JD, Patterson BD, Fox-Dobbs K, Okumura MM, Cerling TE, Moore JW, Koch PL, Dominy NJ. 2009. Cooperation and individuality among man-eating lions. *Proceedings of the National Academy of Sciences* 106: 19040–19043.
- Yob JM, et al. 2001. Nipah virus infection in bats (order Chiroptera) in peninsular Malaysia. *Emerging Infectious Diseases* 7: 439–441.

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