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Widespread Sampling Bias in Herbarium Collections Identified from Comprehensively Sampled Mobilized Herbaria

Herbarium specimens contain a wealth of information about plant diversity, distribution, and ecology, but non-random collecting practices may bias conclusions drawn from herbarium data. We assessed spatial, temporal, trait-based, and phylogenetic sampling biases in 4.6 million herbarium records representing 61,807 vascular plant species from three of the most extensively collected regions of the world: South Africa, Australia, and the New England region of the United States. Our analyses demonstrate several biases in these data. Samples were spatially biased: specimens were overwhelmingly collected close to roads and herbaria. Samples were temporally biased: specimens were collected more frequently in biological spring. Samples were trait-biased: perennial species were collected more often than annuals, woody species more than herbaceous ones, and threatened species were collected significantly less often than common species. Samples were collector-biased: majority of the samples are collections from only a few selected collectors. And lastly, phylogenetic bias was indicated because specimen frequency per species was correlated with relatedness to other taxa in herbarium collections. These results demonstrate common biases in herbarium records spanning vastly different taxa and geographic regions of the world. We recommend that the use of herbarium collections for ecological and evolutionary modeling should account for these common sampling biases, and that future herbarium samples should be collected in ways that are designed to minimize bias and make collections applicable to a broader range of evolutionary and ecological research.

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Digital Curation of Botanical Specimens from Isle Royale National Park

Isle Royale National Park and Pictured Rocks National Lakeshore are iconic scenes of Michigan's natural beauty and Great Lakes ecosystems. The University of Michigan Herbarium has been tasked with the project of bringing the preserved botanical specimens of these locales into the digital age. This project is ongoing, and on schedule to be completed by August 2017. Specimens require physical repair, and are being checked to ensure their correct classification. They will be digitally photographed and their

metadata compiled into a spreadsheet, as this is the format the Forest and Parks Services requested. Suggestions will be provided for the data's dissemination to accessible sources, such as Specify.

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Sharing Research Data: "I need to store and share data, and get recognition"

Researchers are increasingly encouraged, or even mandated, to make research data available, accessible, discoverable, and usable. Elsevier has developed a range of options to fit researchers' needs, ranging from data storage (for preservation and citation purposes), to database linking (for discoverability and accessibility), to data enrichment (for data visualization and exploration), to publication (contextualizing and verifying data in short data articles).

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Visually Representing a Biodiversity Literature Collection Using Metadata and Full Text Analysis

In order to better understand the Biodiversity Heritage Library's (BHL) collection strengths and weaknesses, I am creating visualizations of the collection that will represent the corpus geographically, taxonomically, temporally and topically. While some data points for analysis are readily available in the BHL metadata data tables including publication dates and keywords, information such as taxonomic names and geographic locations have to be mined from the full text. Tools developed in the Mining Biodiversity project, like the Argo workbench, will be used to mine full text for location names while GNRD will be used to mine taxonomic names from OCRd text. The geographic names will be charted onto a global map and tree maps will be built using the taxonomic names. Topical analysis will be performed by using subject headings and keywords that are assigned to materials at ingest (from MARC records of incoming text). The ability to visualize the BHL collection allows members to focus future digitization efforts on filling gaps in the corpus to create more complete biodiversity coverage.

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Consider the Source: A Case Study Using GBIF Data for Research on Entocytherid Ostracods

Entocytherid ostracods are ectosymbionts of other crustaceans including crayfish, freshwater crabs, isopods, and marine amphipods. As such, they provide interesting and unique opportunities to examine host-symbiont global distribution patterns. Unfortunately, these patterns are obscured in available GBIF data due to taxonomic errors, lack of host data, and erroneous localities. As a first step in combating these types of misleading information, researchers at the North Carolina Museum of Natural Sciences (NCSM) are in the process of creating a revised taxonomic history and checklist of valid entocytherid taxa based on a thorough review of all primary sources. By tracing these records back to sources from which they are derived, we have uncovered numerous discrepancies in the GBIF dataset that appear to have resulted from synonymizations and other taxonomic revisions overlooked during the process of data aggregation. Using Specify, we are also working to establish a database for the NCSM Non-Molluscan Invertebrate Collection in which symbionts, including a growing collection of entocytherids, are linked to their host and other associates, and all specimen and locality data will be reviewed using a multi-tiered strategy prior to being made publicly available. This will help preempt compounding of errors in GBIF.

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Research and Management Applications of Online Collection Data: A Case Study of Prairie Fen Biodiversity

Prairie fen wetlands are globally vulnerable wetlands that provide habitat for over 35 listed species and function at the headwaters for several major watersheds. Since 2012, the Prairie Fen Biodiversity Project (PFBP) has collected baseline plant diversity data in prairie fens to investigate drivers of biodiversity in these diverse systems. One priority for PFBP has been to manage our biodiversity data digitally in support of research pipelines. Digitized plant vouchers, species observations, and photographs collected. Annotated species checklists are now available through the Central Michigan University Collection on the Consortium of Midwest Herbaria portal (http://midwestherbaria.org). We illustrated how we have integrated our research, data usage, and digitization workflows and how we assessed this as the project grows and incorporates insect biodiversity data. The PFBP data and checklists have multiple potential uses and we anticipate that our PFBP can use the portal to add, update, or pool data in new ways as the collaboration grows and new tools become available. Online digitized data gives us unprecedented access to biodiversity data and facilitates data accessibility, current data updates, and a broader use of the specimen and research data both within our research team and with associated partners.

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BioBeacon: An Online Field Guide to Digital Biodiversity Information Resources

Managing the biodiversity crisis requires access to credible information on species, as well as their changing abundance and spatio-temporal distributions, among other variables. Technological advances are expanding both the variety and volume of data available, driving the emergence of biodiversity informatics as a new research paradigm. Many online data resources exist however they lack a directory based on fundamental categorization, which inhibits efficient location and use of relevant data for biological research, conservation, education and industrial application. BioBeacon is a student-driven collaboration between the Biodiversity major at University of Guelph and the Biodiversity Institute of Ontario. Its purpose is to shine a light on biodiversity information resources and characterize them according to objective criteria that simplifies their navigation and increases accessibility. Criteria will include data type, source, region of focus, and current status. We envision BioBeacon to be a resource directory that will be cooperatively managed by its creators and steering committee, while inviting input from all stakeholders. Ideally, BioBeacon will grow to incorporate relevant biodiversity information resources that bear diverse types of data from locations around the world, complementing the conceptual development of biodiversity informatics into a mature research discipline.

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Identifying, Cross-referencing, and Extracting Dark Data using GeoDeepDive

Machine learning and text-mining can be used to (1) identify data missing from synoptic databases; (2) link collections in existing databases to scientific literature; and (3) algorithmically populate databases. Here, we describe how we used the GeoDeepDive (geodeepdive.org) high throughput computing infrastructure and digital library to achieve these goals. First, we use natural language processed documents to find co-occurrences of formal rock unit names with phrases indicating the presence of fossils. We then measured the percentage (37%) of these fossiliferous formations that were unrecorded in the Paleobiology Database to evaluate its completeness relative to the published literature. Second, we show how complete bibliographic metadata in GeoDeepDive can be linked to incomplete bibliographic information in the Paleobiology Database and to specific collection records extracted from them. Third, we extract new taxonomic names and fossil occurrence information from documents to augment existing fossil databases. Instances of museum specimens identified by number in the published literature, in particular, can be extracted from the published literature and linked to fossil collections in existing digital databases or aggregated into new databases. Together, these examples illustrate the power of GeoDeepDive for evaluating, enhancing, and building scientific databases.

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Taxonomic Concept Mapping in Support of Floristic Studies

As part of preparing a flora for the state of Oregon, we have developed a database framework to capture the taxonomic concepts encountered. A taxonomic concept, represented by a number, encompasses all scientific names associated with that concept, whether it is the currently accepted name or a synonym(s). We utilize several features that allow us to precisely track and assign concepts. Bare species vs. terminal taxa: When recognized subtaxa occur within a species, each is considered as a unique, terminal taxonomic concept. The corresponding binomial ("bare species") is also tracked in our database. Ambiguities refer to scientific names that refer to more than one taxonomic concept. We have designed processes to capture, manage, and apply taxonomic concepts and to disambiguate names. This is critical for the accurate presentation of floristic data in printed and especially digital formats.

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The Potential Within a Modern Flora

The digital presentation of a floristic work represents more than providing access to a compilation of biodiversity data. A digital flora offers a synthesis of said data within a defined taxonomic framework while providing a biological, ecological, and social context for the data. OregonFlora is working with Symbiota to develop an innovative portal to present digitally the information contained within the Flora of Oregon (Volume 1 of 3 published in 2015), and to make the information useful and useable by a wide audience. The readily available tools such as interactive mapping, image galleries, and interactive keys will be applied to both specimen and observation data, reflecting the taxonomic concepts in our floristic work. Taxonomic accuracy is utilized in newly developed tools for gardeners, making the website an educational vehicle for plant enthusiasts or botanical newcomers. The impact of the OregonFlora website on a diverse audience reinforces the relevance of the written flora as the foundation of interactive and engaging digital resources.

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Imago: Building a Biocollections Repository for Digital Preservation and Scientific Reproducibility

The Imago Biocollections Specimen Repository is a new repository tool built with the Fedora 4.0 digital preservation repository and the Hydra/Sufia 7 front-end interface while utilizing the NSF Jetstream cloud-based supercomputing infrastructure. This poster will focus on collections co-curated between the Indiana University Libraries and the IU Center for Biological Research Collections (Palaeontology, Herbarium, and Zooarchaeology). It showcases why the IUL built Imago to integrate rich metadata that meets the Dublin and Darwin Core standards needed for preservation and interoperability with other biocollection tools such as Symbiota, Specify, and iDigBio.

Academic libraries by nature are funded with institutional base support to supply long-term curation infrastructures for access and preservation of data and the resulting created knowledge by scholars and researchers worldwide. These infrastructures are multi-faceted and include a large amount of technical systems which encapsulates, for the purposes of this discussion, two components: technology - hardware, software, and cloud; and metadata for discovery, access, and preservation. In either case, a great deal of human capital is utilized to maintain the systems. It is the research libraries' duty and responsibility to respond across the institution to collections owners who benefit from library investment in these technical preservation infrastructures.

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Exploring the Untapped Potential of CT Scanning in the Quantitative Analysis of Brachiopod Long Loops

In terebratulide brachiopods, long loops—the calcareous structures supporting the lophophore—are important morphological characters, especially in a phylogenetic, taxonomic, and ontogenetic context. The aim of our research is to provide a quantitative framework for the study of long loop variability in order to test the morphological validity of living named species, a crucial starting point for understanding intra- and interspecific ranges of variability and taxonomic validity of fossil brachiopod species. Given the geometrically complex shape of the loops, we utilized CT scanning technology to image a total of 62 individuals (41 individuals from the genus Laqueus, 16 from Terebratalia, and 4 from Dallinella). These specimens were analyzed using 3D geometric morphometric analyses including exploratory methods such as Principal Component Analysis (PCA) and Canonical Variate Analysis (CVA), and using statistical methods (Procrustes ANOVA) to test the correlation between species with shape. Our results show that all six named species analyzed can be successfully discriminated based on loop morphology—i.e. specimens of each species cluster together in shape space—thus, validating current taxonomic species names. CT technology plays an important role not only in descriptive studies but also in the quantitative analyses of complex 3D structures such as brachiopod long loops.

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Kurator: A scientific workflow tool for data quality improvement of natural science collections data

The Kurator project develops technology and tools (http://github.com/kurator-org) facilitating the development, documentation, and execution of scripts and workflows for standardizing, cleaning, and curating biodiversity data: Kurator-web (http://kurator.acis.ufl.edu/kurator-web) is aimed at non-technical users who want to execute or modify existing curation workflows. For "curation tool-makers" and other technical users, data quality libraries and command-line tools are provided: e.g., Kurator-YW allows authors of data curation scripts to reveal queryable forms of prospective and retrospective provenance, based on simple YesWorkflow annotations inside of scripts. Thus, Kurator tools can expose data dependency and lineage information which allows users to understand why and how certain data quality issues were flagged, and what changes are being suggested by Kurator workflows. As a general principle, these are proposed as amendments, but they are not forced upon the user.

For tool makers, Kurator tools can be linked into the data lifecycle at multiple points, e.g., early during data capture and preprocessing, during aggregation, or in later stages, integrated with data analysis pipelines.

The Kurator team is also working with the TDWG Data Quality Interest Group to (i) develop and integrate a suite of standard data quality tests for biodiversity, and (ii) develop a standard reporting framework.

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Digitizing Archival Data: Ecoinformatics in the Alcohol House

Tucked away under the public galleries of the Carnegie Museum of Natural History are thousands of glass jars containing decades' worth of collections efforts in Herpetology. This collection space, known as the Alcohol House, is the 9th largest herpetology collection in the United States and the most complete collection of Pennsylvanian amphibians and reptiles in existence. The collection is a wealth of information collected across multiple temporal and geographic scales and used by scientists to understand the fitness of herpetofauna in a changing world. This has led the Carnegie Herpetology department to work towards full digitization of all specimen related data.

Ecoinformatics seeks "to integrate and increase the accessibility of multiple lines of environmental data" to advance the usefulness of natural history collections. In the Alcohol House, we are digitizing supplementary environmental data that includes photos from 35mm slides, field notebooks, and locality information; all digitized data is uploaded to iDigBio. Here, we explore the advantages and challenges that such supplementary data can pose for researchers who are using these data to understand current biodiversity questions. We will also explore how digitization of particular Alcohol House collections could be used to understand how herpetofauna are responding to climate change.

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Biodiversity Literacy in Undergraduate Education (BLUE): Opportunities for Collaboration

The biodiversity sciences have experienced a rapid mobilization of data that has increased capacity to investigate large-scale issues of critical importance in the 21st century (e.g. climate change and its impacts, zoonotic disease transmission, sustainable resource management, impacts of invasive species, and biodiversity loss). The volume, complexity, and variation in the biodiversity data requires sophisticated data skills to ensure accurate and reproducible science. Drawing from ongoing efforts across the biodiversity community we will review existing resources and potential needs in the development and integration of collections based educational materials. We will provide details on a new initiative, Biodiversity Literacy in Undergraduate Education (BLUE; biodiversityliteracy.com), that brings together communities of biodiversity, data, and education specialists to develop effective strategies for sustained development and implementation of biodiversity and data literacy education. We will provide examples of activities developed by BLUE, and BLUE partners, that highlight the use of NHC data in undergraduate biology courses. In summation, we will introduce ways one can join the BLUE efforts, participate in BLUE activities, and share and disseminate resources through the growing BLUE network.

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Global Biotic Interactions: A Case Study in Ecological Data Aggregation

Large-scale ecological data sets are essential to enhance our understanding of biodiversity in a changing world, but efforts to aggregate and harmonize ecological data from heterogeneous sources are in their infancy. Global Biotic Interactions (GloBI, www.globalbioticinteractions.org/about.html) contributes to progress in this area by building an extensible, open-source infrastructure for the efficient integration and sharing of species interaction data. GloBI lowers technical barriers for data contributors by accommodating a variety of data types and formats. The GloBI integration infrastructure leverages multiple taxonomic hierarchies, community ontologies, controlled vocabularies, and registries. Integration into the unified GLoBI framework is continuous, and the data are rebuilt and updated from original sources on a daily basis. As novel data and metadata types are incorporated and the volume of interaction records grows, the integration process is optimized to ensure scalability. GloBI currently manages more than 2 million interaction records for over 100,000 taxa from almost 300 sources. These data are openly shared through an application programming interface (API) and various data archives. While the support of scientific analyses is GloBI's main goal, the data also support public outreach through dissemination by the Encyclopedia of Life and Gulf of Mexico Species Interactions (GoMexSI, gomexsi.tamucc.edu).

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Big Data Challenges in Ecological and Biodiversity Informatics: A Functional Trait Perspective

The increasing measurement and collection of a potentially intractable number of functional traits has created a massive volume of data concerning the phenotypic and behavioral attributes of a variety of species across spatial and temporal scales. This trait formulation for an n-dimensional hypervolume, realized as Hutchinsonian Niches, suggests several key challenges hinder a direct “big data” approach to constructing a useful biodiversity knowledge graph. These challenges include 1) the need for an objective means of trait selection for modelling and 2) the ability to apply the resulting models across other spatial and/or temporal scales in more generalized contexts.

We present, for consideration and feedback, the case for utilizing functional trait data to develop a principled framework for integrating bio-ontology driven trait selection into the modeling and analysis of biological systems. We then explore new applications of "big data" analysis techniques that are made possible by this bio-ontological model for trait selection.

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The Value of Digital Morphology for Understanding Plant (paleo) Biodiversity

While plant morphology and anatomy has taken a back seat to genetics for most recent systematic studies, its study remains critical for a) deciphering modern biodiversity by providing phenotypic data that complements genetic data, helps infer character evolution, and provides insights to biotic and abiotic influences on biodiversity; and b) allowing us to analyze biodiversity patterns on long timescales by using the fossil record. In the last decade, computed tomography (CT) has become increasingly used in paleontological and neontological morphology/anatomy studies, using synchrotron-based or industrial microCT. CT studies enhance plant biodiversity studies in several ways. Data are more rapidly produced compared to traditional histology, permitting acquisition of large phenotypic datasets. It is a non-destructive technique, which is critical for rare herbarium specimens or fossils from museums, where original specimens must be kept intact. The 3D datasets permit exploration in 2D (like traditional sectioning) in any plane of section from one specimen. Structures can also be virtually dissected and/or used for virtual taphonomy. These datasets can (and should) be archived and shared, adding to the preservation and value of collections and reproducibility of data. There are numerous examples of how digital morphology has helped to better understand plant paleobiology.

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Automatic Generation of Herbarium Labels from Spreadsheet Data using LaTeX

Producing herbarium labels directly from a field spreadsheet allows for flexibility, as the labels can be generated anywhere a user has access to a computer with the requisite software. Unfortunately, current work-flows are unreliable. Once a spreadsheet is merged in Microsoft Word, any additional edits produce cascading effects which drastically alter the formatting of the document. To mend the changes, requires an un-necessary amount of time and tedious effort. This issue can be alleviated through a reporting template used in intermediary repositories, but these systems are less flexible. A portable, field-ready and reliable solution is required to help botanists avoid time lost and help them to make labels. Additionally, a system that is free and open-source increases the capabilities of botanists and collections managers in countries where herbaria lack extensive resources. LaTeX is a free and robust typesetting platform that fits the needs of entry users while allowing for complex typesetting--a tutorial to generate labels is what follows.

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Wildbook: Computer-assisted Identification of Crowd-sourced Wildlife Imagery

Citizen science can greatly increase the volume of data for wildlife studies and support more detailed analyses, but only if data can be successfully integrated into structured studies and data processing can scale correspondingly. We present Wildbook, an open-source software system for collecting and organizing wildlife data, focusing on imagery as a primary source. Incorporating computer vision techniques, machine learning, and species-specific matching algorithms, Wildbook aides in processing large volumes of crowd-sourced wildlife photos into usable biological data. Wildbook is the core technology behind the recent citizen science project, the Great Grevy's Rally in Kenya, where 120 distributed teams attempted to photograph the Kenyan Grevy's zebra population (99% of the world's Grevy's) to perform the first complete census of this endangered animal. Wildbook has a long history supporting crowd-sourced photo identification projects, such as MantaMatcher and Wildbook for Whale Sharks, which also use computer-assisted photo identification to match individual animals in photos submitted by the public. Wildbook represents a flexible, reusable, and modern architecture for sophisticated wildlife research using crowd-sourced data, computer vision, and machine learning.

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Patterns and Processes in the Evolution of Opisthoglyphous Fangs in Colubrid Snakes

Opisthoglyphous fangs are rearward facing, grooved, and often enlarged teeth found at the posterior of the maxillary bone found in many species of Colubrid snakes. Aiming to understand more about the evolution of this unique character, I investigated the dentition of museum specimens of species both in the family Colubridae and in several other families. Using µCT data, I uncovered much variability in the degree of grooving of the rear fangs across species. By collecting data on the distribution of opisthoglyphous fangs for a subset of species in the family Colubridae, I reconstructed the ancestral state of this trait using likelihood and parsimony methods. I found support for a rear fanged ancestor at the base of the Colubrid radiation, followed by subsequent losses in several groups. I find evidence for strong phylogenetic signal of rear fangs across the species analyzed here. To test the mode of evolution of rear fangs, I fitted two discrete Markov models of character evolution to ascertain the maximum likelihood transition rates for this character. I found similar rates of gain and loss of rear fangs, with the rate of gain being slightly but not significantly larger. However, I present evidence that rear fangs likely did not evolve in a correlated fashion with prey-base at a coarse level.

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Digitization of Strepsirrhine Primates from the Duke Lemur Center

For the past two years, ongoing efforts at Duke University have resulted in microCT scanning of more than 100 strepsirrhine primate cadavers (17 species) from the Duke Lemur Center in Durham, NC. To date, more than 500 scans have been generated, including specimen overviews and zooms of complex anatomical regions (e.g., cranium, hands, feet). Scans have been uploaded to the digital repository Morphosource.org, and will soon be publicly available.

As captive (but free-ranging) individuals, these specimens have a wealth of associated information that is largely unavailable for wild populations, including detailed life history data, longitudinal body mass, and records of use in experiments. This collection is also exceptional in representation of age categories that are uncommon in museum collections, and maintains associations in indistinct anatomical regions (e.g., caudal vertebrae, manual and pedal phalanges).

The primary goals of this project were to capture osteological and dental information, but initial research projects utilizing this dataset have also successfully reconstructed soft tissue structures (i.e., muscle ligaments). Currently, these specimens are stored frozen and are available for a fee to research projects that require destructive sampling. This digital collection maximizes the information obtained from rare and endangered animals without degradation of the original specimens."